Global Mapping of Infectious Disease Risk

Supplementary Information: Systematic Review of Diseases of Clinical Significance

Contents

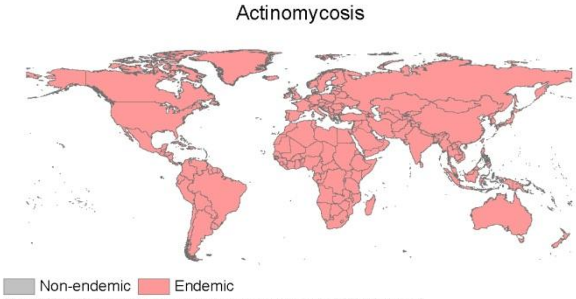
Disease: Actinomycosis.

ICD-10 Code: A42.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Actinomycetaceae, Actinomyces spp. (typically *A. israelii*) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Trauma or oral contact; endogenous [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,874.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Actinomycosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

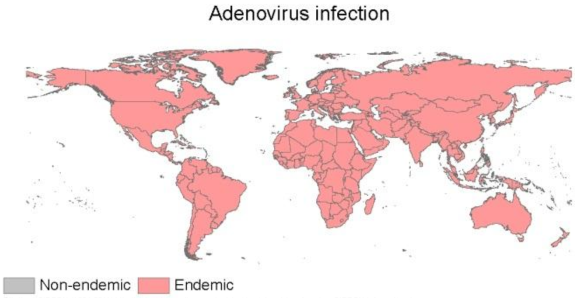
Disease: Adenovirus infection.

ICD-10 Code: B34.0.

Transmission category: Respiratory.

Agent: Virus-DNA.

Taxonomy: Adenoviridae, Group I, Various mastadenoviruses [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets; contact with contaminated water [1].

Reservoir*: Humans and non human primates [1].

Incubation period: 8 days (range 4-12 days) [1].

Significant epidemiological characteristics:

Vaccine: Adenovirus (types 4 and 7; military use only) [1].

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 1,358.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 111.
- **ProMED feeds 1994-2011:** 31.
- **BioCaster feeds 2006-2011:** 106.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Adenovirus infections are endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

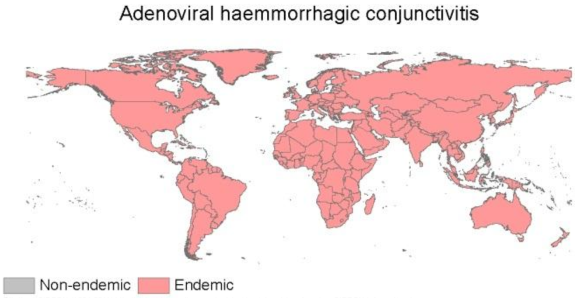
<u>**Disease**</u>**:** Adenoviral haemmorrhagic conjunctivitis.

<u>**ICD-10 Code:**</u> B30.1.

<u>**Transmission category:**</u> Respiratory/close contact.

<u>**Agent**</u>**:** Virus-DNA.

<u>**Taxonomy:**</u> Adenoviridae, Group I,
Adenovirus, Types 3, 4, and 7 [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Swimming in contaminated pools; direct contact [1].

Reservoir*: Humans [1].

Incubation period: 8 days (range 4-12 days) [1].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: Adenovirus (types 4 and 7; military use only) [1].

Estimated R_0 value(s) from published literature:

Human: 2.64 [3].

Reservoir: There is no animal reservoir for this disease.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

PubMed hits on 04/11/11: 220 for "Haemorrhagic Conjunctivitis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>**Mapping recommendation:**</u> Option 1; do not map. Adenoviral haemmorrhagic conjuctivitis is endemic worldwide and potentially vaccine preventable.

<u>**Future mapping potential**</u>**:** None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

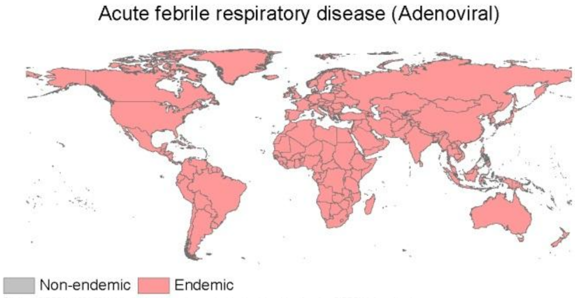
<u>Disease</u>: Acute febrile respiratory disease (Adenoviral).

<u>ICD-10 Code:</u> B34.0.

<u>Transmission category:</u> Respiratory/close contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Adenoviridae, Group I,
Adenovirus, Types 1-5, 7, 14, and 21 [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Faecal-oral route; direct contact or contact with fomites [1].

Reservoir*: Humans [1].

Incubation period: 5.5 days (range 1-10 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: Adenovirus (types 4 and 7; military use only) [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 13.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Acute febrile respiratory disease (Adenoviral) is endemic worldwide and potentially vaccine preventable.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

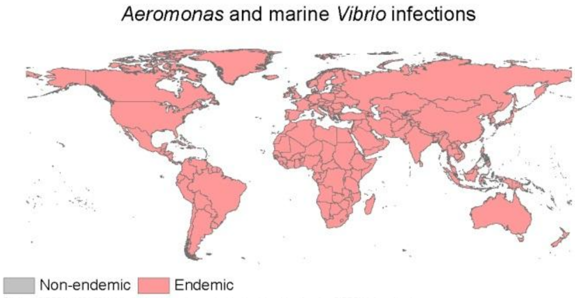
Disease: *Aeromonas* and marine *Vibrio* infections.

ICD-10 Code: A05, A05.9, A05.B98.1.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria,
Aeromonadales, Aeromonadaceae,
Aeromonas hydrophila.
Vibrionales, Vibrionaceae,
Vibrio vulnificus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Trauma; consumption of infected shellfish [1].

Reservoir*: Fish and shellfish [1].

Incubation period: 4.5 days (range 2-7 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 5,439 for “Aeromonas,” 168 for “Marine Vibrio,” 2,288 for “*Aeromonas hydrophila*” and 1,218 for “*Vibrio vulnificus*.”

GenBank hits on 22/02/12: 5,382.

HealthMap feeds 2006-2011: 9 for “*Vibrio vulnificus*”.

ProMED feeds 1994-2011: 40 for “*Vibrio vulnificus*”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >204 [1].

Previously published maps: Not found.

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 26 occurrence points per country based on 5,439 results for “Aeromonas” in PubMed and 204 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

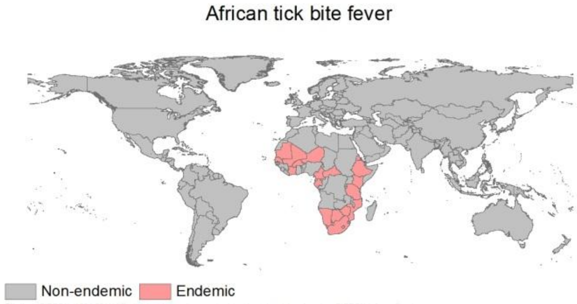
Disease: African tick bite fever.

ICD-10 Code: A77.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia africae* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Amblyomma hebreum*; *Rhiphicephalus* spp. and *Haemaphysalis* spp. also implicated) [1].

Reservoir*: Dogs, rodents, sheep, goats, cattle and ticks [1].

Incubation period: 6.5 days (range 3-18 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 78 for "*Rickettsia africae*" and 93 for "African tick bite fever".

GenBank hits on 22/02/12: 79.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >26 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	24	4.5	2	8	[4]
Vector	100	3.5	2	26	[5]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 4 occurrence points per country based on 93 results for "African tick bite fever" in PubMed and 26 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

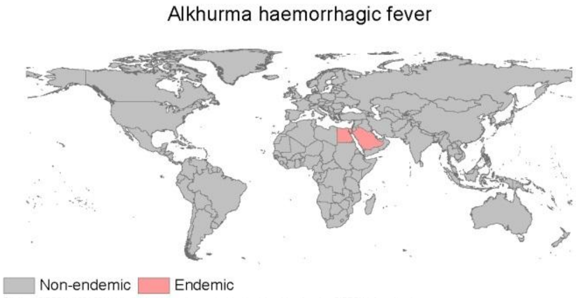
Disease: Alkhurma haemorrhagic fever.

ICD-10 Code: A98.8.

Transmission category: Soil contact.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, Flavivirus, Flavivirus, Alkhurma haemorrhagic fever virus (AHFV) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Ornithodoros savignyi*); consumption of infected meat or camel milk [1].

Reservoir*: Cattle, buffaloes and ticks [1].

Incubation period: 7.5 days (range 3-12 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [6].

Reservoir: 0-23 (crows) [7].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 10.

GenBank hits on 22/02/12: 49.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

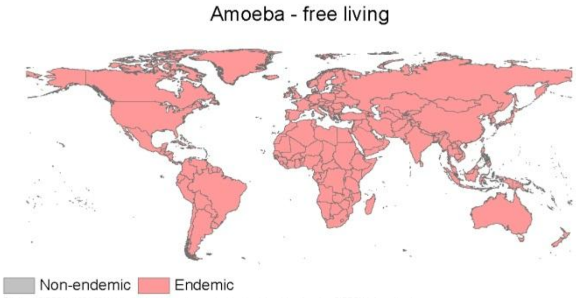
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	25	5.5	2	15	[8]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 10 occurrence points per country based on 8 results for Alkhurma haemorrhagic fever in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Amoeba - free living.

<u>ICD-10 Code:</u> B60.1, B60.8, B60.2.

<u>Transmission category:</u> Water contact

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Protista, Amoebozoa, Centramoebida, Centramoebida, Acanthamoebidae,

Acanthamoeba, several (*A. culbertsoni*, *A. polyphaga*, *A. castellanii*, *A. astronyxis*) [1, 2].

Balamuthia mandrillaris [1, 2].

Protista, Percolozoa, Heterolobosea, Schizopyrenida, Vahkampfidae,

Naegleria fowleri [1, 2].

<u>Natural history</u>:

Mode of transmission: Contact with contaminated water; possibly direct contact [1].

Reservoir*: None [1].

Incubation period: 5.5 days (range 2-14 days), 5 days (range 3-7 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 3,169 for “Acanthamoeba,” 129 for “*Balamuthia mandrillaris*” and 484 for “*Naegleria fowleri*.”

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 2 for “Free Living Amoeba” and 152 for “Amebiasis”.

ProMED feeds 1994-2011: 1 for “Free Living Amoeba” and 46 for “Amebiasis”.

BioCaster feeds 2006-2011: 7.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Free living amoeba are endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

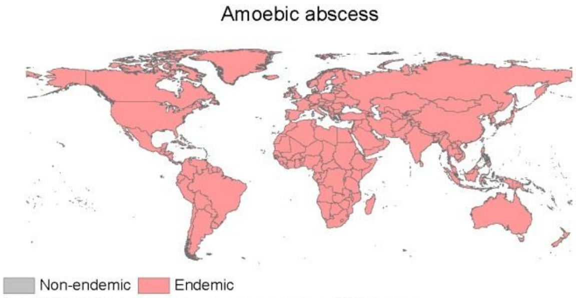
Disease: Amoebic abscess.

ICD-10 Code: A06.4 to A06.6.

Transmission category: Direct contact.

Agent: Parasite.

Taxonomy: Protista, Protozoa, Sarcomastigophora, Lobosea, Amoebida, Endamoebidae, *Entamoeba histolytica* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated water; faecal-oral route; consumption of contaminated food; sexual contact; flies [1].

Reservoir*: Humans [1].

Incubation period: 97 days (range 14-180 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 131.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Amoebic abscesses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

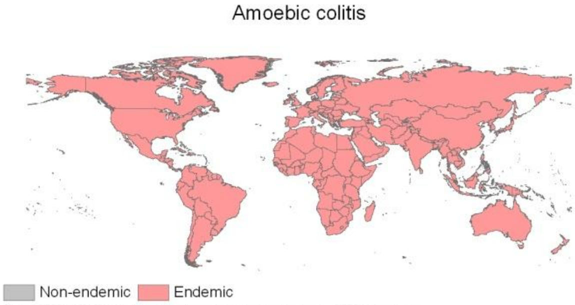
Disease: Amoebic colitis.

ICD-10 Code: A06.2.

Transmission category: Direct contact.

Agent: Parasite.

Taxonomy: Protista, Protozoa, Sarcomastigophora, Lobosea, Amoebida, Endamoebidae, *Entamoeba histolytica* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated water; faecal-oral route; consumption of contaminated food; sexual contact; flies [1].

Reservoir*: Humans [1].

Incubation period: 14 days (range 3-90 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 151.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Amoebic colitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

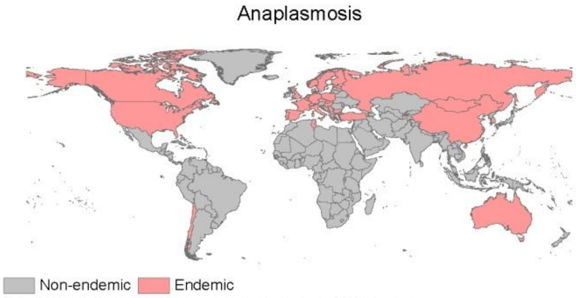
Disease: Anaplasmosis.

ICD-10 Code: A79.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Ehrlichiaceae, *Anaplasma phagocytophilum* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (Various ixodids including *Ixodes dammini/scapularis, I. pacifcus* and *I. ricinus*) [1].

Reservoir*: Rodents, rabbits, ticks and deer [1].

Incubation period: 14 days (range 7-21 days) [1].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [9].

Reservoir: 0-3.9 (multiple species) [9, 10].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,426.

GenBank hits on 22/02/12: 2,735.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 201.

Approximate number of endemic countries: >38 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	12	8.5	3	9	[11]
Vector	18	4.5	2	5	[4]
Vector	1	8	3	1	[12]
Vector	12	7.5	3	8	[13]
Vector	14	4.5	2	3	[4]
Vector	36	4.5	2	9	[4]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 38 occurrence points per country based on 1,426 results for "Anaplasmosis" in PubMed and 38 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

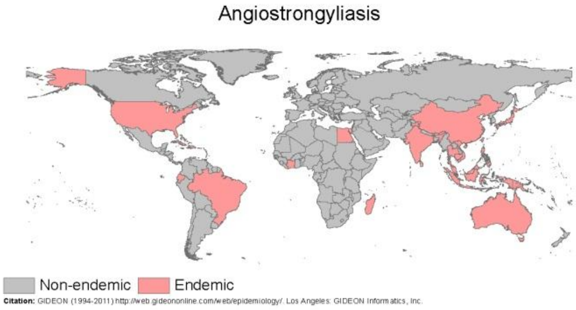
Disease: Angiostrongyliasis.

ICD-10 Code: B83.2.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Metastrongylidae, *Angiostrongylus* [*Parastrongylus*] *cantonensis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Ingestion of infected food [1].

Reservoir*: Rats, prawns and frogs [1].

Incubation period: 14 days (range 5-35 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [14].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 260.

GenBank hits on 22/02/12: 17.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >47 [1].

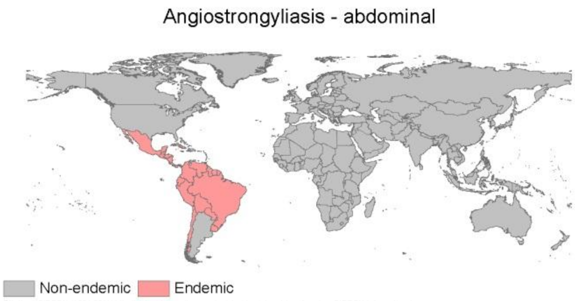
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	34	8.5	2	32	[15]
Disease	97	5	2	54	[14]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 6 occurrence points per country based on 24 results for “Angiostrongyliasis” in PubMed and 47 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.


Angiostrongyliasis - abdominal

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Angiostrongyliasis - abdominal.

ICD-10 Code: B81.3.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Metastrongylidae, *Parastrongylus* [*Angiostrongylus, Morerastrongylus*] *costaricensis* [1, 2].

Natural history:

Mode of transmission: Ingestion of infected food; contact with infectious secretions [1].

Reservoir*: Cotton rats (*Sigmodon*) and slugs [1].

Incubation period: 12 days (range 10-14 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [14].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 52 for “Angiostrongyliasis and abdominal”.

GenBank hits on 22/02/12: 17.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

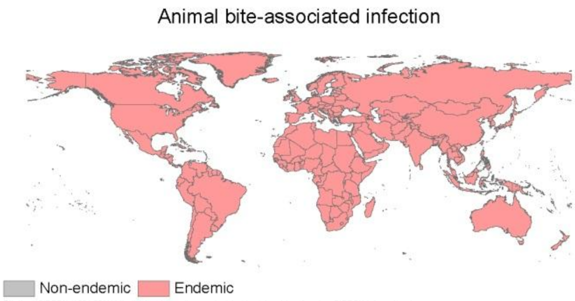
Approximate number of endemic countries: >24 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were 2 occurrence points per country based on 24 results for “Angiostrongyliasis and abdominal” in PubMed and 24 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Animal bite-associated infection.

ICD-10 Code: A28.9.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae, Many (e.g. *Pasteurella multocida*) [1, 2].

Natural history:

Mode of transmission: Usually dog or cat bites [1].

Reservoir*: Cats, dogs, marsupials (Tazmanian devil), other mammals and birds (rarely) [1].

Incubation period: 2 days (range 0.125-3 days) [1].

Significant epidemiological characteristics:

Vaccine: None [1].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [16, 17].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4 for “Animal bite infections”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 28 for “Pasteurellosis”.

ProMED feeds 1994-2011: 16 for “Pasteurellosis”.

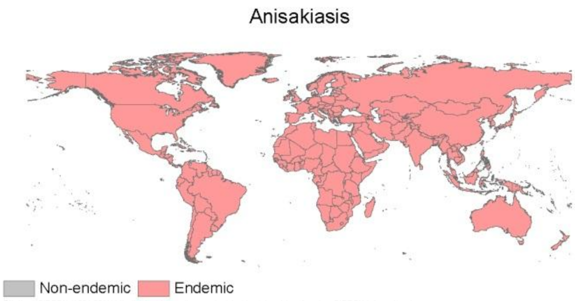
BioCaster feeds 2006-2011: 36 for “Pasteurellosis”.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Animal bite-associated infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Anisakiasis.

ICD-10 Code: B81.0.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Anisakidae,

Anisakis simplex [1, 2].

Pseudoterranova decipiens [1, 2].

Natural history:

Mode of transmission: Consumption of undercooked infected fish [1].

Reservoir*: Sea mammals and fish [1].

Incubation period: 7 days (range 0.25-14 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [18].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 610 for "Anisakiasis" and 437 for "*Anisakis simplex*".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 1.

ProMED feeds 1994-2011: 0.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	2	8	2	N/A	[19]

Mapping recommendation: Option 1; do not map. Anisakiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

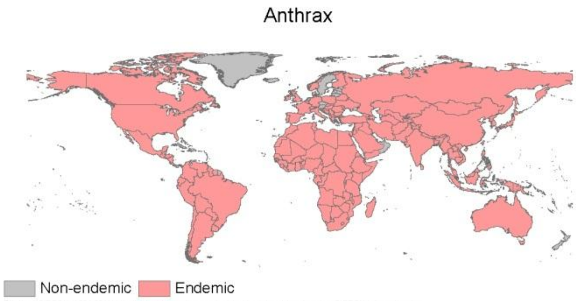
Disease: Anthrax.

ICD-10 Code: A22.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae,
Bacillus anthracis [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation; consumption of contaminated food; flies; fomites [1].

Reservoir*: Goats, cattle, sheep and horses [1].

Incubation period: 3.5 days (range 1-7 days) [1].

Significant epidemiological characteristics:

Vaccine: Anthrax [1].

Estimated R_0 value(s) from published literature:

- **Human:** 0 [20].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 5,461.
- **GenBank hits on 22/02/12:** 3,404.
- **HealthMap feeds 2006-2011:** 1,692.
- **ProMED feeds 1994-2011:** 1,873.
- **BioCaster feeds 2006-2011:** 3,980.

Approximate number of endemic countries: >147 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	7	2	<1	[21]
Disease	100	4.5	2	25	[22]
Disease	13	5	2	4	[23]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 37 occurrence points per country based on 5,461 results for “Anthrax” in PubMed and 147 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

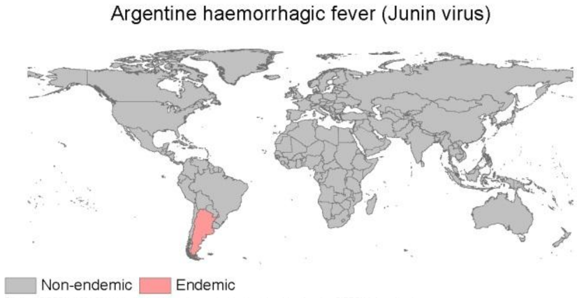
Disease: Argentine haemorrhagic fever (Junin virus).

ICD-10 Code: A96.0.

Transmission category: Soil contact.

Agent: Virus-RNA.

Taxonomy: Arenaviridae, Group V, Arenavirus Junin virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious rodent secretions [1].

Reservoir*: Rodents (*Calomys musculinus*) [1].

Incubation period: 11.5 days (range 7-16 days) [1].

Significant epidemiological characteristics:

Vaccine: Argentine haemorrhagic fever [1].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [24].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 169 for "Argentine haemorrhagic fever" and 499 for "Junin virus".

GenBank hits on 22/02/12: 205.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4.5	2	25	[25]
Disease	100	4.5	2	25	[26]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 499 occurrence points per country based on 499 results for "Junin virus" in PubMed and 1 endemic country listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Ascariasis.

ICD-10 Code: B77.

Transmission category: Soil contact.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Ascarididae, *Ascaris lumbricoides* [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food or soil; flies [1].

Reservoir*: Humans and dogs [1].

Incubation period: 14 days (range 7->200 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-8.6 [27, 28].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 5,268.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 2.

ProMED feeds 1994-2011: 2.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	51	4.5	2	N/A	[29]

Mapping recommendation: Option 1; do not map. Ascariasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

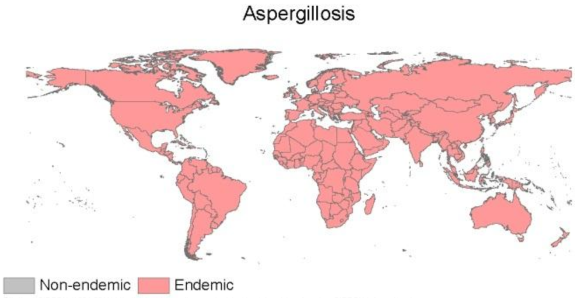
Disease: Aspergillosis.

ICD-10 Code: B44.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Euascomycetes, Eurotiales, Trichocomaceae, *Aspergillus fumigatus, A. flavus* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of spores [1].

Reservoir*: None [1].

Incubation period: 12.5 days (range 3-21 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Some evidence for person to person [30].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 13,688 for “Aspergillosis,” 7,020 for “*Aspergillus fumigatus*” and 2,860 for “*Aspergillus flavus*”.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 21.
- **ProMED feeds 1994-2011:** 21.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Aspergillosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Astrakhan fever.

ICD-10 Code: A77.1.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia conorii* subspp *caspia* [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Rhipicephalus pumilio*) [1].

Reservoir*: Dogs, cats, hedgehogs, hares and small rodents [1].

Incubation period: 6.5 days (range 3-18 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [31].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 18.

GenBank hits on 22/02/12: 72.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >3 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	87	1.5	2	10	[32]
Vector	100	3.5	2	26	[4]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 6 occurrence points per country based on 18 results for “Astrakhan fever” in PubMed and 3 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vector. If occurrence data for this tick species is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

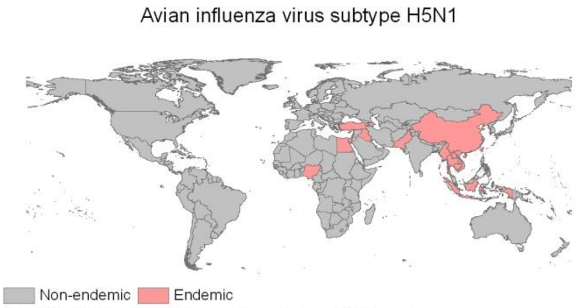
Disease: Avian influenza virus subtype H5N1.

ICD-10 Code: J09

Transmission category: Animal contact

Agent: Virus-RNA.

Taxonomy: Orthomyxoviridae, Group V, Orthomyxovirus, H5N1 (subtype A) [1, 2].



Avian influenza virus subtype H5N1

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious secretions; contact with avian infectious secretions [1].

Reservoir*: Waterfowl, chickens, pigeons, crows and others [1].

Incubation period: 2.5 days (range 2-3 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease; 0-2.4 (Pandemic flu) [33-38].

Reservoir: 0-3 (birds) [39, 40].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,300.

GenBank hits on 22/02/12: 21,346.

HealthMap feeds 2006-2011: 11,774 for “Avian influenza”.

ProMED feeds 1994-2011: 5,286 for “Avian influenza”.

BioCaster feeds 2006-2011: 8,006 for “H5N1”.

Approximate number of endemic countries: >14 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	22	[41]
Disease	100	5	2	28	[42]
Disease	100	5	2	28	[43]
Disease	100	5	2	28	[43]
Disease	100	5	2	28	[44]
Disease	100	6.5	2	36	[45]
Disease	4	7	2	1	[46]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 304 occurrence points per country based on 4,300 results for “H5N1 avian influenza” in PubMed and 14 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

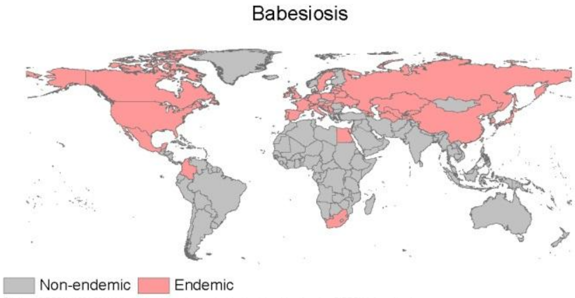
Disease: Babesiosis.

ICD-10 Code: B60.0.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Alveolata, Apicomplexa, Aconoidasida, Piroplasmida, Babesiidae, *Babesia* spp. [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Ixodes* spp.); blood transfusion; rarely vertical transmission [1].

Reservoir*: Rodents (usually *Peromyscus leucopus*), rabbits, deer, cattle and ticks [1].

Incubation period: 10 days (range 7-63 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [47].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,217.

GenBank hits on 22/02/12: 679.

HealthMap feeds 2006-2011: 16 for “Babesiosis”.

ProMED feeds 1994-2011: 31 for “Babesiosis”.

BioCaster feeds 2006-2011: 117.

Approximate number of endemic countries: >45 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	22	[4]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 71 occurrence points per country based on 3,217 results for “Babesiosis” in PubMed and 45 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

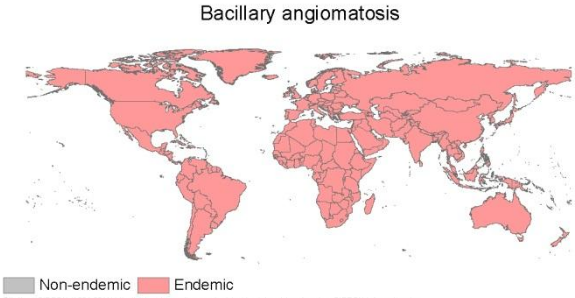
Disease: Bacillary angiomatosis.

ICD-10 Code: A44.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rhizobiales, Bartonellaceae, *Bartonella henselae* and *B.quintana* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Cat flea vector; rarely tick vector [1].

Reservoir*: Humans, cats and ticks [1].

Incubation period: 19 days (range 16-22 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [48, 49].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 562.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 5 for "*Bartonella*".

ProMED feeds 1994-2011: 3 for "*Bartonella*".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacillary angiomatosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Disease: *Bacillus cereus* food poisoning.

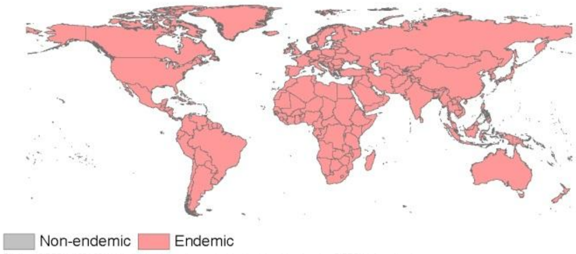
ICD-10 Code: A05.4.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae,

Bacillus cereus [1, 2].



Bacillus cereus food poisoning

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food [1].

Reservoir*: None [1].

Incubation period: 0.23 days (range 0.083-0.375 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,191 for "*Bacillus cereus*" and 23 for "*Bacillus cereus* food poisoning".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Bacillus cereus* food poisoning is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

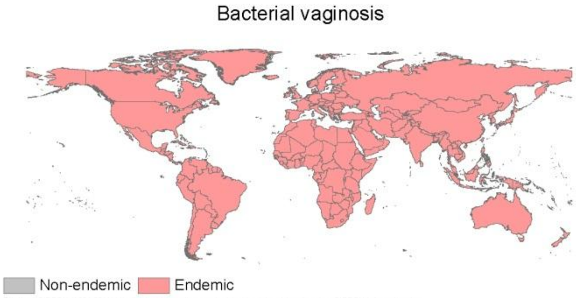
Disease: Bacterial vaginosis.

ICD-10 Code: N76, B96.8.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Many (e.g. *Gardenella vaginalis*, *Mobiluncus curtisii*, *M. mulieris* and *Prevotella* spp.) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,958.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacterial vaginosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

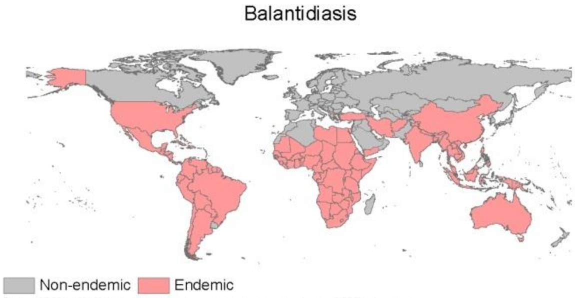
<u>Disease</u>: Balantidiasis.

<u>ICD-10 Code:</u> A07.0.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Chromalveolata, Alveolata, Ciliophora, Litostomatea, Vestibuliferida, Balantiididae, *Balantidium coli* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of contaminated food or water [1].

Reservoir*: Pigs, non-human primates and rodents [1].

Incubation period: 3.5 days (range 1-7 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [50].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 303.

GenBank hits on 22/02/12: 25.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >109 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were 3 occurrence points per country based on 303 results for “Balantidiasis” in PubMed and 109 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

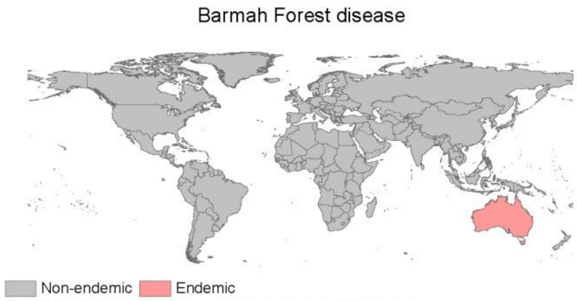
Disease: Barmah Forest disease.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, Alphavirus, Bamah Forest virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (e.g. *Aedes* spp., *Culex* spp., *Coquillettidia* spp.) [1].

Reservoir*: Marsupials (wallaby, kangaroo), cattle and horses [1].

Incubation period: 7 days (range 3-11 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [51].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 65.

GenBank hits on 22/02/12: 48.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	7	2	39	[52]
Disease	100	8	2	44	[53]
Disease	100	8	2	44	[54]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 65 occurrence points per country based on 65 results for “Barmah Forest disease” in PubMed and 1 endemic country listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Bartonellosis - cat borne.

<u>ICD-10 Code:</u> A44.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rhizobiales,

Many (e.g. *Afipia feliz, Bartonella henselae, B. clarridgeiae*) [1, 2].

<u>Natural history</u>:

Mode of transmission: Cat or thorn scratches [1].

Reservoir*: Cats and ticks (possibly) [1].

Incubation period: 7.5 days (range 3-14 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [55].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

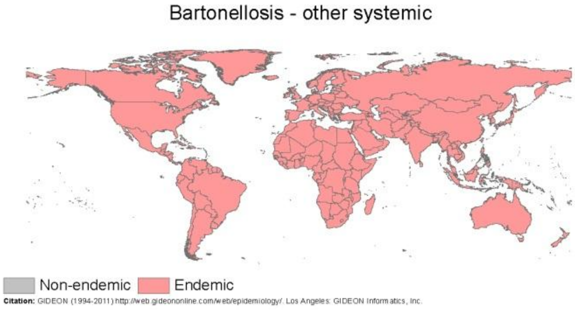
- **PubMed hits on 04/11/11:** 200 for “Bartonellosis” and 74 for “Bartonellosis and cat”.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0 for “Cat Scratch Fever”.
- **ProMED feeds 1994-2011:** 13 for “Cat Scratch Fever”.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Bartonellosis (cat borne) is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Bartonellosis - other systemic.

ICD-10 Code: A44.0.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rhizobiales, Bartonellaceae,

Many (e.g. *Bartonella quintana, B. koehlerare, B. elizabethae, B. tamiae, B. wahoensis, B. bacillformis, B. procyonis*) [1, 2].

Natural history:

Mode of transmission: Contact with lice faeces through wound or eye [1].

Reservoir*: Humans, lice, rats, cats, dogs and sheep [1].

Incubation period: 17 days (range 9-25 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [48].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 200 for “Bartonellosis” and 18 for “Bartonellosis and systemic”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 5 for “Bartonella”.

ProMED feeds 1994-2011: 3 for “Bartonella”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bartonellosis (other systemic) is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

<u>Disease</u>: Bartonellosis - South American.

<u>ICD-10 Code:</u> A44.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rhizobiales, Bartonellaceae, *Bartonella bacilliformis* [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Sandfly vector (*Lutzomyia* spp.) [1].

Reservoir*: Humans [1].

Incubation period: 21 days (range 14-28 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [55].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 200 for “Bartonellosis” and 176 for “*Bartonella bacilliformis*”.
- **GenBank hits on 22/02/12:** 140.
- **HealthMap feeds 2006-2011:** 5 for “Bartonella”.
- **ProMED feeds 1994-2011:** 3 for “Bartonella”.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >5 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 40 occurrence points per country based on 200 results for “Bartonellosis” in PubMed and 5 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

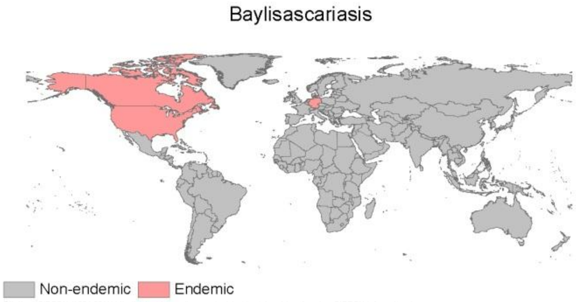
Disease: Baylisascariasis.

ICD-10 Code: B77.9.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Ascarididae, *Baylisascaris procyonis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated animal faeces (e.g. racoon) [1].

Reservoir*: Mammals (>40) and birds [1].

Incubation period: Not found [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [56].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 10.

GenBank hits on 22/02/12: 15.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 2.

Approximate number of endemic countries: >4 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were 3 occurrence points per country based on 303 results for “Balantidiasis” in PubMed and 109 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

<u>Disease</u>: *Bertiella* and *Inermicapsifer*.

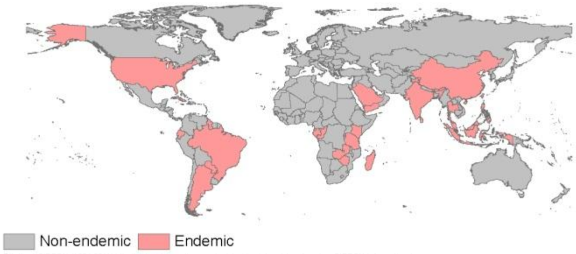
<u>ICD-10 Code:</u> B71.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Anoplocephalidae,
Bertiella and *Inermicapsifer* spp. [1, 2].

Bertiella and *Inermicapsifer*



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Ingestion of infected mites [1].

Reservoir*: Rodents and non-human primates [1].

Incubation period: Not found.

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [57].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 45 for "*Bertiella*" and 26 for "*Inermicapsifer*".

GenBank hits on 22/02/12: 17.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

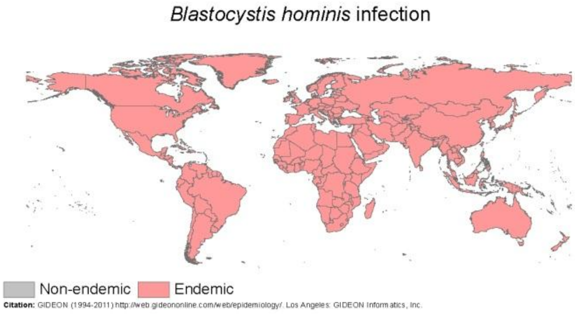
Approximate number of endemic countries: >29 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 45 results for "*Bertiella"* in PubMed and 29 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Blastocystis hominis* infection.

ICD-10 Code: A07.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Chromista, Heterokontophyta, Blastocystea, Blastocystida, Blastocystidae,
Blastocystis hominis [1, 2].

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated water [1].

Reservoir*: Humans [1].

Incubation period: Not found.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 721 for "*Blastocystis* and hominis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

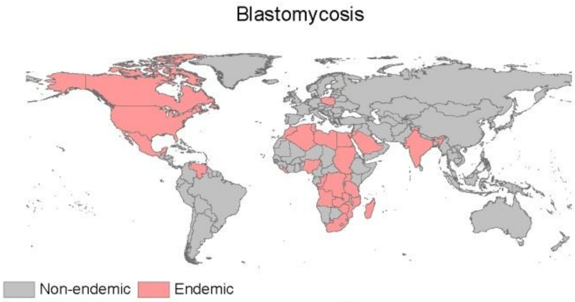
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Blastocystis hominis* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Blastomycosis.

ICD-10 Code: B40.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Ascomycetes, Incertae sedis, Incertae sedis, *Blastomyces dermatitidis* [1, 2].

Natural history:

Mode of transmission: Inhalation of spores [1].

Reservoir*: Beavers, dogs and rodents [1].

Incubation period: 29 days (range 14-44 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0 (point source) [58].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,666.

GenBank hits on 22/02/12: 17,337.

HealthMap feeds 2006-2011: 10 for "Blastomycosis".

ProMED feeds 1994-2011: 15 for "Blastomycosis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >28 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	14	7.5	2	6	[59]
Disease	13	4.5	2	3	[60]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 95 occurrence points per country based on 2,666 results for "Blastomycosis" in PubMed and 5 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

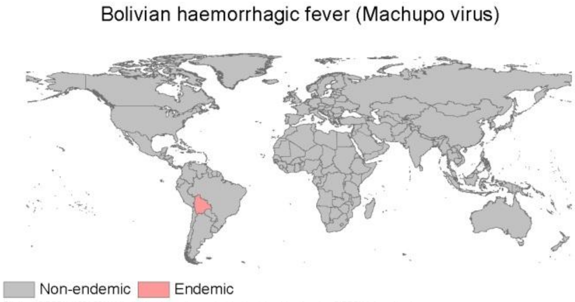
<u>Disease</u>: Bolivian haemorrhagic fever (Machupo virus).

<u>ICD-10 Code:</u> A96.1.

<u>Transmission category:</u> Soil contact.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Arenaviridae, Tacaribe complex, Group V, Arenavirus, Machupo virus [1, 2].


Bolivian haemorrhagic fever (Machupo virus)

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious rodent secretions; direct contact [1].

Reservoir*: Rodents (*Calomys callosus*) [1].

Incubation period: 12 days (range 5-19 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [24].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 39 for "Bolivian hemorrhagic fever" and 69 for "Machupo virus".

GenBank hits on 22/02/12: 122.

HealthMap feeds 2006-2011: 0 for "Machupo Virus".

ProMED feeds 1994-2011: 0 for "Machupo Virus".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	1	2	6	[61]
Disease	100	3.5	2	19	[62]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 69 occurrence points per country based on 69 results for "Machupo virus" in PubMed and 1 endemic country listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

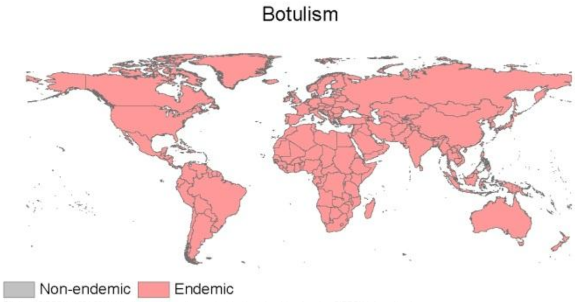
<u>**Disease**</u>**:** Botulism.

<u>**ICD-10 Code:**</u> A05.1.

<u>**Transmission category:**</u> Food/water-borne.

<u>**Agent**</u>**:** Bacterium.

<u>**Taxonomy:**</u> Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium botulinum* [1, 2].



Botulism

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Consumption of contaminated food; rare contamination of wound by soil [1].

Reservoir*: Animals and fish [1].

Incubation period: 1.5 days (range 1-2 days) [1].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: Botulism antitoxin [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

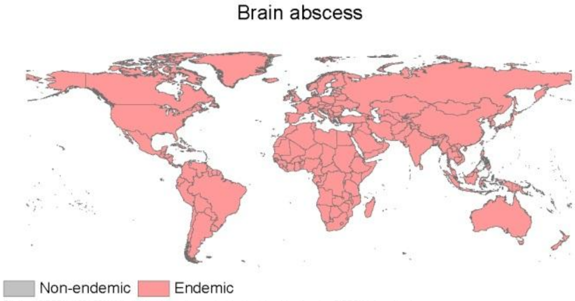
- **PubMed hits on 04/11/11:** 3,161.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 538 for “Botulism”.
- **ProMED feeds 1994-2011:** 561 for “Botulism”.
- **BioCaster feeds 2006-2011:** 1,121.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>**Mapping recommendation:**</u> Option 1; do not map. Botulism is endemic worldwide and vaccine preventable.

<u>**Future mapping potential**</u>**:** None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Brain abscess.

ICD-10 Code: A48.8.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae,
Mixed oral anaerobes / streptococci (e.g. *Staphylococcus aureus*) [1, 2].

Natural history:

Mode of transmission: Endogenous [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not applicable - majority acquired from trauma or other infection in body [63].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,168.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Brain abscesses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.


Brainerd diarrhoea

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Brainerd diarrhoea.

ICD-10 Code: A09.9.

Transmission category: Unknown.

Agent: Unknown [1, 2].

Natural history:

Mode of transmission: Consumption of contaminated water or milk [1].

Reservoir*: Unknown [1].

Incubation period: 12.5 days (range 10-15 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 6 occurrence points per country based on 6 results for “Brainerd Diarrhea” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

<u>Disease</u>: Brazilian haemorrhagic fever (Sabia virus).

<u>ICD-10 Code:</u> A96.8.

<u>Transmission category:</u> Soil contact.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Arenaviridae, Tacaribe complex, Group V, Arenavirus,
Sabia virus [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption or inhalation of infected rodent excreta [1].

Reservoir*: Rodents (presumed) [1].

Incubation period: 11.5 days (range 7-16 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [64].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 0 for “Brazilian haemorrhagic fever” and 17 for “Sabia virus”.

GenBank hits on 22/02/12: 16.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 17 occurrence points per country based on 17 results for “Sabia virus” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Brazilian purpuric fever.

ICD-10 Code: A48.4.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae, *Haemophilus influenzae* biogroup *aegyptius* [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with oral or ocular secretions; fomites; possible flies [1].

Reservoir*: Humans [1].

Incubation period: 10.5 days (range 7-14 days) [1].

Significant epidemiological characteristics:

Vaccine: H. influenzae (HbOC-DTP or -DTaP, HbOC, PRP-D, PRP-OMP, PRP-T) [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 75.

GenBank hits on 22/02/12: 42.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >2 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	90	5.5	2	27	[65]
Disease	90	5.5	2	27	[66]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 38 occurrence points per country based on 75 results for "Brazilian Purpuric Fever" in PubMed and 2 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

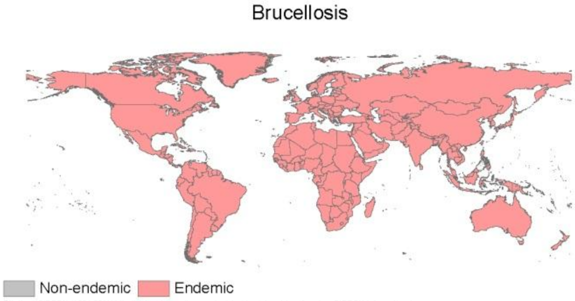
Disease: Brucellosis.

ICD-10 Code: A23.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rhizobiales, Brucellaceae, *Brucella arbortus*, *B.suis* or *B.canis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated food or infected dairy products; inhalation of infectious droplets [1].

Reservoir*: Pigs, cattle, sheep, goats, dogs, coyotes and caribou [1].

Incubation period: 12 days (range 10-14 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [67, 68].

Reservoir: 0-1.7 (bison) [67, 68].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11,016.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 448.

ProMED feeds 1994-2011: 372.

BioCaster feeds 2006-2011: 926.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	71	6	2	N/A	[69]

Mapping recommendation: Option 1; do not map. Brucellosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

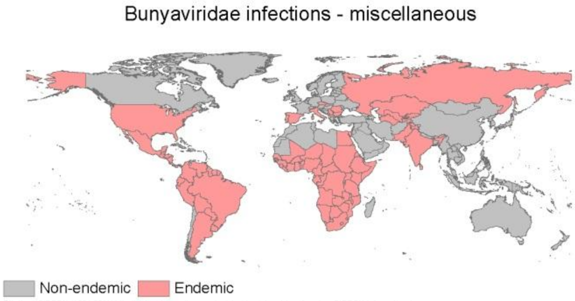
<u>Disease</u>: Bunyaviridae infections - miscellaneous.

<u>ICD-10 Code:</u> A92.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Bunyaviridae, Group V, Orthobunyavirus, >30 strains [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito, midge and tick vectors [1].

Reservoir*: Rats, birds, marsupials, chipmunks, cattle, sheep, horses and bats [1].

Incubation period: 12.5 days (range 10-15 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 462 for “Bunyaviridae infections” and 179 for “Orthobunyavirus”.

GenBank hits on 22/02/12: 10,994.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >88 [1].

Previously published maps: None.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 5 occurrence points per country based on 462 results for “Bunyaviridae infections” in PubMed and 88 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: California encephalitis group.

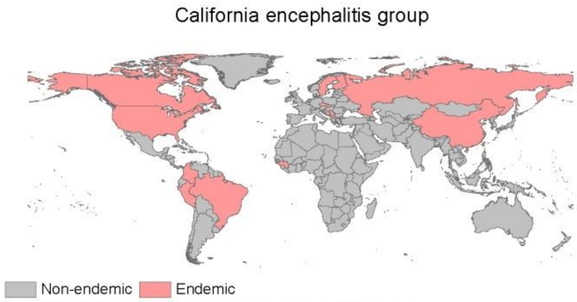
ICD-10 Code: A83.5.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, Orthobunyavirus

Many [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Various mosquito vectors species including *Aedes, Anopheles, Culex, Psorophora* spp. [1].

Reservoir*: Chipmunks, squirrels, rodents and foxes [1].

Incubation period: 10 days (range 5-15 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 179 for “Orthobunyavirus,” 442 for “California encephalitis” and 402 for “La Crosse”.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: 16 for “La Crosse Encephalitis”.

ProMED feeds 1994-2011: 1 for “La Crosse Encephalitis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [1].

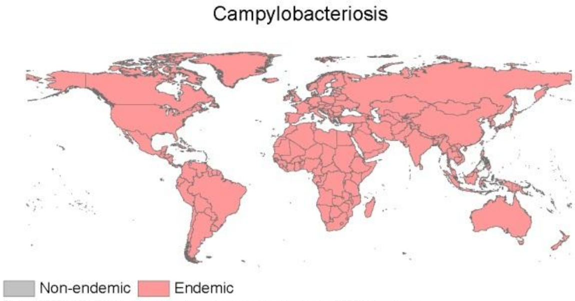
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	14	5.5	2	4	[70]
Disease	14	1.5	2	1	[71]
Vector	21	2.5	2	3	[71]
Disease	14	7.5	2	6	[72]
Disease	14	7	2	6	[73]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 34 occurrence points per country based on 442 results for “California encephalitis” in PubMed and 13 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Campylobacteriosis.

ICD-10 Code: A04.5.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Epsilon Proteobacteria, Campylobacterales, Campylobacteraceae, *Campylobacter jejuni* subspp. *jejuni* [1, 2].

Natural history:

Mode of transmission: Consumption of contaminated food; contact with contaminated water [1].

Reservoir*: Humans, mammals and birds [1].

Incubation period: 3 days (range 2-4 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0 [74].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 12,504 for "*Campylobacter*," 1806 for "*Campylobacter* and diarrhea" and 637 for "Campylobacteriosis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 85 for "*Campylobacter*".

ProMED feeds 1994-2011: 59 for "*Campylobacter*".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	<1	9	2	N/A	[75]

Mapping recommendation: Option 1; do not map. Campylobacteriosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

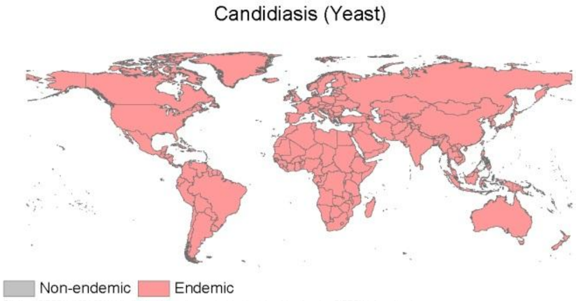
<u>Disease</u>: Candidiasis (Yeast).

<u>ICD-10 Code:</u> B37.

<u>Transmission category:</u> Endogenous.

<u>Agent</u>: Fungus.

<u>Taxonomy:</u> Fungi, Ascomycota, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, *Candida albicans* (and others) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct contact; vertical transmission; endogenous [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

> **Human:** Often endogenous, but need more information as it can transmit person to person in hospital and via contact [76].
>
> **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

> **PubMed hits on 04/11/11:** 27,651 for “Candidiasis” and 25,580 for “*Candida albicans*”.
>
> **GenBank hits on 22/02/12:** N/A.
>
> **HealthMap feeds 2006-2011:** 14 for “Thrush”.
>
> **ProMED feeds 1994-2011:** 0 for “Thrush”.
>
> **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Candidiasis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Capillariasis - extraintestinal.

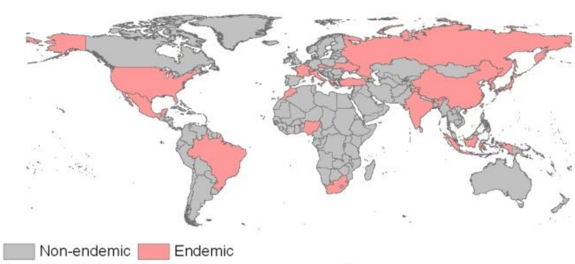
ICD-10 Code: B83.3.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Adenophorea, Many (e.g. *Capillaria hepatica*, *C. aerophila*, and *Antrichosoma cutaneum*) [1, 2].

Capillariasis - extraintestinal



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated liver; contact with infected earthworms [1].

Reservoir*: Rats, dogs, cats, monkeys and earthworms [1].

Incubation period: 24.5 days (range 21-28 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 139 for "Capillariasis".

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >22 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 6 occurrence points per country based on 139 results for “Capillariasis” in PubMed and 22 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

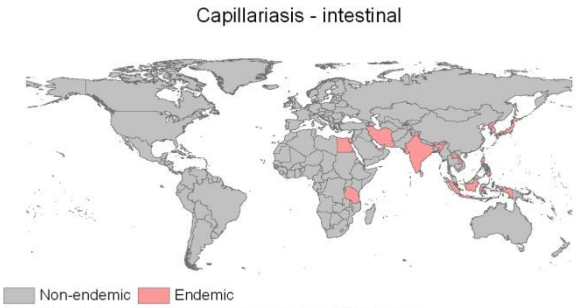
Disease: Capillariasis - intestinal.

ICD-10 Code: B81.1.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Adenophorea, Trichurida, Trichinellidae,
Capillaria [*Aonchotheca*] *philippinensis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food [1].

Reservoir*: Birds and fish [1].

Incubation period: 21 days [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 139 for “Capillariasis” and 49 for “*Capillaria philippinensis*”.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [1].

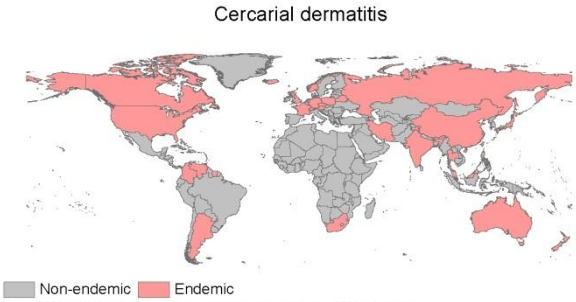
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	4	7	2	3	[77]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 11 occurrence points per country based on 139 results for “Capillariasis” in PubMed and 13 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Cercarial dermatitis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Cercarial dermatitis.

ICD-10 Code: B65.3.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Strigeidida, Schistosomatidae, Avian schistosomes such as *Trichobilharzia*, *Heterobilharzia* and *Orientobilharzia* spp. [1, 2].

Natural history:

Mode of transmission: Contact with contaminated water [1].

Reservoir*: Aquatic birds and snails [1].

Incubation period: 0.5 days (range 0.042-1 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [78].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 122.

GenBank hits on 22/02/12: 497.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >30 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 4 occurrence points per country based on 122 results for “Cercarial dermatitis” in PubMed and 30 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

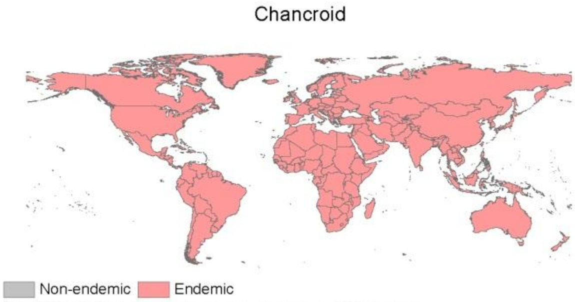
Disease: Chancroid.

ICD-10 Code: A57.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae, *Haemophilus ducreyi* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact [1].

Reservoir*: Humans [1].

Incubation period: 6.5 days (range 3-13 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** ~1 (0.96) [79, 80].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 1,114.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Chancroid is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

<u>Disease</u>: Chandipura and Vesicular stomatitis viruses.

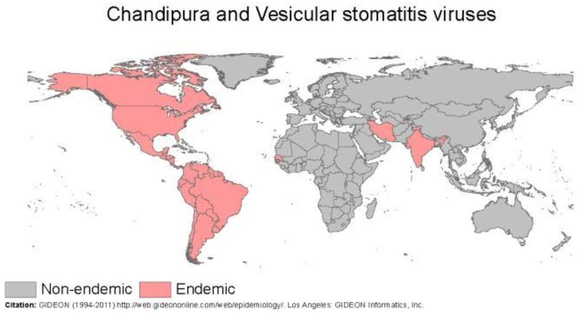
<u>ICD-10 Code:</u> A92.8, A93.8.

<u>Transmission category:</u> Animal contact.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Mononegavirales, Rhabdoviridae, Group V, Vesiculovirus,

Chandipura virus and Vesicular stomatitis virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of aerosol from infected animals [1].

Reservoir*: Horses, pigs and cattle [1].

Incubation period: 4 days (range 2-6 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [81].

Reservoir: 0-0.74 [81].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 103 for “Chandipura” and 7,591 for “Vesicular stomatitis”.

GenBank hits on 22/02/12: 810.

HealthMap feeds 2006-2011: 47 for “Vesicular Stomatitis”.

ProMED feeds 1994-2011: 110 for “Vesicular Stomatitis”.

BioCaster feeds 2006-2011: 23 for “Vesicular Stomatitis”.

Approximate number of endemic countries: >26 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	56	8.5	2	26	[82]
Disease	56	8.5	2	26	[83]
Disease	33	5	2	9	[84]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 292 occurrence points per country based on 7,591 results for “Vesicular stomatitis” in PubMed and 26 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

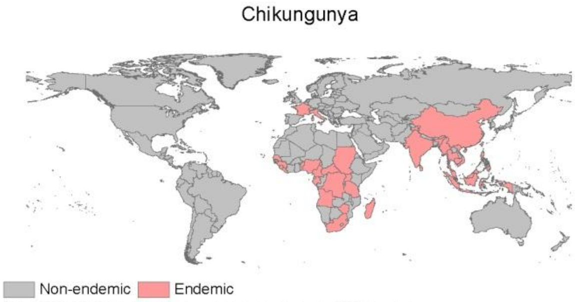
Disease: Chikungunya.

ICD-10 Code: A92.0.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, Alphavirus, Chikungunya virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (e.g. *Ae. aegypti*, *Ae. furcifer-taylori* group in Africa) [1].

Reservoir*: Non-human primates [1].

Incubation period: 7 days (range 2-12 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-3.3 [85, 86].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,314.

GenBank hits on 22/02/12: 1,691.

HealthMap feeds 2006-2011: 792.

ProMED feeds 1994-2011: 477.

BioCaster feeds 2006-2011: 1,038.

Approximate number of endemic countries: >37 [1].

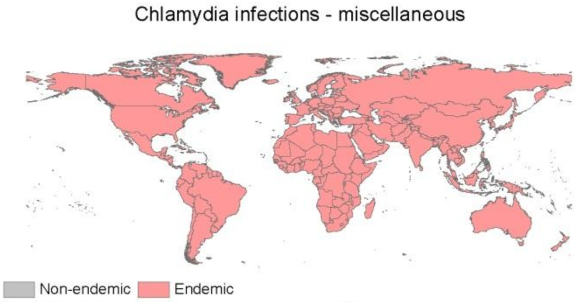
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	9	4	100	[87]
Disease	76	7	2	30	[88]
Disease	76	7	2	30	[89]
Disease	57	6.5	2	20	[90]
Vector	100	4.5	2	25	[90]
Disease	2	4.5	2	<1	[91]
Disease	33	5.5	2	10	[92]
Vector	20	4.5	2	5	[93]
Disease	47	5.5	2	14	[94]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 36 occurrence points per country based on 1,314 results for “Chikungunya” in PubMed and 37 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Chlamydia infections - miscellaneous.

ICD-10 Code: A56.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Chlamydiae, Chlamydiae, Chlamydiales, Chlamydiaceae, *Chlamydia trachomatis* [1, 2].

Natural history:

Mode of transmission: Sexual contact [1].

Reservoir*: Humans [1].

Incubation period: 7.5 days (range 5-15 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-3.6 [95-97].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 21,933.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 114.

ProMED feeds 1994-2011: 38.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	<1	7.5	2	N/A	[98]
Disease	<1	6.5	2	N/A	[99]
Disease	<1	6.5	2	N/A	[100]
Disease	<1	7.5	2	N/A	[101]

Mapping recommendation: Option 1; do not map. Chlamydia infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

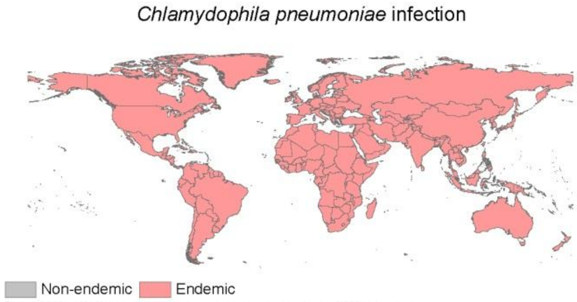
Disease: *Chlamydophila pneumoniae* infection.

ICD-10 Code: J16.0.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Chlamydiae, Chlamydiae, Chlamydiales, Chlamydiaceae, *Chlamydophila pneumoniae* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets [1].

Reservoir*: Humans [1].

Incubation period: 17.5 days (range 7-28 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,399.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Chlamydophila pneumoniae* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

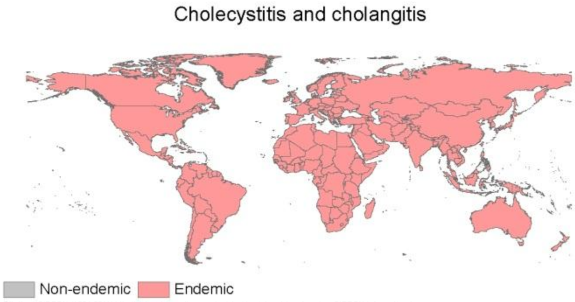
<u>Disease</u>: Cholecystitis and cholangitis.

<u>ICD-10 Code:</u> K81, K83.0.

<u>Transmission category:</u> Endogenous.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Many (e.g. *Escherichia coli, Klebsiella pneumoniae, Enterococcus* spp.) [1, 2].


Cholecystitis and cholangitis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Endogenous [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 15,308 for “Cholecystitis” and 11,941 for “Cholangitis”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Cholecystitis and cholangitis are endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

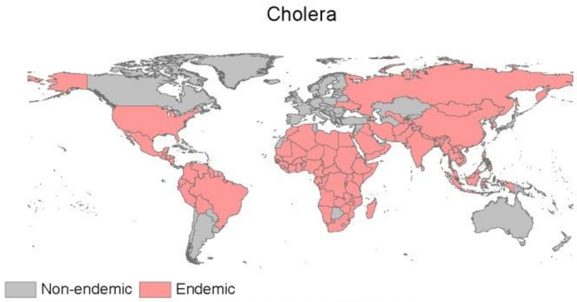
Disease: Cholera.

ICD-10 Code: A00.0.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Vibrionales, Vibrionaceae, *Vibrio cholerae* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food; faecal-oral route; contact with contaminated water; flies [1].

Reservoir*: Humans [1].

Incubation period: 2.5 days (range 2-3 days) [1].

Significant epidemiological characteristics:

Vaccine: Cholera - injectible or oral [1].

Estimated R_0 value(s) from published literature:

Human: 0-19 [102-109].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 21,746.

GenBank hits on 22/02/12: 22,106.

HealthMap feeds 2006-2011: 9,196.

ProMED feeds 1994-2011: 3,953.

BioCaster feeds 2006-2011: 23,694.

Approximate number of endemic countries: >95 [1].

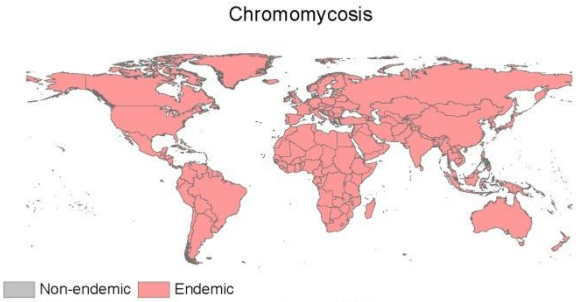
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	98	5	2	27	[110]
Disease	3	8	3	2	[111]
Disease	17	6	2	6	[112]
Disease	3	8	4	2	[113]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 229 occurrence points per country based on 21,746 results for “Cholera” in PubMed and 95 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Chromomycosis.

ICD-10 Code: B43.

Transmission category: Soil contact.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Euascomycetes, Chaetothyriales,

Many (e.g. *Phialophora verrucosa, Cladophialophora verrucosa, Fonsecaea pedrosi, F. compacta,* and *Rhinocladiella aquaspersa*) [1, 2].

Natural history:

Mode of transmission: Minor trauma [1].

Reservoir*: Non-human primates [1].

Incubation period: 52 days (range 14-90 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 293.

GenBank hits on 22/02/12: 91.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >229 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 1 occurrence point per country based on 293 results for "Chromomycosis" in PubMed and 229 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Chronic fatigue syndrome.

ICD-10 Code: G93.3.

Transmission category: Unknown.

Agent: Unknown [1, 2].

Natural history:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,586.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Chronic fatigue syndrome is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

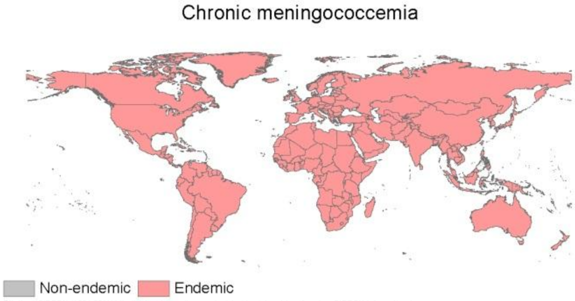
Disease: Chronic meningococcemia.

ICD-10 Code: A39.3.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Neisseriales, Neisseriaceae, *Neisseria meningitidis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious airborne particles; direct contact [1].

Reservoir*: Humans [1].

Incubation period: 6 days (range 2-10 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 60.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 0 for “Meningococcemia”.

ProMED feeds 1994-2011: 1 for “Meningococcemia”.

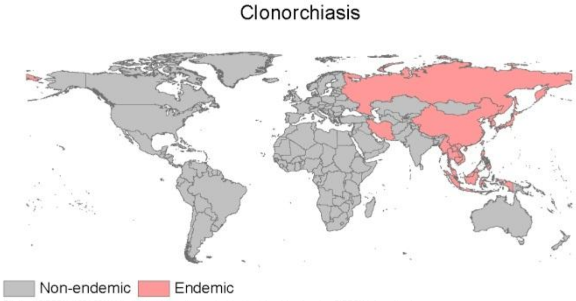
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Chronic meningococcemia is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Clonorchiasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Clonorchiasis.

ICD-10 Code: B66.1.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Plagiorchiida, Opisthorchiidae, *Clonorchis sinensis* [1, 2].

Natural history:

Mode of transmission: Consumption of infected freshwater fish or crayfish [1].

Reservoir*: Humans, cats, dogs, pigs and snails (*Bythnia*, *Alocinma*, *Semisulcospira*) [1].

Incubation period: 24.5 days (range 21-28 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [114].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 794.

GenBank hits on 22/02/12: 3,113.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >19 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	57	7	2	22	[114]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 42 occurrence points per country based on 794 results for "Clonorchiasis" in PubMed and 19 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

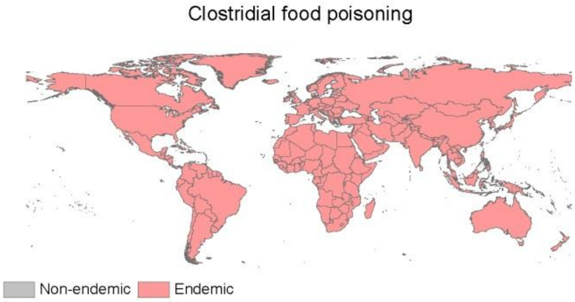
Disease: Clostridial food poisoning.

ICD-10 Code: A05.2.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium perfringens* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food [1].

Reservoir*: Humans, pigs, cattle, fish and poultry [1].

Incubation period: 0.45 days (range 0.3-0.6 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 7,398 for "*Clostridium perfringens*" and 454 for "Clostridium and food poisoning".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.
- **Approximate number of endemic countries:** Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Clostridial food poisoning is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

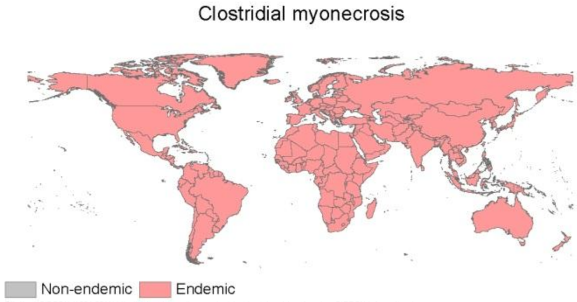
Disease: Clostridial myonecrosis.

ICD-10 Code: A48.0.

Transmission category: Soil contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium perfringens* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated soil; trauma [1].

Reservoir*: Humans [1].

Incubation period: 1.6 days (range 0.25-3 days) [1].

Significant epidemiological characteristics:

Vaccine: Gas gangrene antitoxin [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,398 for "*Clostridium perfringens*" and 165 for "Clostridial myonecrosis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Clostridial myonecrosis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

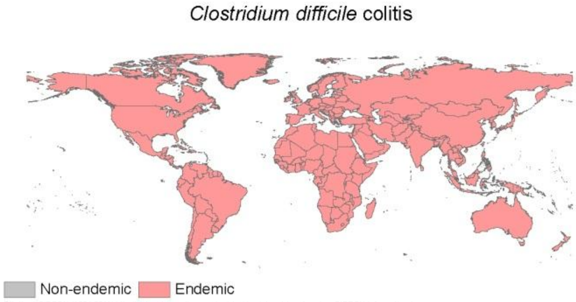
Disease: *Clostridium difficile* colitis.

ICD-10 Code: A04.7.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium difficile* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not applicable.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,594 for "*Clostridium difficile*" and 353 for "*Clostridium difficile* colitis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 536 for "*C. difficile*".

ProMED feeds 1994-2011: 101 "*C. difficile*".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Clostridium difficile* colitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

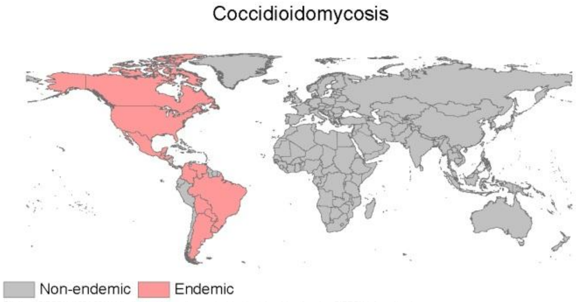
Disease: Coccidioidomycosis.

ICD-10 Code: B38.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Euascomycetes, Onygenales, Onygenaceae, *Coccidioides immitis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious particles [1].

Reservoir*: Envronmental sources. [1].

Incubation period: 12 days (range 10-14 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0 (not contagious) [115].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,782.

GenBank hits on 22/02/12: 11,246.

HealthMap feeds 2006-2011: 0.

ProMED feeds 1994-2011: 0.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	0	2	0	[116]
Disease	52	4.5	2	13	[117]
Disease	52	2.5	2	7	[118]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 214 occurrence points per country based on 2,782 results for “Coccidioidomycosis” in PubMed and 13 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

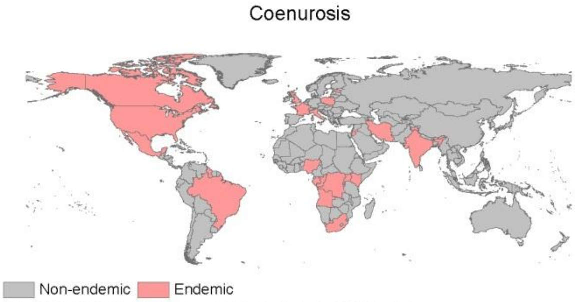
<u>Disease</u>: Coenurosis.

<u>ICD-10 Code:</u> B71.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae, *Taenia multiceps* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of contaminated food; contact with contaminated soil or water [1].

Reservoir*: Sheep, wild carnivores, horses and dogs [1].

Incubation period: Variable (months-years) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 75.
- **GenBank hits on 22/02/12:** 63.
- **HealthMap feeds 2006-2011:** 3 for “Taeniasis”.
- **ProMED feeds 1994-2011:** 2 for “Taeniasis”.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >24 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 3 occurrence points per country based on 75 results for “Coenurosis” in PubMed and 24 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Colorado tick fever.

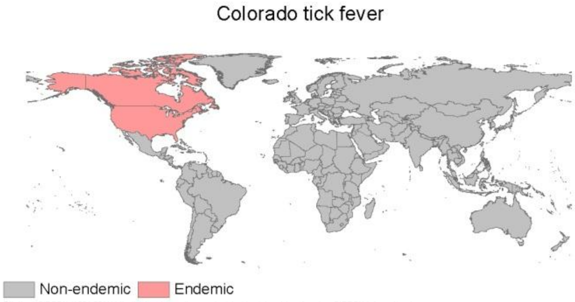
ICD-10 Code: A93.2.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Reoviridae, Spinareovirinae, Group III, Coltivirus,

Colorado tick fever (CTF) virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Dermacentor andersoni*) [1].

Reservoir*: Ground squirrels, porcupines, chipmunks, ticks, mice, rabbits, hares and woodchucks [1].

Incubation period: 4.5 days (range 4-5 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 179.

GenBank hits on 22/02/12: 102.

HealthMap feeds 2006-2011: 0.

ProMED feeds 1994-2011: 3.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >2 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	4.5	2	25	[4]
Vector	90	6.5	2	33	[119]
Disease	90	7.5	2	38	[120]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 90 occurrence points per country based on 179 results for “Colorado Tick Fever” in PubMed and 2 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Coltiviruses - Old World.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Reoviridae, Spinareovirinae, Group III, Coltiviruses A and B,
Banna virus and Eyach virus, Seadornavirus [1, 2].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (e.g. *Culex*, *Anopheles* and *Aedes* spp.) [1].

Reservoir*: Pigs, cattle, rabbits and mice [1].

Incubation period: 5 days (range 3-7 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 44 for “Coltivirus,” 22 for “Banna virus,” 13 for “Eyach virus” and 11 for “Seadornavirus”.

GenBank hits on 22/02/12: 267.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >6 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	92	8	2	81	[121]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 7 occurrence points per country based on 44 results for “Coltivirus” in PubMed and 6 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

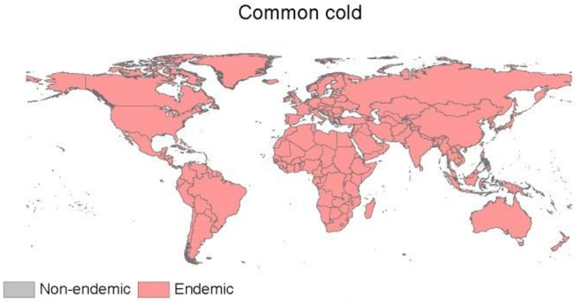
<u>Disease</u>: Common cold.

<u>ICD-10 Code:</u> J00.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Picornavirales, Picornaviridae, Group IV, Various (e.g. Rhinoviruses, Coronavirus) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious particles; direct contact [1].

Reservoir*: Humans [1].

Incubation period: 2 days (range 1-3 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** 0-4 [122].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 4,315.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 454.
- **ProMED feeds 1994-2011:** 8.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. The common cold is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

<u>Disease</u>: Conjunctivitis - viral.

<u>ICD-10 Code:</u> B30.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Virus.

<u>Taxonomy:</u> Many (e.g. Picornavirus, Adenovirus) [1, 2].

Conjunctivitis - viral

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct contact [1].

Reservoir*: Humans [1].

Incubation period: 2 days (range 1-3 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: Adenovirus (types 4 and 7; military use only) [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 12,869 for “Conjunctivitis” and 1,044 for “Conjunctivitis and viral”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 814”.

ProMED feeds 1994-2011: 131.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Conjunctivitis (viral) is endemic worldwide and potentially vaccine preventable.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

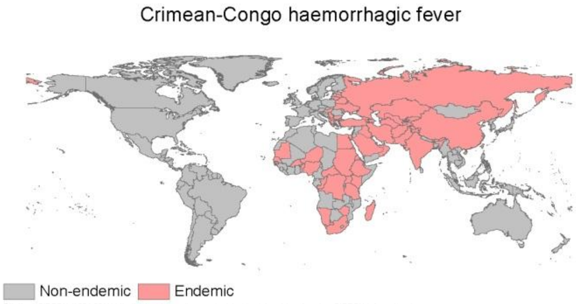
<u>**Disease**</u>**:** Crimean-Congo haemorrhagic fever.

<u>**ICD-10 Code:**</u> A98.0.

<u>**Transmission category:**</u> Vector-borne.

<u>**Agent**</u>**:** Virus-RNA.

<u>**Taxonomy:**</u> Bunyaviridae, Group V, Nairovirus, Crimean-Congo haemorrhagic fever virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Contact with secretions from patients or livestock; Tick vector (e.g. *Hyalomma* spp.) [1].

Reservoir*: Hares, birds, ticks, cattle, sheeps and goats [1].

Incubation period: 3.5 days (range 1-6 days) [1].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: Inactive virus vaccines used in Europe and Russia [1].

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [10, 123]
- **Reservoir:** 0-2.2 (Multispecies) [10, 123].

<u>**Map(s) from published literature**</u>**:**

Total available literature:

- **PubMed hits on 04/11/11:** 384.
- **GenBank hits on 22/02/12:** 701.
- **HealthMap feeds 2006-2011:** 251.
- **ProMED feeds 1994-2011:** 428.
- **BioCaster feeds 2006-2011:** 196.

Approximate number of endemic countries: >52 [1].

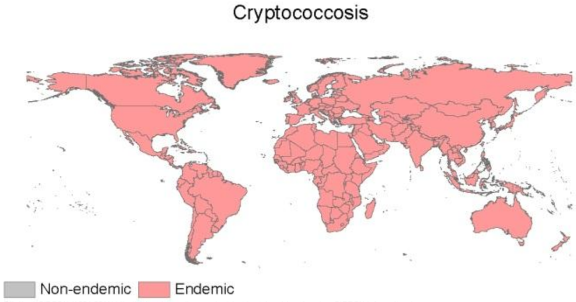
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	2	2	11	[124]
Disease	64	4.5	2	16	[123]
Disease	100	6	2	33	[125]
Disease	2	8	3	1	[126]

<u>**Mapping recommendation:**</u> Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 7 occurrence points per country based on 384 results for “Crimean-Congo haemorrhagic fever” in PubMed and 52 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Cryptococcosis.

ICD-10 Code: B45.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Basidiomycota, Tremellomycetes, Tremellales, Tremellaceae, *Cryptococcus neoformans* [1, 2].

Natural history:

Mode of transmission: Inhalation of infectious particles [1].

Reservoir*: Pigeons [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0 (sporadic human infections that rarely transmit person to person) [49].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,632.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 45.

ProMED feeds 1994-2011: 36.

BioCaster feeds 2006-2011: 8.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Cryptococcosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

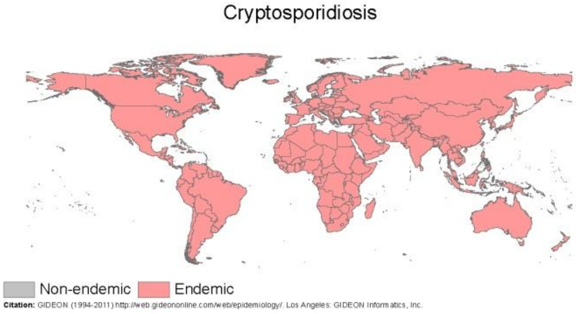
Disease: Cryptosporidiosis.

ICD-10 Code: A07.2.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Apicomplexa, Conoidasida, Eucoccidiorida, Cryptosporidiidae, *Cryptosporidium hominis*, *C.parvum*, rarely: *C.muris*, *C. felis*, *C.meleagridis* [1, 2].


Cryptosporidiosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated oysters; flies [1].

Reservoir*: Mammals (>150 species) [1].

Incubation period: 7.5 days (range 5-10 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1 [127, 128]

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,529 for “Cryptosporidiosis” and 6,141 for “*Cryptosporidium*”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 190 for “*Cryptosporidium*”.

ProMED feeds 1994-2011: 142 for “*Cryptosporidium*”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	9	2	N/A	[129]

Mapping recommendation: Option 1; do not map. Cryptosporidiosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Cutaneous larva migrans.

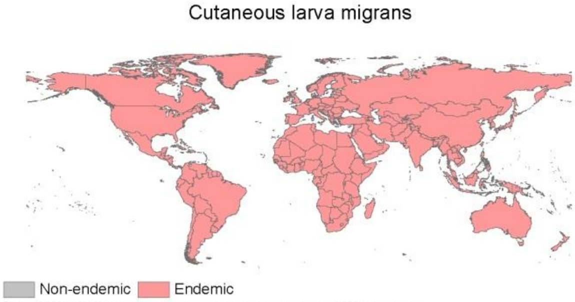
ICD-10 Code: B76.9.

Transmission category: Soil contact.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea,

Many (e.g. *Ancylostoma braziliense, A. caninum, Bunostomum phlebotomum, Strongyloides myopotami*) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Direct or soil contact [1].

Reservoir*: Cats, dogs and cattle [1].

Incubation period: 2.5 days (range 2-3 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 289.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	5	2.5	2	N/A	[130]

Mapping recommendation: Option 1; do not map. Cutaneous larva migrans is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

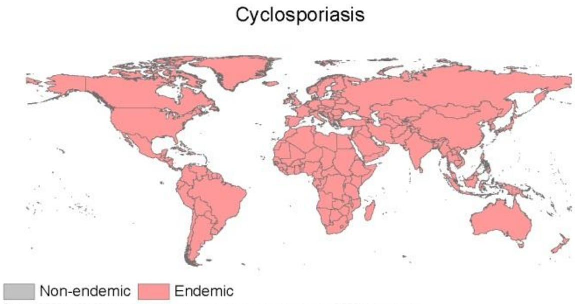
Disease: Cyclosporiasis.

ICD-10 Code: A07.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Apicomplexa, Conoidasida, Eucoccidiorida, Eimeriidae, *Cyclospora cayetanensis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food and water; contact with contaminated water [1].

Reservoir*: Humans and non-human primates [1].

Incubation period: 6 days (range 1-11 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [131].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 208.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 4.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	36	5	2	N/A	[132]

Mapping recommendation: Option 1; do not map. Cyclosporiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

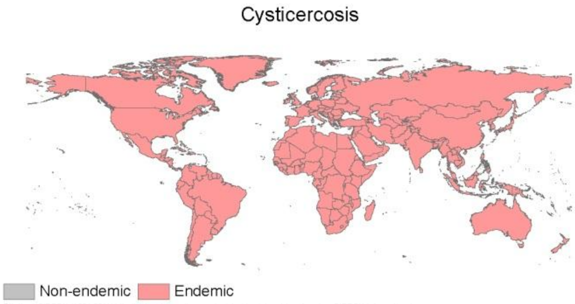
Disease: Cysticercosis.

ICD-10 Code: B69.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae,
Taenia solium [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; soil contact; flies [1].

Reservoir*: Pigs and humans [1].

Incubation period: 225 days (range 90-365 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-1.75 (pig-human) [133].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,516.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 23.

ProMED feeds 1994-2011: 19.

BioCaster feeds 2006-2011: N/A.

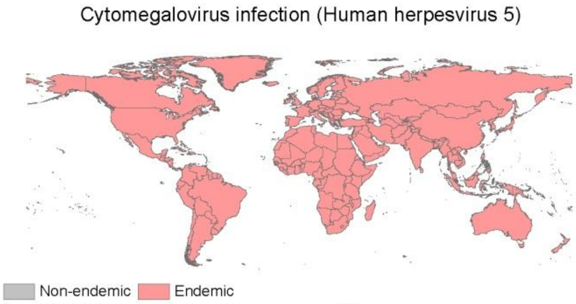
Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	74	5	2	N/A	[134]
Disease	74	5	2	N/A	[135]

Mapping recommendation: Option 1; do not map. Cysticercosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.


Cytomegalovirus infection (Human herpesvirus 5)

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Cytomegalovirus infection (Human herpesvirus 5).
ICD-10 Code: B25.
Transmission category: Respiratory.
Agent: Virus-DNA.
Taxonomy: Herpesviridae, Betaherpesvirinae, Group I, Cytomegalovirus,
Human (beta) herpes virus 5 [1, 2].

Natural history:

Mode of transmission: Contact with infectious secretions; inhalation of infectious droplets; consumption of contaminated dairy products [1].

Reservoir*: Humans [1].

Incubation period: 28 days (range 21-35 days) [1].

Significant epidemiological characteristics:

Vaccine: Cytomegalovirus immunoglobulin [1].

Estimated R_0 value(s) from published literature:

Human: 0-8.89; 0-15 in immunocompromised patients [136-138].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 36,807 for “Cytomegalovirus” and 326 for “Human herpesvirus 5”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 35.

ProMED feeds 1994-2011: 6.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	35	6.5	2	N/A	[139]

Mapping recommendation: Option 1; do not map. Cytomegalovirus infections are endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

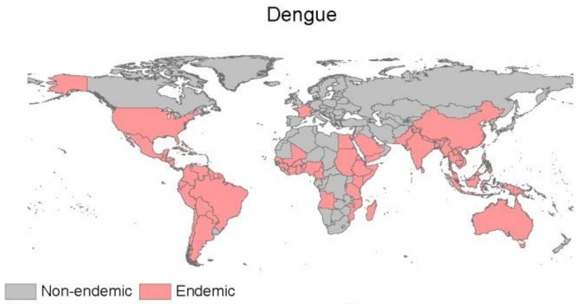
Disease: Dengue.

ICD-10 Code: A90, A91.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, Flavivirus, Dengue fever virus serotypes 1, 2, 3, 4 [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors (e.g. *Aedes aegypti, Ae. albopictus, Ae. polynesiensis, Ae. scutellaris*); rare direct contact [1].

Reservoir*: Humans, mosquitoes and monkeys (Malaysia, Africa) [1].

Incubation period: 6.5 days (range 5-8 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-22 [85, 140-150].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 9,115.

GenBank hits on 22/02/12: 11,473.

HealthMap feeds 2006-2011: 13,614.

ProMED feeds 1994-2011: 4,814.

BioCaster feeds 2006-2011: 17,993 for “Dengue” and 2 for “Haemorrhagic dengue fever”.

Approximate number of endemic countries: >119 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	85	8.5	4	80	[151]
Vector	100	9	4	100	[87]
Disease	91	4	2	20	[152]
Disease	61	4	2	14	[153]
Disease	66	4	2	15	[154]
Vector	74	4	2	16	[154]
Disease	66	3	2	11	[155]
Vector	74	3	2	12	[155]
Disease	92	2	2	10	[156]
Vector	13	4	2	3	[93]
Disease	100	6	2	33	[157]

Disease	26	4.5	2	6	[158]
Vector	26	4.5	2	6	[158]
Disease	11	4.5	2	3	[159]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 77 occurrence points per country based on 9,115 results for “Dengue” in PubMed and 119 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Dermatophytosis.

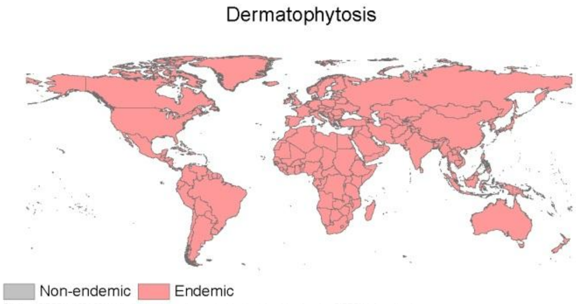
ICD-10 Code: B35.

Transmission category: Animal contact.

Agent: Fungus.

Taxonomy: Fungi,

Many (e.g. *Epidermophyton floccosum*, *Microsporum* spp., *Trichophyton schoeleinii, T. tonsurans, T. audouinii, Trichosporon* spp., *Arthroderma* spp.) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Direct or soil contact [1].

Reservoir*: Humans, dogs, cats, rabbits, marsupials and other mammals [1].

Incubation period: 12 days (range 10-14 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [160].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,188.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Dermatophytosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

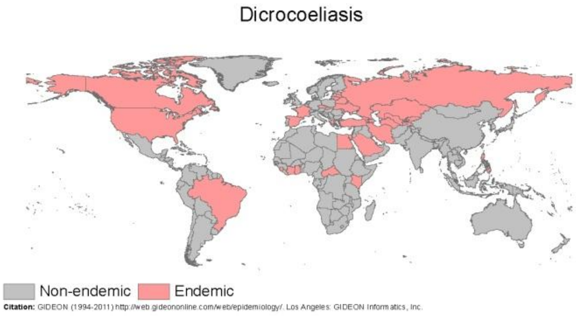
<u>Disease</u>: Dicrocoeliasis.

<u>ICD-10 Code:</u> B66.2.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Trematoda, Plagiorchiida, Dicrocoeliidae, *Dicrocoelium dendriticum* and *D. hospes* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of infected ants [1].

Reservoir*: Sheeps, snails and ants [1].

Incubation period: Unknown [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 200.

GenBank hits on 22/02/12: 11.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

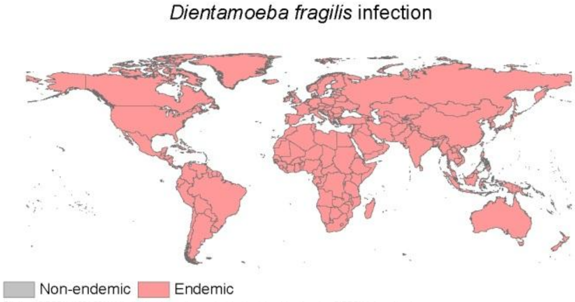
Approximate number of endemic countries: >32 [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 6 occurrence points per country based on 200 results for “Dicrocoeliasis” in PubMed and 32 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Dientamoeba fragilis* infection.

ICD-10 Code: A07.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Excavata, Metamonada, Parabasalia, Trichomonadida, Monocercomonadidae, *Dientamoeba fragilis* [1, 2].

Natural history:

Mode of transmission: Faecal-oral route [1].

Reservoir*: Humans and gorillas [1].

Incubation period: 16.5 days (range 8-25 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

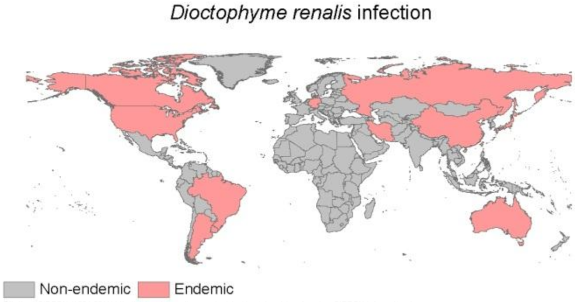
- **PubMed hits on 04/11/11:** 186.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Dientamoeba fragilis* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Dioctophyme renalis* infection.

ICD-10 Code: B83.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Dioctophymatidae, *Dioctophyme renale* [1, 2].

Natural history:

Mode of transmission: Consumption of infected fish [1].

Reservoir*: Dogs and mink [1].

Incubation period: 135 days (range 90-180 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 17 for "*Dioctophyme*" and 0 for "*Dioctophyme renalis*".

GenBank hits on 22/02/12: 3.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

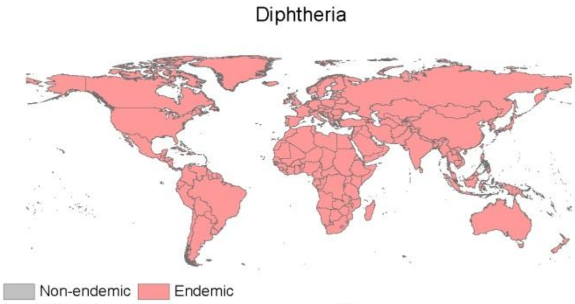
Approximate number of endemic countries: >11 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 17 results for "*Dioctophyme*" in PubMed and 11 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Diphtheria.

ICD-10 Code: A36.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Corynebacteriaceae, *Corynebacterium diphtheriae* [1, 2].

Natural history:

Mode of transmission: Inhalation of infectious droplets; consumption of contaminated dairy products; fomites; direct contact [1].

Reservoir*: Humans [1].

Incubation period: 3.5 days (range 2-5 days) [1].

Significant epidemiological characteristics:

Vaccine: Diphtheria antitoxin, Diphtheria, DTP, DT, DTaP, Td [1].

Estimated R_0 value(s) from published literature:

Human: 0-5 [28].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 16,416.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 469.

ProMED feeds 1994-2011: 134.

BioCaster feeds 2006-2011: 11.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Diphtheria is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

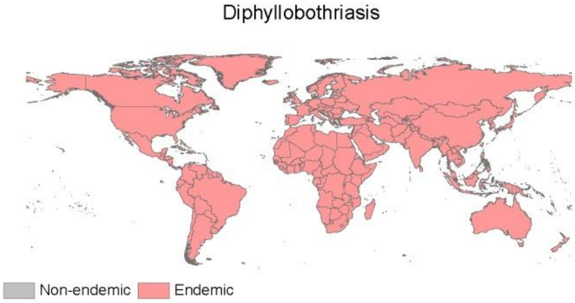
Disease: Diphyllobothriasis.

ICD-10 Code: B70.0.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Pseudophyllidea, Diphyllobothriidae, *Diphyllobothrium latum* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated fish [1].

Reservoir*: Humans, dogs, bears and fish-eating mammals [1].

Incubation period: 35 days (range 28-42 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [161].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 527.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 0".

ProMED feeds 1994-2011: 8.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	4	6	2	N/A	[162]
Disease	5	6.5	2	N/A	[163]

Mapping recommendation: Option 1; do not map. Diphyllobothriasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

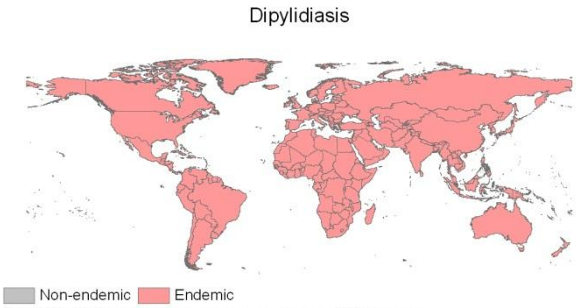
<u>**Disease**</u>**:** Dipylidiasis.

<u>ICD-10 Code:</u> B71.1.

<u>Transmission category:</u> Food/water-borne.

<u>**Agent**</u>**:** Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Dipylidiidae,
Dipylidium caninum [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Consumption of infected fleas (*Ctenocephalides* spp.) [1].

Reservoir*: Dogs and cats [1].

Incubation period: 24.5 days (range 21-28 days) [1].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [164].
- **Reservoir:** Not found.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

- **PubMed hits on 04/11/11:** 21.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Dipylidiasis is endemic worldwide.

<u>**Future mapping potential**</u>**:** None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Dirofilariasis.

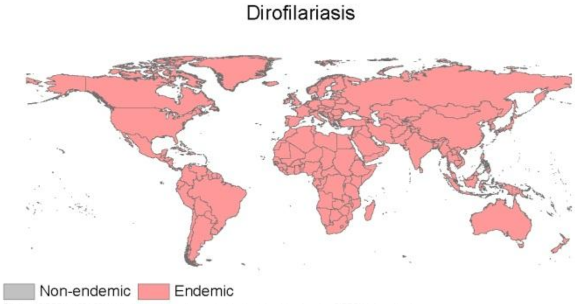
ICD-10 Code: B74.8.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Filariidae,

Many [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors [1].

Reservoir*: Mammals, dogs and wild carnivores (*D. tenuis* in raccoons; *D. ursi* in Bears) [1].

Incubation period: 75 days (range 60-90 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,862.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	6	5	2	N/A	[165]
Disease	6	5	2	N/A	[166]
Disease	3	6	2	N/A	[166]

Mapping recommendation: Option 1; do not map. Dirofilariasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Disease: Dracunculiasis (Guinea worm).

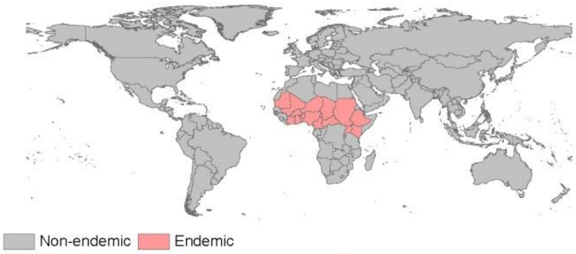
ICD-10 Code: B72.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Camallanida, Dracunculidae, *Dracunculus medinensis* [1, 2].

Dracunculiasis (Guinea worm)



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Drinking water contaminated with infected copepods (e.g. *Mesocyclops* and *Thermocyclops*) [1].

Reservoir*: Humans [1].

Incubation period: 450 days (range 360-540 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 754 for “Dracunculiasis” and 274 for “Guinea worm”.

GenBank hits on 22/02/12: 8.

HealthMap feeds 2006-2011: 16 for “Guinea Worm”.

ProMED feeds 1994-2011: 34 for “Guinea Worm”.

BioCaster feeds 2006-2011: 3 for “Guinea Worm”.

Approximate number of endemic countries: >16 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5	2	28	[167]
Disease	77	4.5	2	19	[168]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 47 occurrence points per country based on 754 results for “Dracunculiasis” in PubMed and 16 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

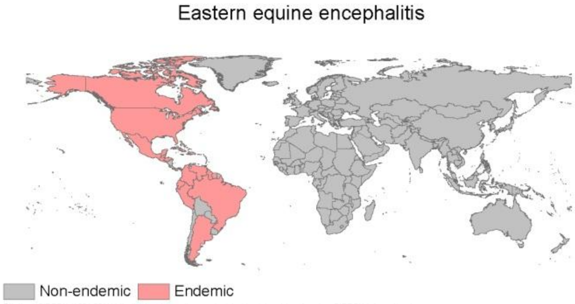
Disease: Eastern equine encephalitis.

ICD-10 Code: A83.2.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, Alphavirus, Eastern equine encephalitis (EEE) virus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors (e.g. *Aedes, Culiseta, Coquillettidia* spp.) [1].

Reservoir*: Wild birds, horses, cattle and pigs [1].

Incubation period: 8.5 days (range 7-10 days) [1].

Significant epidemiological characteristics:

Vaccine: Eastern equine encephalitis [1].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [169].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 326.

GenBank hits on 22/02/12: 879.

HealthMap feeds 2006-2011: 317.

ProMED feeds 1994-2011: 271.

BioCaster feeds 2006-2011: 983.

Approximate number of endemic countries: >19 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	76	1.5	2	8	[71]
Disease	79	8	2	47	[170]
Disease	36	7.5	2	20	[171]
Vector	36	9	3	36	[172]
Disease	36	7.5	2	20	[72]
Vector	36	8.5	3	34	[173]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 17 occurrence points per country based on 326 results for “Eastern Equine Encephalitis” in PubMed and 19 endemic countries listed in the GIDEON database. With fewer than

25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors. If occurrence data for these mosquito species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

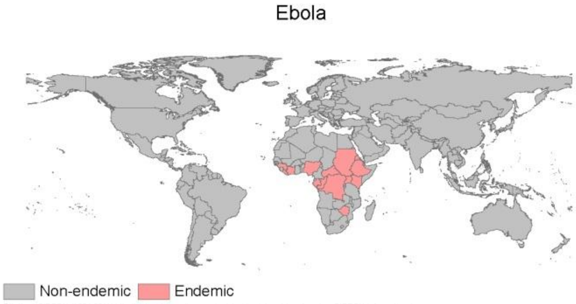
<u>Disease</u>: Ebola.

<u>ICD-10 Code:</u> A98.4.

<u>Transmission category:</u> Blood/body fluid contact.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Mononegavirales, Filoviridae, Group V, Filovirus,
Ebolavirus [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious droplets; contact with secretions or blood; fomites [1].

Reservoir*: Bats, possibly primates and guinea pigs [1].

Incubation period: 8.5 days (range 5-12 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; 0-2.7 (outbreaks) [174-177]
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 1,485.
- **GenBank hits on 22/02/12:** 89.
- **HealthMap feeds 2006-2011:** 567.
- **ProMED feeds 1994-2011:** 815.
- **BioCaster feeds 2006-2011:** 1,440.

Approximate number of endemic countries: >14 [1].

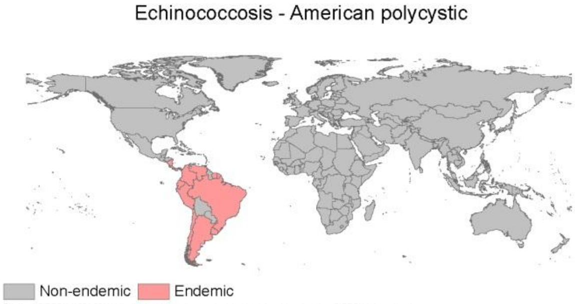
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	35	4.5	2	9	[178]
Disease	35	6	2	12	[179]
Disease	44	6.5	2	16	[180]
Disease	54	8	2	24	[181]
Disease	31	8	2	14	[182]
Disease	1	6.5	2	<1	[183]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 106 occurrence points per country based on 1,485 results for “Ebola” in PubMed and 14 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Echinococcosis - American polycystic.

ICD-10 Code: B67.9.

Transmission category: Soil contact.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae,
Echinococcus vogeli, E. oligarthrus [1, 2].

Natural history:

Mode of transmission: Contact with contaminated soil; faecal-oral route [1].

Reservoir*: Bush dogs, pacas and rodents [1].

Incubation period: 2,373 days (range 365-3,650 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 35 for "*Echinococcus vogeli*," 24 for "*Echinococcus oligarthrus*" and 43 for "Echinococcosis and American".

GenBank hits on 22/02/12: 58.

HealthMap feeds 2006-2011: 64 for "Echinococcosis".

ProMED feeds 1994-2011: 30 for "Echinococcosis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Host	100	3.5	2	39	[184]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 3 occurrence points per country based on 35 results for "*Echinococcus vogeli*" in PubMed and 13 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

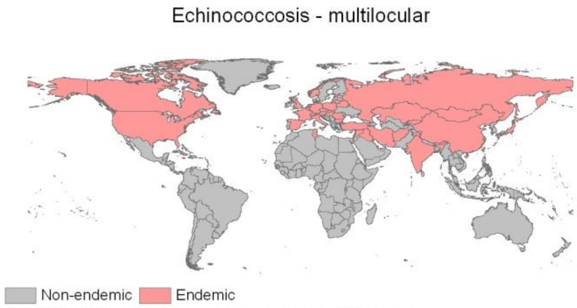
<u>Disease</u>: Echinococcosis - multilocular.

<u>ICD-10 Code:</u> B67.5 to B67.7.

<u>Transmission category:</u> Soil contact.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae,
Echinococcus multilocularis [1, 2].


Echinococcosis - multilocular

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Faecal-oral route; fomites [1].

Reservoir*: Foxes, wolves, coyotes, dogs, cats, voles, lemmings, shrews and mice [1].

Incubation period: 3,833 days (range 365-7,300 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [185, 186]

Reservoir: 0-4 (foxes) [185]

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 8 for "*Echinococcus multiocularis*" and 98 for "Echinococcosis and multilocular".

GenBank hits on 22/02/12: 389.

HealthMap feeds 2006-2011: 64 for "Echinococcosis".

ProMED feeds 1994-2011: 30 for "Echinococcosis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >38 [1].

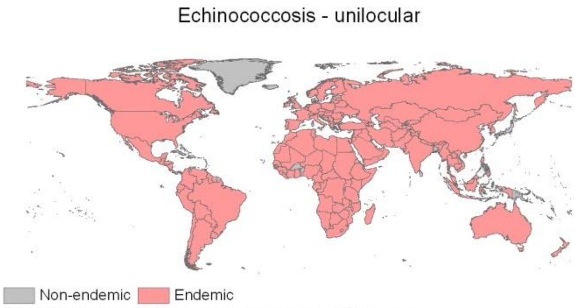
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	63	4.5	2	32	[187]

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 3 occurrence points per country based on 98 results for "Echinococcosis and multilocular" in PubMed and 38 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Echinococcosis - unilocular.

<u>ICD-10 Code:</u> B67.

<u>Transmission category:</u> Soil contact.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae,
Echinococcus granulosus, E.canadensis [1, 2].

<u>Natural history</u>:

Mode of transmission: Faecal-oral route; contact with contaminated water and soil; fomites; consumption of contaminated food; direct contact with infected dogs; flies [1].

Reservoir*: Dogs, wolves, dingoes, cats, sheep, horses, pigs, camels and others [1].

Incubation period: 3,833 days (range 365-7,300 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [188-190].

Reservoir: 0-1.8 (goats, sheep) [188-190].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 2537 for "*Echinococcus granulosus*," 17 for "*Echinococcus canadensis*" and 98 for "Echinococcosis and unilocular".

GenBank hits on 22/02/12: 2,334.

HealthMap feeds 2006-2011: 64 for "Echinococcosis".

ProMED feeds 1994-2011: 30 for "Echinococcosis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >153 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5	2	56	[191]
Disease	87	4.5	2	43	[192]

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 17 occurrence points per country based on 2537 results for "*Echinococcus granulosus*" in PubMed and 153 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

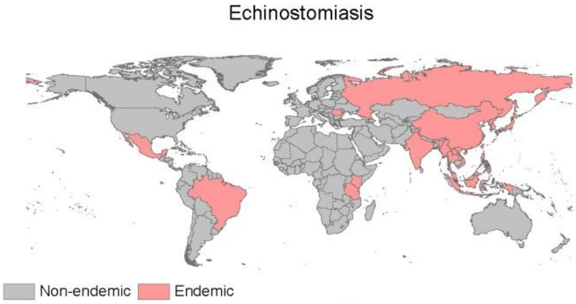
<u>Disease</u>: Echinostomiasis.

<u>ICD-10 Code:</u> B66.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Eumetazoa, Platyhelminthes, Trematoda, Echinostomatida, Echinostomatidae, *Echinostoma ilocanum, E. malayanum* and *E. revolutum* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Contact with contaminated water; consumption of infected clams, fish, snail, tadpoles and frogs; contact with infected snails [1].

Reservoir*: Mammals, birds, humans, frogs, cats and snails [1].

Incubation period: 14 days (range 7-21 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [193].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 253.

GenBank hits on 22/02/12: 93.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >22 [1].

Previously published maps: None.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 12 occurrence points per country based on 253 results for “Echinostomiasis” in PubMed and 22 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

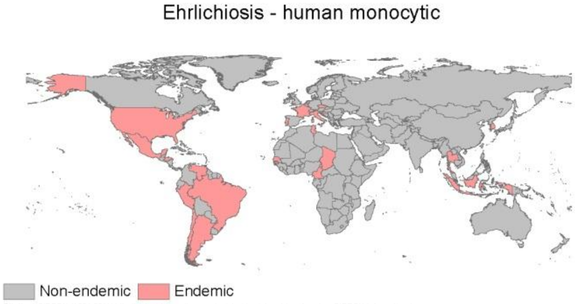
Disease: Ehrlichiosis - human monocytic.

ICD-10 Code: A79.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Anaplasmataceae, *Ehrlichia chaffeensis* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vectors (e.g. *Dermacentor variablis, Ambylomma americanum, Ixodes scapularis*) [1].

Reservoir*: Dogs, ticks, deer and coyotes [1].

Incubation period: 14 days (range 7-21 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [194].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,947 for "Ehrlichiosis" and 297 for "Ehrlichiosis and monocytic".

GenBank hits on 22/02/12: 505.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 18.

Approximate number of endemic countries: >24 [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	23	7	2	9	[195]
Disease	23	7	2	9	[194]
Disease	34	4.5	2	9	[194]
Disease	23	6.5	2	8	[196]
Disease	23	6.5	2	8	[197]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 81 occurrence points per country based on 1,947 results for “Ehrlichosis” in PubMed and 24 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

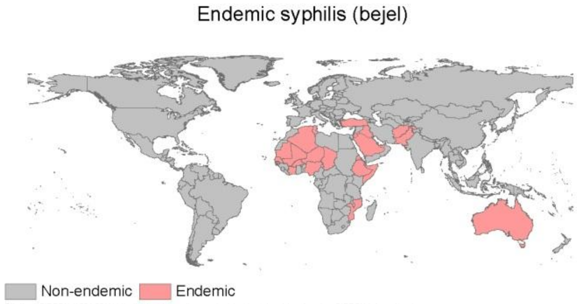
Disease: Endemic syphilis (bejel).

ICD-10 Code: A65.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Spirochaetaceae, *Treponema pallidum* subspp. *endemicum* [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; fomites [1].

Reservoir*: Humans [1].

Incubation period: 52 days (range 14-90 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 109 for “Endemic syphilis” and 66 for “Bejel”.

GenBank hits on 22/02/12: 1,304.

HealthMap feeds 2006-2011: 284.

ProMED feeds 1994-2011: 58.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >24 [1].

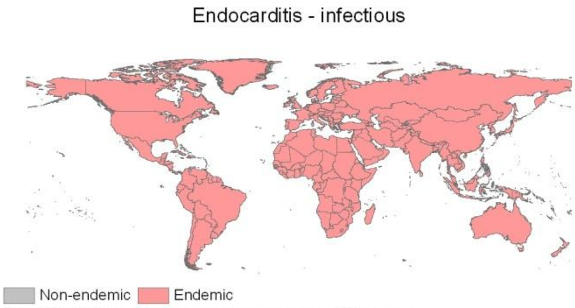
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	6	2	67	[113]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 5 occurrence points per country based on 109 results for “Endemic syphilis” in PubMed and 24 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Endocarditis - infectious.

<u>ICD-10 Code:</u> I33.0, B37.8.

<u>Transmission category:</u> Endogenous.

<u>Agent</u>: Bacterium; Fungus

<u>Taxonomy:</u> Eubacteria, Firmicutes, Bacilli,
Lactobacillales, Streptococcaceae,
Streptococcus spp. [1, 2].
Lactobacillales, Enteroccaceae,
Enterococcus spp. [1, 2].
Bacillales, Staphylococcaceae,
Staphylococcus aureus [1, 2].
Fungi, Ascomycota, Saccharomycetes, Saccharomycetales, Saccharomycetaceae,
Candida albicans [1, 2].

<u>Natural history</u>:

Mode of transmission: Endogenous; contact [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

> **Human:** 0-0.7 (possible >1) for MRSA [198]; 0-~1 (3-4 in one model) for vancomycin resistant enterococci [199, 200].
>
> **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

> **PubMed hits on 04/11/11:** "Endocarditis" - 29278
>
> **GenBank hits on 22/02/12:** N/A.
>
> **HealthMap feeds 2006-2011:** N/A.
>
> **ProMED feeds 1994-2011:** N/A.
>
> **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Endocarditis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

<u>Disease</u>: *Entamoeba polecki* infection.

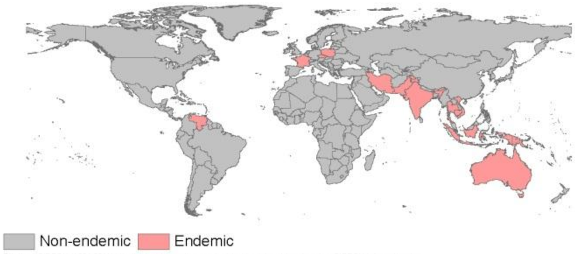
<u>ICD-10 Code:</u> A07.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Protista, Protozoa, Sarcomastigophora, Lobosea, Amoebida, Entamoebidae, *Entamoeba polecki* [1, 2].

Entamoeba polecki infection



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of contaminated food [1].

Reservoir*: Pigs and monkeys [1].

Incubation period: Unknown.

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [201].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 34.

GenBank hits on 22/02/12: 33.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >16 [1].

Previously published maps: None.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 34 results for "*Entamoeba polecki*" in PubMed and 16 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Enteritis necroticans.

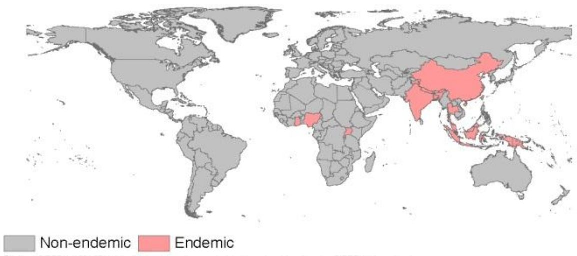
ICD-10 Code: A05.2.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium perfringens* [1, 2].

Enteritis necroticans



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food [1].

Reservoir*: Mammals [1].

Incubation period: 0.625 days (range 0.25-1 days) [1].

Significant epidemiological characteristics:

Vaccine: Gas gangrene antitoxin [1].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 82.

GenBank hits on 22/02/12: 7,384.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [1].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 6 occurrence points per country based on 82 results for “Enteritis necroticans” in PubMed and 13 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

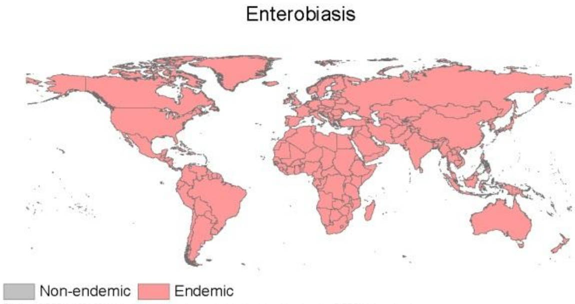
Disease: Enterobiasis.

ICD-10 Code: B80.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Oxyurida, Oxyuridae,
Enterobius vermicularis [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; inhalation of dust containing eggs; fomites; sexual contact [1].

Reservoir*: Humans [1].

Incubation period: 28 days (range 14-42 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 681.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 2.
- **ProMED feeds 1994-2011:** 0.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Enterobiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

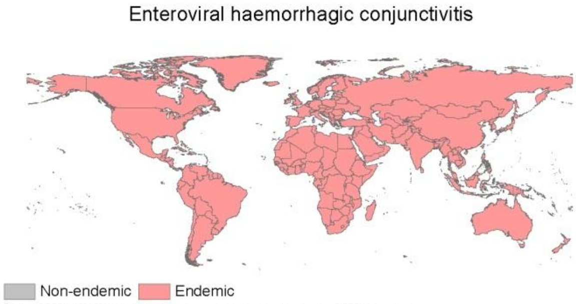
<u>Disease</u>: Enteroviral haemorrhagic conjunctivitis.

<u>ICD-10 Code:</u> B30.3.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Adenoviridae, Group I, Adenovirus, Type 70 [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct contact; swimming in contaminated pools [1].

Reservoir*: Humans [1].

Incubation period: 8 days (range 4-12 days) [1].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 220 for “Hemorrhagic conjunctivitis”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Enteroviral haemorrhagic conjunctivitis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

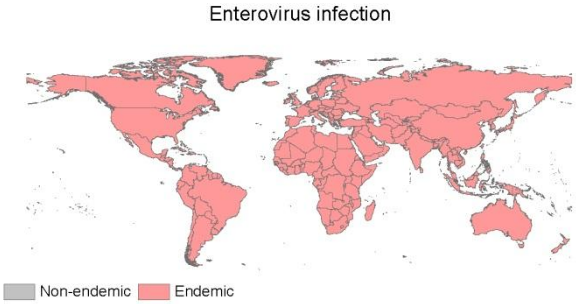
Disease: Enterovirus infection.

ICD-10 Code: B34.1.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Picornaviridae, Group IV, Coxsackievirus, Enterovirus, Parechovirus (e.g. ECHO virus) [1, 2].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets; faecal-oral route [1].

Reservoir*: Humans [1].

Incubation period: 4.5 days (range 2-7 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** 0-5.5 [202].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

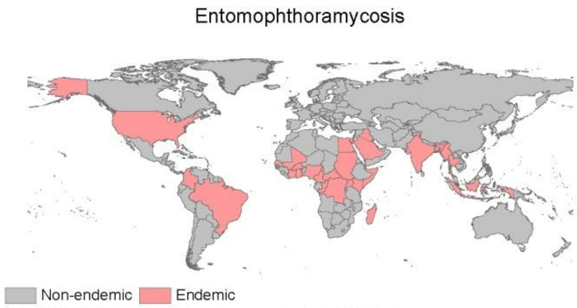
- **PubMed hits on 04/11/11:** 5,002 for “Coxsackievirus,” 11,704 for “Enterovirus” and 169 for “Parechovirus”.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 200.
- **ProMED feeds 1994-2011:** 145.
- **BioCaster feeds 2006-2011:** 8.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: None.

Mapping recommendation: Option 1; do not map. Enterovirus infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Entomophthoramycosis.

ICD-10 Code: B46.8.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Zygomycota, Zygomycetes, Entomophthorales, Basidiobolaceae, *Basidiobolus ranarum* (haptosporus) [1, 2].
Fungi, Zygomycota, Zygomycetes, Entomophthorales, Anylistaceae, *Conidiobolus coronatus* [1, 2].

Natural history:

Mode of transmission: Inhalation of infectious particles; blood inoculation [1].
Reservoir*: Amphibians and reptiles [1].
Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.
Estimated R_0 value(s) from published literature:
- **Human:** Not found.
- **Reservoir:** Not found.

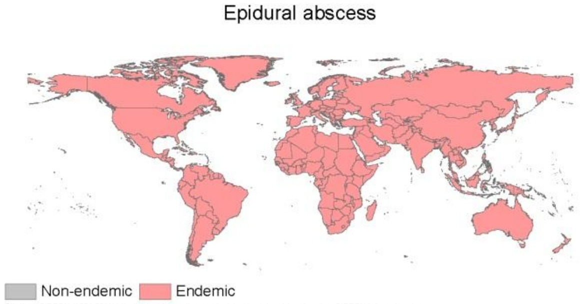
Map(s) from published literature:

Total available literature:
- **PubMed hits on 04/11/11:** 23 for “Entomophthoramycosis,” 62 for “*Basidiobolus ranarum*” and 79 for “*Conidiobolus coronatus*”.
- **GenBank hits on 22/02/12:** 7,417.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >32 [1].
Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.
There were approximately 2 occurrence points per country based on 79 results for “*Conidiobolus coronatus”* in PubMed and 32 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Epidural abscess.

ICD-10 Code: G06.0.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus* [1, 2].

Natural history:

Mode of transmission: Trauma [1].

Reservoir*: Humans [1].

Incubation period: Variable [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,477.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

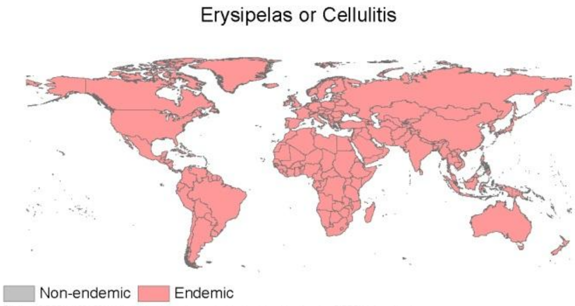
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Epidural abscesses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Erysipelas or Cellulitis.

ICD-10 Code: L03.

Transmission category: Direct contact

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pyogenes* [1, 2].

Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus* [1, 2].

Natural history:

Mode of transmission: Inhalation of infectious droplets; fomites; trauma [1].

Reservoir*: Humans [1].

Incubation period: 4 days (range 1-7 days) [1].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not applicable (endogenous).

Reservoir: 0-3 (pigs) [203].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,034 for “Erysipelas” and 8,909 for “Cellulitis”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

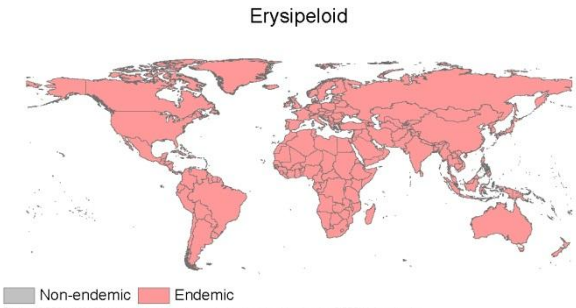
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Erysipelas and Cellulitis are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.


Erysipeloid

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Erysipeloid.

ICD-10 Code: A26.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Mollicutes, Erysipelotrichales, Erysipelotrichidae, *Erysipelothrix rhusiopathiae* [1, 2].

Natural history:

Mode of transmission: Contact with contaminated meat, poultry and fish [1].

Reservoir*: Mammals, birds and fish [1].

Incubation period: 2.5 days (range 1-5 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 435.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

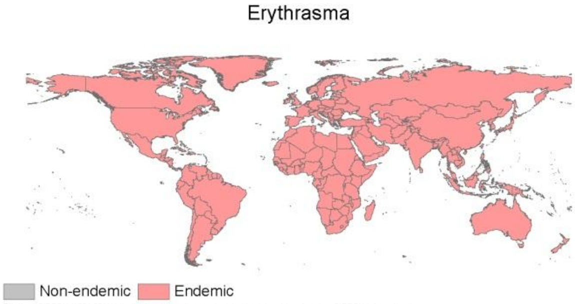
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Erysipeloid is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Erythrasma.

ICD-10 Code: L08.1.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Corynebacteriaceae, *Corynebacterium minutissimum* [1, 2].

Natural history:

Mode of transmission: Endogenous [1].

Reservoir*: Humans [1].

Incubation period: 2 days [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 181.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [1].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Erythrasma is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Disease: *Escherichia coli* diarrhoea.

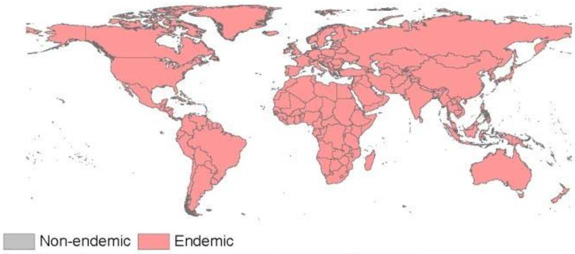
ICD-10 Code: A04.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Escherichia coli* [1, 2].

Escherichia coli diarrhoea



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food; faecal-oral route [1].

Reservoir*: Humans and mammals [1].

Incubation period: 2 days (range 1-3 days) [1].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11,0656 for "*E. coli*" and 3,539 for "*E. coli* and diarrhea".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 5,838 for "*E. coli*".

ProMED feeds 1994-2011: 1,111 for "*E. coli*".

BioCaster feeds 2006-2011: 3,370.

Approximate number of endemic countries: Worldwide [1].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	8	2	N/A	[129]

Mapping recommendation: Option 1; do not map. *Escherichia coli* diarrhoea is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

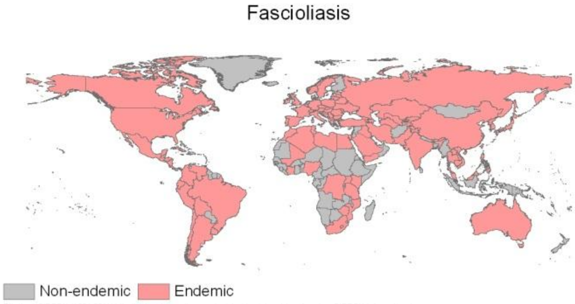
Disease: Fascioliasis.

ICD-10 Code: B66.3.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Echinostomatida, Fasciolidae, *Fasciola hepatica* and *F. gigantica* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food, notably aquatic plants and watercress (*Nasturtium officinale*) [204].

Reservoir*: Sheep, cattle and snails (*Lymnaea* spp., *Fossaria* spp.) [204].

Incubation period: 52 days (range 14-90 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [206].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 3,202.
- **GenBank hits on 22/02/12:** 1,667.
- **HealthMap feeds 2006-2011:** 3 for "Fascioliasis".
- **ProMED feeds 1994-2011:** 7 for "Fascioliasis".
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >95 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	10	8.5	3	7	[207]
Disease	1	6.5	3	1	[208]
Disease	3	7.5	2	1	[209]
Disease	<1	7	3	<1	[210]
Disease	<1	6.5	2	<1	[211]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 34 occurrence points per country based on 3,202 results for “Fascioliasis” in PubMed and 95 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

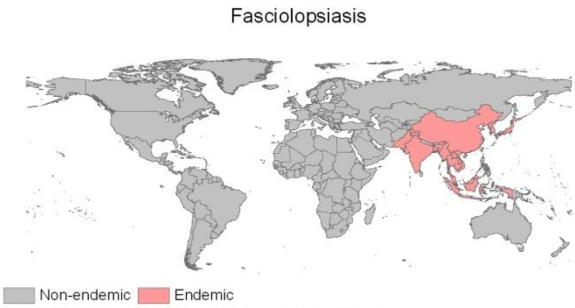
<u>Disease</u>: Fasciolopsiasis.

<u>ICD-10 Code:</u> B66.5.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Trematoda, Echinostomatida, Fasciolidae, *Fasciolopsis buski* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of contaminated food, notably aquatic plants (e.g. water-chestnut (*Eliocharis tuberosa*), water-caltrop (*Tropan natans*) and water fern (*Salvinia natans*)) [204].

Reservoir*: Pigs, humans, dogs and snails (*Hippeutis* spp., *Segmentina* spp.) [204].

Incubation period: 60 days (range 30-90 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 35.

GenBank hits on 22/02/12: 11.

HealthMap feeds 2006-2011: 0 for “Fasciolopsiasis”.

ProMED feeds 1994-2011: 0 for “Fasciolopsiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >16 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Host	100	8	3	53	[212]

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 35 results for “Fasciolopsiasis” in PubMed and 16 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

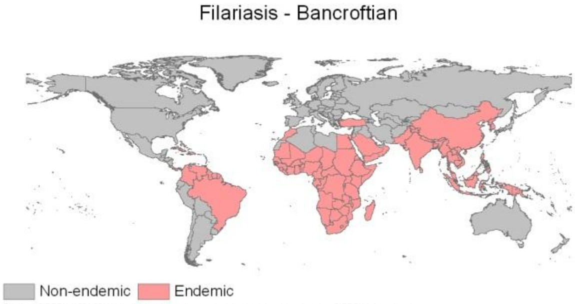
Disease: Filariasis - Bancroftian.

ICD-10 Code: B74.0.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Onchocercidae, *Wuchereria bancrofti* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors (e.g. *Culex. quinquefasciatus*, *Anopheles. gambiae*, *An. funestus, Aedes. polynesiensis*, *Ae. scapularis*, and *Ae. pseudoscutellaris*) [204].

Reservoir*: Humans [204].

Incubation period: 345 days (range 150-540 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-~5.5 [213-215].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,390 for "*Wuchereria bancrofti*".

GenBank hits on 22/02/12: 188.

HealthMap feeds 2006-2011: 28 for "Filariasis".

ProMED feeds 1994-2011: 15 for "Filariasis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >117 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	62	5	2	14	[216]
Disease	21	6	3	9	[217]
Disease	56	4.5	2	11	[218]
Disease	<1	8.5	2	<1	[219]
Disease	1	7	2	<1	[220]
Disease	1	6	2	<1	[221]
Disease	37	7	2	11	[222]
Disease	81	4	2	14	[223]
Disease	<1	7.5	2	<1	[224]
Disease	2	6	2	1	[225]

Disease	80	4	2	14	[226]

Mapping recommendation: Option 5; map limits using prevalence data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys. The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Build upon current ecological niche modelling results [227] using additional occurrence data and aggregate systematically prevalence data to implement MBG.

Disease: Filariasis - *Brugia malayi*.

ICD-10 Code: B74.1.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Onchocercidae, *Brugia malayi* [204, 205].

Filariasis - *Brugia malayi*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors (e.g. *Mansonia* spp., *Aedes* spp., *Anopheles* spp.) [204].

Reservoir*: Humans, non-human primates, cats and civets [204].

Incubation period: 345 days (range 150-540 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 824 for “Filariasis and *Brugia malayi*” and 1,481 for “*Brugia malayi*”.
- **GenBank hits on 22/02/12:** 60,397.
- **HealthMap feeds 2006-2011:** 28 for “Filariasis”.
- **ProMED feeds 1994-2011:** 15 for “Filariasis”.
- **BioCaster feeds 2006-2011:** N/A.

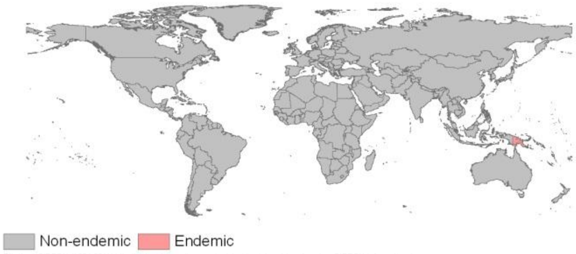
Approximate number of endemic countries: >16 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	53	7	2	16	[222]
Disease	3	6	2	1	[225]
Disease	89	4	2	16	[226]

Mapping recommendation: Option 5; map limits using prevalence data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys. The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Build upon current ecological niche modelling results [227] using additional occurrence data and aggregate systematically prevalence data to implement MBG.



Filariasis - *Brugia timori*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Filariasis - *Brugia timori*.

ICD-10 Code: B74.2.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Onchocercidae, *Brugia timori* [204, 205].

Natural history:

Mode of transmission: Mosquito vectors (e.g. *Anopheles. barbirostris*, *Aedes. oceanicus* and *Ae. samoanus*) [204].

Reservoir*: Humans [204].

Incubation period: 345 days (range 150-540 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 40 for "*Brugia timori*".

GenBank hits on 22/02/12: 25.

HealthMap feeds 2006-2011: 28 for "Filariasis".

ProMED feeds 1994-2011: 15 for "Filariasis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >2 [204].

Previously published maps: Not found.

Mapping recommendation: Option 5; map limits using prevalence data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys. The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Build upon current ecological niche modelling results [227] using additional occurrence data and aggregate systematically prevalence data to implement MBG.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Flinders Island spotted fever.

ICD-10 Code: A77.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia honei* [204, 205].

Natural history:

Mode of transmission: Tick vectors [204].

Reservoir*: Ticks and rodents [204].

Incubation period: 6.5 days (range 6-7 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [228].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 15.

GenBank hits on 22/02/12: 34.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

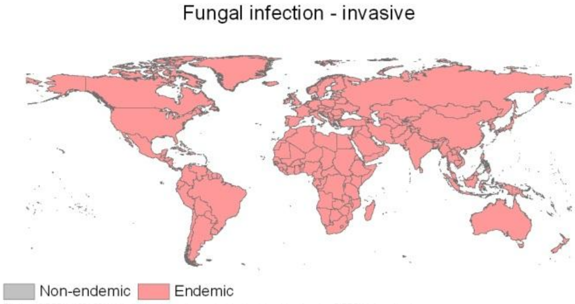
Approximate number of endemic countries: >1 [204].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 15 occurrence points per country based on 15 results for "Flinders Island spotted fever" in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Fungal infection - invasive.

ICD-10 Code: B35 to B49.

Transmission category: Endogenous.

Agent: Fungus.

Taxonomy: Various fungi [204, 205].

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans [204].

Incubation period: Variable [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not applicable.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 672 for “Invasive fungal infection”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Invasive fungal infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Gastrodiscoidiasis.

ICD-10 Code: B66.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Echinostomida, Paramphistomatidae, *Gastrodiscoides hominis* [204, 205].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of, or contact with, contaminated fresh water plants [204].

Reservoir*: Pigs, herbivores and snails (*Helicorbis coenosis*) [204].

Incubation period: Unknown [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1 for "Gastrodiscoidiasis" and 21 for "*Gastrodiscoides hominis*".

GenBank hits on 22/02/12: 7.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

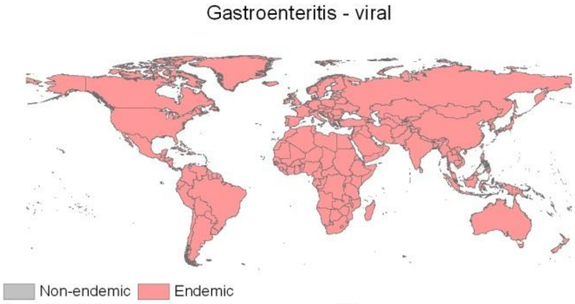
Approximate number of endemic countries: >11 [204].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 21 results for "*Gastrodiscoides hominis*" in PubMed and 11 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Gastroenteritis - viral.

ICD-10 Code: A08.4.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Coronaviridae, Group VI,
Calicivirus, Norwalk virus [204, 205].
Coronaviridae, Torovirinae, Group VI,
Torovirus [204, 205].
Astroviridae, Group VI,
Astrovirus [204, 205].

Natural history:

Mode of transmission: Ingestion of contaminated food or water [204].

Reservoir*: Humans [204].

Incubation period: 1.5 days (range 1-2 days); 3.5 days (range 3-4 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 16,604 for “Gastroenteritis,” 790 for “Norwalk virus,” 1,027 for “Calicivirus,” 96 for “Torovirus” and 632 for “Astrovirus”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 1,838 for “Norovirus” and 1,738 for “Gastroenteritis”.

ProMED feeds 1994-2011: 511 for “Norovirus” and 491 for “Gastroenteritis”.

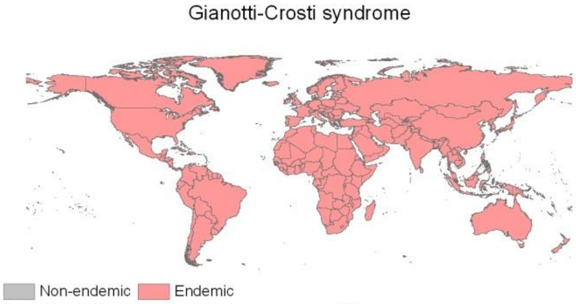
BioCaster feeds 2006-2011: 264 for “Norovirus” and 3,677 for “Gstroenteritis”.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Viral gastroenteritis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Gianotti-Crosti syndrome.

ICD-10 Code: L44.4.

Transmission category: Unknown.

Agent: Unknown.

Taxonomy: Unknown [204, 205].

Natural history:

Mode of transmission: Unknown [204].

Reservoir*: Unknown [204].

Incubation period: No incubation period [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no known animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 163.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

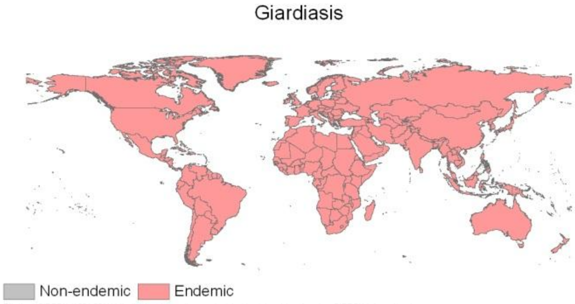
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Gianotti-Crosti syndrome is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Giardiasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Giardiasis.

ICD-10 Code: A07.1.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Protista, Archezoa, Metamonada, Metamonada, Diplomonadida, Hexamitidae, *Giardia lamblia* (*G. intestinalis*, *G. duodenalis*) [204, 205].

Natural history:

Mode of transmission: Contact with contaminated water; faecal-oral route; consumption of contaminated food; flies [204].

Reservoir*: Humans, beavers and muskrats [204].

Incubation period: 14 days (range 7-21 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,737.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 723.

ProMED feeds 1994-2011: 35.

BioCaster feeds 2006-2011: 8.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	9	2	N/A	[229]

Mapping recommendation: Option 1; do not map. Giardiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

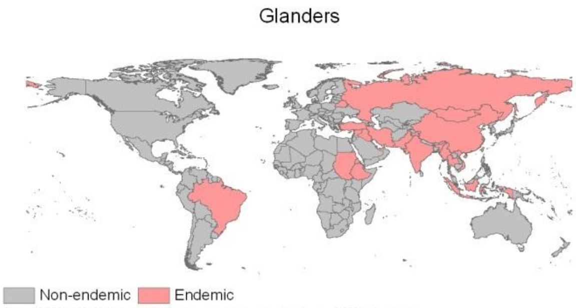
Disease: Glanders.

ICD-10 Code: A24.0.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Burkholderiales, Burkholderiaceae, *Burkholderia mallei* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with infectious secretions [204].

Reservoir*: Horses, mules and donkeys [204].

Incubation period: 9.5 days (range 5-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [230].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 314.

GenBank hits on 22/02/12: 2,580.

HealthMap feeds 2006-2011: 68.

ProMED feeds 1994-2011: 31.

BioCaster feeds 2006-2011: 70.

Approximate number of endemic countries: >22 [204].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 14 occurrence points per country based on 314 results for "Glanders" in PubMed and 22 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

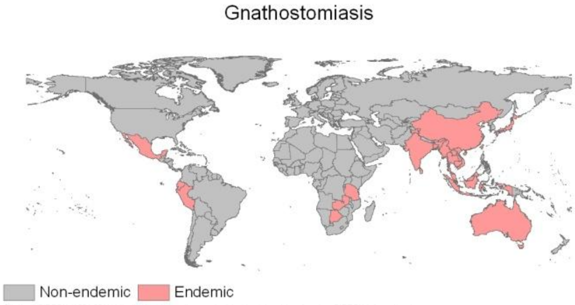
Disease: Gnathostomiasis.

ICD-10 Code: B83.1.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Gnathostomatidae, *Gnathostoma spinigerum* (rarely *G. hispidum*, *G. doloresi* and *G. nipponicum*) [204, 205].


Gnathostomiasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of infected fish, reptiles and amphibians [204].

Reservoir*: Cats, dogs, poultry, frogs and fishes [204].

Incubation period: 24.5 days (range 21-28 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [231].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 271.

GenBank hits on 22/02/12: 53.

HealthMap feeds 2006-2011: 4 for “Gnathostomiasis” and 3 for “Gnathostoma”.

ProMED feeds 1994-2011: 4 for “Gnathostomiasis” and 3 for “Gnathostoma”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >22 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	88	5	2	49	[232]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 12 occurrence points per country based on 271 results for “Gnathostomiasis” in PubMed and 22 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

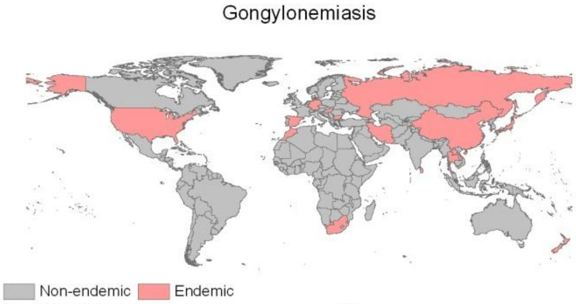
Disease: Gongylonemiasis.

ICD-10 Code: B83.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Spirurida, Gongylonematidae, *Gongylonema pulchrum* [204, 205].


Gongylonemiasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of infected insects [204].

Reservoir*: Sheep, cattle, pigs, bears and monkeys [204].

Incubation period: 70 days (range 60-80 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [233].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 10.
- **GenBank hits on 22/02/12:** 184.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

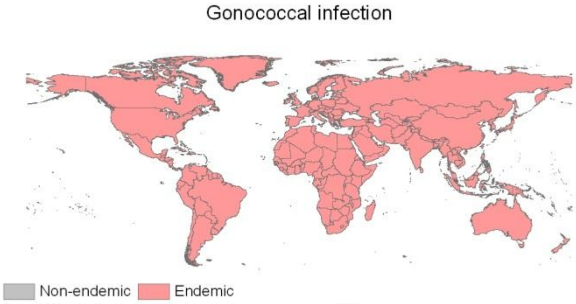
Approximate number of endemic countries: >15 [204].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 1 occurrence point per country based on 10 results for “Gongylonemiasis” in PubMed and 15 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.


Gonococcal infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Gonococcal infection.

ICD-10 Code: A54.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Neisseriales, Neisseriaceae, *Neisseria gonorrhoeae* [204, 205].

Natural history:

Mode of transmission: Sexual contact or exudates; vertical transmission at childbirth [204].

Reservoir*: Humans [204].

Incubation period: 4.5 days (range 2-7 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-2 [234-239].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 12,946.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 79 for “Gonorrhea”.

ProMED feeds 1994-2011: 41 for “Gonorrhea”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	7.5	2	N/A	[240]
Disease	5	6.5	2	N/A	[241]
Disease	5	6.5	2	N/A	[242]
Disease	20	7.5	2	N/A	[243]

Mapping recommendation: Option 1; do not map. Gonococcal infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

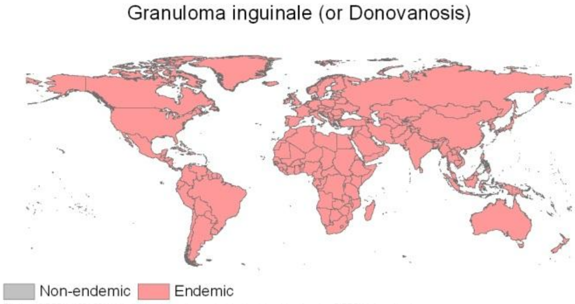
<u>Disease</u>: Granuloma inguinale (or Donovanosis).

<u>ICD-10 Code:</u> A58.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Klebsiella granulomatis* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct or sexual contact [204].

Reservoir*: Humans [204].

Incubation period: 18.5 days (range 7-30 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 601 for “Granuloma inguinale” and 193 for “Donovanosis”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

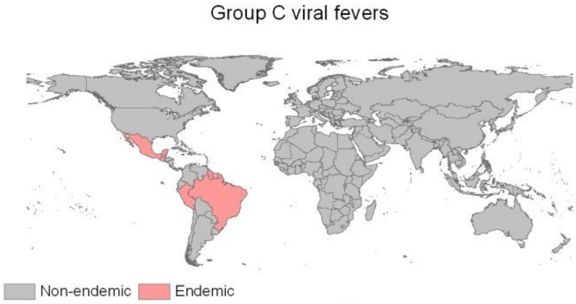
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Granuloma inguinale is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Group C viral fevers.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, Orthobunyavirus, Apeu, Caraparu, Itaqui, Madrid, Marituba, Murutucu, Nepuyo, Oriboca, Ossa, and Restan viruses [204, 205].

Natural history:

Mode of transmission: Unknown [204].

Reservoir*: Rodents, marsupials and (possibly) bats [204].

Incubation period: 7.5 days (range 3-12 days) [204].

Significant epidemiological characteristics:

Vaccine: Live and inactive virus vaccines for livestock.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 0 for “Group C viral fevers,” 5 for “Apeu,”, 20 for “Carapeu,” 8 for “Itaqui,” 1 for “Madrid virus,” 12 for “Marituba,” 3 for “Murutucu,” 12 for “Nepuyo,” 28 for “Oriboca,” 116 for “Ossa” and 8 for “Restan”.

GenBank hits on 22/02/12: 47.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >9 [204].

Previously published maps: None.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 13 occurrence points per country based on 116 results for “Ossa” in PubMed and 9 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

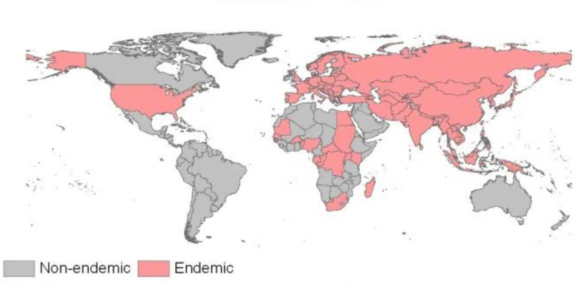
Disease: Hantavirus - Haemorrhagic fever with renal sydrome (HFRS).

ICD-10 Code: A98.5

Transmission category: Soil contact.

Agent: Virus-RNA

Taxonomy: Bunyaviridae, Group V,
Hantavirus (more than >25 species) [204, 205].


Hantavirus - HFRS

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission:

Reservoir*: Field mice (*Apodemus agrarius* - Hantaan), voles (*Myodes glareolus* - Puumala), rats (*Rattus norvegicus* - Seoul), possibly bats and birds [204].

Incubation period: 16.5 days (range 12-21 days) [204].

Significant epidemiological characteristics:

Vaccine: Hantavirus (old world) [204].

Estimated R_0 value(s) from published literature:

Human: 0-4.24 [244, 245].

Reservoir: 0-4.2 (rodent-human) [244].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,160 for “Hantavirus and renal syndrome”.

GenBank hits on 22/02/12: 4,388.

HealthMap feeds 2006-2011: 861 for “Hantavirus”.

ProMED feeds 1994-2011: 1,106 for “Hantavirus”.

BioCaster feeds 2006-2011: 313 for “Hantavrius” and 4 for “Hantavirus – HFRS”.

Approximate number of endemic countries: >93 [204].

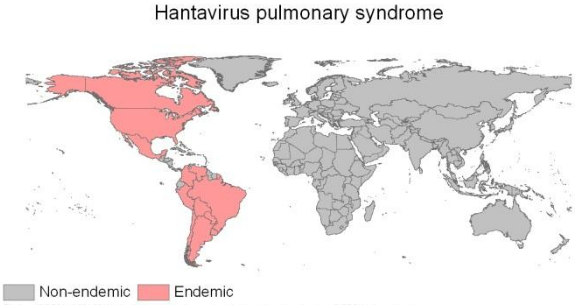
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	37	1.5	2	3	[246]
Disease	32	4	2	7	[247]
Disease	62	4	2	14	[248]
Host	67	6.5	2	24	[248]
Disease	24	8	2	11	[249]
Disease	<1	8	2	<1	[250]
Disease	12	6	2	4	[251]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 12 occurrence points per country based on 1,160 results for “Hantavirus and renal syndrome” in PubMed and 93 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of reservoir distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mouse reservoirs. If occurrence data for these mouse species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Hantavirus pulmonary syndrome.

ICD-10 Code: B33.4+.

Transmission category: Soil contact.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, Hantavirus, Andes virus; Laguna Negra virus; Juquitiba virus; Black Creek Canal virus; Bayou virus; New York-1 virus; Monongahela virus; Sin Nombre virus [204, 205].

Natural history:

Mode of transmission: Inhalation of contaminated rodent secretions; contact with contaminated animal secretions; (rare) direct contact or bites [204].

Reservoir*: Rodents - deer mice (*Peromyscus maniculatus*), pinon mice, harvest mice, cotton rats, brush mice, western chipmunks and (rare) humans [204].

Incubation period: 21.5 days (range 9-33 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [244, 252]

Reservoir: 0-1.6 (rodents) [244, 252].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 661 for "Hantavirus and pulmonary syndrome".

GenBank hits on 22/02/12: 567.

HealthMap feeds 2006-2011: 861 for "Hantavirus".

ProMED feeds 1994-2011: 1,106 for "Hantavirus".

BioCaster feeds 2006-2011: 313 for "Hantavrius" and 2 for "Hantavirus pulmonary syndrome".

Approximate number of endemic countries: >14 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	81	1.5	2	7	[246]
Disease	75	4	2	17	[247]
Disease	74	4	2	16	[248]
Host	100	6.5	2	36	[248]
Disease	88	3.5	2	17	[253]
Disease	37	7	2	14	[254]
Disease	5	6.5	3	3	[255]

Host	55	1	2	3	[256]
Disease	37	7	2	14	[257]
Disease	23	7	4	18	[258]
Disease	23	7.5	2	10	[259]
Disease	100	7.5	2	42	[260]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 47 occurrence points per country based on 661 results for “Hantavirus and pulmonary syndrome” in PubMed and 14 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Hendra virus disease.

ICD-10 Code: A86.

Transmission category: Animal contact.

Agent: Virus-RNA.

Taxonomy: Mononegavirales, Paramyxoviridae, Group V, *Henipavirus*, Hendra virus [204, 205].

Natural history:

Mode of transmission: Contact with contaminated animal secretions [204].

Reservoir*: Horses, fruit bats (*Pteropus* spp.), (possibly) cats and guinea pigs [204].

Incubation period: 9.5 days (range 5-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [261, 262].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 193.

GenBank hits on 22/02/12: 52.

HealthMap feeds 2006-2011: 216 for "Nipah/Hendra Virus".

ProMED feeds 1994-2011: 284 for "Nipah/Hendra Virus".

BioCaster feeds 2006-2011: 89.

Approximate number of endemic countries: >1 [204].

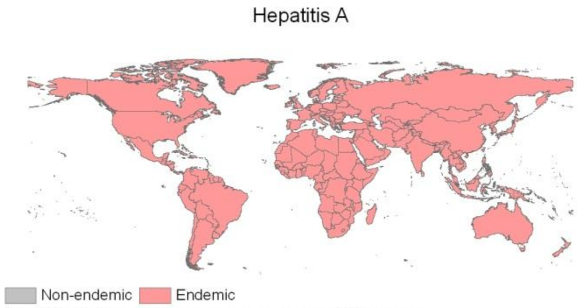
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4.5	2	25	[263]
Disease	100	3.5	2	19	[264]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 193 occurrence points per country based on 193 results for "Hendra Virus" in PubMed and 1 endemic country listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Hepatitis A.

ICD-10 Code: B15.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Picornavirales, Picornaviridae, Group IV, *Hepatovirus*, Hepatitis A virus (HAV) [204, 205].

Natural history:

Mode of transmission: Consumption of contaminated food or water; faecal-oral route; flies [204].

Reservoir*: Humans and non-human primates [204].

Incubation period: 25.5 days (range 21-30 days) [204].

Significant epidemiological characteristics:

Vaccine: Hepatitis A, Hepatitis A + B [204].

Estimated R_0 value(s) from published literature:

Human: 0-4 [265-268].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 21,140.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 157.

ProMED feeds 1994-2011: 30.

BioCaster feeds 2006-2011: 617.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5.5	2	N/A	[269]
Disease	100	5.5	2	N/A	[270]
Disease	100	2.5	2	N/A	[271]
Disease	<1	7	3	N/A	[272]
Disease	100	6.5	2	N/A	[273]

Mapping recommendation: Option 1; do not map. Hepatitis A is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

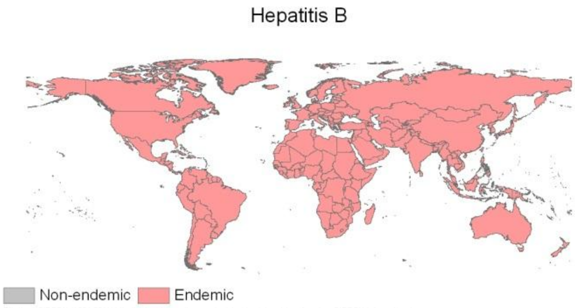
Disease: Hepatitis B.

ICD-10 Code: B16.

Transmission category: Sexual contact.

Agent: Virus-DNA.

Taxonomy: Hepadnaviridae, Group VII, *Orthohepadnavirus*, Hepatitis B virus (HBV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; contact with infected secretions; blood-borne transmission; vertical transmission [204].

Reservoir*: Humans and non-human primates [204].

Incubation period: 75 days (range 60-90 days) [204].

Significant epidemiological characteristics:

Vaccine: Hepatitis B, Hepatitis A + Hepatitis B, Hepatitis B + *Haemophilus influenzae*, and Hepatitis B immunoglobulin [204].

Estimated R_0 value(s) from published literature:

Human: 0-10 [234, 237, 274-276].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 67,648.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 236.

ProMED feeds 1994-2011: 16.

BioCaster feeds 2006-2011: 646.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4.5	2	N/A	[277]
Disease	89	5	2	N/A	[278]
Disease	100	5	2	N/A	[279]
Disease	100	6	2	N/A	[280]
Disease	<1	5.5	2	N/A	[281]

Mapping recommendation: Option 1; do not map. Hepatitis B is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

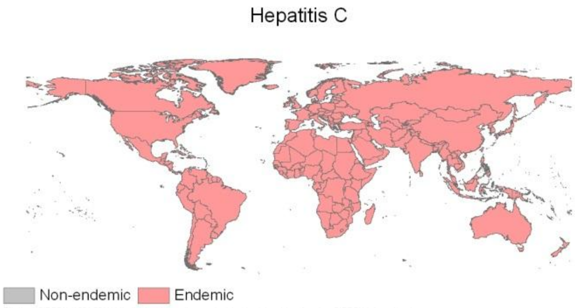
Disease: Hepatitis C.

ICD-10 Code: B17.1.

Transmission category: Blood/body fluid contact.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Hepacivirus*, Hepatitis C virus (HCV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; blood-borne transmission; vertical transmission [204].

Reservoir*: Humans [204].

Incubation period: 52.5 days (range 35-70 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-7.96 [282-286].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 53,810.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 127.

ProMED feeds 1994-2011: 26.

BioCaster feeds 2006-2011: 478.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	49	7	2	N/A	[287]
Disease	100	6.5	2	N/A	[288]
Disease	100	5	2	N/A	[289]
Disease	67	2	2	N/A	[290]

Mapping recommendation: Option 1; do not map. Hepatitis C is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

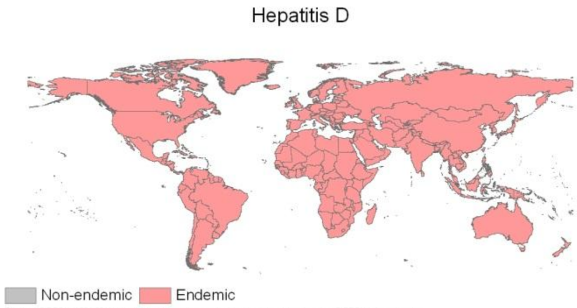
Disease: Hepatitis D.

ICD-10 Code: B17.8.

Transmission category: Blood/body fluid contact.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group V, *Deltavirus*, Hepatitis D virus (HDV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; contact with infectious secretions; blood-borne transmission [204].

Reservoir*: Humans [204].

Incubation period: 42 days (range 28-56 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,114.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 0.

ProMED feeds 1994-2011: 0.

BioCaster feeds 2006-2011: 9.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	89	7	2	N/A	[291]
Disease	80	7	2	N/A	[292]
Disease	52	5	2	N/A	[293]
Disease	79	7	2	N/A	[294]

Mapping recommendation: Option 1; do not map. Hepatitis D is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

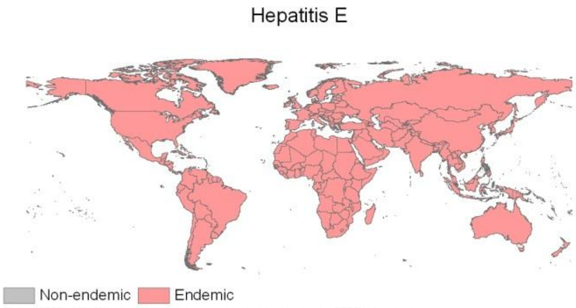
Disease: Hepatitis E.

ICD-10 Code: B17.2.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Caliciviridae, Group IV, *Hepevirus*, Hepatitis E virus (HEV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated shellfish, meat and water; faecal-oral route [204].

Reservoir*: Humans, rodents and pigs [204].

Incubation period: 26-42 days (range 15-64 days) [204].

Significant epidemiological characteristics:

Vaccine: Advances in development [204].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [295-297].

Reservoir: 0-8 (swine) [296].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,473.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 26

ProMED feeds 1994-2011: 9.

BioCaster feeds 2006-2011: 88.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	66	4.5	2	N/A	[298]
Disease	70	4.5	2	N/A	[299]
Disease	61	5	2	N/A	[300]
Disease	60	5	2	N/A	[301]

Mapping recommendation: Option 1; do not map. Hepatitis E is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

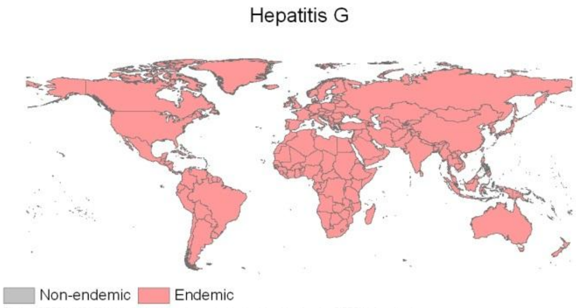
Disease: Hepatitis G.

ICD-10 Code: B17.8.

Transmission category: Blood/body fluid contact.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Hepacivirus*, Hepatitis G virus (HGV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; blood-borne transmission; vertical transmission [204].

Reservoir*: Humans [204].

Incubation period: 81 days (range 50-112 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found,
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

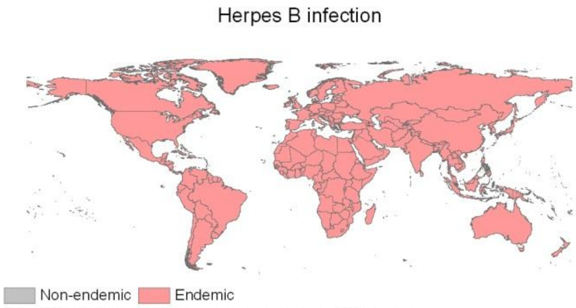
- **PubMed hits on 04/11/11:** 1,008.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Hepatitis G is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Herpes B infection.

<u>ICD-10 Code:</u> B00.8.

<u>Transmission category:</u> Animal contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Herpesviridae, Group I, *Herpesvirus 1*, Herpes simplex virus (HSV) 1 [204, 205].

<u>Natural history</u>:

Mode of transmission: Direct contact; bites [204].

Reservoir*: Monkeys (usually *Macaca* spp. and *Cynomolgus* spp.) [204].

Incubation period: 15 days (range 10-20 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [302, 303].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 71.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 468 for “Herpes”.

ProMED feeds 1994-2011: 82 for “Herpes”.

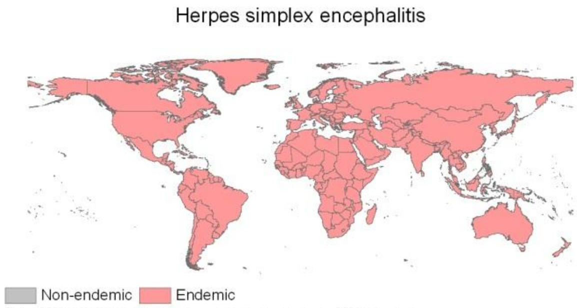
BioCaster feeds 2006-2011: 888 for “Herpes”.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Herpes B infections are endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Herpes simplex encephalitis.

<u>ICD-10 Code:</u> B00.4.

<u>Transmission category:</u> Blood/body fluid contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Herpesviridae, Group I, *Herpesvirus* (usually *type I*), Herpes simplex virus (HSV) 1 (occasionally type 2) [204, 205].

<u>Natural history</u>:

Mode of transmission: Sexual contact; contact with infectious secretions [204].

Reservoir*: Humans [204].

Incubation period: 12 days (range 3-21 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 1,621.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 468 for “Herpes”.
- **ProMED feeds 1994-2011:** 82 for “Herpes”.
- **BioCaster feeds 2006-2011:** 888 for “Herpes”.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Herpes simplex encephalitis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

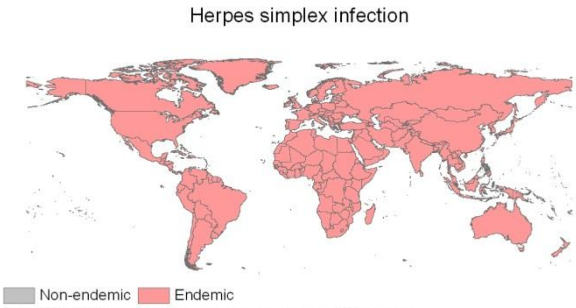
Disease: Herpes simplex infection.

ICD-10 Code: B00.

Transmission category: Blood/body fluid contact.

Agent: Virus-DNA.

Taxonomy: Herpesviridae, Group I, *Herpesvirus I* and *II*, Herpes simplex virus (HSV) 1 and 2 [204, 205].


Herpes simplex infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; contact with infectious secretions [204].

Reservoir*: Humans [204].

Incubation period: 7.5 days (range 1-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-5, 0-18; HSV1, HSV2, [304-307].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 36,271.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 468 for “Herpes”.

ProMED feeds 1994-2011: 82 for “Herpes”.

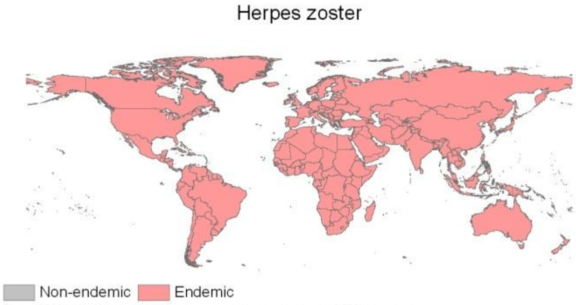
BioCaster feeds 2006-2011: 888 for “Herpes”.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Herpes simplex infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Herpes zoster.

<u>ICD-10 Code:</u> B02.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Herpesviridae, Alphaherpesvirinae, Group I,

Herpesvirus 3, Varicella-zoster virus (VZV) [204, 205].

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious particles; direct contact [204].

Reservoir*: Humans [204].

Incubation period: 17.5 days (range 14-21 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: Herpes zoster [204].

Estimated R_0 value(s) from published literature:

- **Human:** 0-16.9 [237, 308, 309].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 10,649.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 8 for “Herpes Zoster”.
- **ProMED feeds 1994-2011:** 1 for “Herpes Zoster”.
- **BioCaster feeds 2006-2011:** N/A.

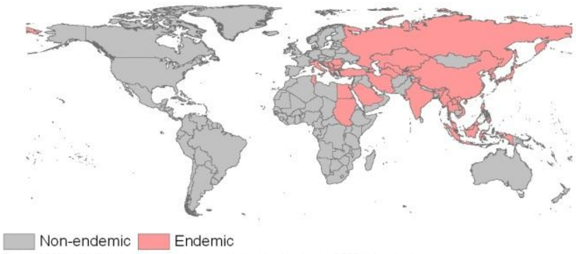
Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Herpes zoster is endemic worldwide and vaccine preventable

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Heterophyid infections



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Heterophyid infections.

ICD-10 Code: B66.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Opisthorchiida, Heterophyidae, *Heterophyes heterophyes*, *H. nocens* and others [204, 205].

Natural history:

Mode of transmission: Consumption of contaminated fish (particularly, mullet and tilapia) [204].

Reservoir*: Snails (*Cerithidea cingulata*, *Pirenella conica*) and fish [204].

Incubation period: 10.5 days (range 7-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [310, 311].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 99.

GenBank hits on 22/02/12: 2.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

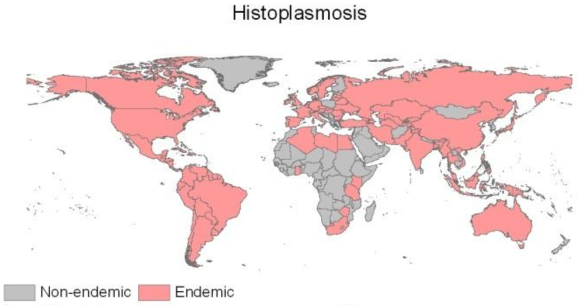
Approximate number of endemic countries: >38 [204].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 3 occurrence points per country based on 99 results for “Heterophyid infections” in PubMed and 38 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Histoplasmosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Histoplasmosis.

ICD-10 Code: B39.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Ascomycetes, Onygenales, Onygenaceae, *Histoplasma capsulatum* var. *capsulatum* [204, 205].

Natural history:

Mode of transmission: Inhalation of infectious particles [204].

Reservoir*: Bats [204].

Incubation period: 12 days (range 10-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 5,843.

GenBank hits on 22/02/12: 5.

HealthMap feeds 2006-2011: 23.

ProMED feeds 1994-2011: 19.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >93 [204].

Previously published maps: Not found.

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 63 occurrence points per country based on 5,843 results for “Histoplasmosis” in PubMed and 93 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

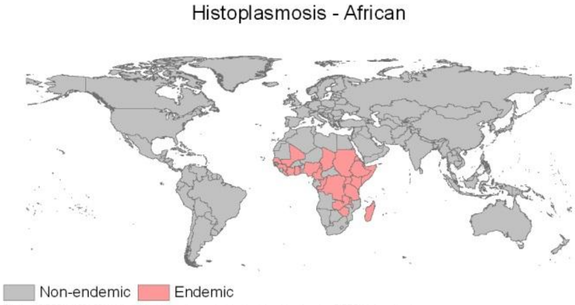
<u>Disease</u>: Histoplasmosis - African.

<u>ICD-10 Code:</u> B39.5.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Fungus.

<u>Taxonomy:</u> Fungi, Ascomycota, Ascomycetes, Onygenales, Onygenaceae, *Histoplasma capsulatum* var. *duboisii* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious particles [204].

Reservoir*: Baboons, birds and (possibly) bats [204].

Incubation period: Unknown [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 127.
- **GenBank hits on 22/02/12:** 20.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

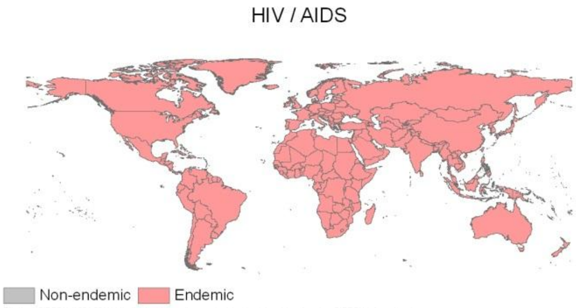
Approximate number of endemic countries: >25 [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 5 occurrence points per country based on 127 results for "African Histoplasmosis" infection in PubMed and 25 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: HIV / AIDS.

ICD-10 Code: B20-B24.

Transmission category: Sexual contact.

Agent: Virus-RNA.

Taxonomy: Retroviridae, Lentivirinae, Group VI, *Lentivirus*, Human immunodeficiency virus (HIV) [204, 205].

Natural history:

Mode of transmission: Sexual contact; blood-borne transmission; vertical transmission; breast feeding [204].

Reservoir*: Humans [204].

Incubation period: 25.5 days (range 7-42 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-12 [234, 237, 274, 275, 312-319].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 230,277.

GenBank hits on 22/02/12: 447,821.

HealthMap feeds 2006-2011: 4,467.

ProMED feeds 1994-2011: 721.

BioCaster feeds 2006-2011: 79 for “AIDS”.

Approximate number of endemic countries: Worldwide [204].

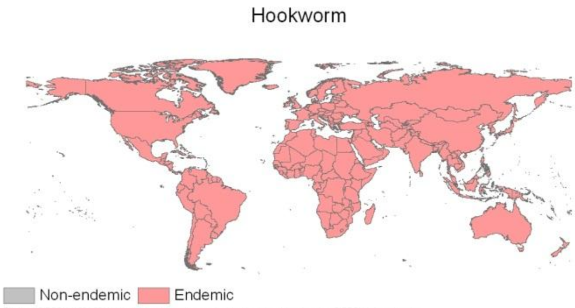
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	18	[320]
Disease	100	4	2	18	[321]
Disease	100	4	2	18	[322]
Disease	100	6	2	27	[323]
Disease	<1	7.5	5	<1	[324]
Disease	<1	6.5	5	<1	[325]
Disease	1	8.5	5	1	[326]
Disease	1	8	3	1	[327]
Disease	1	8	2	<1	[328]
Disease	1	7.5	2	<1	[329]

Disease	1	7	2	<1	[330]
Disease	12	5	2	3	[331]
Disease	5	6	2	1	[332]

Mapping recommendation: Option 5; map limits using annual prevalence data and model-based geostatistics (MBG) on infection prevalence surveys conditioned by human population density maps. The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: A huge effort would be required to undertake this work but in time would be the first application of MBG to a sexually transmitted disease.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Hookworm.

ICD-10 Code: B76.

Transmission category: Soil contact.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Ancylostomatidae,
Necator americanus
Ancylostoma duodenale [204, 205].

Natural history:

Mode of transmission: Direct contact; contact with contaminated soil [204].

Reservoir*: Humans [204].

Incubation period: 368.5 days (range 7-730 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-3.7 [237, 333-336].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,023 for "Hookworm," 550 for "*Necator americanus*" and 275 for "*Ancylostoma duodenale*".

GenBank hits on 22/02/12: 250.

HealthMap feeds 2006-2011: 7.

ProMED feeds 1994-2011: 5.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

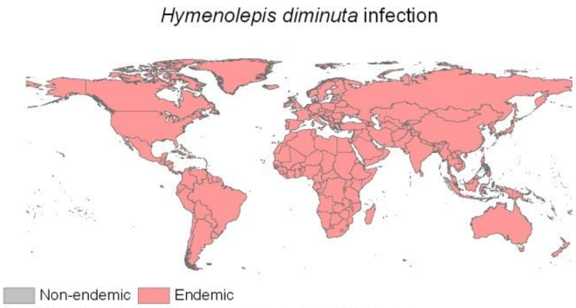
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	70	4.5	2	14	[337]
Disease	74	5.5	2	18	[338]
Disease	75	5.5	2	18	[339]
Disease	12	7.5	5	10	[340]
Disease	2	8	5	2	[341]
Disease	2	8	5	2	[342]
Disease	<1	6.5	2	<1	[343]
Disease	<1	8	5	<1	[344]
Disease	<1	8	5	<1	[345]

Disease	<1	8	5	<1	[346]
Disease	1	7	2	<1	[347]

<u>Mapping recommendation</u>: Option 5; map limits using prevalence data and biological mask and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys.

The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

<u>Future mapping potential</u>: Revisit current maps as the survey data becomes available from http://www.thiswormyworld.org [340].



Hymenolepis diminuta infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Hymenolepis diminuta* infection.

ICD-10 Code: B71.0.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Hymenolepididae, *Hymenolepis diminuta* [204, 205].

Natural history:

Mode of transmission: Consumption of infected arthropods [204].

Reservoir*: Rodents and various insects [204].

Incubation period: 21 days (range 14-28 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [348].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 878.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0 for “Hymenolepiasis”.
- **ProMED feeds 1994-2011:** 0 for “Hymenolepiasis”.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Hymenolepis diminuta* is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: *Hymenolepis nana* infection.

ICD-10 Code: B71.0.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Hymenolepididae, *Hymenolepis nana* [204, 205].

Hymenolepis nana infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food and water; faecal-oral route [204].

Reservoir*: Humans and rodents (especially hamsters) [204].

Incubation period: 21 days (range 14-28 days) [204].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [349].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 710.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0 for "Hymenolepiasis".
- **ProMED feeds 1994-2011:** 0 for "Hymenolepiasis".
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Hymenolepis nana* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

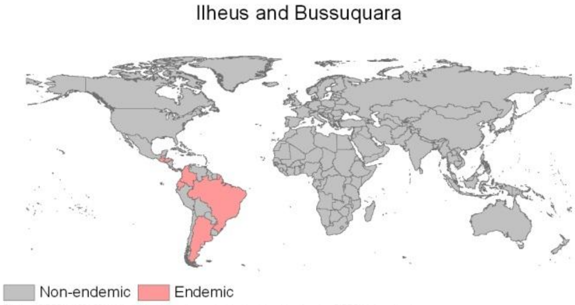
Disease: Ilheus and Bussuquara.

ICD-10 Code: A83.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Ilheus virus (ILHV) and Bussuquara virus [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors including *Aedes*, *Culex*, *Coquillettidia*, *Haemagogus*, *Psorophora*, *Sabethes*, *Trichoprosopon*, *Wyeomyia* spp. [204].

Reservoir*: (Possibly) Wild birds [204].

Incubation period: 6 days [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [350].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 76 for "Ilheus" and 13 for "Bussuquara".

GenBank hits on 22/02/12: 40.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

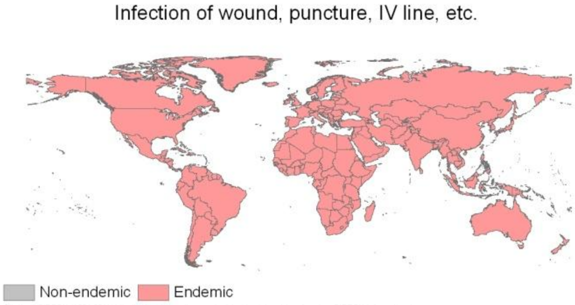
Approximate number of endemic countries: >9 [204].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 8 occurrence points per country based on 76 results for Ilheus in PubMed and 9 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Infection of wound, puncture, IV line, etc.

<u>ICD-10 Code:</u> A49.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Various (e.g. *Staphylococcus aureus*, streptococci, facultative or aerobic gram negative bacilli and anaerobes) [204, 205].

<u>Natural history</u>:

Mode of transmission: Contact with contaminated water; trauma; autoinoculation; fomites [204].

Reservoir*: Humans [204].

Incubation period: Variable [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

> **Human:** *Staphylococcus* - 0-0.7 (possible >1) for MRSA / *Streptococcus* - 0-0.29 (resistant)/Gram negative - 0-0.05 (resistant) [351, 352].
>
> **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

> **PubMed hits on 04/11/11:** Not a specific agent to search for.
>
> **GenBank hits on 22/02/12:** N/A.
>
> **HealthMap feeds 2006-2011:** N/A.
>
> **ProMED feeds 1994-2011:** N/A.
>
> **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Infections of wounds, puncture, IV line, etc. are endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

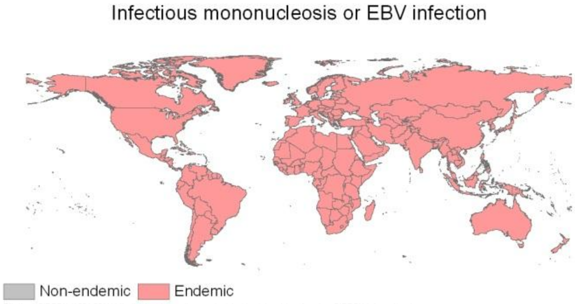
<u>**Disease**</u>**:** Infectious mononucleosis or EBV infection.

<u>**ICD-10 Code:**</u> B27, B27.0.

<u>**Transmission category:**</u> Blood/body fluid contact.

<u>**Agent**</u>**:** Virus-DNA.

<u>**Taxonomy:**</u> Herpesviridae, Gammaherpesvirinae, Group I, *Lymphocryptovirus*, Epstein-Barr virus (EBV) [204, 205].


Infectious mononucleosis or EBV infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Blood-borne transmission; contact with infectious saliva [204].

Reservoir*: Humans [204].

Incubation period: 35 days (range 28-42 days) [204].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found,

Reservoir: There is no animal reservoir for this disease.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

PubMed hits on 04/11/11: 8,020 for “Mononucleosis,” 7,663 for “Infectious mononucleosis” and 24,027 for “Epstein-Barr virus”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 89 for “Mononucleosis”.

ProMED feeds 1994-2011: 1 for “Mononucleosis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	15	4	2	N/A	[353]

<u>**Mapping recommendation:**</u> Option 1; do not map. Infectious mononucleosis or EBV infections are endemic worldwide.

<u>**Future mapping potential**</u>**:** None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

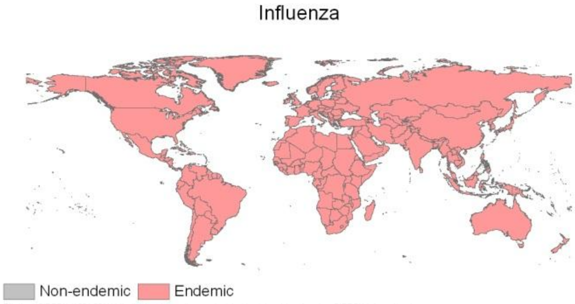
<u>Disease</u>: Influenza.

<u>ICD-10 Code:</u> J09 to J11

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Orthomyxoviridae, Group V, *Orthomyxovirus*, A, B and C types (H1N1, H2N2, H3N2) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious droplets [204].

Reservoir*: Humans, (occassionally) ferrets, birds and pigs [204].

Incubation period: 2 days (range 1-3 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: Influenza - inactivated, Influenza - live [204].

Estimated R_0 value(s) from published literature:

Human: Pandemic: 0-4.3 / Seasonal: 0-2.0 [354-373]

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 64,377.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 30,317.

ProMED feeds 1994-2011: 2,138.

BioCaster feeds 2006-2011: 82 for “Influenza” and 24,904 for “H1N1”.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	41	4	2	N/A	[374]

<u>Mapping recommendation:</u> Option 1; do not map. Influenza is endemic worldwide and vaccine preventable.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

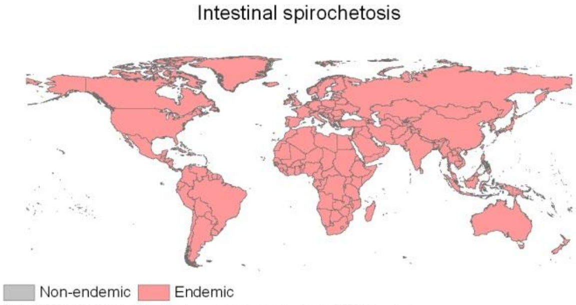
Disease: Intestinal spirochetosis.

ICD-10 Code: A69.8.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Brachyspiraceae, *Brachyspira pilosicoli* and *B. aalborgi* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans, fowl and pigs [204].

Incubation period: 9.5 days (range 3-16 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [375].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 87.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Intestinal spirochetosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

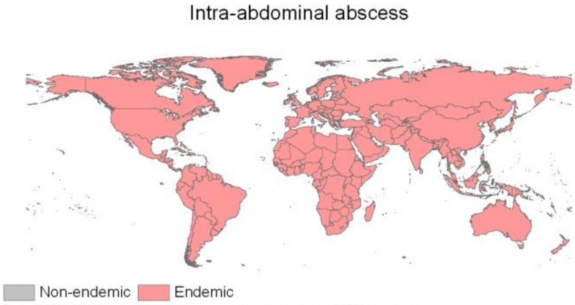
Disease: Intra-abdominal abscess.

ICD-10 Code: T81.4.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various including mixed anaerobic/aerobic, staphylococci, *Neisseria gonorrhoeae*, *Chlamydia trachomatis*, etc. [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans [204].

Incubation period: Variable [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 776.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

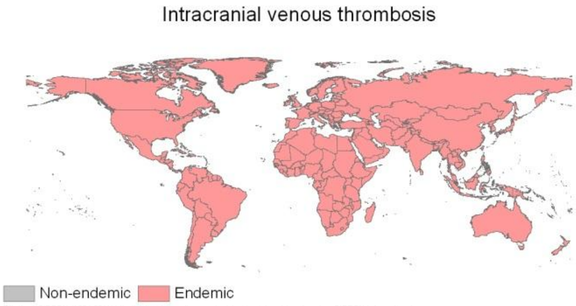
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Intra-abdominal abscesses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Intracranial venous thrombosis.

ICD-10 Code: G08.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various including oral anaerobes, streptococci, etc. [204, 205].

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans [204].

Incubation period: Variable [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 80.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Intracranial venous thromboses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

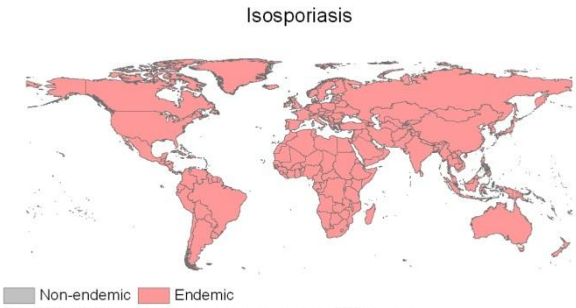
Disease: Isosporiasis.

ICD-10 Code: A07.3.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Apicomplexa, Conoidasida, Eucoccidiorida, Eimeriidae, *Isospora* [*Cystoisospora*] *belli* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; sexual contact [204].

Reservoir*: Humans [204].

Incubation period: 8.5 days (range 7-10 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 209.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0 for “Isosporiasis”.
- **ProMED feeds 1994-2011:** 0 for “Isosporiasis”.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Isosporiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

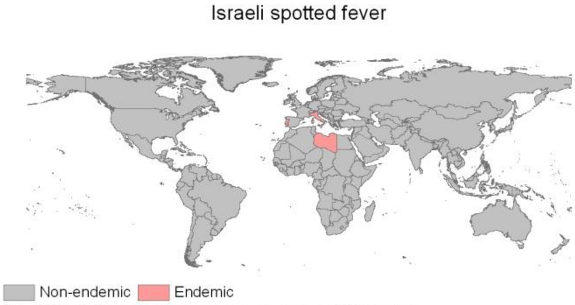
Disease: Israeli spotted fever.

ICD-10 Code: A77.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia conorii* subspp. *Israelensis* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Rhipicephalus sanguineus*) [204].

Reservoir*: Dogs, rodents and ticks [204].

Incubation period: 7.5 days (range 7-8 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [376, 377].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 27.

GenBank hits on 22/02/12: 5.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >4 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4.5	2	33	[378]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 7 occurrence points per country based on 27 results for “Israeli spotted fever” in PubMed and 4 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vector. If occurrence data for this tick species is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

Disease: Japanese encephalitis.

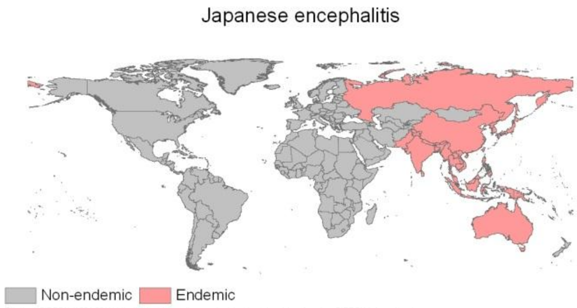
ICD-10 Code: A83.0.

Transmission category: Vector-borne.

Agent: Virus-RNA

Taxonomy: Flaviviridae, Group IV

Flavivirus, Japanese encephalitis (JE) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vectors including *Aedes* spp., *Anopheles barbirostris* and *An. hyrcanus* groups, *Culex tritaeniorhynchus* group, *Cu. vishnui*, *Cu. gelidus*, and *Cu. annulus* [204].

Reservoir*: Pigs and birds [204].

Incubation period: 7 days (range 6-8 days) [204].

Significant epidemiological characteristics:

Vaccine: Japanese encephalitis [204].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [379, 380].

Reservoir: 0-1.4 [380].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,448.

GenBank hits on 22/02/12: 1,825.

HealthMap feeds 2006-2011: 435.

ProMED feeds 1994-2011: 359.

BioCaster feeds 2006-2011: 626.

Approximate number of endemic countries: >32 [204].

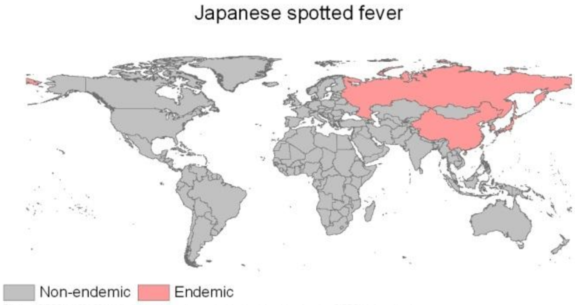
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	3	2	17	[381]
Disease	96	4	2	21	[382]
Disease	96	4.5	2	24	[383]
Vector	100	9	4	100	[384]
Vector	1	8.5	4	1	[385]
Disease	1	8	2	<1	[386]
Disease	34	6	2	11	[387]
Disease	3	7.5	2	1	[388]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 108 occurrence points per country based on 3,448 results for “Japanese encephalitis” in PubMed and 32 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Japanese spotted fever.

ICD-10 Code: A77.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia japonica* [204, 205].

Natural history:

Mode of transmission: Tick vectors (e.g. *Haemaphysalis longicornis*, *Dermacentor taiwanensis*; possibly *Ixodes ovatus* and *Ha*. *flava*) [204].

Reservoir*: Dogs, rodents and ticks [204].

Incubation period: 7.5 days (range 6-8 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [389].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 58 for "Japanese spotted fever" and 67 for "*Rickettsia japonica*".

GenBank hits on 22/02/12: 40.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >4 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	3.5	2	26	[378]
Vector	94	3.5	2	24	[378]
Disease	8	6	2	3	[390]
Disease	8	7	2	4	[389]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 17 occurrence points per country based on 67 results for "*Rickettsia japonica*" in PubMed and 4 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available Digitized versions of expert opinions of their ranges could usefully inform future mapping.

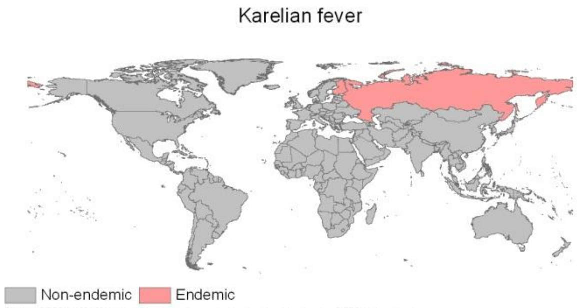
<u>Disease:</u> Karelian fever.

<u>ICD-10 Code:</u> A92.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Togaviridae, Group IV,
Alphavirus, Karelian fever virus (KFV) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vectors [204].

Reservoir*: Birds [204].

Incubation period: 4.5 days (range 3-6 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [391].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 15.
- **GenBank hits on 22/02/12:** 2.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >2 [204].

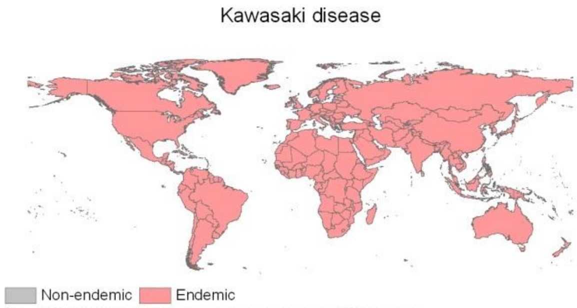
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	96	2.5	2	18	[392]

<u>Mapping recommendation:</u> Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 8 occurrence points per country based on 15 results for “Karelian fever” in PubMed and 2 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

<u>Future mapping potential</u>: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors and bird reservoirs. If occurrence data for these species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping. There is also the potential to link occurrence data with the distribution of other Sindbis virus (SINV) diseases.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Kawasaki disease.

ICD-10 Code: M30.3.

Transmission category: Unknown.

Agent: Unknown.

Taxonomy: Postulated *Staphylococcus aureus* or Group A Streptococci [204, 205].

Natural history:

Mode of transmission: Unknown [204].

Reservoir*: Only found in humans to date [204].

Incubation period: Unknown [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not applicable.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,432.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Kawasaki disease is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Disease: Keratoconjunctivitis - Adenoviral.

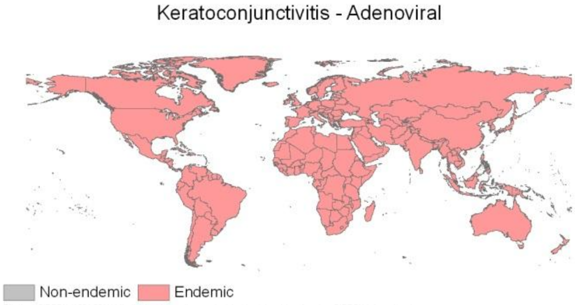
ICD-10 Code: B30.0.

Transmission category: Respiratory.

Agent: Virus-DNA

Taxonomy: Adenoviridae, Group I

Adenovirus, Types 8, 19, and 37 (severe: 8, 5, 19) [204, 205].



Keratoconjunctivitis - Adenoviral

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Fomites; direct contact [204].

Reservoir*: Humans [204].

Incubation period: 8.5 days (range 5-12 days) [204].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,855.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

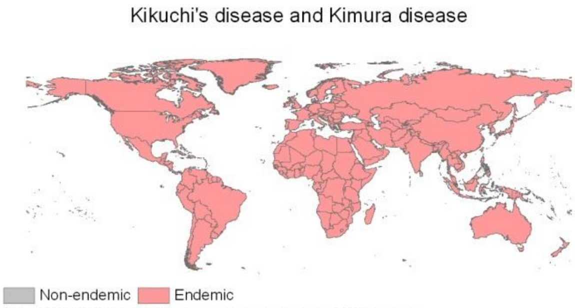
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Adenoviral Keratoconjunctivitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Kikuchi's disease and Kimura disease.

ICD-10 Code: I88.8.

Transmission category: Unknown.

Agent: Unknown [204, 205].

Natural history:

Mode of transmission: Unknown [204].

Reservoir*: Unknown [204].

Incubation period: Unknown [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 246 for “Kikuchi's disease” and 99 for “Kimura disease”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

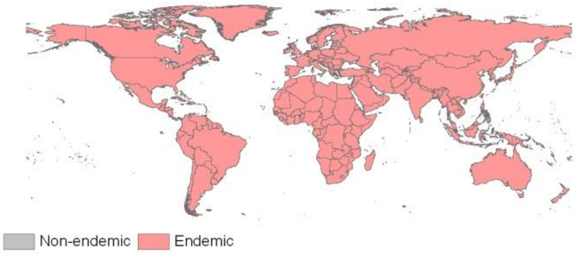
Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	20	7.5	2	33	[393]

Mapping recommendation: Option 1; do not map. Kikuchi’s disease and Kimura disease are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.


Kingella infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Kingella* infection.

ICD-10 Code: A48.8.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Neisseriales, Neisseriaceae, *Kingella kingae* [204, 205].

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans [204].

Incubation period: Unknown [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 313.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Kingella* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Kyasanur Forest disease.

ICD-10 Code: A98.2.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Kyasanur Forest disease (KFD) virus [204, 205].

Natural history:

Mode of transmission: Tick vectors (e.g. *Haemaphysalis spiniger, Ha.turturis, Ha.papuana* [*kinneari*]) [204].

Reservoir*: Rodents, shrews, mokneys, bats, birds and ticks [204].

Incubation period: 7.5 days (range 3-12 days) [204].

Significant epidemiological characteristics:

Vaccine: Kyasanur Forest disease [204].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [394, 395].

Reservoir: 0-1.47 (Multispecies) [395].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 142 for "Kyasanur Forest disease".

GenBank hits on 22/02/12: 153.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >2 [204].

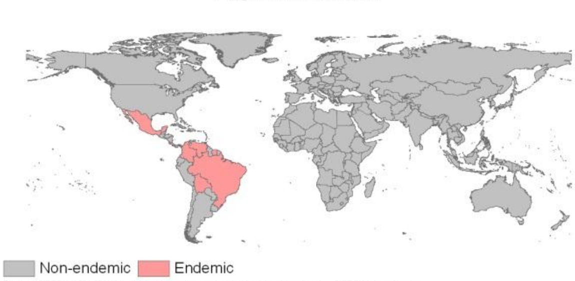
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	48	0	2	0	[394]
Vector	100	3.5	2	19	[378]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 71 occurrence points per country based on 142 results for “Kyasanur Forest Disease” in PubMed and 2 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.


Lagochilascariasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Lagochilascariasis.

ICD-10 Code: B77.9.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Ascarididae, *Lagochilascaris minor* [204, 205].

Natural history:

Mode of transmission: Consumption of ova [204].

Reservoir*: Humans [204].

Incubation period: >30 days [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 12.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

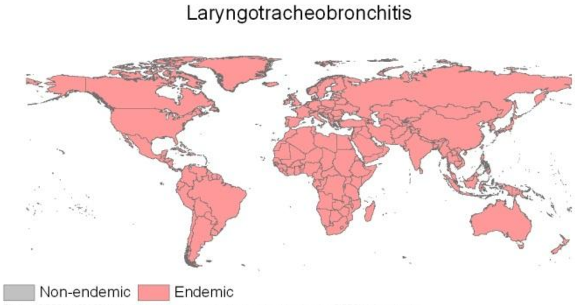
Approximate number of endemic countries: >8 [204].

Previously published maps: None.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 2 occurrence points per country based on 12 results for "Lagochilascariasis" in PubMed and 8 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data. There is the potential the link occurrence data with the distribution of *Ascaris* in the Americas.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Laryngotracheobronchitis.

ICD-10 Code: J20.4, J20.0.

Transmission category: Respiratory.

Agent: Virus.

Taxonomy: Orthomyxoviridae, Group V, *Parainfluenzavirus* and *Influenzavirus*, Parainfluenza virus types 1 and 2 and Influenza virus types A and B [204, 205].

Bacterium

Eubacteria, Firmicutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, *Mycoplasma pneumoniae*

Natural history:

Mode of transmission: Inhalation of infectious droplets [204].

Reservoir*: Humans [204].

Incubation period: 5.5 days (range 3-8 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Seasonal Influenzavirus: 0-2.0 [396-398].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 298 for “Laryngotracheobronchitis”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Laryngotracheobronchitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Lassa fever.

ICD-10 Code: A96.2.

Transmission category: Soil contact.

Agent: Virus-RNA.

Taxonomy: Arenaviridae, Group V, *Arenavirus*, Lassa virus [204, 205].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of rodent excreta; direct contact with secretions [204].

Reservoir*: Multimammate rats (*Mastomys natalensis*) [204].

Incubation period: 11 days (range 8-14 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [399, 400]
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 595.
- **GenBank hits on 22/02/12:** 299.
- **HealthMap feeds 2006-2011:** 113.
- **ProMED feeds 1994-2011:** 196.
- **BioCaster feeds 2006-2011:** 138.

Approximate number of endemic countries: >13 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	79	8.5	4	75	[401]
Disease	70	4.5	2	17	[402]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 46 occurrence points per country based on 595 results for “Lassa fever” in PubMed and 13 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

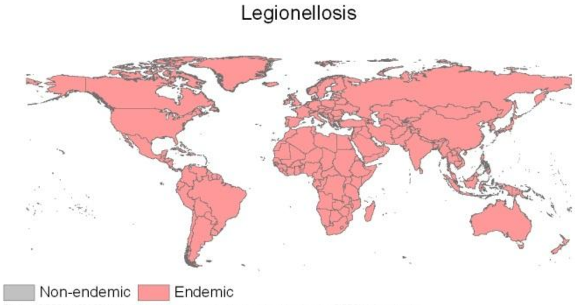
Disease: Legionellosis.

ICD-10 Code: A48.1.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Legionellales, Legionellaceae, *Legionella pneumophila* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated water; inhalation of infectious droplets [204].

Reservoir*: Environmental sources[204].

Incubation period: 5.5 days (range 5-6 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0 [400].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,352.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 972.

ProMED feeds 1994-2011: 535.

BioCaster feeds 2006-2011: 739.

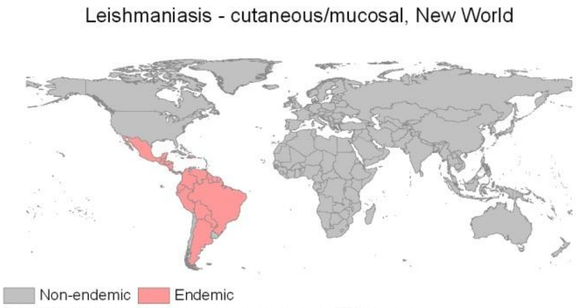
Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	<1	8.5	2	N/A	[403]
Disease	5	5	2	N/A	[404]

Mapping recommendation: Option 1; do not map. Legionellosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.


Leishmaniasis - cutaneous/mucosal, New World

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Leishmaniasis - cutaneous/mucosal, New World.

ICD-10 Code: B55.1/B55.2.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Excavata, Euglenozoa, Kinetoplastida, Trypanosomatida,
Leishmania braziliensis, L.mexicana, *L.amazonensis*, et al. [204, 205].

Natural history:

Mode of transmission: Sandfly vectors (*Lutzomyia* spp.); (rare) direct contact; sexual contact; blood transfusions [204].

Reservoir*: Humans, marsupials, dogs, sloths, anteaters and armadillos [204].

Incubation period: 35 days (range 14-56 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-1.4 [405, 406].

Reservoir: 0-1.9 (dogs)[406].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,088 for "Cutaneous leishmaniasis" and 1,133 for "Mucocutaneous leishmaniasis".

GenBank hits on 22/02/12: 9,135.

HealthMap feeds 2006-2011: 495 for "Leishmaniasis".

ProMED feeds 1994-2011: 349 for "Leishmaniasis".

BioCaster feeds 2006-2011: 261 for "Leishmaniasis".

Approximate number of endemic countries: >20 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	98	0	2	0	[407]
Disease	100	3	2	17	[408]
Disease	100	4	2	22	[409]
Disease	100	6	2	33	[410]
Disease	98	4	2	22	[411]
Disease	36	7.5	2	15	[412]
Vector	36	7	2	14	[412]
Disease	9	6.5	4	6	[413]

Disease	36	7.5	2	15	[414]
Disease	36	7.5	2	15	[415]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 304 occurrence points per country based on 6,088 results for Cutaneous leishmaniasis in PubMed and 20 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

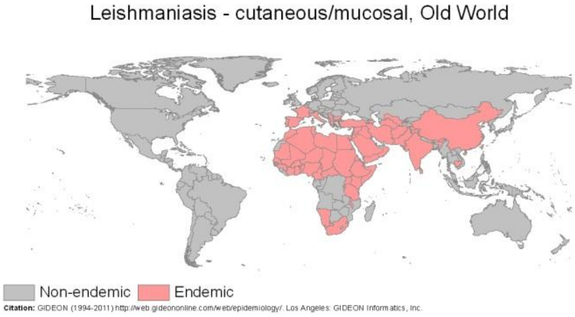
Disease: Leishmaniasis - cutaneous/mucosal, Old World.

ICD-10 Code: B55.1/B55.2.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Excavata, Euglenozoa, Kinetoplastida, Trypanosomatida,
Leishmania tropica, *L.major*, *L.aethiopica*, et al. [204, 205].



Natural history:

Mode of transmission: Sandfly vectors (*Phlebotomus papatasi* etc.); (rare) direct contact; sexual contact; blood transfusions [204].

Reservoir*: Humans, hyraxes, rodents and dogs [204].

Incubation period: 35 days (range 14-56 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-1.4 [405, 416].

Reservoir: 0-1.06 (dogs)[416].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,088 for “Cutaneous leishmaniasis” and 1,133 for “Mucocutaneous leishmaniasis”.

GenBank hits on 22/02/12: 10,309.

HealthMap feeds 2006-2011: 495 for “Leishmaniasis”.

ProMED feeds 1994-2011: 349 for “Leishmaniasis”.

BioCaster feeds 2006-2011: 261 for “Leishmaniasis”.

Approximate number of endemic countries: >64 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	59	3	2	10	[417]
Disease	90	3	2	15	[408]
Disease	57	4	2	13	[409]
Disease	100	6	2	33	[410]
Disease	89	4	2	20	[411]
Disease	53	7	2	21	[418]
Disease	15	5	2	4	[419]
Disease	7	5.5	2	2	[420]

Vector	<1	5.5	2	<1	[421]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 95 occurrence points per country based on 6,088 results for Cutaneous leishmaniasis in PubMed and 64 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Leishmaniasis - visceral.

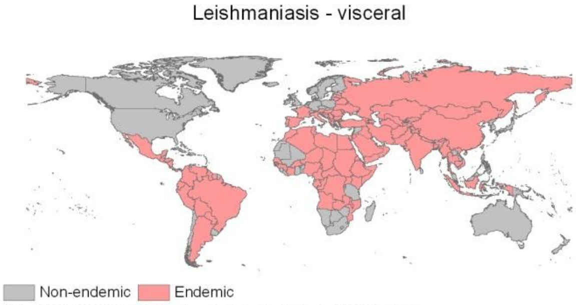
ICD-10 Code: B55.0.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Excavata, Euglenozoa, Kinetoplastida, Trypanosomatida,

Leishmania donovani, *L.infantum*, *L.cruzi* and *L.tropica* [204, 205].



Leishmaniasis - visceral

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sandfly vectors (*Phlebotomous* spp. and *Lutzomyia* spp.); blood transfusion [204].

Reservoir*: Humans, rodents, dogs and foxes [204].

Incubation period: 120 days (range 60-180 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [422].

Reservoir: 0-~10 (dogs), [422].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,391.

GenBank hits on 22/02/12: 11,766.

HealthMap feeds 2006-2011: 495 for “Leishmaniasis”.

ProMED feeds 1994-2011: 349 for “Leishmaniasis”.

BioCaster feeds 2006-2011: 261 for “Leishmaniasis”.

Approximate number of endemic countries: >107 [204].

Previously published maps:

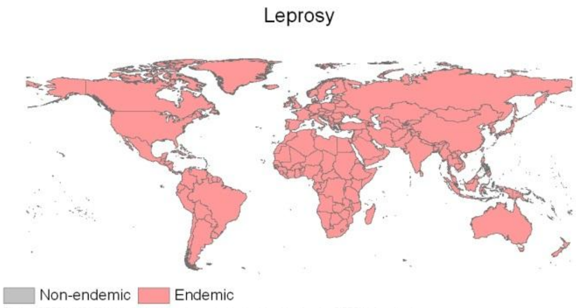
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	69	3	2	12	[417]
Disease	81	4	2	18	[409]
Disease	11	5	2	3	[419]
Disease	22	7.5	4	18	[423]
Disease	4	7.5	2	1	[424]
Disease	1	8.5	4	1	[425]
Vector	<1	5	3	<1	[426]
Disease	1	6.5	2	<1	[427]
Vector	1	8	2	<1	[428]

Disease	2	4	3	1	[429]
Disease	23	6.5	2	8	[430]
Disease	1	6.5	2	<1	[431]
Disease	1	7.5	4	1	[432]
Disease	1	8.5	3	<1	[433]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 69 occurrence points per country based on 7,391 results for “Visceral Leishmaniasis” in PubMed and 107 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Leprosy.

ICD-10 Code: A30.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Corynebacteriaceae, *Mycobacterium leprae* [204, 205].

Natural history:

Mode of transmission: Contact with infectious secretions [204].

Reservoir*: Humans, (possibly) armadillos [204].

Incubation period: 1,460 days (range 1,095-1,825 days) [204].

Significant epidemiological characteristics:

Vaccine: Bacillus Calmette-Guérin (BCG) [204].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 21,695.

GenBank hits on 22/02/12: 639.

HealthMap feeds 2006-2011: 159 for "Leprosy".

ProMED feeds 1994-2011: 54 for "Leprosy".

BioCaster feeds 2006-2011: 113.

Approximate number of endemic countries: >122 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	3	7	2	1	[434]
Disease	78	5	2	22	[435]
Disease	55	5	2	15	[436]
Disease	73	5	2	20	[437]
Disease	24	5	2	7	[438]
Disease	23	4	2	5	[439]
Disease	54	5	2	15	[440]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 178 occurrence points per country based on 21,695 results for “Leprosy” in PubMed and 122 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

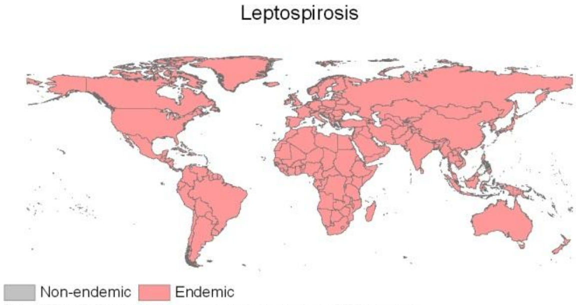
<u>Disease</u>: Leptospirosis.

<u>ICD-10 Code:</u> A27.

<u>Transmission category:</u> Water contact.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Leptospiraceae, *Leptospira interrogans* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Contact with contaminated water and soil; contact with infected urine [204].

Reservoir*: Cattle, dogs, horses, deer, rodents, foxes, marine mammals, cats, marsupials and frogs [204].

Incubation period: 9.5 days (range 7-12 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: Not available worldwide, but some serovar specific vaccines have been used [204].

Estimated R_0 value(s) from published literature:

Human: 0 [441, 442].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 6,744.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 647.

ProMED feeds 1994-2011: 544.

BioCaster feeds 2006-2011: 770.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	61	6	2	N/A	[443]
Disease	3	6.5	2	N/A	[444]
Disease	1	8	2	N/A	[445]
Disease	3	8.5	2	N/A	[446]
Disease	3	6.5	2	N/A	[447]

<u>Mapping recommendation:</u> Option 1; do not map. Leptospirosis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

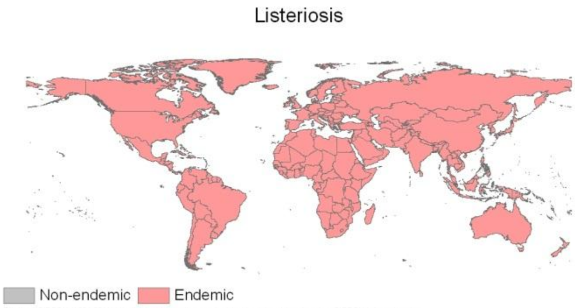
<u>**Disease**</u>**:** Listeriosis.

<u>**ICD-10 Code:**</u> A32.

<u>**Transmission category:**</u> Food/water-borne.

<u>**Agent**</u>**:** Bacterium.

<u>**Taxonomy:**</u> Eubacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae,
Listeria monocytogenes [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Contact with contaminated water; consumption of contaminated foodstuffs; vertical transmission

Reservoir*: Mammals, humans and birds [204].

Incubation period: 12 days (range 3-21 days) [204].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; Indirect zoonosis (food-borne pathogen) [448].

Reservoir: Not found.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

PubMed hits on 04/11/11: 6,502.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 932.

ProMED feeds 1994-2011: 202.

BioCaster feeds 2006-2011: 757.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

<u>**Mapping recommendation:**</u> Option 1; do not map. Listeriosis is endemic worldwide.

<u>**Future mapping potential**</u>**:** None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

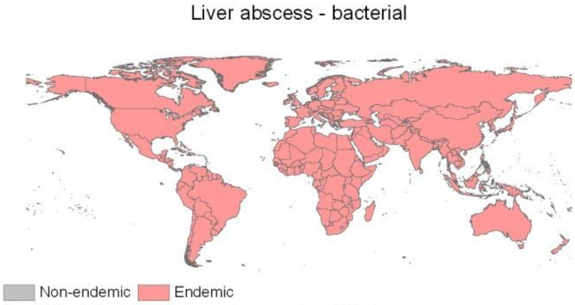
Disease: Liver abscess - bacterial.

ICD-10 Code: K75.0.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various species from portal (Bacteroides, mixed aerobe-anaerobe) or biliary (*Escherichia coli*, etc) source [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [204].

Reservoir*: Humans [204].

Incubation period: Variable [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not applicable.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,679 for "Liver abscess".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Liver abscesses (bacterial) are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

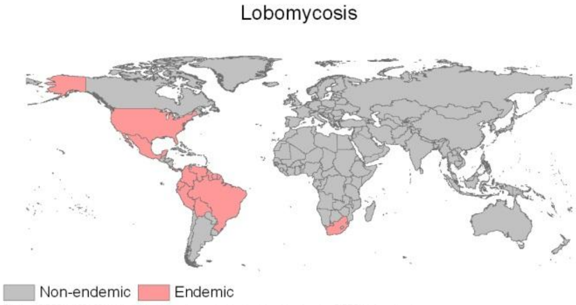
<u>Disease</u>: Lobomycosis.

<u>ICD-10 Code:</u> B48.0.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Fungus.

<u>Taxonomy:</u> Fungi, Ascomycota, Eurotiomycetes, Onygenales, Incertae sedis,
Lacazia (*Loboa*) *loboi* [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious particles; (possibly) skin trauma [204].

Reservoir*: Humans and dolphins (*Tursiops truncatus* and *Sotalia guianensis*) [204].

Incubation period: 547.5 days (range 365-730 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [449].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 79.

GenBank hits on 22/02/12: 95.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >14 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	4	7.5	2	3	[450]

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There was approximately 6 occurrence points per country based on 79 results for “Lobomycosis” in PubMed and 14 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Loiasis.

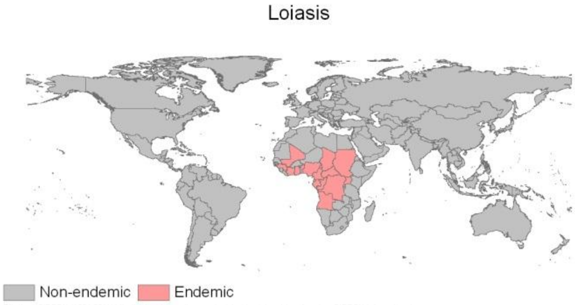
ICD-10 Code: B74.3.

Transmission category: Vector-borne.

Agent: Parasite

Animalia, Nematoda, Chromadorea, Spirurida, Onchocercidae,

Loa loa [204, 205].


Loiasis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Fly vector (*Chrysops* spp.) [204].

Reservoir*: Humans [204].

Incubation period: 607.5 days (range 120-1,095 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 511.

GenBank hits on 22/02/12: 38,529.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >17 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	4	7	2	2	[451]
Disease	93	1	2	5	[452]
Disease	15	7	2	6	[221]
Disease	93	8	2	41	[453]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 30 occurrence points per country based on 511 results for “Loiasis” in PubMed and 17 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

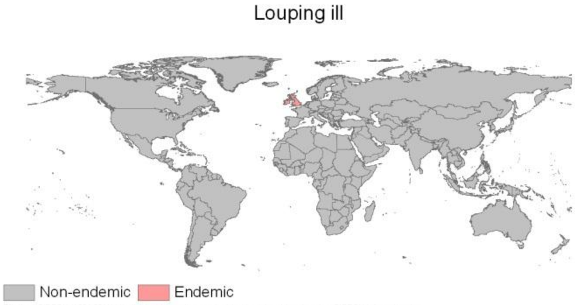
<u>Disease</u>: Louping ill.

<u>ICD-10 Code:</u> A84.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Flaviviridae, Group IV, *Flavivirus*, Louping ill virus [204, 205].


Louping ill

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Tick vector (*Ixodes ricinus*); consumption of contaminated dairy products [204].

Reservoir*: Ticks, sheep, deer and grouse [204].

Incubation period: 5.5 days (range 4-7 days) [204].

<u>Significant epidemiological characteristics</u>:

Vaccine: Inactive virus vaccines used in Europe and Russia [204].

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [454].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 226.
- **GenBank hits on 22/02/12:** 33.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >3 [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	1	2	6	[455]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 75 occurrence points per country based on 226 results for “Louping ill” in PubMed and 3 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

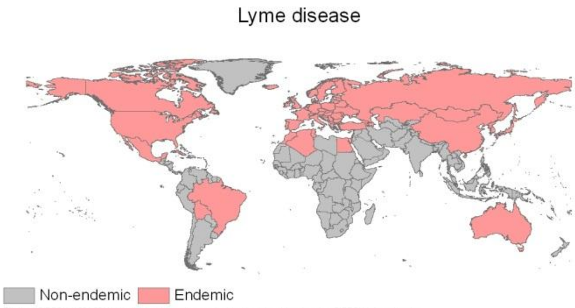
Disease: Lyme disease.

ICD-10 Code: A69.2.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Spirochaetaceae, *Borrelia burgdorferi* [204, 205].


Lyme disease

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Ixodes scapularis*, *I.pacificus*, *Ambylomma* spp.) [204].

Reservoir*: Ticks, deer, rodents and birds [204].

Incubation period: 10.5 days (range 7-14 days) [204].

Significant epidemiological characteristics:

Vaccine: Vaccine had been developed - pulled from market (GSK LYMErix) [204].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [456-459].

Reservoir: 0-11 (mice, multiple species) [457-459].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 8,871.

GenBank hits on 22/02/12: 8,684.

HealthMap feeds 2006-2011: 198.

ProMED feeds 1994-2011: 143.

BioCaster feeds 2006-2011: 501.

Approximate number of endemic countries: >63 [204].

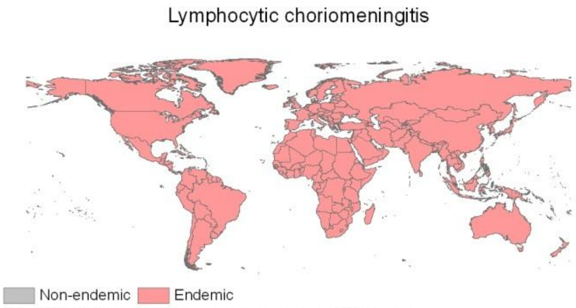
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	11	4.5	2	3	[378]
Vector	10	5.5	2	3	[460]
Vector	10	6.5	2	3	[461]
Disease	10	7.5	2	4	[462]
Disease	10	6.5	2	3	[463]
Vector	10	7.5	4	8	[464]
Disease	10	6.5	2	3	[465]
Vector	1	8	3	1	[466]
Disease	2	8	2	1	[467]
Disease	10	7.5	3	6	[468]
Disease	<1	5.5	3	<1	[469]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 141 occurrence points per country based on 8,871 results for “Lyme disease” in PubMed and 63 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Lymphocytic choriomeningitis.

ICD-10 Code: A87.2.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Arenaviridae, Group V, *Arenavirus*, Lymphocytic choriomeningitis virus [204, 205].

Natural history:

Mode of transmission: Inhalation of dust; faecal-oral route; consumption of contaminated food; contact of contaminated urine, saliva and faeces [204].

Reservoir*: House mice, guinea pigs, hamsters and monkeys [204].

Incubation period: 10 days (range 8-12 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [470].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 3,172.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Lymphocytic choriomeningitis are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

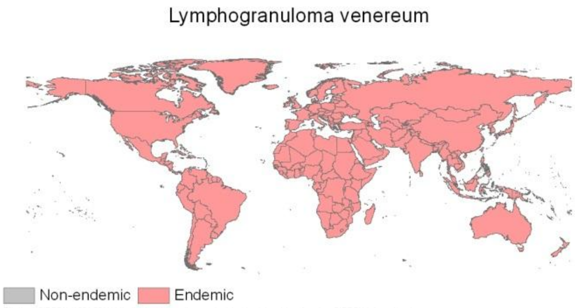
Disease: Lymphogranuloma venereum.

ICD-10 Code: A55.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Chlamydiae, Chlamydiae, Chlamydiales, Chlamydiaceae, *Chlamydia trachomatis* (types L1, L2, L3) [204, 205].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact [204].

Reservoir*: Humans [204].

Incubation period: 9.5 days (range 7-12 days) [204].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,550.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 16 for “LGV”.

ProMED feeds 1994-2011: 21 for “LGV”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [204].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	5	4.5	2	N/A	[471]

Mapping recommendation: Option 1; do not map. Lymphogranuloma venereum is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

<u>Disease:</u> Malaria - *P. falciparum.*

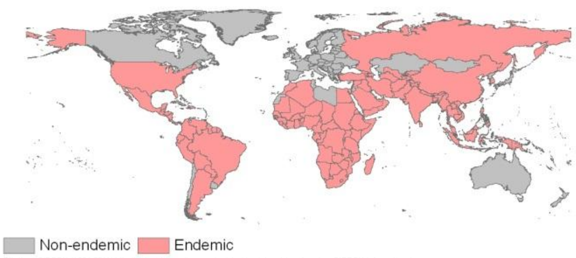
<u>ICD-10 Code:</u> B50.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Protista, Protozoa, Apicomplexa, Sporozoa, Eucoccidiida, Plasmodiidae, *Plasmodium falciparum* [472, 473].

Malaria - all human *Plasmodium* spp.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Anopheles* spp.); blood transfusion [472].

Reservoir*: Humans [472].

Incubation period: 12 days (range 9-14 days) [474].

<u>Significant epidemiological characteristics</u>:

Vaccine: None currently licensed; RTS,S vaccine in development [475, 476].

Estimated R_0 value(s) from published literature:

Human: 0-1000 [477-480].

Reservoir: Primates not thought to be significant in maintaining transmission [481].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 25,158 for "*falciparum".*

GenBank hits on 22/02/12: 84,718.

HealthMap feeds 2006-2011: 4,688 for "Malaria".

ProMED feeds 1994-2011: 1,165 for "Malaria".

BioCaster feeds 2006-2011: 2,299 for "Malaria".

Approximate number of endemic countries: >100 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	5	3	33	[482]
Disease	100	5	3	33	[483]
Disease	100	7	5	78	[484]
Disease	100	8	5	89	[485]
Vector	100	8	4	71	[486]
Vector	15	9	4	12	[487]
Vector	16	9	4	13	[488]
Vector	67	9	4	54	[489]

Mapping recommendation: Option 5; map limits using annual parasite index data and biological mask and endemicity within this range using model-based geostatistics (MBG) on parasite rate surveys.
The availability of a high volume of systematically collected parasite rate data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Revisit current global endemicity maps as new malariometric data becomes available [490]. Ultimately use Bayesian techniques to merge API and PR based estimates in areas of low endemicity.

Disease: Malaria - *P. vivax.*

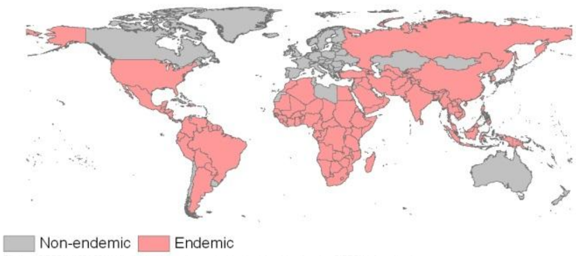
ICD-10 Code: B51.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Protista, Protozoa, Apicomplexa, Sporozoa, Eucoccidiida, Plasmodiidae, *Plasmodium vivax* [472, 473].

Malaria - all human *Plasmodium* spp.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Anopheles* spp.); blood transfusion [472].

Reservoir*: Humans [472].

Incubation period: 18 days (range 12-18 days) [474].

Significant epidemiological characteristics:

Vaccine: None currently licensed; two candidate vaccines (CSP and Pvs25) past phase I trials [491].

Estimated R_0 value(s) from published literature:

Human: 0-100 (38.6) [479, 492].

Reservoir: Primates not thought to be significant in maintaining transmission [481].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,317 for "*vivax*".

GenBank hits on 22/02/12: 22,166.

HealthMap feeds 2006-2011: 4,688 for "Malaria".

ProMED feeds 1994-2011: 1,165 for "Malaria".

BioCaster feeds 2006-2011: 2,299 for "Malaria".

Approximate number of endemic countries: >100 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	5	3	33	[482]
Disease	100	5	3	33	[483]
Disease	100	7	5	78	[493]
Vector	100	8	4	71	[486]
Vector	15	9	4	12	[487]
Vector	16	9	4	13	[488]
Vector	67	9	4	54	[489]

Mapping recommendation: Option 5; map limits using annual parasite index data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on parasite rate surveys.

The availability of a high volume of systematically collected parasite rate data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Revisit current global endemicity maps as new malariometric data becomes available [490]. Ultimately use Bayesian techniques to merge API and PR based estimates in areas of low endemicity.

Disease: Malaria - *P. malariae.*

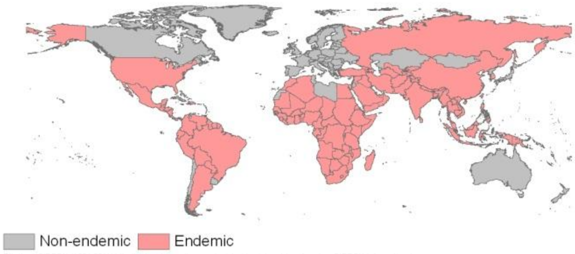
ICD-10 Code: B52.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Protista, Protozoa, Apicomplexa, Sporozoa, Eucoccidiida, Plasmodiidae, *Plasmodium malariae* [472, 473].

Malaria - all human *Plasmodium* spp.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Anopheles* spp.); blood transfusion [472].

Reservoir*: Humans [472].

Incubation period: 29 days (range 18-40 days) [474].

Significant epidemiological characteristics:

Vaccine: None currently licensed.

Estimated R_0 value(s) from published literature:

Human: 0-16 [477].

Reservoir: Primates not thought to be significant in maintaining transmission [481].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 900 for "*malariae*".

GenBank hits on 22/02/12: 105.

HealthMap feeds 2006-2011: 4,688 for "Malaria".

ProMED feeds 1994-2011: 1,165 for "Malaria".

BioCaster feeds 2006-2011: 2,299 for "Malaria".

Approximate number of endemic countries: >100 [472].

Previously published maps:

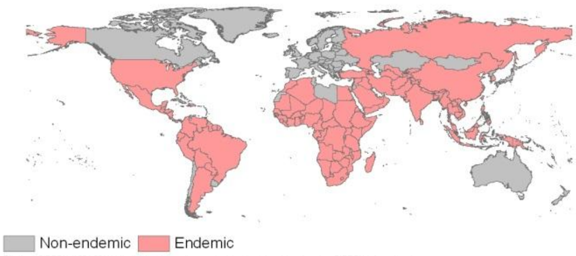
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	5	3	33	[482]
Vector	100	8	4	71	[486]
Vector	15	9	4	12	[487]
Vector	16	9	4	13	[488]
Vector	67	9	4	54	[489]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 9 occurrence points per country based on 900 results for "*malariae*" in PubMed and 100 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its *Anopheles* vectors. Digitized versions of expert opinions of their ranges could usefully inform future mapping.

Malaria - all human *Plasmodium* spp.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Malaria - *P. ovale.*

<u>ICD-10 Code:</u> B53.0.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Protista, Protozoa, Apicomplexa, Sporozoa, Eucoccidiida, Plasmodiidae, *Plasmodium ovale* [472, 473].

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Anopheles* spp.); blood transfusion [472].

Reservoir*: Humans [472].

Incubation period: 18 days (range 12-18 days) [474].

<u>Significant epidemiological characteristics</u>:

Vaccine: None currently licensed.

Estimated R_0 value(s) from published literature:

Human: 0-16 [477].

Reservoir: Primates not thought to be significant in maintaining transmission [481].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 272 for "*ovale*".

GenBank hits on 22/02/12: 189.

HealthMap feeds 2006-2011: 4,688 for "Malaria".

ProMED feeds 1994-2011: 1,165 for "Malaria".

BioCaster feeds 2006-2011: 2,299 for "Malaria".

Approximate number of endemic countries: >100 [472].

Previously published maps:

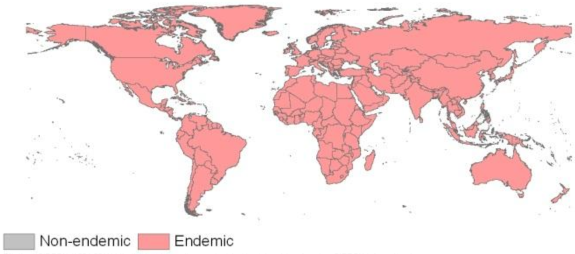
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	5	3	33	[482]
Vector	100	8	4	71	[486]
Vector	15	9	4	12	[487]
Vector	16	9	4	13	[488]
Vector	67	9	4	54	[489]

<u>Mapping recommendation:</u> Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 3 occurrence points per country based on 272 results for "*ovale*" in PubMed and 100 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its *Anopheles* vectors. Digitized versions of expert opinions of their ranges could usefully inform future mapping.

Malignant otitis externa



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Malignant otitis externa.

ICD-10 Code: H60.2.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pseudomonadales, Pseudomonadaceae, *Pseudomonas aeruginosa* [472, 473].

Natural history:

Mode of transmission: Endogenous; direct contact [472].

Reservoir*: Humans [472].

Incubation period: 2 days (range 1-3 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-0.14 (*Pseudomonas*, in hosptial) [494].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 131.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Malignant otitis externa is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

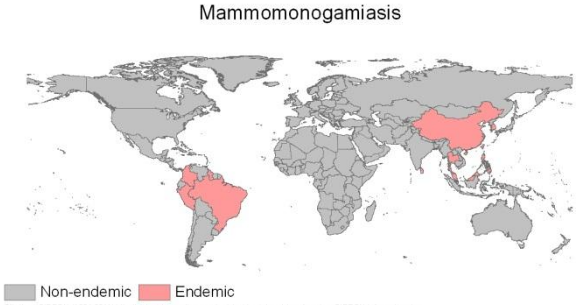
Disease: Mammomonogamiasis.

ICD-10 Code: B83.3.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Syngamidae, *Mammomonogamus* (*Syngamus*) *laryngeus* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated uncooked vegetables or water [472].

Reservoir*: Mammals (coyotes, cats, cattle, orangutans) and birds [472].

Incubation period: 8.5 days (range 6-11 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [495, 496].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 1.
- **GenBank hits on 22/02/12:** 0.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >17 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was less 1 occurrence point per country based on the 1 result for “Mammomonogamiasis” in PubMed and 17 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Generate global thumbnail map using systematic searches of occurrence data.

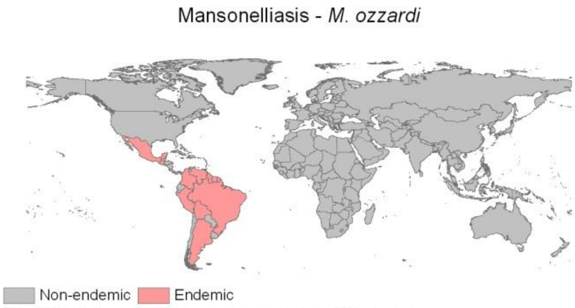
<u>Disease</u>: Mansonelliasis - *M. ozzardi*.

<u>ICD-10 Code:</u> B74.4.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Nematoda, Secernentea, Strongylida, Onchocercidae, *Mansonella ozzardi* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Black fly (*Simulium* spp.) or midge (*Culicoides* spp.) vector [472].

Reservoir*: Humans [472].

Incubation period: 345 days (range 150-540 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 193 for “Mansonelliasis” or 105 for “*Mansonella ozzardi*”.
- **GenBank hits on 22/02/12:** 62.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >23 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 8 occurrence points per country based on 193 PubMed results for “Mansonelliasis” and 23 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

<u>Future mapping potential</u>: Generate known distribution map using systematic searches of occurrence data for the disease and its *Simulium* or *Culicoides* vectors. Digitized versions of expert opinions of their ranges could usefully inform future mapping.

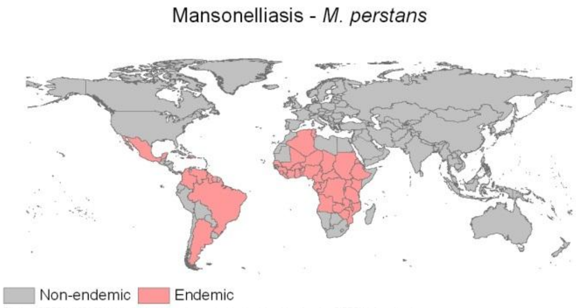
Disease: Mansonelliasis - *M. perstans.*

ICD-10 Code: B74.4.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Onchocercidae, *Mansonella* (*Esslingeria*) *perstans* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Midge vector (*Culicoides* spp.) [472].

Reservoir*: Humans [472].

Incubation period: 345 days (range 150-540 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 193 for "Mansonelliasis" or 125 for "*Mansonella perstans*".
- **GenBank hits on 22/02/12:** 7.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: > 49 [472].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 4 occurrence points per country based on 193 PubMed results for "Mansonelliasis" and 49 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its *Culicoides* vectors. Digitized versions of expert opinions of their ranges could usefully inform future mapping.

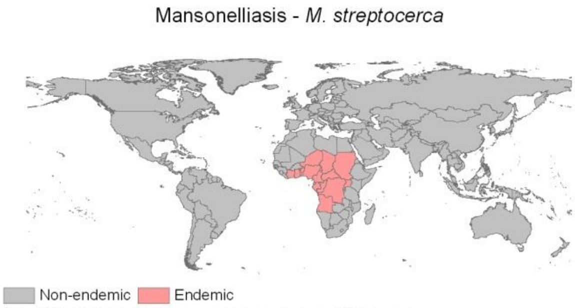
Disease: Mansonelliasis - *M. streptocerca.*

ICD-10 Code: B74.4.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Onchocercidae, *Mansonella* (*Esslingeria*) *streptocerca* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Midge vector (*Culicoides grahami*, *C. milnei*) [472].

Reservoir*: Non-human primates [472].

Incubation period: 345 days (range 150-540 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: None.

Reservoir: None.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 193 for "Mansonelliasis"or 16 for "*Mansonella streptocerca*".

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >16 [472].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 12 occurrence points per country based on 193 PubMed results for "Mansonelliasis" and 16 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its *Culicoides* vectors. Digitized versions of expert opinions of their ranges could usefully inform future mapping.

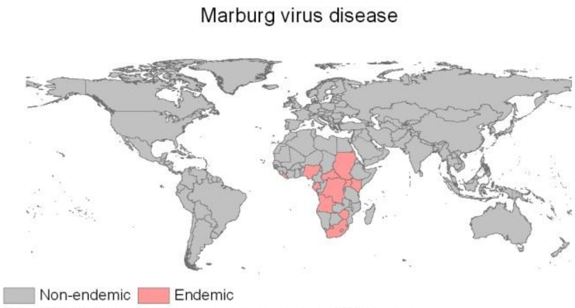
<u>**Disease**</u>**:** Marburg virus disease.

<u>**ICD-10 Code:**</u> A98.3.

<u>**Transmission category:**</u> Blood/body fluid contact.

<u>**Agent**</u>**:** Virus-RNA.

<u>**Taxonomy:**</u> Mononegavirales, Filoviridae, Group V, *Filovirus*, Marburgvirus [472, 473].



Marburg virus disease

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Inhalation of infectious droplets; contact with secretions or blood [472].

Reservoir*: Bats and (possibly) African green monkeys [472].

Incubation period: 6 days (range 5-7 days) [472].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1 (0.96) [497].

Reservoir: Not known.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

PubMed hits on 04/11/11: 1,498.

GenBank hits on 22/02/12: 224.

HealthMap feeds 2006-2011: 141.

ProMED feeds 1994-2011: 148.

BioCaster feeds 2006-2011: 97.

Approximate number of endemic countries: >11 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	70	4	2	15	[498]
Disease	25	3.5	2	5	[499]
Disease	40	6	2	13	[500]
Disease	30	6	4	20	[501]
Disease	100	8	2	44	[502]

<u>**Mapping recommendation:**</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 136 occurrence points per country based on 1,498 results for “Marburg virus” in PubMed and 11 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

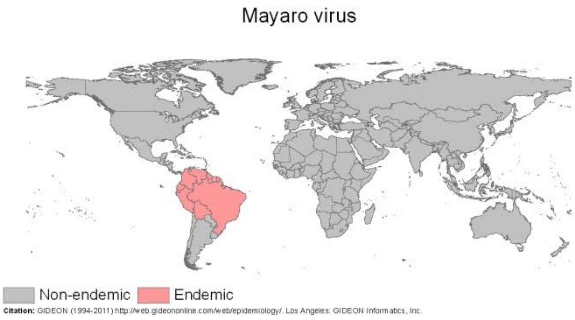
<u>Disease</u>: Mayaro virus.

<u>ICD-10 Code:</u> A92.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Togaviridae, Group IV, *Alphavirus*, Mayaro (Uruma) virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Haemagogus* spp.) [472, 474].

Reservoir*: Possibly non-human primates and birds [472].

Incubation period: 7.5 days (range 3-12 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [503].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 92.

GenBank hits on 22/02/12: 81.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >11 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	89	[504]
Disease	2	3.5	2	7	[503]

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 8 occurrence points per country based on 92 results for “Mayaro virus” in PubMed and 11 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current maps using systematic searches of occurrence data.

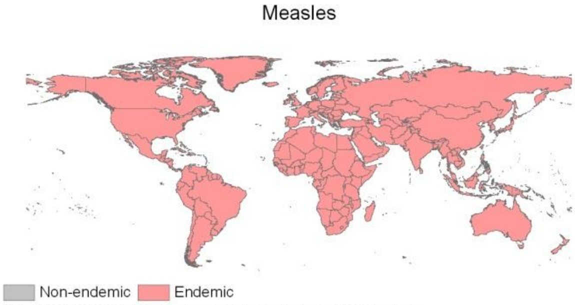
<u>Disease</u>: Measles.

<u>ICD-10 Code:</u> B05.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Mononegavirales, Paramyxoviridae, Group V, *Morbillivirus*, Measles virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious droplets; close contact [472].

Reservoir*: Humans [472].

Incubation period: 11 days (range 8-14 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: Measles, Measles-Mumps-Rubella and Measles-Rubella [472].

Estimated R_0 value(s) from published literature:

- **Human:** 0-18 [477].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 21,268.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 7,308.
- **ProMED feeds 1994-2011:** 1.568.
- **BioCaster feeds 2006-2011:** 8,727.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Measles is endemic worldwide and vaccine preventable.

<u>Future mapping potential</u>: There is perhaps some utility for this condition in providing surfaces of permanent fresh water bodies in proximity to human populations where contamination is likely

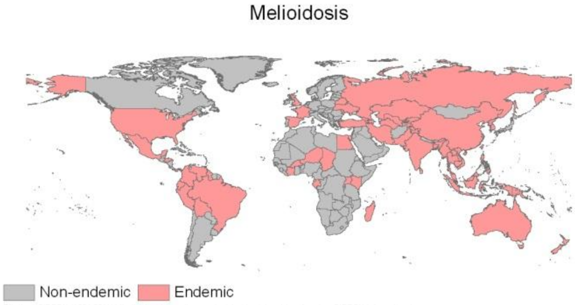
Disease: Melioidosis.

ICD-10 Code: A24.1 to A24.4.

Transmission category: Soil contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Burkholderiales, Burkholderiaceae, *Burkholderia pseudomallei* [472, 473].


Melioidosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated soil [472].

Reservoir*: Sheep, goats, horses, pigs, rodents, monkeys and marsupials [472].

Incubation period: 12 days (range 3-21 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,690.

GenBank hits on 22/02/12: 32,311.

HealthMap feeds 2006-2011: 50.

ProMED feeds 1994-2011: 66.

BioCaster feeds 2006-2011: 45.

Approximate number of endemic countries: >73 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	94	4	2	42	[505]
Disease	87	6	2	58	[506]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 23 occurrence points per country based on 1,690 results for “Meliodosis” in PubMed and 73 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current maps using systematic searches of occurrence data.

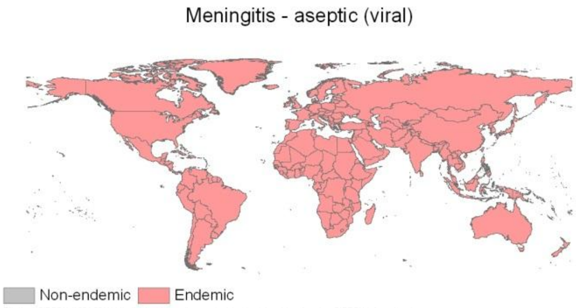
Disease: Meningitis - aseptic (viral).

ICD-10 Code: A87.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Picornavirales, Picornaviridae, Group IV *Enterovirus*, various [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets; close contact; faecal/oral route [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: Dependent on infectious agent (e.g. mumps, varicella or influenza) [472, 474]

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 48,597 for “Meningitis” and 4,010 for “Meningitis and viral”.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 137 for “Viral Meningitis”.

ProMED feeds 1994-2011: 5 for “Viral Meningitis”.

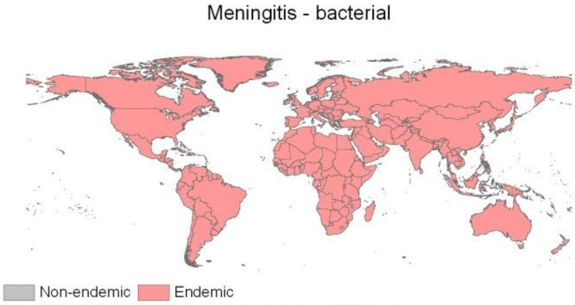
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Aseptic viral meningitis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Meningitis - bacterial.

ICD-10 Code: A39.0.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria,
Proteobacteria, Beta Proteobacteria, Neisseriales, Neisseriaceae,
Neisseria meningitidis
Firmicutes, Bacilli, Lactobacillales, Streptococcaceae,
Streptococcus pneumoniae
Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae,
Haemophilus influenzae [472, 473].

Natural history:

Mode of transmission: Inhalation of infectious droplets; close contact; contact with infectious secretions [472].

Reservoir*: Humans [472].

Incubation period: 6 days (range 2-10 days) [472].

Significant epidemiological characteristics:

Vaccine: Meningococcal; Pneumococcal; *H. influenzae* (HbOC-DTP or -DTaP, HbOC, PRP-D, PRP-OMP, PRP-T) [472].

Estimated R_0 value(s) from published literature:

Human: 0-1.36 (*N. meningitis*); 0-2.2 (*S. pneumoniae*); 0-3.3 [507-510].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 48,597 for "Meningitis" and 15,628 for "Meningitis and bacterial".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 557 for “Meningitis - *Neisseria*”.

ProMED feeds 1994-2011: 4,366 for “Meningitis - *Neisseria*”.

BioCaster feeds 2006-2011: 1,765.

Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	50	4.5	2	13	[511]
Disease	62	6	2	21	[512]
Disease	17	6	2	6	[513]
Disease	14	5.5	4	8	[514]

Disease	14	6.5	4	10	[515]
Disease	14	6.5	4	10	[516]
Disease	100	5	2	33	[517]
Disease	100	5	2	33	[518]

Mapping recommendation: Option 1; do not map. Bacterial meningitis is endemic worldwide and vaccine preventable.

Option 4;

Future mapping potential: Although meningitis is endemic worldwide, it is a vaccine preventable disease that remains epidemic in some parts of the world [519]. It is possible to apply modelling techniques such as niche mapping of high risk regions using modelling techniques such as Boosted Regression Trees (BRT) and the 48,597 PubMed results for meningitis. Systematic searches of occurrence data and digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

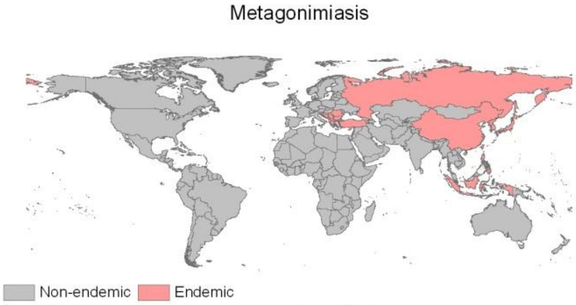
Disease: Metagonimiasis.

ICD-10 Code: B66.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Opisthorchiida, Heterophyidae, *Metagonimus yokogawai* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of infected fish (e.g. trout) [472].

Reservoir*: Snails (*Thiara* spp., *Semisulcospira* spp.), fish, dogs and cats [472].

Incubation period: 14 days (range 14-14 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [520].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 41.

GenBank hits on 22/02/12: 20.

HealthMap feeds 2006-2011: 1.

ProMED feeds 1994-2011: 1.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >19 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	2	2.5	2	1	[521]
Disease	2	5.5	2	1	[522]
Disease	2	5.5	2	1	[523]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 41 results for “Metagonimiasis” in PubMed and 19 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current maps using systematic searches of occurrence data.

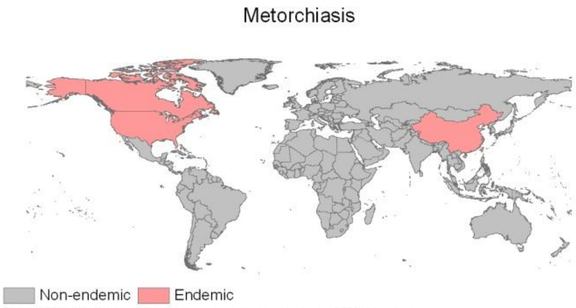
<u>Disease</u>: Metorchiasis.

<u>ICD-10 Code:</u> B66.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Platyhelminthes, Trematoda, Opisthorchiida, Opisthorchiidae,
Metorchis conjunctus, *M. orientalis* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of infected fish (e.g. white sucker (*Catostomus commersoni*); rarely brook trout and other species) [472].

Reservoir*: Snails (*Amnicola limosa*), fish, cats, dogs, minks, foxes, racoons, voles, wolves, bears and coyotes [472].

Incubation period: 5.5 days (range 5-6 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [520].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 7.
- **GenBank hits on 22/02/12:** 19.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >3 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 7 results for “Metorchiasis” in PubMed and 3 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current maps using systematic searches of occurrence data.

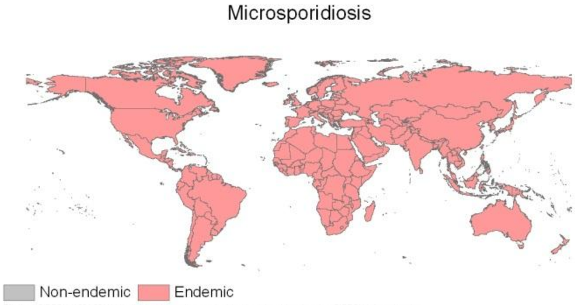
Disease: Microsporidiosis.

ICD-10 Code: B60.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Fungi, Microspora, Microsporea, Microsporida, Enterocytozoonidae, *Enterocytozoon bieneusi* or
Nosematidae, *Vittaforma corneae* or
Pleistophoridae, *Pleistophora* spp. or
Trachipleistophora hominis or
Apansporoblastina, Unikaryonidae,
Encephalitozoon intestinalis [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; contact with contaminated water [472].

Reservoir*: Rabbits, rodents, carnivores, non-human primates, fish, dogs or birds [472].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [524, 525].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

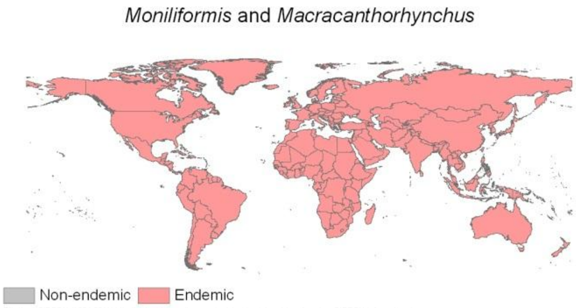
- **PubMed hits on 04/11/11:** 1,052
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Microsporidiosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Moniliformis* and *Macracanthorhynchus.*

ICD-10 Code: B83.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Acanthocephala, Archiacanthocephala, Moniliformida, Moniliformidae

Moniliformis moniliformis

Oligocanthorhynchida, Oligocanthorhynchidae,

Macracanthorhynchus hirudinaceus [472, 473].

Natural history:

Mode of transmission: Ingestion of infected insect [472].

Reservoir*: Rats, foxes and pigs [472].

Incubation period: 27.5 days (range 15-40 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [526, 527].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 430 for "*Moniliformis*" and 73 for "*Macracanthorhynchus*".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Moniliformis* and *Macracanthorhynchus* are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

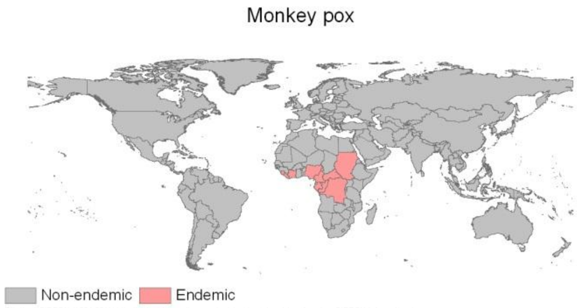
Disease: Monkey pox.

ICD-10 Code: B04.

Transmission category: Direct contact.

Agent: Virus-DNA.

Taxonomy: Poxviridae, Chordopoxvirinae, Group I, *Orthopoxvirus*, Monkeypox virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Close contact [472].

Reservoir*: Monkeys, squirrels and rodents [472].

Incubation period: 11 days (range 10-12 days) [472].

Significant epidemiological characteristics:

Vaccine: Smallpox vaccine effective in some instances (not recommended by WHO, but used in an outbreak in USA) [472, 474].

Estimated R_0 value(s) from published literature:

Human: <1 (0.38); primarily a zoonotic disease [528-530].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 45.

GenBank hits on 22/02/12: 208.

HealthMap feeds 2006-2011: 39.

ProMED feeds 1994-2011: 101.

BioCaster feeds 2006-2011: 36.

Approximate number of endemic countries: >10 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	87	9	4	100	[531]
Disease	100	4	2	33	[529]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 5 occurrence points per country based on 45 results for “Monkey pox” in PubMed and 10 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Generate global thumbnail map using systematic searches of occurrence data.

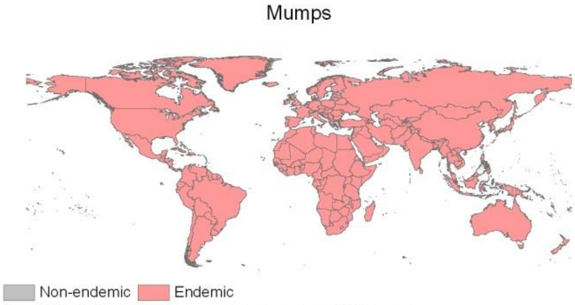
Disease: Mumps.

ICD-10 Code: B26.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Mononegavirales, Paramyxovirinae, Group V, *Rubulavirus*, Mumps virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious aerosol [472].

Reservoir*: Humans [472].

Incubation period: 19 days (range 14-24 days) [472].

Significant epidemiological characteristics:

Vaccine: Measles-Mumps-Rubella, Mumps and Rubella-Mumps [472].

Estimated R_0 value(s) from published literature:

- **Human:** 0-14 [477].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 8,568.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 1,160.
- **ProMED feeds 1994-2011:** 230.
- **BioCaster feeds 2006-2011:** 1,080.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Mumps is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

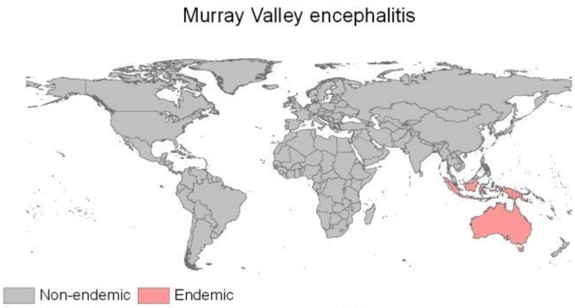
<u>Disease</u>: Murray Valley encephalitis.

<u>ICD-10 Code:</u> A83.4.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Flaviviridae, Group IV, *Flavivirus*, Murray Valley (Australian) encephalitis [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Aedes normanensis, Culex annulirostris*, *Cx. bitaeniorhynchus*) [472].

Reservoir*: Birds [472].

Incubation period: 16.5 days (range 5-28 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [532].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 291.
- **GenBank hits on 22/02/12:** 97.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** 89.

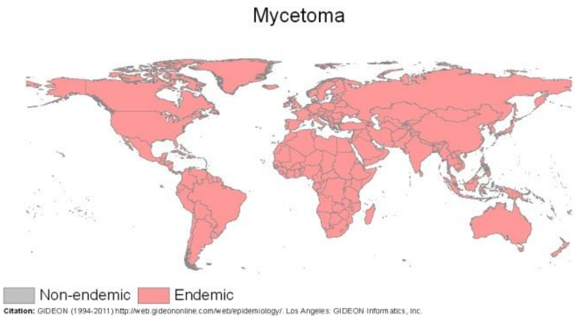
Approximate number of endemic countries: >4 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 73 occurrence points per country based on 291 results for “Murray Valley encephalitis” in PubMed and 4 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Mycetoma

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Mycetoma.

ICD-10 Code: B47.

Transmission category: Soil contact.

Agent: Bacterium or Fungus.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Streptomycetaceae, *Streptomyces somaliensis* or Nocardiaceae, *Nocardia* spp or Fungi, Ascomycota, Sordariomycetes, Sordariales, Incertae sedis, *Madurella mycetomatis* [472, 473].

Natural history:

Mode of transmission: Direct contact; contact with contaminated soil [472].

Reservoir*: None.

Incubation period: 372 days (range 14-730 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,985.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	<1	6	2	N/A	[533]
Disease	<1	6	2	N/A	[534]
Disease	29	2.5	2	N/A	[535]

Mapping recommendation: Option 1; do not map. Mycetoma is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Mycobacteriosis - *M. marinum.*

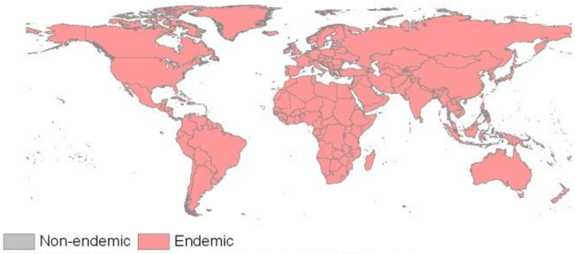
ICD-10 Code: A31.1.

Transmission category: Water contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Mycobacteriaceae, *Mycobacterium marinum* [472, 473].

Mycobacteriosis - *M. marinum*



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Trauma; contact with contaminated water [472].

Reservoir*: Fish (e.g. ornamental, salmon, sturgeon or bass) [472].

Incubation period: 21 days (range 5-270 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic diseasem [536].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 781 for "*Mycobacterium marinum*" and 1,063 for "Mycobacteriosis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

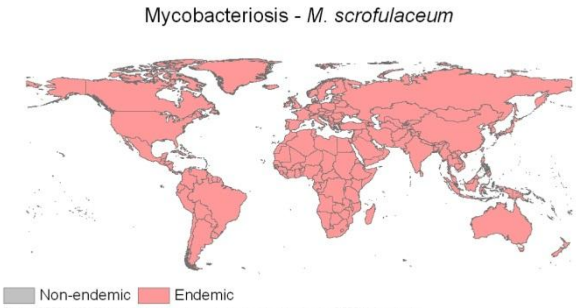
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Mycobacteriosis - *M. marinum* is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Mycobacteriosis - *M. scrofulaceum*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Mycobacteriosis - *M. scrofulaceum.*

<u>ICD-10 Code:</u> A31.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Mycobacteriaceae, *Mycobacterium scrofulaceum* [472, 473].

<u>Natural history</u>:

Mode of transmission: Trauma; contact with contaminated soil or water [472].

Reservoir*: Ruminants, monkeys and rodents [537].

Incubation period: Unknown.

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [537].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 253 for "*Mycobacterium scrofulaceum*" and 1,063 for "Mycobacteriosis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

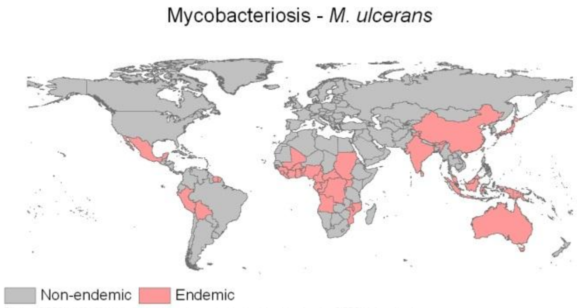
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Mycobacteriosis - *M. scrofulaceum* is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Mycobacteriosis - *M. ulcerans.*

ICD-10 Code: A31.1.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Mycobacteriaceae, *Mycobacterium ulcerans*[472, 473].

Natural history:

Mode of transmission: Contact with contaminated vegetation; (possibly) mosquito vector [472].

Reservoir*: Aquatic insects (*Naucoridae* spp.) [538].

Incubation period: 55.5 days (range 21-90 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [538].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 648 for "*Mycobacterium ulcerans*".

GenBank hits on 22/02/12: 233.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >37 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	65	5	2	36	[539]
Disease	71	5	2	40	[540]
Disease	66	4	2	29	[541]
Disease	14	4	2	6	[542]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 18 occurrence points per country based on 648 results for "*Mycobacterium ulcerans"* in PubMed and 37 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Generate global thumbnail map using systematic searches of occurrence data.

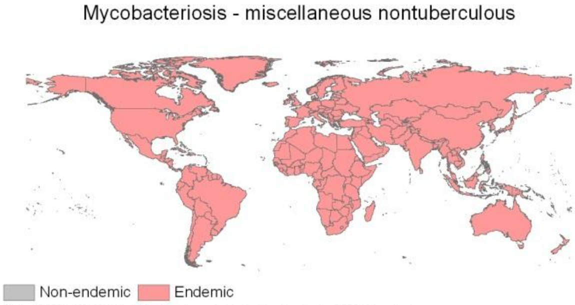
Disease: Mycobacteriosis - miscellaneous nontuberculous.

ICD-10 Code: A31.8.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Mycobacteriaceae, *Mycobacterium* spp [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Ingestion of contaminated food or water, contact with an infected animal or patient or though inhalation of bacterium from close contact [472].

Reservoir*: Fish, mammals and birds [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [537].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 138 for "Mycobacteriosis and nontuberculous" .

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 21 for “Mycobacteria, non-TB”.

ProMED feeds 1994-2011: 68 for “Mycobacteria, non-TB”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Mycobacteriosis - miscellaneous nontuberculous is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: *Mycoplasma* (miscellaneous) infections.

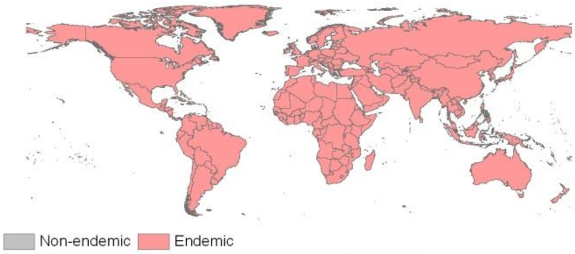
ICD-10 Code: A49.3.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, *Mycoplasma genitalium*, *M. hominis*, *M. fermentans*, *M. penetrans* and *Ureaplasma urealyticum* [472, 473].

Mycoplasma (miscellaneous) infections



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; contact with infectious secretions [472].

Reservoir*: Human [472].

Incubation period: 17.5 days (range 14-21 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,621 for "*Mycoplasma* infections," 666 for "*Mycoplasma genitalium*," 1,396 for "*Mycoplasma hominis*," 363 for "*Mycoplasma fermentans*," 90 for "*Mycoplasma penetrans*" and 1784 for "*Ureaplasma urealyticum*" .

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Mycoplasma* (miscellaneous) infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

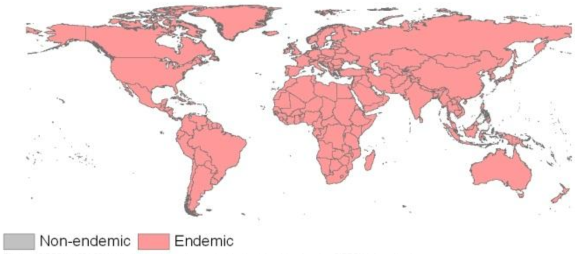
<u>Disease</u>: *Mycoplasma pneumoniae* infection.

<u>ICD-10 Code:</u> B96; J15.7.

<u>Transmission category:</u> Respiratory.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Firmicutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, *Mycoplasma pneumoniae* [472, 473].



Mycoplasma pneumoniae infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Inhalation of infectious droplets [472].

Reservoir*: Humans [472].

Incubation period: 14.5 days (range 6-23 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 4,577 for "*Mycoplasma pneumoniae*" and 831 for "*Mycoplasma pneumoniae* infection".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. *Mycoplasma pneumoniae* is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

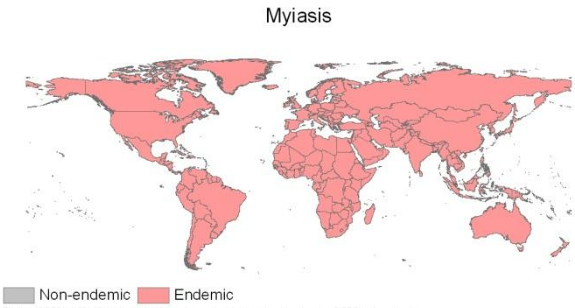
<u>Disease</u>: Myiasis.

<u>ICD-10 Code:</u> B87.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Diptera, many [472].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Fly eggs deposited by biting arthropods [472].

Reservoir*: Mammals [472].

Incubation period: 14 days (range 7-21 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [543].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 2,557.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 14.
- **ProMED feeds 1994-2011:** 35.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Myiasis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

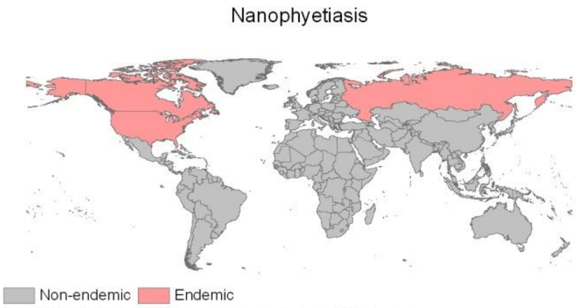
Disease: Nanophyetiasis.

ICD-10 Code: B66.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Plagiorchiida, Nanophyetidae, *Nanophyetus salminocola* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of infected fish (e.g. salmon) [472].

Reservoir*: Snails (*Semisulcospira*) and fish [472].

Incubation period: 7 days [472].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [544].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

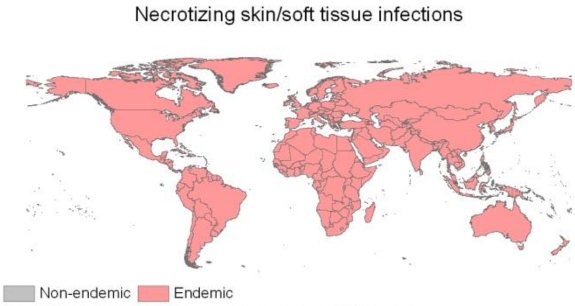
Approximate number of endemic countries: >3 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 1 occurrence point per country based on 3 results for “Nanophyetiasis” in PubMed and 3 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Generate global thumbnail map using systematic searches of occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Necrotizing skin/soft tissue infections.

ICD-10 Code: M72.6.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, mixed anaerobic and/or gram-negative bacilli (e.g. *Streptococcus pyogenes*) or

Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, *Clostridium perfringens* [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: Gas gangrene antitoxin [472].

Estimated R_0 value(s) from published literature:

Human: Not applicable.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 0 for "Necrotizing skin infection" and 117 for "Necrotizing soft tissue infection".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Necrotizing skin and soft tissue infections is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

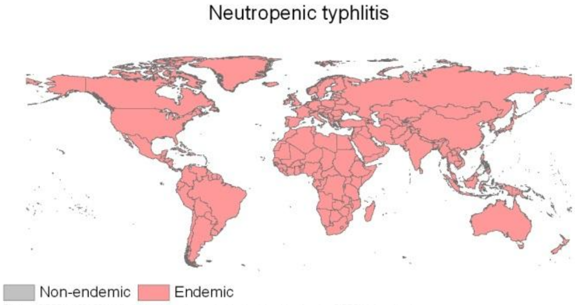
Disease: Neutropenic typhlitis.

ICD-10 Code: A09.0.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium septicum (occasionally *C. tertium*, *C. sporogenes*, *C. sordellii* or *C. tertium*) [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: Gas gangrene antitoxin [472].

Estimated R_0 value(s) from published literature:

Human: Not applicable.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 10.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Neutropenic typhlitis and soft tissue infections is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

New World phleboviruses

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: New World phleboviruses.

<u>ICD-10 Code:</u> A93.1.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Bunyaviridae, n.a., Group V, Orthobunyavirus,

Alenquer, Arboledas, Bujaru, Cacao, Candiru, Chagres and Punta Toro viruses [472, 473].

<u>Natural history</u>:

Mode of transmission: Sandfly (*Lutzomyia* spp.) vector [472].

Reservoir*: Sandfly (*Lutzomyia trapidoi*, *Lu. ylephiletor*) and potentially rodents [472].

Incubation period: 3.5 days (range 3-4 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 0
- **GenBank hits on 22/02/12:** 52.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

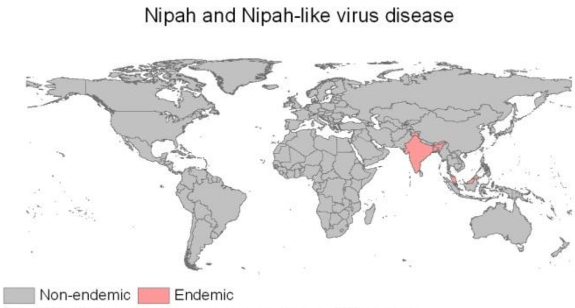
Approximate number of endemic countries: >3 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were 0 occurrence points per country based on 0 results for “New World phleboviruses” in PubMed and 3 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Generate global thumbnail map using systematic searches of occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Nipah and Nipah-like virus disease.

ICD-10 Code: A86.

Transmission category: Animal contact.

Agent: Virus-RNA.

Taxonomy: Mononegavirales, Paramyxoviridae, Group V, *Megamyxovirus* [*Henipavirus*], Nipah virus [472, 473].

Natural history:

Mode of transmission: Potentially through inhalation of infectious droplets; contact with urine or secretions or fruit sap contaminated with bat faeces [472].

Reservoir*: Pigs and bats [472].

Incubation period: 11 days (range 4-18 days) [472].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1 (0.45); primarily a zoonotic disease [545, 546].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 438.

GenBank hits on 22/02/12: 116.

HealthMap feeds 2006-2011: 216 for “Nipah/Hendra Virus”.

ProMED feeds 1994-2011: 284 for “Nipah/Hendra Virus”.

BioCaster feeds 2006-2011: 261.

Approximate number of endemic countries: >4 [472].

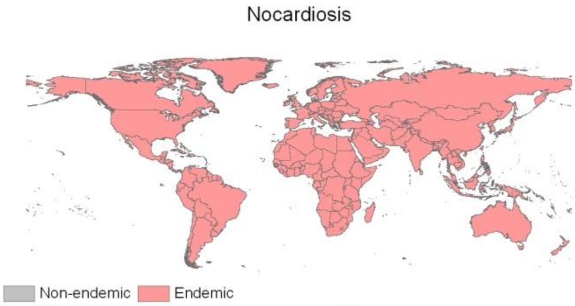
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Host	100	4	2	22	[547]
Disease	100	5	2	28	[547]
Disease	2	3.5	2	<1	[548]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 110 occurrence points per country based on 438 results for “Nipah virus” PubMed and 4 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Nocardiosis.

ICD-10 Code: A43.

Transmission category: Soil contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Nocardiaceae, *Nocardia* spp. [472, 473].

Natural history:

Mode of transmission: Close contact; contact with contaminated soil [472].

Reservoir*: None.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,173.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Nocardiosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

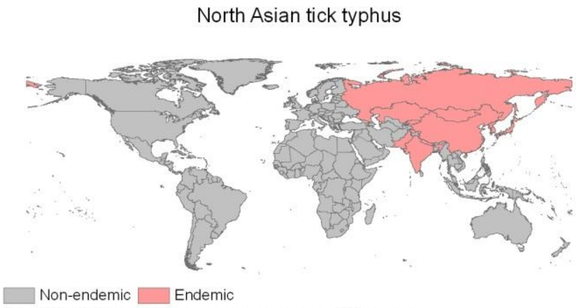
Disease: North Asian tick typhus.

ICD-10 Code: A77.2.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiaceae, *Rickettsia sibirica* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Dermacentor* spp., *Haemaphysalis* spp.) [472].

Reservoir*: Rodents and dogs [472].

Incubation period: 6.5 days (range 6-7 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [549].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 5.

GenBank hits on 22/02/12: 198.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

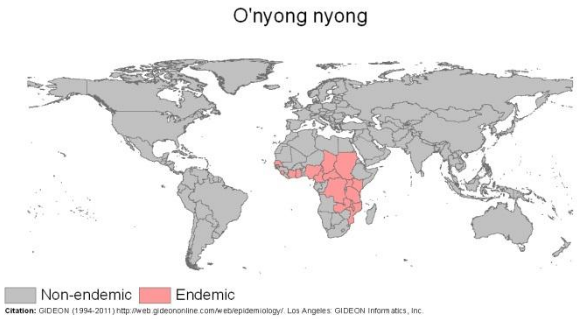
Approximate number of endemic countries: >12 [472].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There was less than 1 occurrence point per country based on 5 results for “North Asian tick typhus” in PubMed and 12 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: O'nyong nyong.

ICD-10 Code: A92.1.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, *Alphavirus*, O'nyong-nyong virus [472, 473].

Natural history:

Mode of transmission: Mosquito vector (*Anopheles* spp.) [472].

Reservoir*: Unknown.

Incubation period: 7.5 days (range 3-15 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 72.

GenBank hits on 22/02/12: 20.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >16 [472].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 5 occurrence points per country based on 72 results for “O'nyong nyong” in PubMed and 16 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors. If occurrence data for these mosquito species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

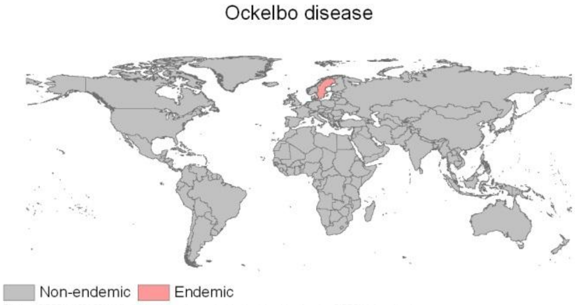
Disease: Ockelbo disease.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, *Alphavirus*, Ockelbo virus [472, 473].



Ockelbo disease

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Culiseta* spp. (*Culiseta morsitans*), *Culex* spp. (*Culex pipiens*), *Aedes* spp. (*Aedes communis*)) [472].

Reservoir*: Human and birds [472].

Incubation period: 4.5 days (range 3-6 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [550].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 21.

GenBank hits on 22/02/12: 1.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	2.5	2	19	[551]
Disease	100	5.5	2	41	[552]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 21 occurrence points per country based on 32 results for “Ockelbo” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors. If occurrence data for these mosquito species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping. There is also the potential to link occurrence data with the distribution of other Sindbis virus (SINV) diseases.

Disease: Oesophagostomiasis.

ICD-10 Code: B81.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Strongyloidae, *Oesophagostomum bifurcum*, *O. apiostomum* or *O. stephanostomum* [472, 473].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; contact with contaminated water or soil [472].

Reservoir*: Non-human primates [472].

Incubation period: 37 days (range 14-60 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [553].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 381 for "Oesophagostomiasis," 45 for "*Oesophagostomum bifurcum*," 2 for "*Oesophagostomum apiostomum*" and 3 for "*Oesophagostomum stephanostomum*".

GenBank hits on 22/02/12: 23.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >35 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	6.5	2	<1	[554]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 11 occurrence points per country based on 381 results for Oesophagostomiasis in PubMed and 35 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Old World phleboviruses.

ICD-10 Code: A93.1.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, *Phlebovirus*, Sandfly fever virus or Dabie Mountain virus [472, 473].

Natural history:

Mode of transmission: Sandfly vector (*Phlebotomus* spp.) [472].

Reservoir*: Fly (*Phlebotomus* spp.) and potentially rodents [472].

Incubation period: 3.5 days (range 3-4 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 0.

GenBank hits on 22/02/12: 33.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >53 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were less than one occurrence point per country based on 0 results for Old World phleboviruses in PubMed and 53 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Omsk haemorrhagic fever.

ICD-10 Code: A98.1.

Transmission category: Vector-borne.

Agent: Virus-RNA

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Omsk haemorrhagic fever (OHF) virus [472, 473].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Dermacentor pictus, D. marginatus*) [472].

Reservoir*: Rodents, muskrats (*Ondrata zibethica*) and ticks [472].

Incubation period: 6 days (range 3-9 days) [472].

Significant epidemiological characteristics:

Vaccine: Formalinized mouse-brain OHF virus vaccine reported [474]

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [555].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 66.

GenBank hits on 22/02/12: 41.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >2 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	87	1	2	5	[556]
Vector	100	3.5	2	19	[557]
Vector	100	3.5	2	19	[557]
Disease	87	4.5	2	22	[558]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 33 occurrence points per country based on 66 results for “Omsk haemorrhagic fever” in PubMed and 2 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

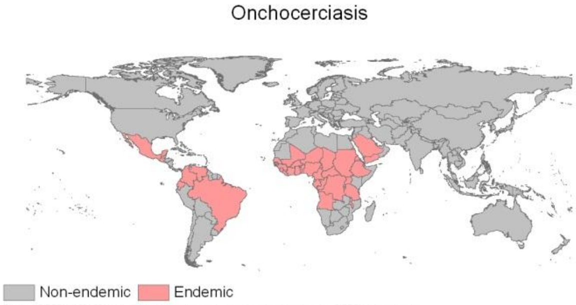
Disease: Onchocerciasis.

ICD-10 Code: B73.

Transmission category: Vector-borne.

Agent: Parasite

Taxonomy: Animalia, Nematoda, Secernentea, Strongylida, Onchocercidae, *Onchocerca volvulus* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Black fly vector (*Simulium* spp.) [472].

Reservoir*: Humans [472].

Incubation period: 450 days (range 360-540 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-74 [477].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,999.

GenBank hits on 22/02/12: 579.

HealthMap feeds 2006-2011: 2 for “Onchocerciasis” and 20 for “River Blindness”.

ProMED feeds 1994-2011: 2 for “Onchocerciasis” and 20 for “River Blindness”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >36 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	86	4.5	2	22	[559]
Disease	2	5	2	1	[560]
Disease	4	5.5	3	2	[561]
Disease	17	3.5	2	3	[562]
Vector	17	3.5	2	3	[562]
Disease	33	2.5	2	5	[563]
Disease	86	4.5	2	22	[564]
Disease	99	0	2	0	[565]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 111 occurrence points per country based on 3,999 results for “Onchocerciasis” in PubMed and 36 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

<u>Disease</u>: Opisthorchiasis.

<u>ICD-10 Code:</u> B66.0.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite

<u>Taxonomy:</u> Animalia, Platyhelminthes, Trematoda, Opisthorchiata, Opisthorchiidae, *Opisthorchis felineus*, *O. guayaquilensis* and *O. viverrini* [472, 473].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of infected freshwater fish [472].

Reservoir*: Cats, civets, dogs, other-fish-eating-mammals and snails (*Bythinia*) [472].

Incubation period: 24.5 days (range 21-28 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [520].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 1,267 for “Opisthorchiasis,” 149 for "*Opisthorchis felineus*,” 0 for "*Opisthorchis guayaquilensis*" and 507 for "*Opisthorchis viverrini*".

GenBank hits on 22/02/12: 646.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >17 [472].

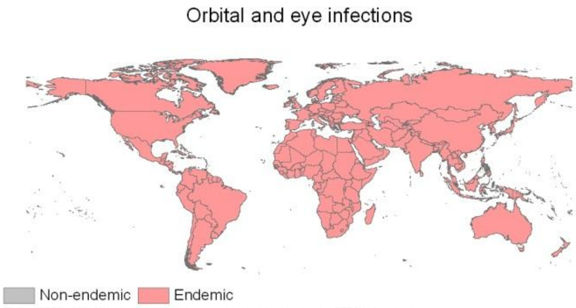
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	92	5	2	26	[566]
Disease	3	7	2	1	[567]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 74 occurrence points per country based on 1,267 results for “Opisthorchiasis” in PubMed and 17 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Orbital and eye infections.

ICD-10 Code: H05.0.

Transmission category: Endogenous.

Agent: Bacterium or Fungus.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae,
Streptococcus pyogenes
Fungi, Ascomycota, Eurotiomycetes, Eurotiales, Trichocomaceae,
Aspergillus spp [472, 473].

Natural history:

Mode of transmission: Endogenous; trauma; blood contact [472].

Reservoir*: Non-human primates [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 106 for "Orbital infection" and 242 for "Eye infection"

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Orbital eye infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

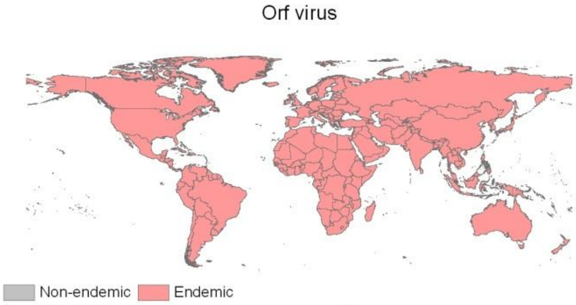
<u>Disease</u>: Orf virus.

<u>ICD-10 Code:</u> B08.0.

<u>Transmission category:</u> Animal contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Poxviridae, Group I, *Parapoxvirus*, Orf virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Contact with infectious secretions or fomites [472].

Reservoir*: Sheep, goats, reindeer and musk oxen [472].

Incubation period: 4.5 days (range 3-6 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [568].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 317.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Orf virus is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

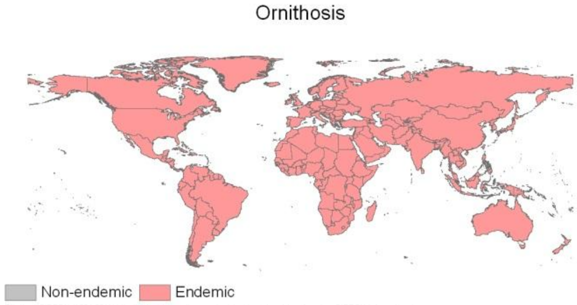
Disease: Ornithosis.

ICD-10 Code: A70.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Chlamydiae, Chlamydiae, Chlamydiales, Chlamydiaceae, *Chlamydia psittaci* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with contaminated bird faeces; inhalation of infectious dust or aerosol from cat (rare) [472].

Reservoir*: Parakeets, parrots, pigeons, turkeys, ducks, cats, sheep, goats, cattle and possibly dogs [472].

Incubation period: 10.5 days (range 7-14 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [569].

Reservoir: Not found

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,098.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Ornithosis virus is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

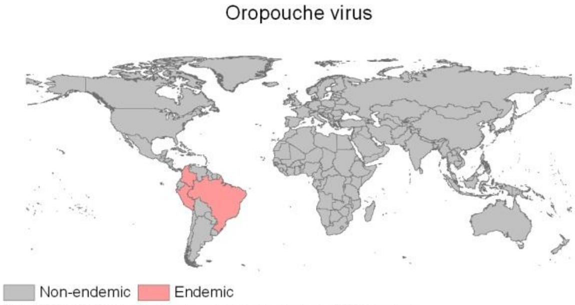
Disease: Oropouche virus.

ICD-10 Code: A93.0.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, Orthobunyavirus, Oropouche virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Midge (*Culicoides paraensis*) and mosquito (*Culex quinquefasciatus*, *Aedes serratus*, *Coquillettidia venezuelensis*) vectors [472].

Reservoir*: Unknown; (possibly) midges (*Culicoides* spp.) [472].

Incubation period: 6 days (range 4-8 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; epidemics in urban setting only last ~6 months [570].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 67.

GenBank hits on 22/02/12: 222.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >5 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	71	5.5	2	29	[571]
Disease	71	5	2	26	[570]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 22 occurrence points per country based on 67 results for “Oropouche” in PubMed and 5 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its midge and mosquito vectors. If occurrence data for these mosquito and midge species are not available Digitized versions of expert opinions of their ranges could usefully inform future mapping.

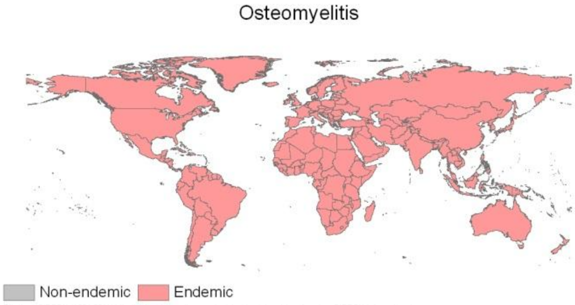
<u>Disease</u>: Osteomyelitis.

<u>ICD-10 Code:</u> M86 B95.6.

<u>Transmission category:</u> Endogenous.

<u>Agent</u>: Bacterium or Fungus.

<u>Taxonomy:</u> Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae,
Staphylococcus aureus
Fungi, Ascomycota, Saccharomycetes, Saccharomycetales, Saccharomycetaceae,
Candida albicans[472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Endogenous; trauma; blood contact [472].

Reservoir*: None.

Incubation period: Variable [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

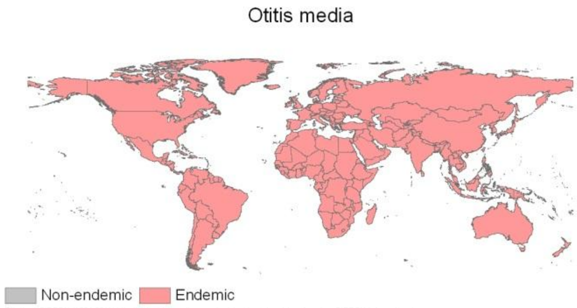
- **PubMed hits on 04/11/11:** 20,930.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Osteomyelitis virus is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Otitis media.

ICD-10 Code: H66.

Transmission category: Endogenous.

Agent: Bacterium or Virus-RNA.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae, *Haemophilus influenzae*
Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pneumoniae*
Mononegavirales, Paramyxoviridae, Group V, *Respiratory syncytial virus* (RSV), *Parainfluenza*, et al [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: *Haemophilus influenzae* (HbOC-DTP or -DTaP, HbOC, PRP-D, PRP-OMP, PRP-T), pneumococcal conjugate or RSV immunoglobulin [472].

Estimated R_0 value(s) from published literature:

Human: 0-3.3 (*H. influenza*); 0-2.2 (*S. pneumoniae*); 0-2.81 (RSV) [508-510, 572-574].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 23,152.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 38.

ProMED feeds 1994-2011: 4.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Otitis media virus is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Paracoccidioidomycosis.

ICD-10 Code: B41.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Eurotiomycetes, Onygenales, Ajellomycetaceae, *Paracoccidioides braziliensis*[472, 473].

Natural history:

Mode of transmission: Inhalation of spores [472].

Reservoir*: Armadillos [472].

Incubation period: 307.5 days (range 30-585 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,506.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: 0.

ProMED feeds 1994-2011: 0.

BioCaster feeds 2006-2011: N/A.

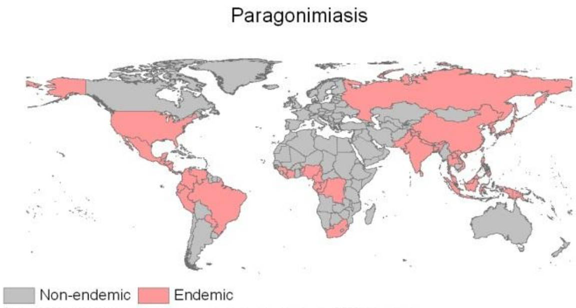
Approximate number of endemic countries: >11 [472].

Previously published maps: Not found.

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 137 occurrence points per country based on 1,506 results for “Paracoccidioidomycosis” in PubMed and 11 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Paragonimiasis.

ICD-10 Code: B66.4.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Trematoda, Plagiorchiformes, Troglotrematidae, *Paragonimus westermani*, *P. heterotremus*, *P. skrjabini*, *P. miyazakii* and *P. africanus* [472, 473].

Natural history:

Mode of transmission: Consumption of infected fresh-water crab (at least 8 species) or crayfish (*Cambaroides* spp.) [472].

Reservoir*: Humans, dogs, cats, pigs, wild carnivores and snails (*Semisulcospira* spp., *Thiara* spp. and others) [472].

Incubation period: 111 days (range 42-222 days) [472].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [575].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,133 for "Paragonimiasis," 418 for "*Paragonimus westermani*," 45 for "*Paragonimus heterotremus*," 13 for "*Paragonimus skrjabini*," 37 for "*Paragonimus miyazakii*" and 17 for "*Paragonimus africanus*".

GenBank hits on 22/02/12: 408.

HealthMap feeds 2006-2011: 3.

ProMED feeds 1994-2011: 6.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >47 [472].

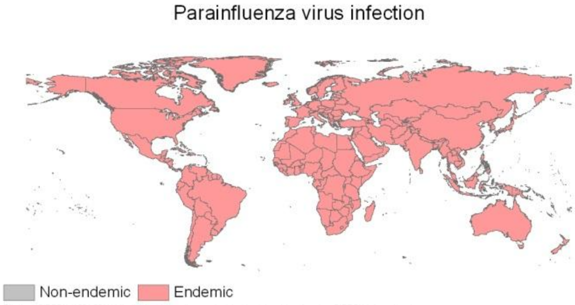
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	71	5.5	2	29	[571]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 24 occurrence points per country based on 1,133 results for "Paragonimiasis" in PubMed and 47 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Parainfluenza virus infection.

ICD-10 Code: J12.2.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Mononegavirales, Paramyxoviridae, Group V, *Respirovirus* and *Rubulavirus*,
Human Parainfluenza virus 1 and 3 and Human Parainfluenza virus 2 and 4 [472, 473].

Natural history:

Mode of transmission: Inhalation of infectious droplets or close contact [472].

Reservoir*: Humans [472].

Incubation period: 5.5 days (range 3-8 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 4,722.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Parainfluenza virus infection is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

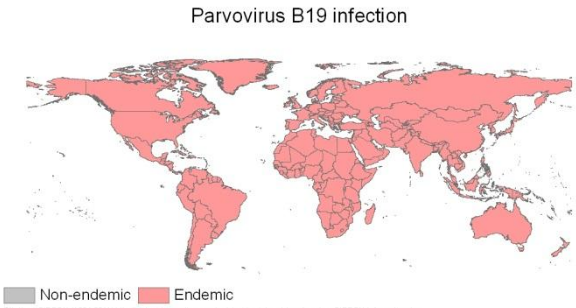
Disease: Parvovirus B19 infection.

ICD-10 Code: B34.3.

Transmission category: Respiratory.

Agent: Virus-DNA.

Taxonomy: Parvoviridae, Group III, *Erythrovirus*, Human parovirus B19 [472, 473].



Parvovirus B19 infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets or close contact [472].

Reservoir*: Humans [472].

Incubation period: 9 days (range 4-14 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-8 [576-579].

Reservoir: There are no animal reservoirs for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,049.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 270.

ProMED feeds 1994-2011: 23.

BioCaster feeds 2006-2011: 170.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Parvovirus B19 infection is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

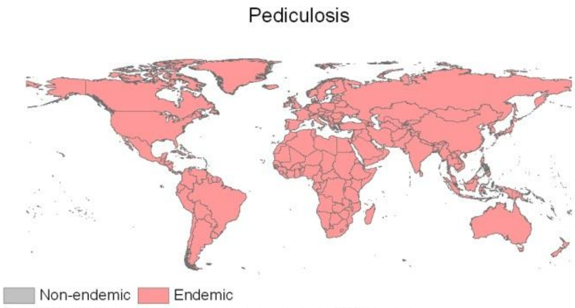
Disease: Pediculosis.

ICD-10 Code: B85.0 - B85.2.

Transmission category: Direct contact.

Agent: Parasite.

Taxonomy: Animalia, Arthropoda, Insecta, Phthiraptera, Pediculidae,
Pediculus humanus or
Pthiridae,
Phthirus pubis [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Direct contact [472].

Reservoir*: Humans [472].

Incubation period: 7 days [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 676 for "Pediculosis," 286 for "*Pediculus humanus*" and 59 for "*Phthirus pubis*".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 63 for “Lice”.
- **ProMED feeds 1994-2011:** 10 for “Lice”.
- **BioCaster feeds 2006-2011:** 2.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pediculosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

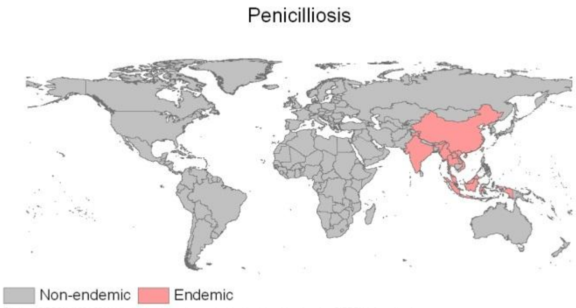
Disease: Penicilliosis.

ICD-10 Code: B85.0 - B85.2.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Eurotiomycetes, Eurotiales, Trichocomaceae, *Penicillium marneffei* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of spores [472].

Reservoir*: Rodents (e.g. *Rhizomys* spp., bamboo rats) [472].

Incubation period: 19.5 days (range 9-30 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 199.
- **GenBank hits on 22/02/12:** 14,388.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

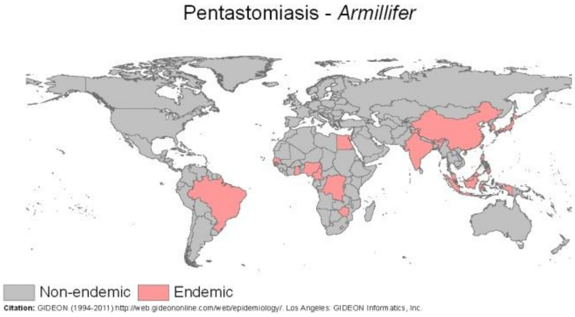
Approximate number of endemic countries: >12 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 17 occurrence points per country based on 199 results for “Penicilliosis” in PubMed and 12 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.


Pentastomiasis - *Armillifer*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Pentastomiasis - *Armillifer.*

<u>ICD-10 Code:</u> B88.8.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Arthropoda, Maxillopoda, Porocephalida, Porocephalidae, *Armillifer moniliformis*, *Porocephalus taiwana*, *Armillifer* [*Porocephalus*] *armillatus* and *Armillifer grandis* [472, 473].

<u>Natural history</u>:

Mode of transmission: Consumption foods such as infected snake meat or contaminated uncooked vegetation [472].

Reservoir*: Rodents and reptiles [472].

Incubation period: Variable [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [580, 581].

Reservoir: Not found

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 60 for "Pentastomiasis," 56 for "*Armillifer*," 8 for "*Armillifer moniliformis*," 0 for "*Porocephalus taiwana*," 28 for "*Armillifer armillatus*" and 3 for "*Armillifer grandis*".

GenBank hits on 22/02/12: 48.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

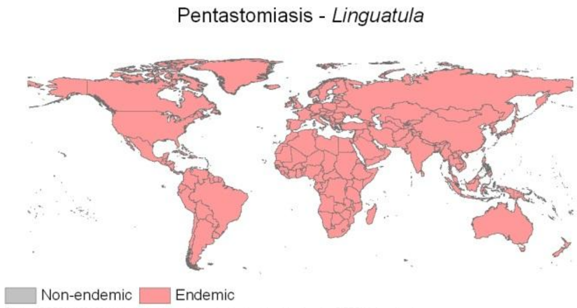
Approximate number of endemic countries: >19 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 3 occurrence points per country based on 56 results for “*Armillifer*” in PubMed and 19 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Pentastomiasis - *Linguatula.*

ICD-10 Code: B88.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Arthropoda, Maxillopoda, Pentastomida, Linguatulidae, *Linguatula serrata* [472, 473].

Natural history:

Mode of transmission: Consumption of infected meats such as the liver or lymph nodes of sheep or goats [472].

Reservoir*: Herbivores [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [580].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 60 for "Pentastomiasis" and 74 for "*Linguatula*".

GenBank hits on 22/02/12: 1.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >184 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was less than 1 occurrence point per country based on 74 results for “*Linguatula*” in PubMed and 184 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

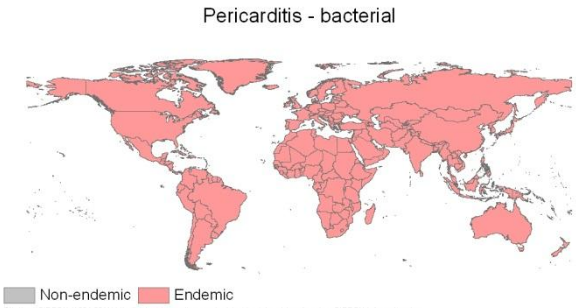
Disease: Pericarditis - bacterial.

ICD-10 Code: I30.1.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae,
Streptococcus pneumoniae
Bacillales, Staphylococcaceae,
Staphylococcus aureus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: Pneumococcal [472].

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 12,255.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

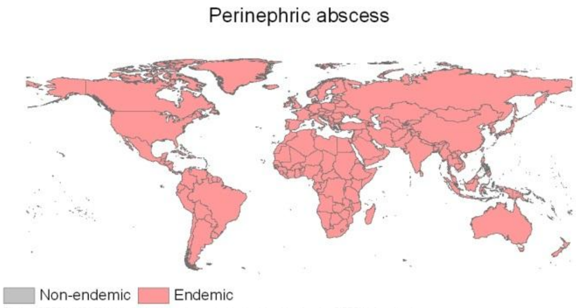
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacterial pericarditis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Perinephric abscess.

ICD-10 Code: N15.1.

Transmission category: Endogenous.

Agent: Bacterium or Fungus.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Escherichia coli*
Other facultative gram negative bacilli (various)
Fungi, Ascomycota, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, *Candida albicans* [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans[472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: 0-0.05 (highly resistant gram-negative strains) [582].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 262.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Perinephric abscesses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

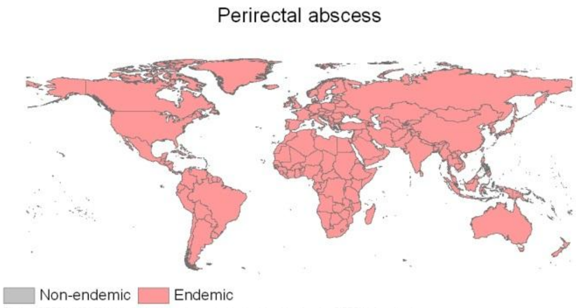
<u>Disease</u>: Perirectal abscess.

<u>ICD-10 Code:</u> K61.1.

<u>Transmission category:</u> Endogenous.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Various (often mixed anaerobic and aerobic flora) [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 109.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

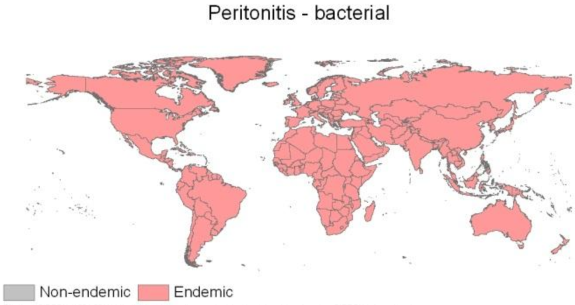
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Perirectal abscesses are endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Peritonitis - bacterial.

ICD-10 Code: K65.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various (often mixed anaerobic and aerobic flora) [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 30,560.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacterial peritonitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

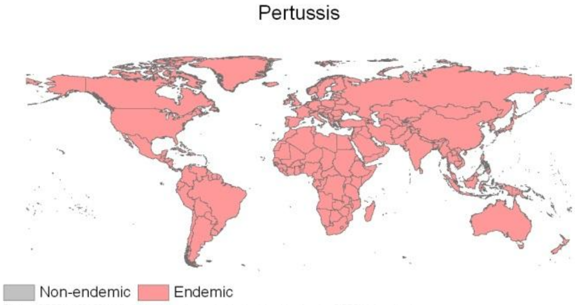
Disease: Pertussis.

ICD-10 Code: A37.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Burkholderiales, Alcaligenaceae, *Bordetella pertussis* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with infectious secretions or close contact [472].

Reservoir*: Humans [472].

Incubation period: 8.5 days (range 7-10 days) [472].

Significant epidemiological characteristics:

Vaccine: DTaP or DTP [472].

Estimated R_0 value(s) from published literature:

Human: 0-18 [477].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 24,598.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 1,916 for "Whooping Cough".

ProMED feeds 1994-2011: 157 for "Whooping Cough".

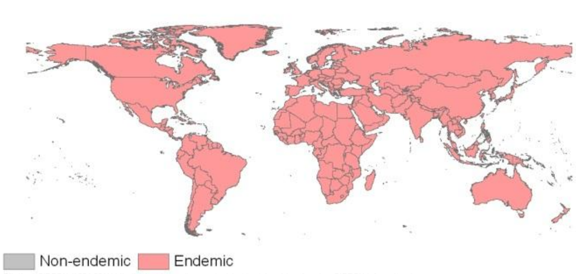
BioCaster feeds 2006-2011: 1,759 for "Whooping Cough".

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pertussis is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Pharyngeal and cervical space infections

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Pharyngeal and cervical space infections.

ICD-10 Code: A49.1.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pyogenes* and mixed oral anaerobes [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

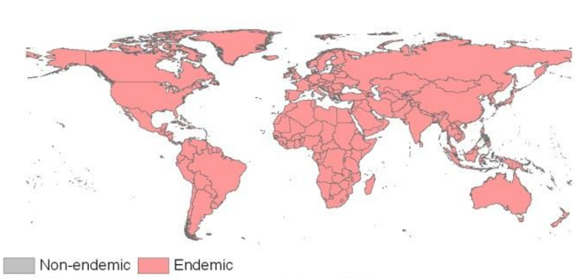
- **PubMed hits on 04/11/11:** 126 for "Pharyngeal infection" and 0 for "Cervical space infection".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pharyngeal and cervical space infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Pharyngitis - bacterial

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Pharyngitis - bacterial.

ICD-10 Code: J02.0.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pyogenes* [472, 473].

Natural history:

Mode of transmission: Inhalation of infectious droplets; rarely from consumption of contaminated food [472].

Reservoir*: Humans [472].

Incubation period: 3 days (range 1-5 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 7,864.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacterial pharyngitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

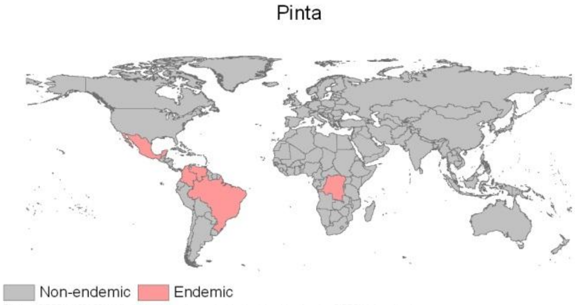
Disease: Pinta.

ICD-10 Code: A67.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Spirochaetaceae, *Treponema carateum* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Close contact ;(possibly) black fly vector (*Simulium* spp.) [472].

Reservoir*: Humans [472].

Incubation period: 14 days (range 7-21 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 188 for "Pinta" and 9 for "*Treponema carateum*".

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >7 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	96	3.5	2	19	[583]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 27 occurrence points per country based on 188 results for “Pinta” in PubMed and 7 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Pityriasis rosea.

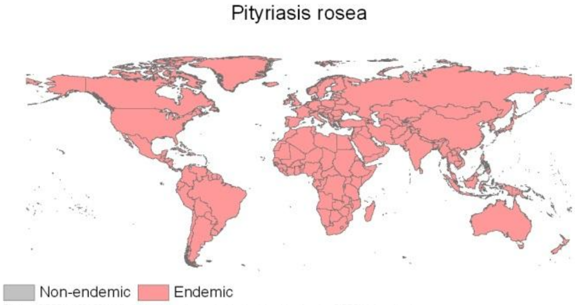
ICD-10 Code: L42.

Transmission category: Unknown.

Agent: Unknown.

Taxonomy: Herpesvirales, Herpesviridae, Group I

Human herpesvirus 7 has been implicated [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 470.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

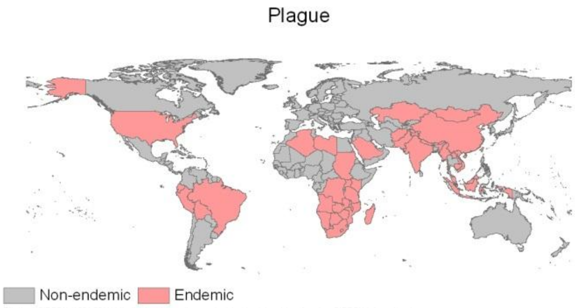
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pityriasis rosea is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Plague.

ICD-10 Code: A20.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Yersinia pestis* [472, 473].

Natural history:

Mode of transmission: Flea vector (*Pulex irritans*, *Xenopsylla cheopis*, *Oropsylla montana*) [472].

Reservoir*: Rodents, rabbits, cats and wild carnivores [472].

Incubation period: 4.5 days (range 2-7 days) [472].

Significant epidemiological characteristics:

Vaccine: Plague [472].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease; up to 3.5 in epidemic settings [584-586].

Reservoir: 0-3.5 (rats and gerbils) [587, 588].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,707.

GenBank hits on 22/02/12: 4,242.

HealthMap feeds 2006-2011: 1,182.

ProMED feeds 1994-2011: 574.

BioCaster feeds 2006-2011: 1,874.

Approximate number of endemic countries: >38 [472].

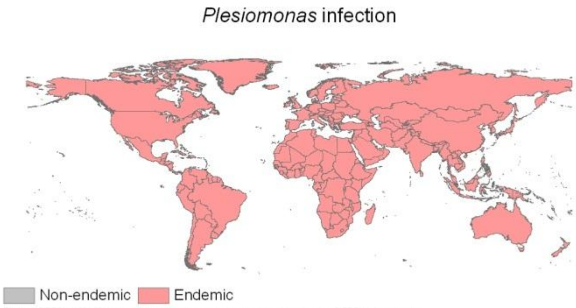
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Host	100	1	2	6	[589]
Disease	92	2	2	10	[589]
Disease	85	3	2	14	[590]
Disease	96	3	2	16	[590]
Disease	91	4	2	20	[591]
Disease	89	4	2	20	[592]
Disease	7	5.5	2	2	[593]
Disease	1	4	2	0	[594]
Disease	7	6	4	5	[595]
Disease	1	6	4	1	[596]
Disease	18	6.5	2	6	[597]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 203 occurrence points per country based on 7,707 results for “Plague” in PubMed and 38 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: *Plesiomonas* infection.

ICD-10 Code: K92.8.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Plesiomonas shigelloides* [472, 473].

Natural history:

Mode of transmission: Consumption of contaminated food or water [472].

Reservoir*: Fish, animals, reptiles and birds [472].

Incubation period: 1.5 days (range 1-2 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 509.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Plesiomonas* infection is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

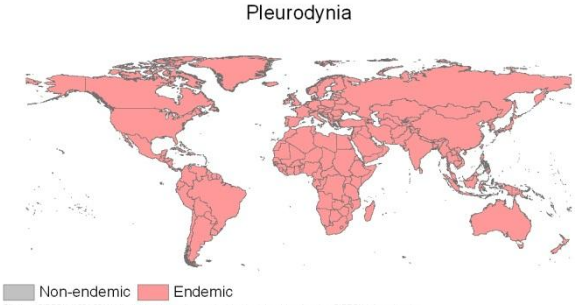
Disease: Pleurodynia.

ICD-10 Code: B33.0.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Picornaviridae, Group IV, *Coxsackievirus*, Types 1-3, 5, and 6 [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Close contact; faecal-oral route; fomites [472].

Reservoir*: Humans [472].

Incubation period: 4 days (range 3-5 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 357.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pleurodynia is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: *Pneumocystis* pneumonia.

ICD-10 Code: B59+.

Transmission category: Respiratory.

Agent: Fungus.

Taxonomy: Fungi, Ascomycota, Pneumocystidomycetes, Pneumocystidales, Pneumocystidaceae, *Pneumocystis jiroveci* [472, 473].

Pneumocystis pneumonia

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of spores [472].

Reservoir*: Humans [472].

Incubation period: 30 days (range 4-56 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7,680.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

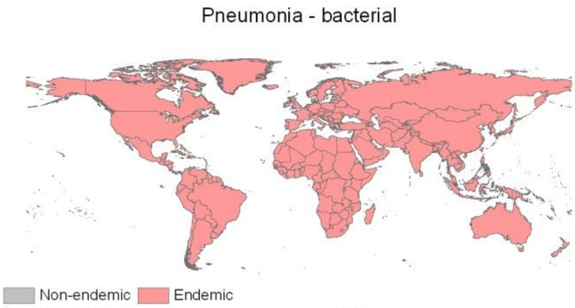
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Pneumocystis* pneumonia is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Pneumonia - bacterial.

ICD-10 Code: J13.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae,
Streptococcus pneumoniae
Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae,
Klebsiella pneumoniae spp *pneumoniae*
Other aerobic and facultative gram negative bacilli [472, 473].

Natural history:

Mode of transmission: Endogenous [472].

Reservoir*: Humans [472].

Incubation period: 2 days (range 1-3 days) [472].

Significant epidemiological characteristics:

Vaccine: Pneumococcal [472].

Estimated R_0 value(s) from published literature:

Human: 0-2.2; 0-0.05 (highly resistant gram-negative strains) [509, 510, 582].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 8698

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 2,162 for “Pneumonia”.

ProMED feeds 1994-2011: 208 for “Pneumonia”.

BioCaster feeds 2006-2011: 1,735 for “Pneumonia”.

Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5	2	N/A	[517]

Mapping recommendation: Option 1; do not map. Bacterial pneumonia is endemic worldwide and is potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Pogosta disease.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, *Alphavirus*, Pogosta virus [472, 473].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (many species) [472].

Reservoir*: Birds [472].

Incubation period: 4.5 days (range 3-6 days)

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [598].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 24.
- **GenBank hits on 22/02/12:** 6.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >1 [472].

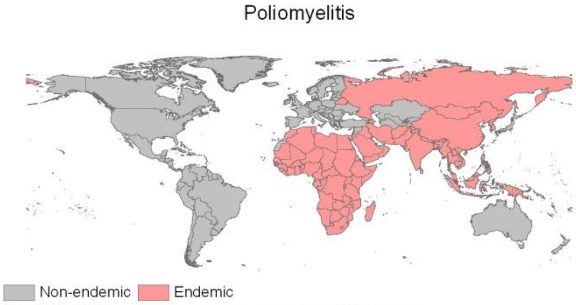
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	6.5	2	48	[599]
Disease	100	2.5	2	19	[551]
Disease	100	7.5	2	56	[600]
Disease	100	7.5	2	56	[601]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 24 occurrence points per country based on 24 results for Pogosta disease in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, but knowledge of vector and host distribution, it is possible to map the maximum potential range of this disease.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors. If occurrence data for these mosquito species are not available, digitized versions of expert opinions of their ranges could usefully inform future mapping. There is also the potential to link occurrence data with the distribution of other Sindbis virus (SINV) diseases.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Poliomyelitis.

<u>ICD-10 Code:</u> A80.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Picornavirales, Picornaviridae, Group IV, *Picornavirus*, Poliovirus types 1, 2, and 3 [472, 473].

<u>Natural history</u>:

Mode of transmission: Faecal-oral route; consumption of contaminated water or food (e.g. dairy) [472].

Reservoir*: Humans [472].

Incubation period: 10.5 days (range 7-14 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: Poliomyelitis - injectable, Poliomyelitis - oral [472].

Estimated R_0 value(s) from published literature:

Human: 0-7 [477].

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 19,742.

GenBank hits on 22/02/12: 3,189.

HealthMap feeds 2006-2011: 5,126.

ProMED feeds 1994-2011: 731.

BioCaster feeds 2006-2011: 3,326.

Approximate number of endemic countries: >87 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	27	6.5	2	10	[602]
Disease	39	5	2	11	[603]
Disease	44	5	2	12	[604]
Disease	28	6.5	2	10	[605]
Disease	40	6.5	2	15	[606]
Disease	64	4	2	14	[607]
Disease	4	7	2	2	[608]
Disease	34	5	2	9	[609]
Disease	44	4	2	10	[610]
Disease	75	4	2	17	[611]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 227 occurrence points per country based on 19,742 results for Poliomyelitis in PubMed and 87 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

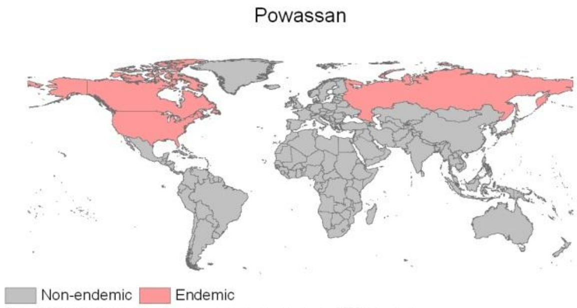
Disease: Powassan.

ICD-10 Code: A84.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Powassan virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Ixodes* spp., *Dermacentor* spp. (*I. cookei*, *I. marxi* and *D. andersoni* in the United States)) ; consumption of dairy products [472].

Reservoir*: Ticks (*Ixodes* spp., *Dermacentor andersoni*), mammals, rodents (woodchuck) and carnivores [472].

Incubation period: 19 days (range 4-30 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [612].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 143.

GenBank hits on 22/02/12: 144.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >3 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	64	8	2	28	[613]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 48 occurrence points per country based on 143 results for “Powassan” in PubMed and 3 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Protothecosis and chlorellosis.

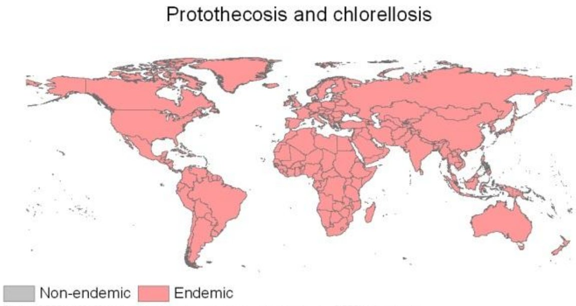
ICD-10 Code: B88.8.

Transmission category: Food/water-borne.

Agent: Alga.

Taxonomy: Plantae, Chlorophyta, Trebouxiophyceae, Chlorellales, Chlorellaceae.

Prototheca wickerhamii (rarely *Pr. zopfii* or *Pr. cutis*) [472, 473].


Protothecosis and chlorellosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated food or water; trauma [472].

Reservoir*: Rarely in domestic cats, dogs and cattle [472].

Incubation period: Unknown [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 176 for "Protothecosis" and 8 for "Chlorellosis".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 266 for “Algae”.

ProMED feeds 1994-2011: 182 for “Algae”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Protothecosis and chlorellosis are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

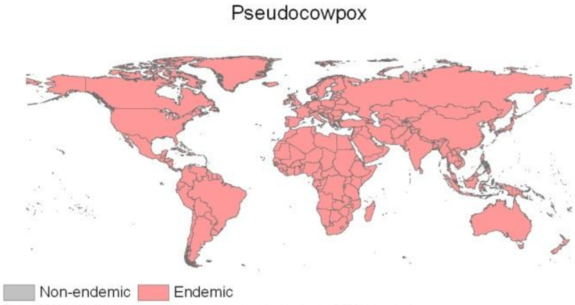
<u>Disease</u>: Pseudocowpox.

<u>ICD-10 Code:</u> B08.0.

<u>Transmission category:</u> Animal contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Poxviridae, Group I, *Parapoxvirus*, Pseudocowpox virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Contact with infected cattle [472].

Reservoir*: Cattle [472].

Incubation period: 9.5 days (range 5-14 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [614].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 58.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

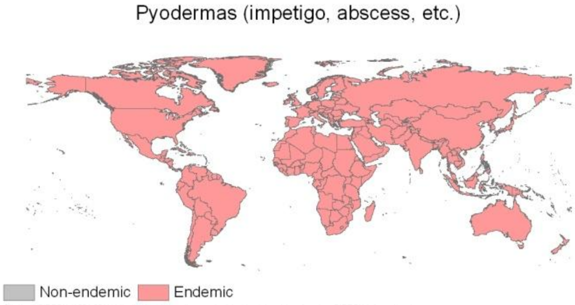
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Pseudocowpox is endemic worldwide.

<u>Future mapping potential</u>: None. However, human and cattle population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Pyodermas (impetigo, abscess, etc.).

ICD-10 Code: L08.0.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Many, such as:

Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus*
Lactobacillales, Streptococcaceae,
Streptococcus pyogenes [472, 473].

Natural history:

Mode of transmission: Endogenous; contact with infectious secretions [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 161.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Pyodermas (impetigo, abscess, etc) is endemic worldwide.

Future mapping potential: None. However, human and cattle population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

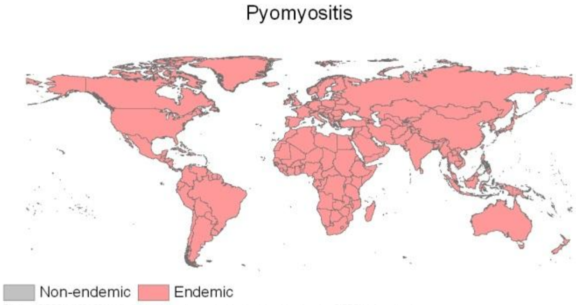
<u>Disease</u>: Pyomyositis.

<u>ICD-10 Code:</u> M60.0.

<u>Transmission category:</u> Blood/body fluid contact.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae,
Staphylococcus aureus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Blood contact or inoculation [472].

Reservoir*: Humans [472].

Incubation period: Variable [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** 0-0.7 (possibly >1) for Methicillin-resistant *Staphylococcus aureus* [615].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 798.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Pyomyositis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

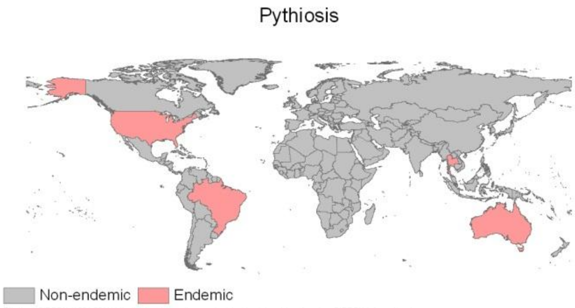
Disease: Pythiosis.

ICD-10 Code: B99.

Transmission category: Blood/body fluid contact.

Agent: Protoctista.

Taxonomy: Chromalveolata, Heterokontophyta, Oomycetes, Pythiales, Pythiaceae, *Pythium insidiosum* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Trauma; direct inoculation or blood transfusion [472].

Reservoir*: Horses, humans, cattle, dogs and cats [472].

Incubation period: Unknown [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 123.

GenBank hits on 22/02/12: 254.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >4 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	12	7.5	2	5	[616]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 31 occurrence points per country based on 123 results for “Pythiosis” in PubMed and 4 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

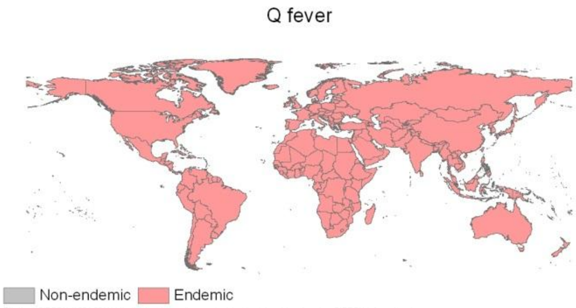
Disease: Q fever.

ICD-10 Code: A78.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Legionellales, Coxiellaceae, *Coxiella burnetii* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of infected dairy products; trauma; blood contact; close contact with an infected animal [472].

Reservoir*: Cattle, sheep, goats, birds, fish, rodents, rabbits, ticks, bandicoots, marsupials, dogs and cats [472].

Incubation period: 19.5 days (range 18-21 days) [472].

Significant epidemiological characteristics:

Vaccine: Q fever [472].

Estimated R_0 value(s) from published literature:

Human: 0 [617].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,067.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 248.

ProMED feeds 1994-2011: 148.

BioCaster feeds 2006-2011: 316.

Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	<1	6	2	N/A	[618]
Disease	5	7	2	N/A	[619]
Disease	1	7	2	N/A	[620]
Disease	<1	7	2	N/A	[621]
Disease	<1	8.5	2	N/A	[622]
Disease	<1	8.5	2	N/A	[623]

Mapping recommendation: Option 1; do not map. Q fever is endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

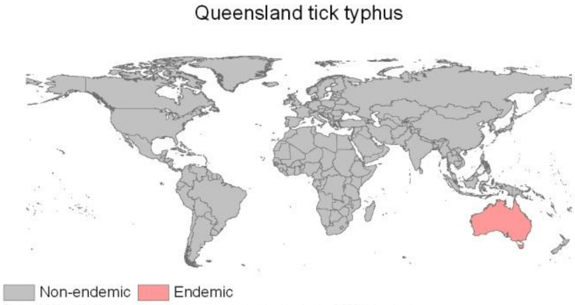
Disease: Queensland tick typhus.

ICD-10 Code: A77.3.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia australis* [472, 473].


Queensland tick typhus

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Ixodes holocyclus*) [472].

Reservoir*: Ticks and rodents [472].

Incubation period: 6.5 days (range 6-7 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [624].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 24.

GenBank hits on 22/02/12: 35.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	2.5	2	19	[557]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 24 occurrence points per country based on 24 results for “Queensland tick typhus” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease, its tick vector and its rodent reservoir. If occurrence data for these tick species or rodent reservoirs are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

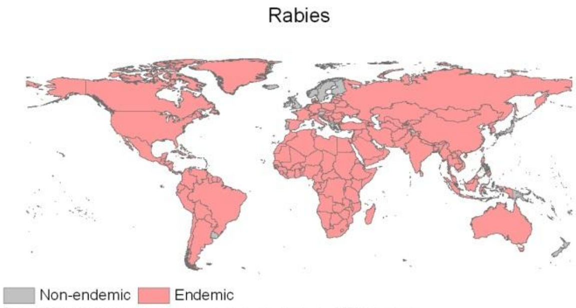
Disease: Rabies.

ICD-10 Code: A82.

Transmission category: Animal contact.

Agent: Virus-RNA.

Taxonomy: Mononegavirales, Rhabdoviridae, Group V, *Lyssavirus*, Rabies virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Animal bites and saliva (particularly bats); inhalation of bat aerosol; rarely from tissue transplant (cornea) [472, 625].

Reservoir*: Dogs, foxes, skunks, jackals, wolves, cats, raccoons, mongooses and bats; rarely rodents and rabbits [472].

Incubation period: 60 days (range 30-90 days) [472].

Significant epidemiological characteristics:

Vaccine: Rabies, rabies immunoglobulin [472].

Estimated R_0 value(s) from published literature:

Human: Human to human transmission extremely rare [625]; 0-2 in dogs to humans [626].

Reservoir: 0-3 (dogs) [627-629]; 0-5 (foxes) [630].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11,568

GenBank hits on 22/02/12: 13,403.

HealthMap feeds 2006-2011: 3,248.

ProMED feeds 1994-2011: 2,125.

BioCaster feeds 2006-2011: 2,887.

Approximate number of endemic countries: >150 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	22	[631]
Disease	100	4	2	22	[631]
Disease	100	4	2	22	[632]
Disease	5	7	2	2	[633]
Disease	1	7	2	1	[634]
Host	3	8.5	2	1	[635]
Disease	0	7.5	2	0	[636]
Disease	5	7	2	2	[637]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).
There were approximately 77 occurrence points per country based on 11,568 results for “Rabies” in PubMed and 150 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Revisit current global risk map [631] using BRT modelling techniques and updated systematic searches occurrence data. Digitized expert opinion of known absence areas (of infection and/or known reservoir species) would be useful to constrain the prediction extent for the BRT.


Rat bite fever - spirillary

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Rat bite fever - spirillary.

ICD-10 Code: A25.0.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Beta Proteobacteria, Nitrosomonadales, Spirillaceae, *Spirillum minus* [472, 473].

Natural history:

Mode of transmission: Animal bite [472].

Reservoir*: Rats, mice and cats [472].

Incubation period: 14 days (range 7-21 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [638].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 243 for "Rat bite fever" and 0 for "Spirillary rat bite fever".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Spirillary rat bite fever is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

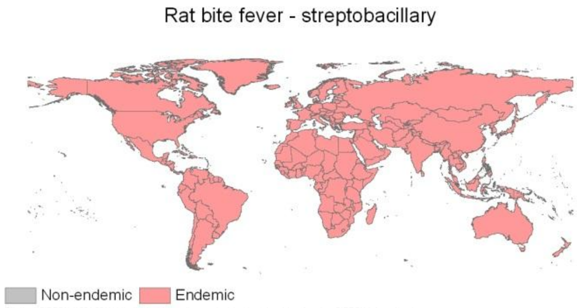
Disease: Rat bite fever - streptobacillary.

ICD-10 Code: A25.1.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Fusobacteria, Fusobacteria, Fusobacteriales, Fusobacteriaceae, *Streptobacillus moniliformis* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Animal bite; contact with infectious secretions; consumption of contaminated dairy products [472].

Reservoir*: Rats, squirrels, weasels and turkeys [472].

Incubation period: 6.5 days (range 3-10 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [638].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 243 for "Rat bite fever" and 7 for "Streptobacillary rat bite fever".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

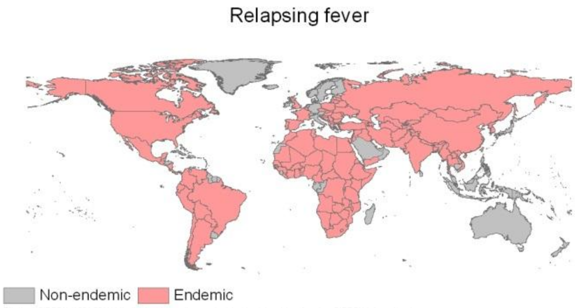
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Streptobacillary rat bite fever is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Relapsing fever.

ICD-10 Code: A68.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetales, Spirochaetaceae, *Borrelia* spp. [472, 473].

Natural history:

Mode of transmission: Tick or louse vectors (*Ornithodoros moubata, O. hispanica, O. rudis, O. talaje, O. tholozani, O. hermsii, O. turicata, Pediculus humanus*); blood transfusion [472].

Reservoir*: Humans, ticks and rodents [472].

Incubation period: 7.5 days (range 7-8 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,081.

GenBank hits on 22/02/12: 2,161.

HealthMap feeds 2006-2011: 1.

ProMED feeds 1994-2011: 0.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >118 [472].

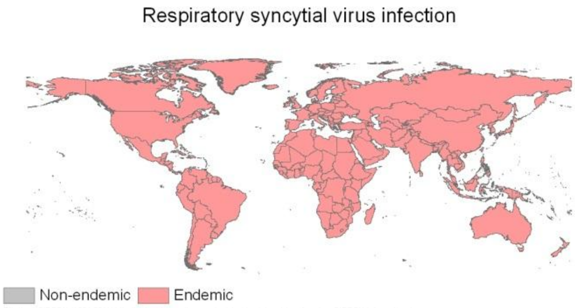
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	4.5	2	33	[639]
Vector	100	4	2	30	[640]
Disease	5	7	2	3	[641]
Disease	92	0	2	0	[642]
Disease	83	2.5	2	15	[643]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 9 occurrence points per country based on 1,081 results for “Relapsing fever” in PubMed and 118 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick and louse vectors. If occurrence data for these tick and lice species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Respiratory syncytial virus infection.

ICD-10 Code: J12.1.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Paramyxoviridae, Pneumovirinae, *Pneumovirus*,
Human respiratory syncytial virus [472, 473].

Natural history:

Mode of transmission: Contact with infectious secretions; inhalation of infectious droplets [472].

Reservoir*: Humans [472].

Incubation period: 5 days (range 2-8 days) [472].

Significant epidemiological characteristics:

Vaccine: RSV immunoglobulin [472].

Estimated R_0 value(s) from published literature:

Human: 0-2.81 [572-574].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 8,519.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 201.

ProMED feeds 1994-2011: 23.

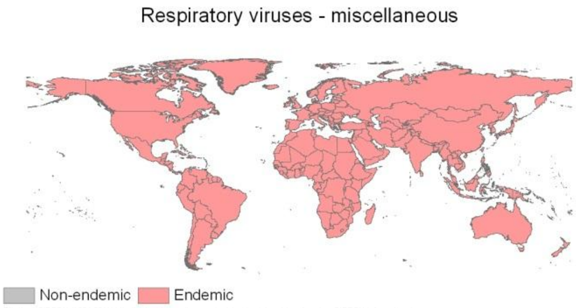
BioCaster feeds 2006-2011: 99.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Respiratory syncytial virus infection is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Respiratory viruses - miscellaneous.

ICD-10 Code: J12.3/B34.2/B34.3.

Transmission category: Respiratory/close contact.

Agent: Virus-RNA and DNA.

Taxonomy: Mononegavirales, Paramyxoviridae, Pneumovirinae, Group V,
Metapneumovirus, Human Metapneumovirus
Nidovirales, Coronaviridae, Coronaviridae, Group IV,
Coronavirus, New Haven HKU1
Parvovirinae, Group III,
Bocavirus, Human Bocavirus [472, 473].

Natural history:

Mode of transmission: Contact with infectious secretions; inhalation of infectious droplets [472].

Reservoir*: Humans [472].

Incubation period: 4 days (range 3-5 days) for human etapneumovirus, 2.75 days (range 0.5-5 days) for New Haven HKU1 and unknown for human bocavirus [472].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: N/A.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Miscellaneous respiratory viruses are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.


Reye's syndrome

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Reye's syndrome.

<u>ICD-10 Code:</u> G93.7.

<u>Transmission category:</u> Unknown.

<u>Agent</u>: Unknown.

<u>Taxonomy:</u> Unknown.

<u>Natural history</u>:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 1,250.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Reye's syndrome is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

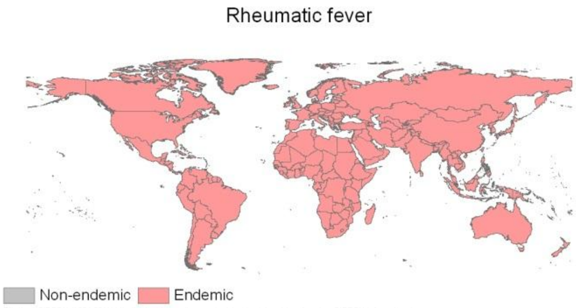
Disease: Rheumatic fever.

ICD-10 Code: I00 - I02.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pyogenes* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious droplets [472].

Reservoir*: Humans [472].

Incubation period: 21 days (range 7-35 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11,202.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 27.

ProMED feeds 1994-2011: 3.

BioCaster feeds 2006-2011: N/A.

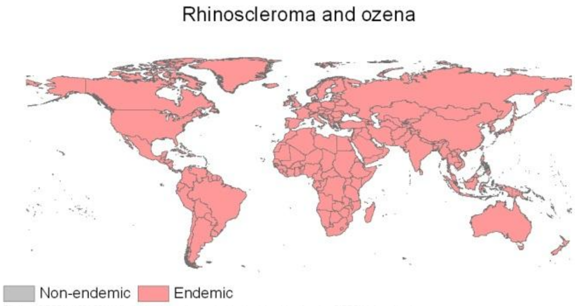
Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5	2	N/A	[644]

Mapping recommendation: Option 1; do not map. Rheumatic fever is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Rhinoscleroma and ozena

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Rhinoscleroma and ozena.

ICD-10 Code: A48.8.

Transmission category: Blood/body fluid contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Klebsiella pneumoniae* subspp *ozaenae* or *K. pneumoniae* subspp *rhinoscleromatis* [472, 473].

Natural history:

Mode of transmission: Contact with infectious secretions [472].

Reservoir*: Humans [472].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 745 for "Rhinoscleroma" and 405 for "Ozena".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

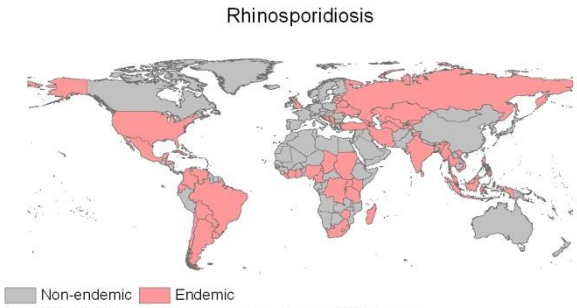
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Rhinoscleroma and ozena are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Rhinosporidiosis.

ICD-10 Code: B48.1.

Transmission category: Respiratory.

Agent: Protoctista.

Taxonomy: Protista, Choanozoa, Ichthyosporea, Dermocystida,
Rhinosporidium seeberi
(may in fact be *Microcystis*, a cyanobacterium) [472, 473].

Natural history:

Mode of transmission: Soil or water contact; inhalation of infectious aerosol [472].

Reservoir*: None.

Incubation period: 97 days (range 14-180 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 463.

GenBank hits on 22/02/12: 17.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >65 [472].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 7 occurrence points per country based on 463 results for “Rhinosporidiosis” in PubMed and 65 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: *Rhodococcus equi* infection.

ICD-10 Code: A43.8.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Nocardiaceae, *Rhodococcus equi* [472, 473].

Rhodococcus equi infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated food; close contact [472].

Reservoir*: Farm animals [472].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 917.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. *Rhodococcus equi* infection is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

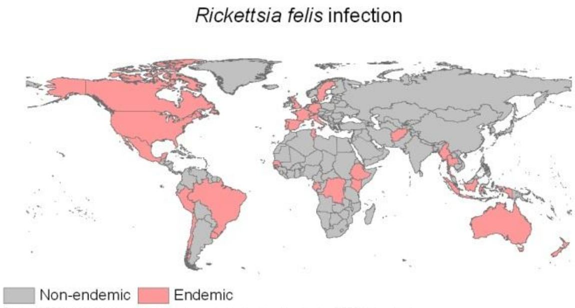
Disease: *Rickettsia felis* infection.

ICD-10 Code: A79.8.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia felis* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Flea vector (*Ctenocephalides felis*; also found in *Pulex irritans*) [472].

Reservoir*: Opossums (*Didelphis marsupialis),* raccoons, fleas and possibly dogs and flying squirrels [472].

Incubation period: 12 days (range 7-14 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [645].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 161.

GenBank hits on 22/02/12: 124.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >31 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	88	5	2	33	[592]
Disease	100	5	2	37	[646]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 5 occurrence points per country based on 161 results for "*Rickettsia felis"* in PubMed and 31 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its flea vectors. If occurrence data for these flea species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

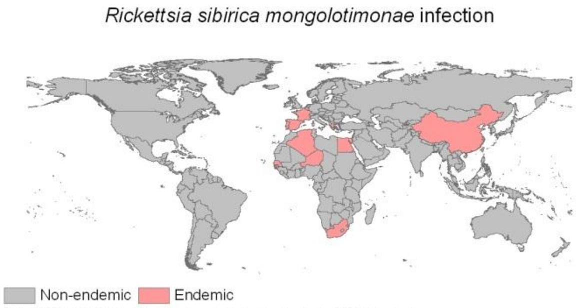
Disease: *Rickettsia sibirica mongolotimonae* infection.

ICD-10 Code: A77.2.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia sibirica mongolotimonae* [472, 473].


Rickettsia sibirica mongolotimonae infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Dermacentor* spp., *Haemaphysalis* spp., *Hyalomma* spp.) [472].

Reservoir*: Rodents and dogs [472].

Incubation period: 4.5 days (range 3-6 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [645].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4.

GenBank hits on 22/02/12: 67.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >11 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	4.5	2	50	[557]

Mapping recommendation: Option 2; map observed occurrence.

There was less than 1 occurrence point per country based on 4 results for "*Rickettsia sibirica mongolotimonae* infection" in PubMed and 11 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

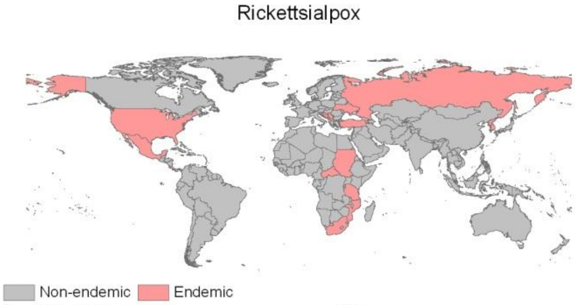
<u>Disease</u>: Rickettsialpox.

<u>ICD-10 Code:</u> A79.1.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae
Rickettsia akari [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mite vector (*Allodermanyssus* (*Liponyssoides*) *sanguineus*) [472].

Reservoir*: Mice (*Mus musculus*), dogs and mites [472].

Incubation period: 11.5 days (range 9-14 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [647].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 96.
- **GenBank hits on 22/02/12:** 156.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

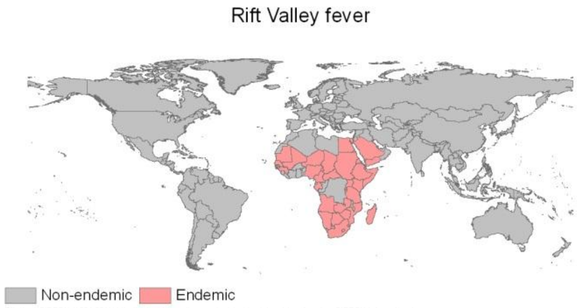
Approximate number of endemic countries: >19 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 5 occurrence points per country based on 96 results for “Rickettsialpox” in PubMed and 19 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

<u>Future mapping potential</u>: Generate known distribution map using systematic searches of occurrence data for the disease and its mite vector. If occurrence data for this mite species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Rift Valley fever.

ICD-10 Code: A92.4.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Bunyaviridae, Group V, *Phlebovirus*, Rift Valley fever virus [472, 473].

Natural history:

Mode of transmission: Mosquito vector (*Culex* spp., *Aedes* spp., *Anopheles* spp., *Erethmapodites* spp., *Mansonia* spp., *Culicoides* spp., *Coquillettidia* spp.) [472].

Reservoir*: Sheep and other ruminants [472].

Incubation period: 4 days (range 3-5 days) [472].

Significant epidemiological characteristics:

Vaccine: Rift Valley fever [472].

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [648].

Reservoir: 0-2.8 (sheep) [649].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,049.

GenBank hits on 22/02/12: 748.

HealthMap feeds 2006-2011: 591.

ProMED feeds 1994-2011: 359.

BioCaster feeds 2006-2011: 358.

Approximate number of endemic countries: >34 [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	1	2	6	[650]
Disease	33	3	4	11	[651]
Disease	100	5	2	28	[652]
Disease	13	5	2	4	[653]
Disease	0	8	2	0	[654]
Disease	3	6.5	2	1	[655]
Disease	2	7	5	2	[656]
Host	2	7	3	1	[657]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 31 occurrence points per country based on 1,049 results for “Rift Valley fever” in PubMed and 34 endemic countries listed in the GIDEON database. With more than 25 hits per country and additional occurrence data obtained from systematic searches (see note below), it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Note there are 1319 point records of occurrence and 516 polygon data to inform the mapping; last updated in February 2010. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

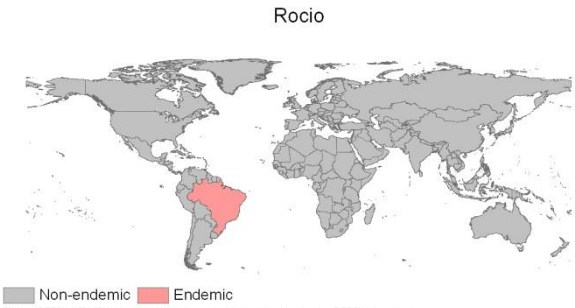
<u>Disease</u>: Rocio.

<u>ICD-10 Code:</u> A83.6.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Flaviviridae, Group IV, *Flavivirus*, Rocio virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Psorophora ferox*, *Aedes scapularis*) [472].

Reservoir*: Possibly wild birds [472].

Incubation period: 12 days (range 7-15 days) [472].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [658].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 89.
- **GenBank hits on 22/02/12:** 11.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >1 [472].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 89 occurrence points per country based on 89 results for “Rocio” in PubMed and 1 endemic country listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

<u>Future mapping potential</u>: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

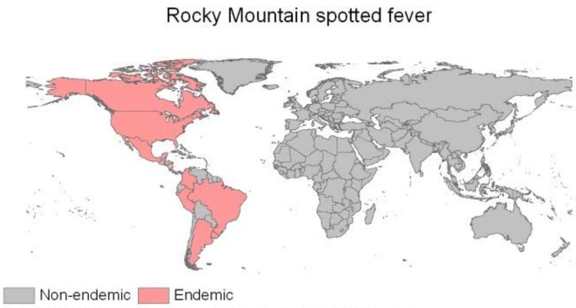
Disease: Rocky Mountain spotted fever.

ICD-10 Code: A77.0.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia rickettsii* [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Dermacentor* spp., *Amblyomma* spp.) [472].

Reservoir*: Ticks, dogs and rodents [472].

Incubation period: 6 days (range 5-7 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [659].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,362.

GenBank hits on 22/02/12: 612.

HealthMap feeds 2006-2011: 34.

ProMED feeds 1994-2011: 48.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >11 [472].

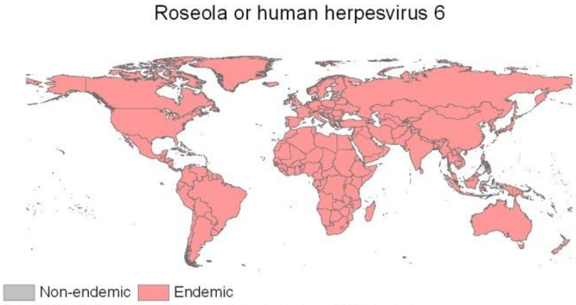
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	39	5.5	2	12	[660]
Disease	100	4.5	2	100	[661]
Disease	39	6.5	2	14	[662]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 124 occurrence points per country based on 1,362 results for “Rocky Mountain spotted fever” in PubMed and 11 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Roseola or human herpesvirus 6.

ICD-10 Code: B09.

Transmission category: Blood/body-fluid contact.

Agent: Virus-DNA.

Taxonomy: Herpesviridae, Betaherpesvirinae, Group I, *Roseolovirus*, Herpesvirus 6 [472, 473].

Natural history:

Mode of transmission: Blood contact or inoculation; inhalation of infectious secretions [472].

Reservoir*: Humans [472].

Incubation period: 12.5 days (range 10-15 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 197 for "Roseola" and 2,562 for "human herpesvirus 6".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 3 for “Roseola”.

ProMED feeds 1994-2011: 0 for “Roseola”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Roseola or human herpesvirus 6 are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

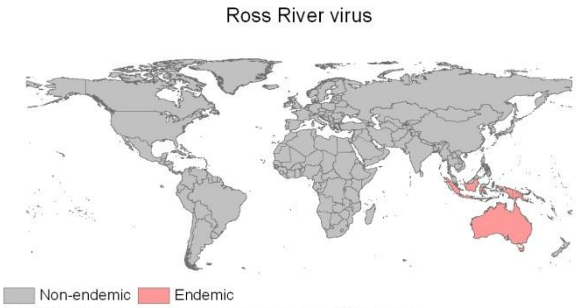
Disease: Ross River virus.

ICD-10 Code: B33.1.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, n.a., Group IV, *Alphavirus*, Ross River virus [472, 473].


Ross River virus

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Aedes vigilax, Ae. polynesiensis, Culex annulirostris*) [472].

Reservoir*: Mosquitoes, birds, horses and possibly rodents and marsupials [472].

Incubation period: 9 days (range 8-10 days) [472].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-100 (0.01-63.5) [663].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 407.

GenBank hits on 22/02/12: 400.

HealthMap feeds 2006-2011: 55.

ProMED feeds 1994-2011: 86.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >13 [472].

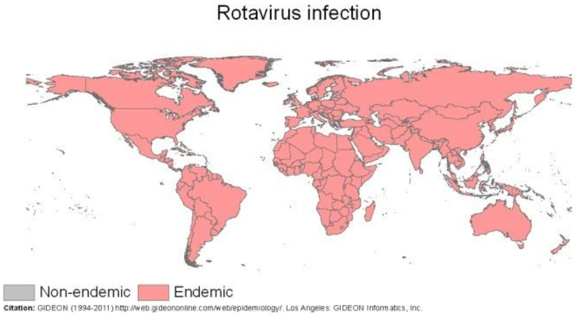
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	3	2	17	[664]
Disease	8	7	2	3	[665]
Disease	8	7	2	3	[666]
Disease	8	6.5	2	3	[667]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 31 occurrence points per country based on 407 results for “Ross River virus” in PubMed and 13 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Rotavirus infection.

ICD-10 Code: A08.0.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Reoviridae, Sedoreovirinae, Group III, Rotavirus,

Group A is most common, Group B is found in adult epidemics and Group C is uncommon in humans [472, 473].

Natural history:

Mode of transmission: Faecal-oral route [472].

Reservoir*: Humans [472].

Incubation period: 1.75 days (range 0.5-3 days) [472].

Significant epidemiological characteristics:

Vaccine: Typhoid – oral [472].

Estimated R_0 value(s) from published literature:

- **Human:** 0-1.84 (0-23 from model prediction based on outbreak data) [668, 669].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 10,118.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 642.
- **ProMED feeds 1994-2011:** 150.
- **BioCaster feeds 2006-2011:** 389.

Approximate number of endemic countries: Worldwide [472].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	1	2	N/A	[670]

Mapping recommendation: Option 1; do not map. Rotavirus is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

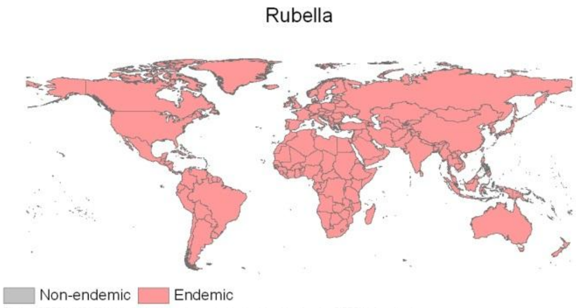
Disease: Rubella.

ICD-10 Code: B06.

Transmission category: Respiratory.

Agent: Virus-RNA.

Taxonomy: Togaviridae, n.a., Group IV, *Rubivirus*, Rubella virus [472, 473].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Close contact; vertical transmission [472].

Reservoir*: Humans [472].

Incubation period: 17 days (range 16-18 days) [472].

Significant epidemiological characteristics:

Vaccine: Rubella, Rubella-Mumps, Measles-Mumps-Rubella, Measles-Rubella [472].

Estimated R_0 value(s) from published literature:

Human: 0-16 [477].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 12,712.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 597.

ProMED feeds 1994-2011: 74.

BioCaster feeds 2006-2011: 162.

Approximate number of endemic countries: Worldwide [472].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Rubella is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

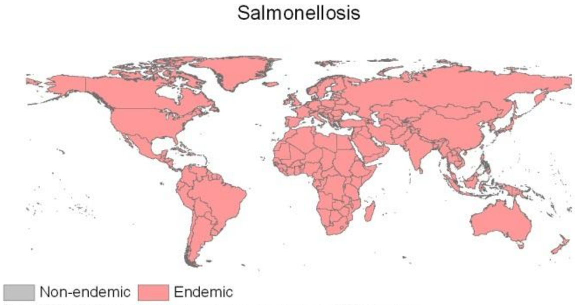
Disease: Salmonellosis.

ICD-10 Code: A02.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Salmonella* spp. [671, 672].


Salmonellosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated food (e.g. milk, eggs, poultry, shellfish, meat, vegetables and fruit) [671].

Reservoir*: Mammals, birds and reptiles [671].

Incubation period: 1 day (range 0.5-1.5 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 70,023 for "Salmonella" and 2,931 for “Salmonella and diarrhoea".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 4,289.

ProMED feeds 1994-2011: 1,255.

BioCaster feeds 2006-2011: 2,128.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	5	7.5	2	N/A	[673]

Mapping recommendation: Option 1; do not map. Salmonellosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

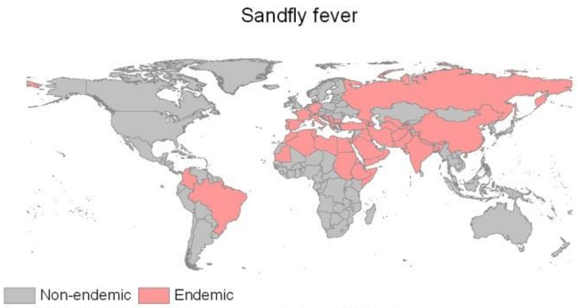
Disease: Sandfly fever.

ICD-10 Code: A93.1.

Transmission category: Vector-borne.

Agent: Virus.

Taxonomy: Bunyaviridae, Group VI, *Phlebovirus*, Sandfly fever virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sandfly vector (*Phlebotomus papatasi*) [671].

Reservoir*: Humans and sand flies [671].

Incubation period: 4.5 days (range 3-6 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 231.

GenBank hits on 22/02/12: 33.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >40

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	6	6	2	3	[674]
Disease	9	5	2	3	[675]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 6 occurrence points per country based on 231 results for “Sandfly fever” in PubMed and 40 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its sandfly vectors. If occurrence data for these sandfly species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

Disease: Sarcocystosis.

ICD-10 Code: A07.8.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Protista, Protozoa, Apicomplexa, Conoidasida, Eucoccidiorida, Sarcocystidae, *Sarcocystis bovihominis, S. suihominis* [671, 672].

Sarcocystosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated water or meat [671].

Reservoir*: Cattle and pigs [671].

Incubation period: 24 days (range 9-39 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [676].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,211 for "Sarcocytosis," 4 for "*Sarcocystis bovihominis*," and 23 for "*Sarcocystis suihominis*" .

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

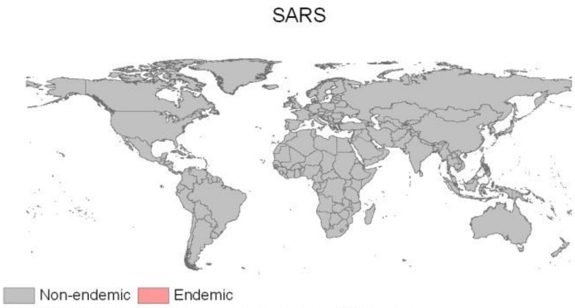
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Sarcocytosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: SARS.

ICD-10 Code: U04.

Transmission category: Food/water-borne.

Agent: Virus-RNA.

Taxonomy: Nidovirales, Coronaviridae, Coronavirinae, Group IV,
Coronavirus, Severe acute respiratory syndrome (SARS) virus [671, 672].

Natural history:

Mode of transmission: Faecal-oral route; possibly through inhalation of infectious droplets [671].

Reservoir*: Humans, bats, civets and cats [671].

Incubation period: 4 days (range 3-5 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-5.6 [677-689]

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 6,077.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 244.

ProMED feeds 1994-2011: 978.

BioCaster feeds 2006-2011: 554.

Approximate number of endemic countries: <1 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	N/A	7.5	2	N/A	[690]

Mapping recommendation: Option 1; do not map. SARS is not endemic in any country.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

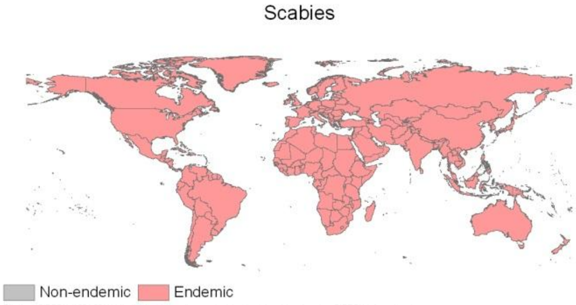
<u>Disease</u>: Scabies.

<u>ICD-10 Code:</u> B86.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Arthropoda, Arachnida, Sarcoptiformes, Sarcoptidae,
Sarcoptes [*Acarus*] *scabiei* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct contact [671].

Reservoir*: Humans [671].

Incubation period: 22.5 days (range 3-42 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 3,344.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 227.

ProMED feeds 1994-2011: 23.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Scabies is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

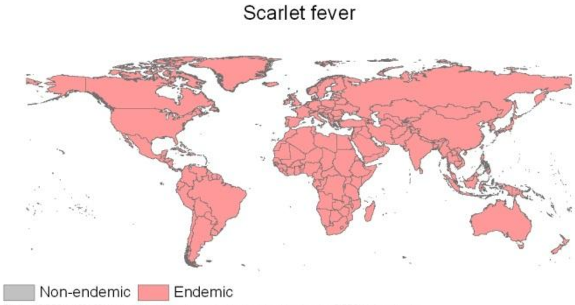
<u>Disease</u>: Scarlet fever.

<u>ICD-10 Code:</u> A38.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pyogenes* [671, 672].


Scarlet fever

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Contact with infectious secretions; (occasionally) consumption of contaminated food [671].

Reservoir*: Humans [671].

Incubation period: 2.5 days (range 1-4 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None

Estimated R_0 value(s) from published literature:

- **Human:** 0-8 [691].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 2,497.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 276.
- **ProMED feeds 1994-2011:** 37.
- **BioCaster feeds 2006-2011:** 293.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Scarlet fever is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

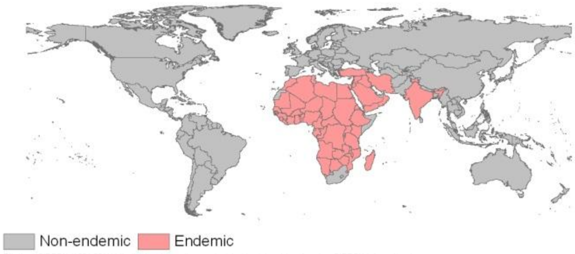
Disease: Schistosomiasis - *S. haematobium.*

ICD-10 Code: B65.0.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma haematobium* [671, 672].


Schistosomiasis - *S. haematobium*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Bulinus* spp., *Planorbarius* spp., *Ferrissia* spp.); rarely baboons or monkeys [671].

Incubation period: 28 days (range 14-42 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-6.5 [691-693].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,551 for "*Schistosoma haematobium*".

GenBank hits on 22/02/12: 213.

HealthMap feeds 2006-2011: 132 for “Schistosomiasis”.

ProMED feeds 1994-2011: 42 for “Schistosomiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >58 [671].

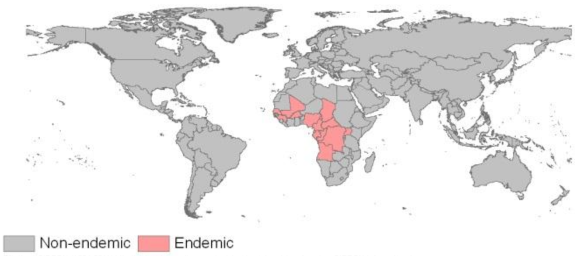
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	51	4	2	9	[694]
Disease	46	5	2	10	[695]
Disease	51	5.5	2	12	[696]
Disease	35	7.5	2	12	[697]
Disease	33	6.5	2	9	[698]
Disease	2	7	4	1	[699]
Disease	5	8	5	4	[700]
Disease	1	8	5	1	[701]
Disease	2	7.5	5	2	[702]
Disease	7	8	3	3	[703]
Host	1	9	4	1	[704]

Mapping recommendation: Option 5; map limits using prevalence data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys.
The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Revisit current global maps as survey data becomes available from http://www.thiswormyworld.org.

Schistosomiasis - *S. intercalatum*



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Schistosomiasis - *S. intercalatum.*

ICD-10 Code: B65.8.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma intercalatum* [671, 672].

Natural history:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Bulinus forskalii* and *Bulinus africanus* group) [671].

Incubation period: 28 days (range 14-42 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 130 for "*Schistosoma intercalatum*".

GenBank hits on 22/02/12: 22.

HealthMap feeds 2006-2011: 132 for “Schistosomiasis”.

ProMED feeds 1994-2011: 42 for “Schistosomiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >15 [671].

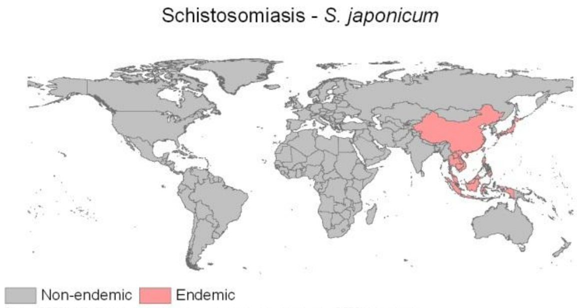
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	97	3.5	2	25	[705]
Disease	5	5.5	2	2	[705]
Disease	100	5.5	2	41	[696]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 9 occurrence points per country based on 130 results for “*Schistosoma intercalatum*” in PubMed and 15 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of reservoir distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its snail reservoirs. If occurrence data for these snail reservoirs is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Schistosomiasis - *S. japonicum.*

ICD-10 Code: B65.2.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma japonicum* [671, 672].

Natural history:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Oncomelania* spp.), water buffalos, dogs, cats, rats, pigs, horses and goats [671].

Incubation period: 28 days (range 14-42 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-12 [691, 693, 706].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,718 for "*Schistosoma japonicum*".

GenBank hits on 22/02/12: 53,595.

HealthMap feeds 2006-2011: 132 for “Schistosomiasis”.

ProMED feeds 1994-2011: 42 for “Schistosomiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >9 [671].

Previously published maps:

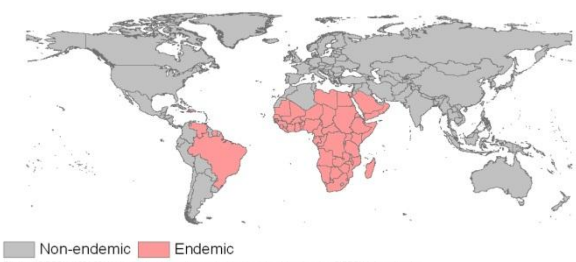
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	18	[694]
Disease	100	5.5	2	24	[696]
Disease	73	5	2	16	[695]
Host	6	7	3	3	[707]
Disease	67	4	2	12	[708]
Disease	67	8.5	5	63	[709]
Disease	67	8.5	5	63	[710]
Host	67	4	3	18	[711]
Disease	67	8.5	3	38	[712]
Disease	83	6	2	22	[713]

Mapping recommendation: Option 5; map limits using prevalence data and biological masks, and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys.

The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Revisit current global maps as survey data becomes available from http://www.thiswormyworld.org.

Schistosomiasis - *S. mansoni*



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Schistosomiasis - *S. mansoni.*

<u>ICD-10 Code:</u> B65.1.

<u>Transmission category:</u> Water contact.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma mansoni* [671, 672].

<u>Natural history</u>:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Biomphalaria* spp.), dogs, cats, pigs, cattle, rodents, horses and non-human primates [671].

Incubation period: 28 days (range 14-42 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: 0-2 [714].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 11,010 for "*Schistosoma mansoni*".

GenBank hits on 22/02/12: 48,160.

HealthMap feeds 2006-2011: 132 for “Schistosomiasis”.

ProMED feeds 1994-2011: 42 for “Schistosomiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >59 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4	2	18	[694]
Disease	100	5.5	2	24	[696]
Disease	100	5	2	22	[695]
Disease	69	7.5	2	23	[697]
Disease	16	8	3	8	[715]
Disease	16	5.5	2	4	[716]
Disease	16	6.5	2	5	[717]
Disease	65	6.5	2	19	[698]
Disease	10	8	5	9	[700]
Disease	10	8	2	3	[700]

Disease	3	8	3	1	[718]
Disease	1	7.5	5	1	[701]
Disease	11	8	5	10	[719]
Disease	16	5.5	3	6	[720]
Disease	3	8	2	1	[721]
Host	7	7.5	3	3	[722]
Disease	7	7	3	3	[723]
Disease	16	7.5	4	11	[724]
Disease	2	8	5	1	[725]
Disease	2	8	5	1	[726]
Disease	2	8	5	1	[727]
Host	3	9	4	2	[704]

Mapping recommendation: Option 5; map limits using prevalence data and biological masks and endemicity within this range using model-based geostatistics (MBG) on prevalence surveys.

The availability of a high volume of systematically collected prevalence data allows for the implementation of MBG to map the limits of infection.

Future mapping potential: Revisit current global maps as survey data becomes available from http://www.thiswormyworld.org.

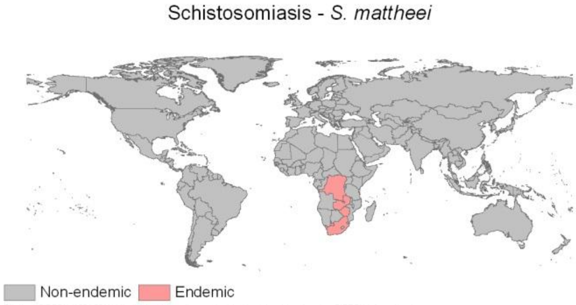
Disease: Schistosomiasis - *S. mattheei.*

ICD-10 Code: B65.8.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma mattheei* [671, 672].



Schistosomiasis - *S. mattheei*

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Bulinus globosus*), sheep, goats, cattle, horses and wild mammals [671].

Incubation period: 28 days (range 14-42 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 92 for "*Schistosoma mattheei*".
- **GenBank hits on 22/02/12:** 23.
- **HealthMap feeds 2006-2011:** 132 for “Schistosomiasis”.
- **ProMED feeds 1994-2011:** 42 for “Schistosomiasis”.
- **BioCaster feeds 2006-2011:** N/A.

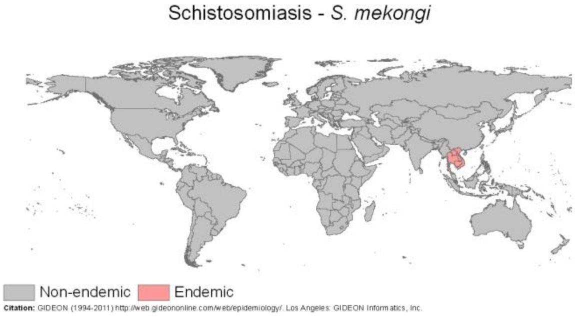
Approximate number of endemic countries: >4 [671].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 23 occurrence points per country based on 92 results for “*Schistosoma mattheei*” in PubMed and 4 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of reservoir distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its snail reservoir. If occurrence data for this snail reservoir is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Schistosomiasis - *S. mekongi.*

ICD-10 Code: B65.8.

Transmission category: Water contact.

Agent: Parasite.

Taxonomy: Animalia, Eumetazoa, Platyhelminthes, Trematoda, Strigeida, Schistosomatidae, *Schistosoma mekongi* [671, 672].

Natural history:

Mode of transmission: Water contact [671].

Reservoir*: Snails (*Neotricula* (*Tricula*) *aperta*); dogs [671].

Incubation period: 28 days (range 14-42 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 75 for "*Schistosoma mekongi*".

GenBank hits on 22/02/12: 25.

HealthMap feeds 2006-2011: 132 for “Schistosomiasis”.

ProMED feeds 1994-2011: 42 for “Schistosomiasis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >4 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	51	2.5	2	9	[728]
Disease	12	5.5	2	5	[729]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 19 occurrence points per country based on 75 results for “*Schistosoma mekongi*” in PubMed and 4 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of reservoir distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its snail reservoir. If occurrence data for this snail reservoir is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

Sennetsu neorickettsiosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Sennetsu neorickettsiosis.

<u>ICD-10 Code:</u> A79.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Anaplasmataceae, *Neorickettsia* (*Ehrlichia*) *sennetsu* [671, 672].

<u>Natural history</u>:

Mode of transmission: Consumption of infected raw fish [671].

Reservoir*: Fish [730].

Incubation period: 11 days (range 8-14 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [730].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 3.

GenBank hits on 22/02/12: 26.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >4 [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There was approximately 1 occurrence point per country based on 3 results for "*Sennetsu neorickettsiosis*" in PubMed and 4 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

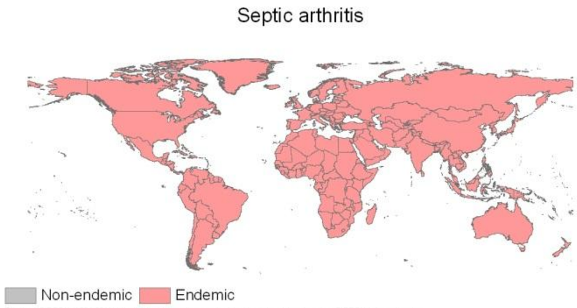
Disease: Septic arthritis.

ICD-10 Code: A41.8.

Transmission category: Endogenous.

Agent: Bacterium or Fungus.

Taxonomy: Gram positive cocci; gram negative bacilli; gonococci; mycobacteria; fungi etc. [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Endogenous [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,626.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Septic arthritis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.


Septicemia - bacterial

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Septicemia - bacterial.

ICD-10 Code: A40/41.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various facultative gram negative bacilli, e.g.:

Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae,

Escherichia coli

Firmicutes, Bacilli, Bacillales, Staphylococcaceae,

Staphylococcus aureus [671, 672].

Natural history:

Mode of transmission: Endogenous [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11,557.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 226 for “Sepsis.”

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Bacterial septicemia is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

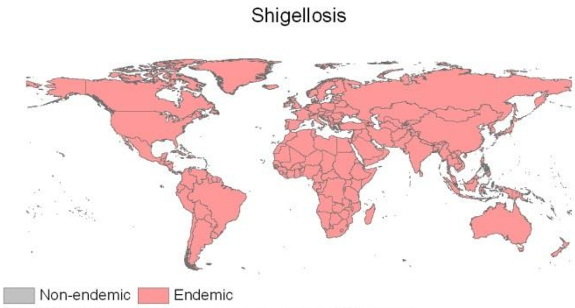
Disease: Shigellosis.

ICD-10 Code: A03.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, many e.g. *Shigella sonnei,S. flexneri, S. boydii, S. dysenteriae* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; fomites; flies; consumption of contaminated water or food (dairy and vegetables) [671].

Reservoir*: Humans and non-human primates [671].

Incubation period: 2.5 days (range 2-3 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 13,585 for "*Shigella*" and 1,780 for "*Shigella* and diarrhoea".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 422.

ProMED feeds 1994-2011: 422.

BioCaster feeds 2006-2011: 87.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	8.5	3	N/A	[731]
Disease	2	8	4	N/A	[732]

Mapping recommendation: Option 1; do not map. Shigellosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

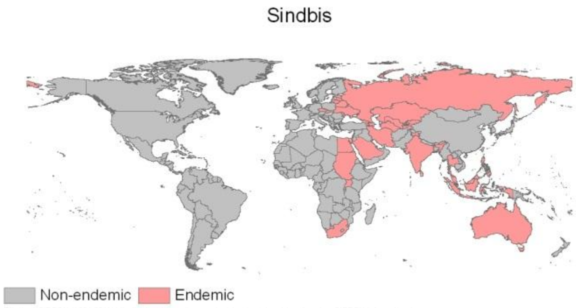
<u>Disease</u>: Sindbis.

<u>ICD-10 Code:</u> A92.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Togaviridae, Group IV, *Alphavirus*, Sindbis virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Culex univittatus*, *Cx. tritaeniorhyncus*) [671].

Reservoir*: Wild birds [671].

Incubation period: 4.5 days (range 3-6 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 2,630.

GenBank hits on 22/02/12: 313.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >33 [671].

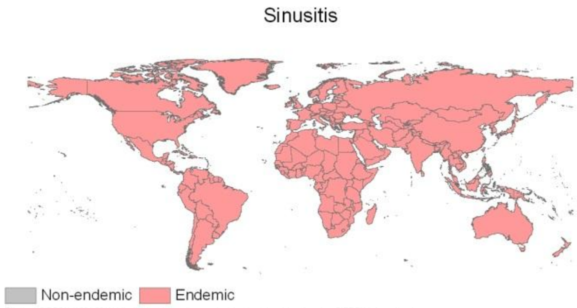
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	6.5	2	1	[733]
Disease	7	2.5	2	1	[734]
Disease	1	7.5	2	1	[735]
Disease	22	6	2	7	[736]
Disease	1	7.5	2	1	[737]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 80 occurrence points per country based on 2,630 results for “Sindbis” in PubMed and 33 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Sinusitis.

ICD-10 Code: J01/J32.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae, *Haemophilus influenzae*
Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus pneumoniae* [671, 672].

Natural history:

Mode of transmission: Contact [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: *Haemophilus influenzae* (HbOC-DTP or -DTaP, HbOC, PRP-D, PRP-OMP, PRP-T); Pneumococcal.

Estimated R_0 value(s) from published literature:

Human: 0-3.3 (*H. influenzae*) [738]; 0-2.2 (*S. pneumonia*) [739, 740].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 18,337.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Sinusitis is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

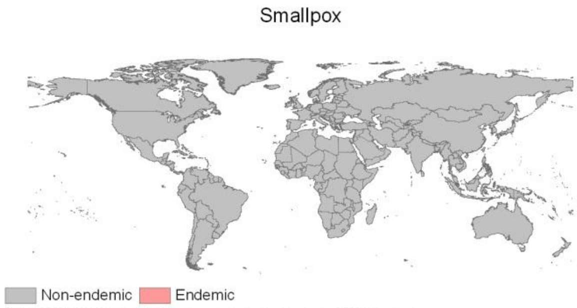
<u>Disease</u>: Smallpox.

<u>ICD-10 Code:</u> B03.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Virus-DNA.

<u>Taxonomy:</u> Poxviridae, Chordopoxvirinae, Group I, *Orthopoxvirus*, Variola virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Fomites; direct contact and contact with infectious secretions [671].

Reservoir*: Humans [671].

Incubation period: 12 days (range 7-17 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: Smallpox

Estimated R_0 value(s) from published literature:

- **Human:** 0-10 [691, 741-743].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

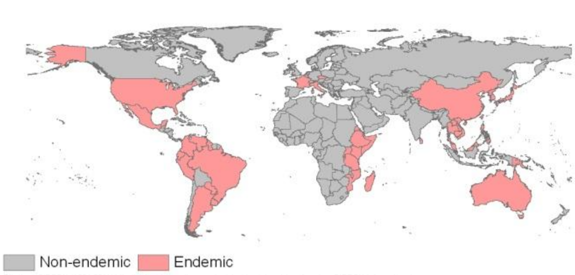
- **PubMed hits on 04/11/11:** 8,653.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 301 for "Smallpox-Related".
- **ProMED feeds 1994-2011:** 163 for "Smallpox-Related".
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: <1 [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Smallpox is not endemic in any country and is vaccine preventable.

<u>Future mapping potential</u>: None.


Sparganosis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Sparganosis.

ICD-10 Code: B70.1.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Pseudophyllidea, Diphyllobothriidae, *Spirometra* spp. [671, 672].

Natural history:

Mode of transmission: Consumption of contaminated water or undercooked infected reptile or amphibian meat [671].

Reservoir*: Birds (from copepods), amphibians and reptiles [671].

Incubation period: 557.5 days (range 20-1,095 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [744].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 391.

GenBank hits on 22/02/12: 157.

HealthMap feeds 2006-2011:N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >48 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 8 occurrence points per country based on 391 results for “Sparganosis” in PubMed and 48 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Spondweni.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Spondweni virus [671, 672].

Natural history:

Mode of transmission: Mosquito vector (*Aedes circumluteolus, Armigeres* spp., *Culex* spp., *Eretmapodites* spp., *Mansonia* spp.) [671].

Reservoir*: Unknown.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** Not found.
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 8.
- **GenBank hits on 22/02/12:** 5.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >10 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was approximately 1 occurrence point per country based on 8 results for “Spondweni” in PubMed and 10 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

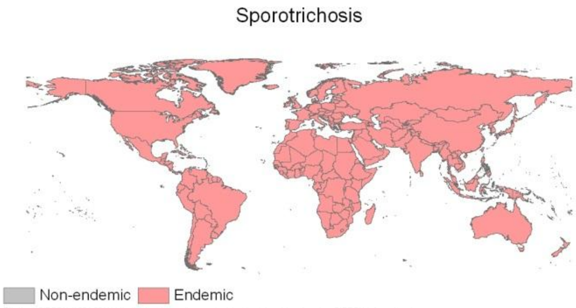
<u>Disease</u>: Sporotrichosis.

<u>ICD-10 Code:</u> B42.

<u>Transmission category:</u> Soil contact.

<u>Agent</u>: Fungus.

<u>Taxonomy:</u> Fungi, Ascomycota, Sordariomycetes, Ophiostomatales, Ophiostomataceae,
Sporothrix schenckii, S. brasiliensis, *S. globosa* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Direct contact; trauma; rarely through inhalation of spores [671].

Reservoir*: None.

Incubation period: 48.5 days (range 7-90 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

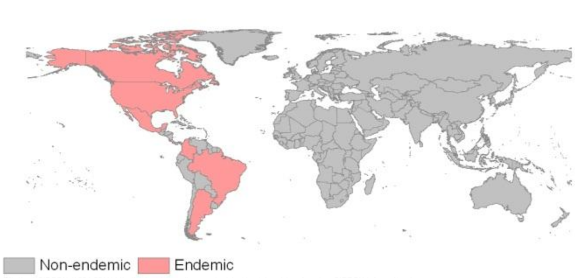
- **PubMed hits on 04/11/11:** 1581 for "*Sporotrichosis*," 621 for "*Sporothrix schenckii*," 5 for "*Sporothrix brasiliensis*," and 4 for "*Sporothrix globosa*".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0 for "Sporotrichosis".
- **ProMED feeds 1994-2011:** 0 for "Sporotrichosis".
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Sporotrichosis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.


Spotted fever group (tick-borne) - Rickettsioses, New World

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Spotted fever group (tick-borne) - Rickettsioses, New World.
ICD-10 Code: A77.
Transmission category: Vector-borne.
Agent: Bacterium.
Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia rickettsii* and others [671, 672].

Natural history:
Mode of transmission: Tick vector (*Dermacentor variablis*, *D. andersoni*, *Amblyomma cajennense*, et al.) [671].
Reservoir*: Dogs, rodents and ticks [671].
Incubation period: 6.5 days (range 6-7 days) [671].

Significant epidemiological characteristics:
Vaccine: None.
Estimated R_0 value(s) from published literature:
Human: <1; primarily a zoonotic disease [745, 746].
Reservoir: 0-8.2 (Multispecies), (Azad and Beard 1998; Matser et al, 2009)

Map(s) from published literature:
Total available literature:
PubMed hits on 04/11/11: 2,531 for "Spotted fever" and 582 for "Rickettsiosis".
GenBank hits on 22/02/12: 612.
HealthMap feeds 2006-2011: N/A.
ProMED feeds 1994-2011: N/A.
BioCaster feeds 2006-2011: N/A.
Approximate number of endemic countries: >7 [671].
Previously published maps:

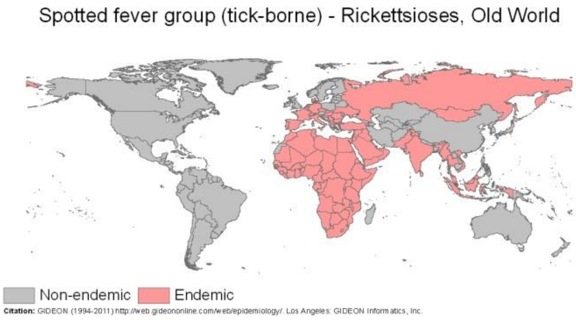
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	96	1.5	2	8	[747]
Vector	100	2.5	2	14	[747]
Disease	93	4	2	21	[748]
Vector	100	4.5	2	25	[749]
Disease	100	5.5	2	31	[750]
Disease	100	7	2	39	[751]
Vector	42	1	2	2	[752]
Disease	42	7	2	16	[753]
Disease	42	8.5	2	20	[754]

Disease	42	5.5	2	13	[755]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 359 occurrence points per country based on 2,531 results for “Spotted Fever” in PubMed and 7 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Spotted fever group (tick-borne) - Rickettsioses, Old World

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Spotted fever group (tick-borne) - Rickettsioses, Old World.

ICD-10 Code: A77.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia africae, R. sibirica mongolitimonae, R. conorii, R. aeschlimannii, R. helvetica, R. massiliae, R. monacensis, R. slovaka,* and others [671, 672].

Natural history:

Mode of transmission: Tick vector (*Rhipicephalus* spp., *Amblyomma* spp., *Ixodes* spp., *Haemaphysalis* spp.) [671].

Reservoir*: Dogs, rodents and ticks [671].

Incubation period: 6.5 days (range 6-7 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [745].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,531 for "Spotted fever" and 582 for "Rickettsiosis".

GenBank hits on 22/02/12: 881.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >40 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	1.5	2	8	[747]
Vector	100	2.5	2	14	[747]
Disease	21	4	2	5	[748]
Vector	100	4.5	2	25	[749]
Disease	12	4.5	2	3	[756]
Disease	100	7	2	39	[751]
Vector	4	1	2	0	[757]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 63 occurrence points per country based on 2,531 results for “Spotted Fever” in PubMed and 40 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

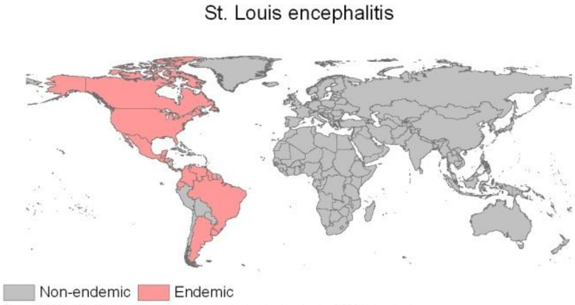
<u>**Disease**</u>**:** St. Louis encephalitis.

<u>**ICD-10 Code:**</u> A83.3.

<u>**Transmission category:**</u> Vector-borne.

<u>**Agent**</u>**:** Virus-RNA.

<u>**Taxonomy:**</u> Flaviviridae, Group IV, *Flavivirus*, St. Louis encephalitis virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>**Natural history**</u>**:**

Mode of transmission: Mosquito vector (*Culex* (*Cx. pipiens, Cx. tarsalis, Cx. nigripalpus, Cx. restuans, Cx. salinarius*), *Aedes* spp., *Sabethes* spp.) [671].

Reservoir*: Birds and mammals [671].

Incubation period: 12.5 days (range 4-21 days) [671].

<u>**Significant epidemiological characteristics**</u>**:**

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [758].

Reservoir: Not found.

<u>**Map(s) from published literature**</u>**:**

Total available literature:

PubMed hits on 04/11/11: 833.

GenBank hits on 22/02/12: 298.

HealthMap feeds 2006-2011: 41.

ProMED feeds 1994-2011: 22.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >21 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	50	1.5	2	4	[759]
Vector	100	2.5	2	14	[759]
Disease	37	7.5	2	15	[760]
Disease	37	6	2	12	[761]
Disease	37	7.5	2	15	[762]
Disease	37	5	2	10	[763]

<u>**Mapping recommendation:**</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 40 occurrence points per country based on 833 results for “St. Louis encephalitis” in PubMed and 21 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

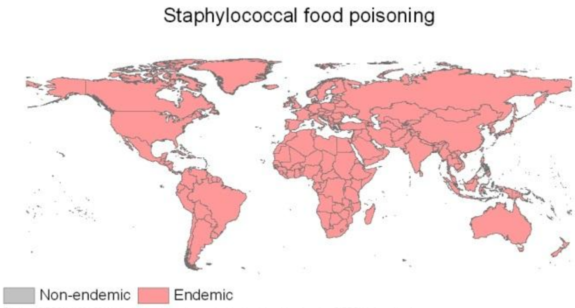
Disease: Staphylococcal food poisoning.

ICD-10 Code: A05.0.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated foods (creams, gravies, sauces) [671].

Reservoir*: Humans (hands) and occasionally cattle (udders) [671].

Incubation period: 0.125 days (range 0.08-0.17 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** 0-0.7 (possible >1) for MRSA [764].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

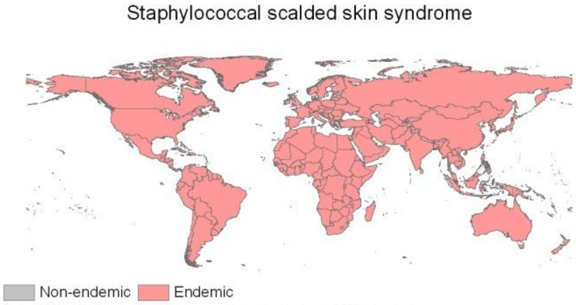
- **PubMed hits on 04/11/11:** 590.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** 111 for “Staphylococcal infection”.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Staphylococcal food poisoning is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Staphylococcal scalded skin syndrome.

ICD-10 Code: L00.

Transmission category: Engogenous.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus* phage group II [671, 672].

Natural history:

Mode of transmission: Endogenous; contact with infectious secretions; consumption of contaminated food [671].

Reservoir*: Humans [671].

Incubation period: 2.5 days (range 1-4 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-0.7 (possible >1 for MRSA) [764].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 430.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Staphylococcal scaled skin syndrome is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

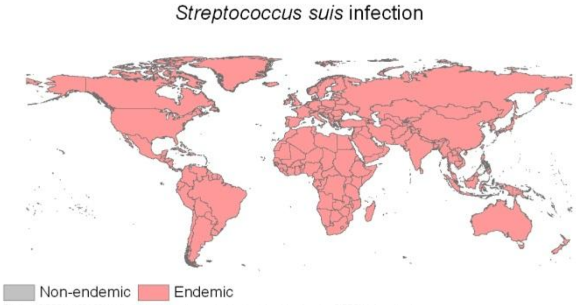
Disease: *Streptococcus suis* infection.

ICD-10 Code: A49.1.

Transmission category: Animal contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, *Streptococcus suis* I and II [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated meat; contact with infectious secretions or wounds; inhalation [671].

Reservoir*: Pigs [671], other ruminants, cats and dogs [765].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [765].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 894.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

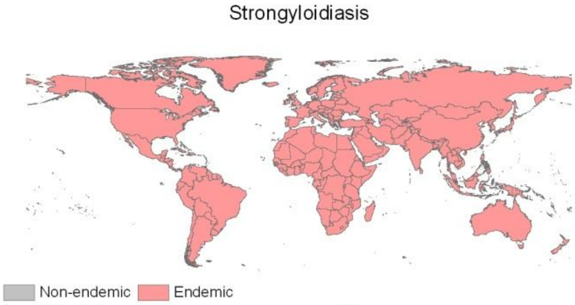
Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	20	7	2	N/A	[766]
Disease	37	6	2	N/A	[767]
Disease	34	6	2	N/A	[768]

Mapping recommendation: Option 1; do not map. *Streptococcus suis* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Strongyloidiasis.

ICD-10 Code: B78.

Transmission category: Soil contact.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Rhabditida, Strongyloididae,

Strongyloides stercoralis (*Strongyloides fulleborni* is occasionally implicated in systemic disease) [671, 672].

Natural history:

Mode of transmission: Soil contact; faecal-oral route; skin contact; (rarely) sexual contact [671].

Reservoir*: Humans, possibly dogs and monkeys (for *Strongyloides fulleborni*) [671].

Incubation period: 22 days (range 14-30 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,151.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

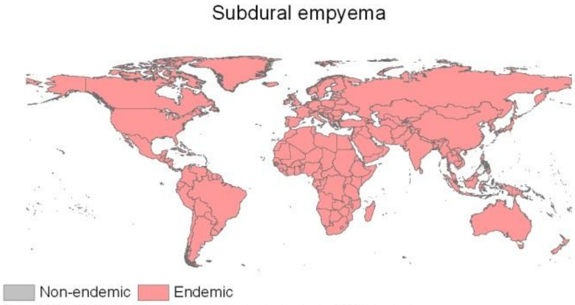
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Strongyloidiasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Subdural empyema.

ICD-10 Code: J86.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Oral anaerobes, streptococci, e.g.: Eubacteria, Proteobacteria, Gamma Proteobacteria, Pasteurellales, Pasteurellaceae
Haemophilus influenzae [671, 672].

Natural history:

Mode of transmission: Endogenous [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: *Haemophilus influenzae* (HbOC-DTP or -DTaP, HbOC, PRP-D, PRP-OMP, PRP-T).

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 813.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

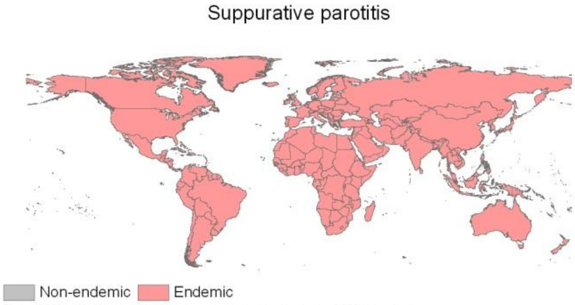
BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Subdural empyema is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Suppurative parotitis.

ICD-10 Code: B26

Transmission category: Endogenous

Agent: Bacterium

Taxonomy: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae,
Staphylococcus aureus [671, 672].

Natural history:

Mode of transmission: Endogenous [671].

Reservoir*: Humans [671].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 138.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 103 for "Parotitis".

ProMED feeds 1994-2011: 58 for "Parotitis".

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Suppurative parotitis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

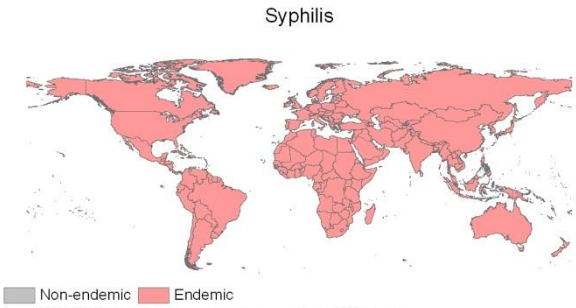
Disease: Syphilis.

ICD-10 Code: A50.

Transmission category: Sexual contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetes, Spirochaetaceae, *Treponema pallidum* ssp. *pallidum* [671, 672].



Syphilis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact; contact with infectious secretions [671].

Reservoir*: Humans [671].

Incubation period: 21 days (range 14-28 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 27,727.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 284.

ProMED feeds 1994-2011: 58.

BioCaster feeds 2006-2011: 239.

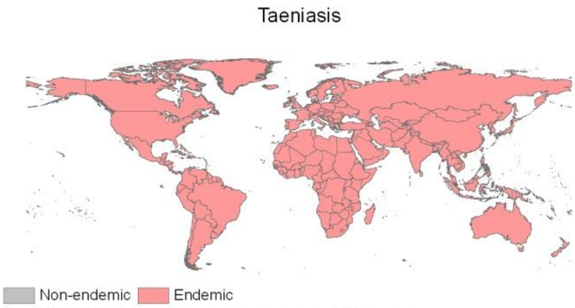
Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	19	7	2	N/A	[769]
Disease	19	7.5	2	N/A	[770]

Mapping recommendation: Option 1; do not map. Syphilis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Taeniasis.

ICD-10 Code: B68.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Platyhelminthes, Cestoda, Cyclophyllidea, Taeniidae,

Taenia solium, T. saginata, T.ovis, T.hydatigena [671, 672].

Natural history:

Mode of transmission: Consumption of contaminated meat [671].

Reservoir*: Cattle and pigs [671].

Incubation period: 70 days (range 42-98 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease (*T. saginata*) [771]; 0-1.75 (*T. solium*) [772]; 0-4 (T.ovis, T.hydatigena)] [771].

Reservoir: (with intervention, 0-0.85) [772].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,732.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 3.

ProMED feeds 1994-2011: 2.

BioCaster feeds 2006-2011: N/A.

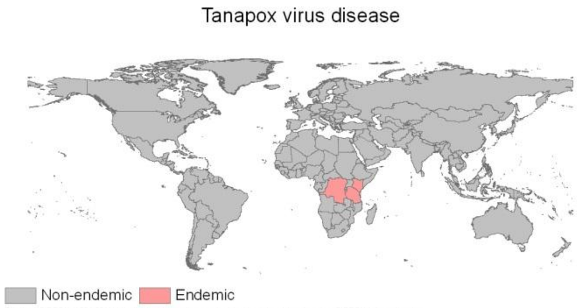
Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	85	5	2	N/A	[773]

Mapping recommendation: Option 1; do not map. Taeniasis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Tanapox virus disease.

ICD-10 Code: B08.8.

Transmission category: Animal contact.

Agent: Virus-DNA.

Taxonomy: Poxviridae, Chordopoxvirinae, Group I, Yatapoxvirus,
Tanapox virus [671, 672].

Natural history:

Mode of transmission: Contact with infected monkeys [671].

Reservoir*: Monkeys [671].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [774, 775].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 28 for "Tanapox".
- **GenBank hits on 22/02/12:** 16.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >3 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 9 occurrence point per country based on 28 results for “Tanapox” in PubMed and 3 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

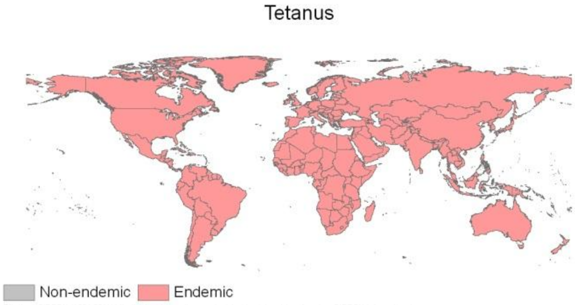
<u>Disease</u>: Tetanus.

<u>ICD-10 Code:</u> A33-35.

<u>Transmission category:</u> Direct contact.

<u>Agent</u>: Bacterium

<u>Taxonomy:</u> Eubacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium tetani [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Trauma [671].

Reservoir*: None [671].

Incubation period: 7 days (range 6-8 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: DT, DTaP, DTP, Td, Tetanus immune globulin, Tetanus.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 23,886.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 513.

ProMED feeds 1994-2011: 32.

BioCaster feeds 2006-2011: 2.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Tetanus is endemic worldwide and is vaccine preventable.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

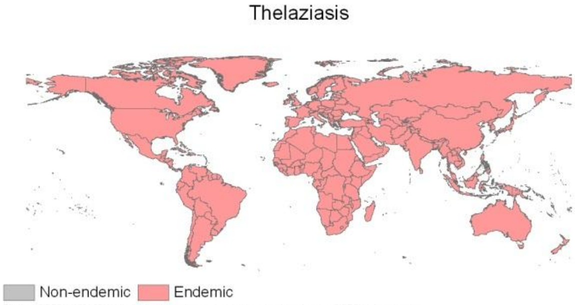
<u>Disease</u>: Thelaziasis.

<u>ICD-10 Code:</u> B83.8.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Nematoda, Secernentea, Spirurida, Thelaziidae,
Thelazia callipaeda, (rarely) *T. californiensis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Fly vector (*Musca* spp.; possibly *Fannia* spp.) [671].

Reservoir*: Dogs, rabbits, deer and cats [671].

Incubation period: 31.5 days (range 21-42 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [776].
- **Reservoir:** Not found.

<u>Map(s) from published literature</u>:

Total available literature:

- **PubMed hits on 04/11/11:** 52.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Thelaziasis is endemic worldwide.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

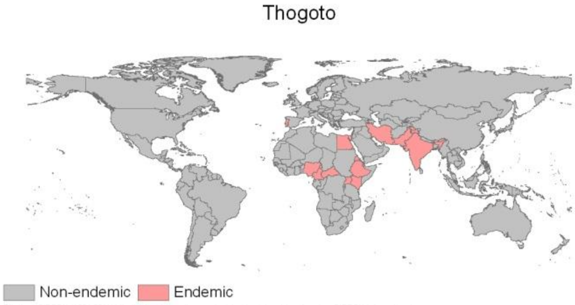
Disease: Thogoto.

ICD-10 Code: A84.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Orthomyxoviridae, Group IV, *Thogotovirus*, Thogoto virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector [671].

Reservoir*: Sheep, ticks, birds [671], cattle, goats and mongooses [777].

Incubation period: 4.5 days (range 4-5 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [777].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 109.

GenBank hits on 22/02/12: 56.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >12 [671].

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 9 occurrence points per country based on 109 results for “Thogoto” in PubMed and 12 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

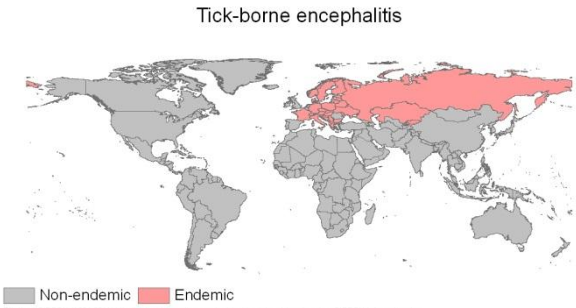
<u>Disease</u>: Tick-borne encephalitis.

<u>ICD-10 Code:</u> A84.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Flaviviridae, Group IV, *Flavivirus*, Tick-borne encephalitis virus (TBEV) [671, 672].



Tick-borne encephalitis

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Tick vector (*Ixodes ricinus*); consumption of contaminated dairy products [671].

Reservoir*: Rodents (*Apodemus flavicollis*, *A. sylvaticus*, *Microtus arvalis*), ticks , birds and cattle [671].

Incubation period: 11.5 days (range 7-14 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: Tick-borne encephalitis, Tick-borne encephalitis globulin.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [746, 778-782].

Reservoir: 0-10.7 (mice; multispecies) [781].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 3,644.

GenBank hits on 22/02/12: 1,095.

HealthMap feeds 2006-2011: 57.

ProMED feeds 1994-2011: 36.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >32 [671].

Previously published maps:

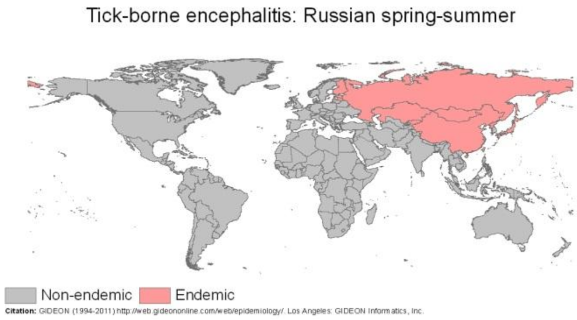
D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	100	3.5	3	29	[783]
Disease	95	4	3	32	[784]
Disease	72	5	2	20	[785]
Disease	57	5	2	16	[786]
Disease	86	5	2	24	[787]
Disease	1	4.5	2	0	[788]
Disease	2	6.5	3	1	[789]
Disease	2	7	2	1	[790]
Vector	2	7	3	1	[791]

Vector	2	6.5	3	1	[792]
Disease	2	8.5	3	1	[793]
Disease	0	7.5	2	0	[794]
Disease	1	7.5	3	1	[795]
Disease	100	6	2	33	[796]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 114 occurrence points per country based on 3,644 results for “Tick-borne encephalitis” in PubMed and 32 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Disease: Tick-borne encephalitis: Russian spring-summer.

ICD-10 Code: A84.0.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, Tick-borne encephalitis virus (TBEV) [671, 672].

Natural history:

Mode of transmission: Tick vector (*Ixodes persulcatus*); consumption of contaminated dairy products [671].

Reservoir*: Rodents, ticks, cattle and goats [671].

Incubation period: 10.5 days (range 7-14 days) [671].

Significant epidemiological characteristics:

Vaccine: Tick-borne encephalitis, Tick-borne encephalitis globulin

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 25 for "Tick-borne encephalitis and Russian spring-summer".

GenBank hits on 22/02/12: 1,095.

HealthMap feeds 2006-2011: 57 for "Tick-borne encephalitis”.

ProMED feeds 1994-2011: 36 for "Tick-borne encephalitis”.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >10 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Vector	99	4.5	2	33	[749]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 9 occurrence points per country based on 25 results for “Tick-borne encephalitis and Russian spring-summer” in PubMed and 10 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

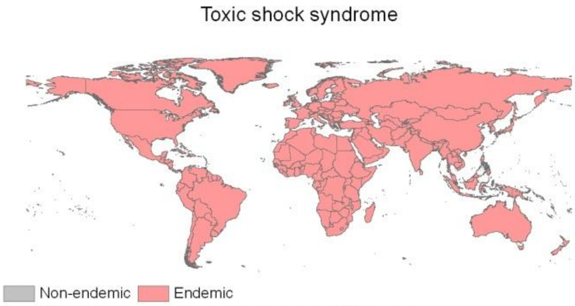
Disease: Toxic shock syndrome.

ICD-10 Code: A48.3.

Transmission category: Endogenous.

Agent: Bacterium.

Taxonomy: Various (toxins), e.g.: Eubacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, *Staphylococcus aureus*, *S. pyrogenes* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Fomites: tampon (occasionally bandage, etc.) which induces toxinosis [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-0.7 (possible >1) for MRSA [764].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,869.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 4.

ProMED feeds 1994-2011: 6.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Toxic shock syndrome is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

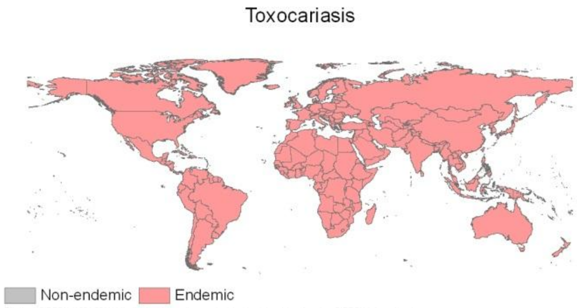
Disease: Toxocariasis.

ICD-10 Code: B83.0.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Secernentea, Ascaridida, Toxocaridae, *Toxocara cati*, *T. canis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of soil (on food) [671].

Reservoir*: Cats, dogs and mice [671].

Incubation period: 368.5 days (range 7-730 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [797].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

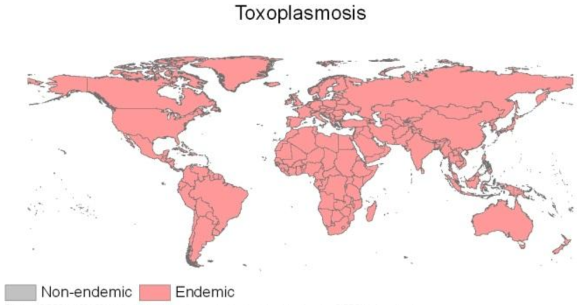
- **PubMed hits on 04/11/11:** 1,667.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 10.
- **ProMED feeds 1994-2011:** 5.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Toxocariasis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Toxoplasmosis.

ICD-10 Code: B58.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Chromalveolata, Apicomplexa, Conoidasida, Eucoccidiorida, Sarcocystidae, *Toxoplasma gondii* [671, 672].

Natural history:

Mode of transmission: Consumption of soil, meat and rarely milk; contact with contaminated water (rare) [671].

Reservoir*: Rodents, pigs, cattle, sheep, chickens, birds, cats and marsupials (kangaroos) [671].

Incubation period: 14 days (range 7-21 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [798].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 17,586.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 30.

ProMED feeds 1994-2011: 40.

BioCaster feeds 2006-2011: 25.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	73	7.5	2	N/A	[799]

Mapping recommendation: Option 1; do not map. Toxoplasmosis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

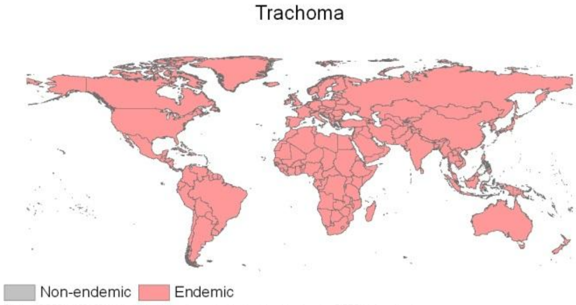
Disease: Trachoma.

ICD-10 Code: A71.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Chlamydiae, Chlamydiae, Chlamydiales, Chlamydiaceae,
Chlamydia trachomatis type A [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Fomites; flies; contact with infectious secretions [671].

Reservoir*: Humans [671].

Incubation period: 8.5 days (range 5-12 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-3.14 [800, 801].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,058.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 17.

ProMED feeds 1994-2011: 2.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	42	5	2	N/A	[802]
Disease	1	7.5	2	N/A	[803]
Disease	1	8	5	N/A	[804]
Disease	?	7	2	N/A	[805]
Disease	43	5	2	N/A	[806]
Disease	42	5	2	N/A	[807]
Disease	42	4	2	N/A	[808]

Mapping recommendation: Option 1; do not map. Trachoma is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

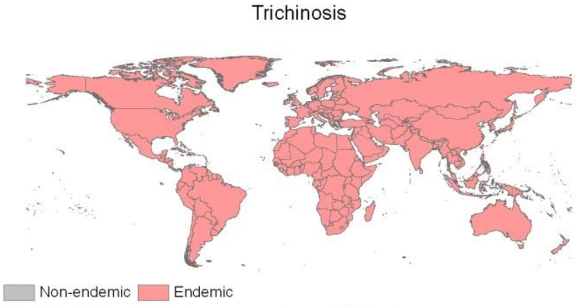
Disease: Trichinosis.

ICD-10 Code: B75.

Transmission category: Food/water-borne.

Agent: Parasite.

Taxonomy: Animalia, Nematoda, Adenophorea, Trichurida, Trichinellidae, *Trichinella spiralis* (occasionally *T. nativa, T. britovi, T. pseudospiralis, T. nelsoni*, et al.) [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated meat [671].

Reservoir*: Wild carnivores, omnivores and marine mammals [671].

Incubation period: 15 days (range 10-20 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: 0-6 [809].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,667.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 227.

ProMED feeds 1994-2011: 227.

BioCaster feeds 2006-2011: 2.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	11	9	2	N/A	[810]
Disease	25	4.5	2	N/A	[811]
Disease	48	4.5	2	N/A	[811]
Disease	1	7	2	N/A	[812]
Disease	24	4.5	2	N/A	[813]
Disease	19	5	2	N/A	[814]
Disease	19	7	2	N/A	[815]

Mapping recommendation: Option 1; do not map. Trichinosis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

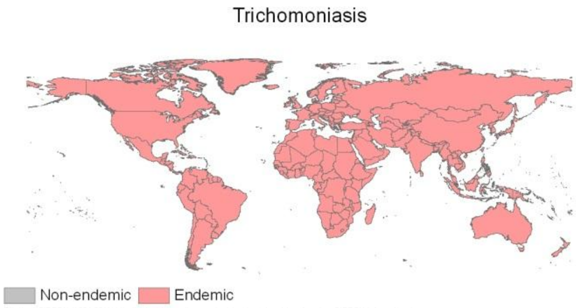
Disease: Trichomoniasis.

ICD-10 Code: A59.

Transmission category: Sexual contact.

Agent: Parasite.

Taxonomy: Excavata, Metamondada, Parabasalia, Trichomonadida, Trichomonadidae, *Trichomonas vaginalis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Sexual contact [671].

Reservoir*: Humans [671].

Incubation period: 16 days (range 4-28 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,661.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Trichomoniasis is endemic worldwide and potentially vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

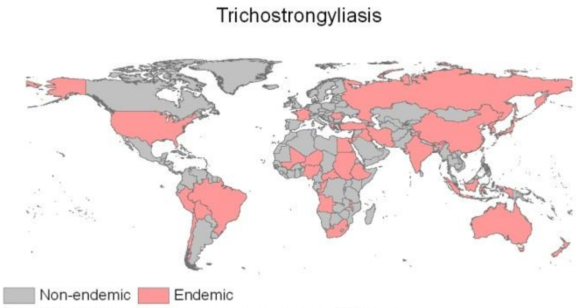
<u>Disease</u>: Trichostrongyliasis.

<u>ICD-10 Code:</u> B81.2.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Nematoda, Secernentea, Strongylida, Trichostrongylidae, *Trichostrongylus colubriformis, T. orientalis, T. probolurus* [671, 672]



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Consumption of contaminated food or water [671].

Reservoir*: Herbivores [671, 816].

Incubation period: 21 days [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [816-818].

Reservoir: 0-13.29 (sheep) [818].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 9 for "Trichostrongyliasis," 809 for "*Trichostrongylus colubriformis*," 19 for ”*Trichostrongylus orientalis*" and 7 for "*Trichostrongylus probolurus*".

GenBank hits on 22/02/12: 66.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >36 [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 22 occurrence points per country based on 809 results for “*Trichostrongylus colubriformis*” in PubMed and 36 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

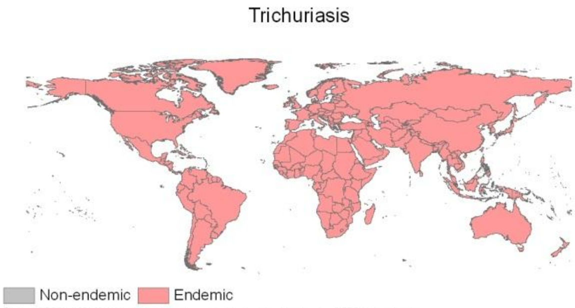
<u>Disease</u>: Trichuriasis.

<u>ICD-10 Code:</u> B79.

<u>Transmission category:</u> Food/water-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Animalia, Nematoda, Adenophorea, Trichocephalida, Trichinellidae, *Trichuris trichiura* [671, 672]



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Sexual contact; flies; consumption of soil on food [671].

Reservoir*: Humans [671].

Incubation period: 395 days (range 60-730 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** 0-6 [691].
- **Reservoir:** There is no animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

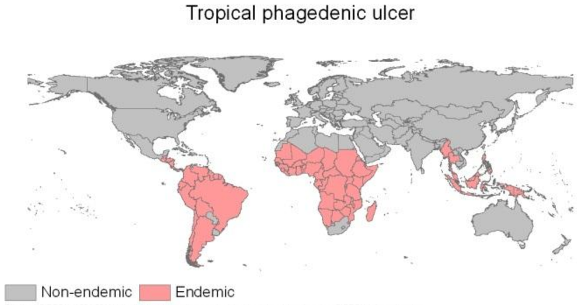
- **PubMed hits on 04/11/11:** 1,951.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 0.
- **ProMED feeds 1994-2011:** 0.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 1; do not map. Trichuriasis is endemic worldwide and potentially vaccine preventable.

<u>Future mapping potential</u>: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Tropical phagedenic ulcer.

ICD-10 Code: L98.4.

Transmission category: Blood/body-fluid contact.

Agent: Bacterium.

Taxonomy: Mixed infection, possibly by *Fusobacterium* spp. and *Borrelia* spp. [671, 672]

Natural history:

Mode of transmission: Direct inoculation to blood; trauma [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 7.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

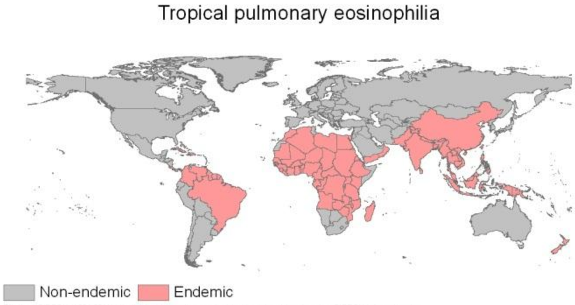
Approximate number of endemic countries: >69 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There was less than 1 occurrence point per country based on 7 results for "Tropical phagedenic ulcer" in PubMed and 69 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Tropical pulmonary eosinophilia.

<u>ICD-10 Code:</u> J82.

<u>Transmission category:</u> Unknown.

<u>Taxonomy:</u> Unknown.

<u>Natural history</u>:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no known animal reservoir for this disease.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 185.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: 0 for “Eosinophilic pneumonia”.

ProMED feeds 1994-2011: 2 for “Eosinophilic pneumonia”.

BioCaster feeds 2006-2011: N/A.

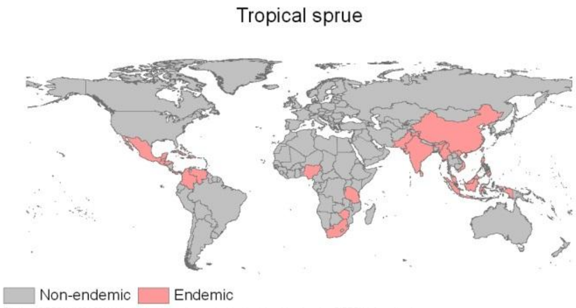
Approximate number of endemic countries: >109 [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 185 results for “Tropical pulmonary eosinophilia” in PubMed and 109 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Tropical sprue.

ICD-10 Code: K90.1.

Transmission category: Unknown.

Agent: Unknown.

Taxonomy: Unknown.

Natural history:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: 6 months [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no known animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 715.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

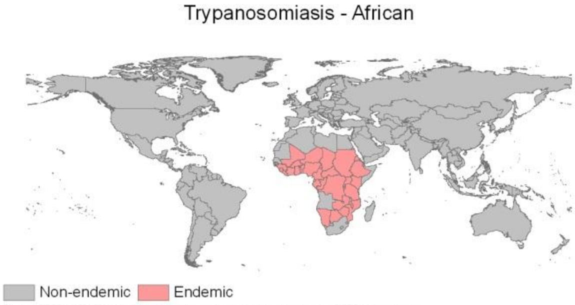
Approximate number of endemic countries: >28 [671].

Previously published maps: Not found.

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 26 occurrence points per country based on 715 results for “Tropical sprue” in PubMed and 28 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.


Trypanosomiasis - African

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Trypanosomiasis - African.

ICD-10 Code: B56.

Transmission category: Vector-borne.

Agent: Parasite.

Taxonomy: Excavata, Euglenozoa, Kinetoplastida, Trypanosomatida,
Trypanosoma brucei gambiense, *T. brucei rhodiense*

Natural history:

Mode of transmission: Tsetse fly vector (*Glossina morsitans, G. palpalis, G. fuscipes, G. tachinoides,G. pallidipes,G. swynnertoni.*) [671].

Reservoir*: Humans, cattle, deer and wild carnivores [671].

Incubation period: 12 days (range 3-21 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: 0-2.65 [819].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,634 for "African trypanosomiasis," 7,469 for "*Trypanosoma brucei*," 943 for "*Trypanosoma brucei gambiense*" and 0 for "*Trypanosoma brucei rhodiense*".

GenBank hits on 22/02/12: 107.

HealthMap feeds 2006-2011: 56 for "Trypanosomiasis".

ProMED feeds 1994-2011: 190 for "Trypanosomiasis".

BioCaster feeds 2006-2011: 119 for "Sleeping sickness".

Approximate number of endemic countries: >30.

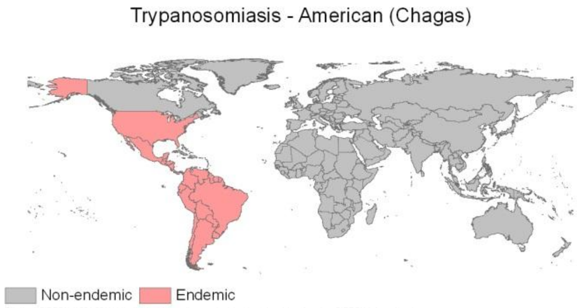
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	99	6	2	33	[816]
Vector	100	4.5	3	38	[820]
Disease	99	6	2	33	[821]
Disease	97	5	2	27	[822]
Disease	97	1	2	5	[823]
Disease	9	8.5	2	4	[824]
Disease	47	6	2	16	[825]
Disease	39	6	2	18	[826]
Disease	31	6	2	14	[827]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 249 occurrence points per country based on 7,469 results for "*Trypanosomoa brucei*" in PubMed and 30 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Trypanosomiasis - American (Chagas).

<u>ICD-10 Code:</u> B57.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Parasite.

<u>Taxonomy:</u> Excavata, Euglenozoa, Kinetoplastida, Trypanosomatida, Trypanosomataceae, *Trypanosoma cruzi* [671, 672].

<u>Natural history</u>:

Mode of transmission: Triatomine bug vector (*Panstrongylus* spp., *Rhodnius* spp., *Triatoma* spp.) [671].

Reservoir*: Humans, dogs, cats, pigs, guinea pigs, armadillos, rats, foxes, opossums, racoons, bats, mice, monkeys and rabbits [671].

Incubation period: 9.5 days (range 5-14 days); 35 days from blood transfusion (range 30-40days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: 0-11 [828-830].

Reservoir: 0-8.2 (dogs) [831]; 0-3.3 (bugs) [832].

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 475 for "American Trypanosomiasis," 11,023 for "Chagas" and 10,662 for "*Trypanosoma cruzi*".

GenBank hits on 22/02/12: 70,089.

HealthMap feeds 2006-2011: 56 for “Trypanosomiasis”.

ProMED feeds 1994-2011: 190 for “Trypanosomiasis”.

BioCaster feeds 2006-2011: 153 for “Chagas”.

Approximate number of endemic countries: >22 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	60	5	2	17	[833]
Disease	46	5	3	19	[834]
Disease	60	5	2	17	[835]
	38	6	2	13	[836]
Vector	16	8.5	3	11	[837]
Vector	23	8.5	4	21	[838]
Vector	2	8.5	3	1	[839]

Disease	13	7.5	2	6	[840]
Disease	13	8.5	3	9	[841]
Vector	49	9	4	49	[842]
Vector	23	9	2	11	[843]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 501 occurrence points per country based on 11,023 results for “Chagas” in PubMed and 22 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

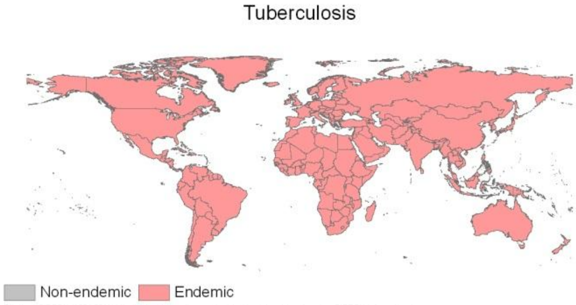
Disease: Tuberculosis.

ICD-10 Code: A15 - A19.

Transmission category: Respiratory.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Mycobacteriaceae, *Mycobacterium tuberculosis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation; consumption of contaminated dairy products [671].

Reservoir*: Humans and cattle [671].

Incubation period: 56 days (range 28-84 days) [671].

Significant epidemiological characteristics:

Vaccine: BCG.

Estimated R_0 value(s) from published literature:

Human: 0-4.47 [844-849].

Reservoir: 0-2.7 (cows) [850, 851]; 0-2 (possums) [850, 852]; 0-1.2 (ferrets) [850, 853]; 0-1.229 (badgers) [850, 854].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 189,049.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 3,112.

ProMED feeds 1994-2011: 697.

BioCaster feeds 2006-2011: 1,928.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	5	2	N/A	[855]
Disease	100	5	2	N/A	[856]
Disease	100	4	2	N/A	[857]
Disease	100	4	2	N/A	[858]

Mapping recommendation: Option 1; do not map. Tuberculosis is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

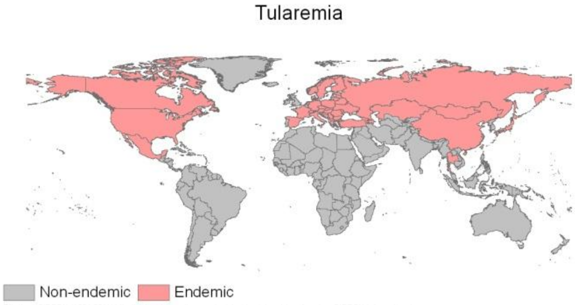
Disease: Tularemia.

ICD-10 Code: A21.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Thiotrichales, Francisellaceae, *Francisella tularensis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick and fly vectors (*Dermacentor* spp., *Amblyomma* spp.; *Chrysops* spp.(deer fly)) [671].

Reservoir*: Muskrats, rabbits, hares, beavers, ticks and mosquitoes [671].

Incubation period: 4 days (range 3-5 days) [671].

Significant epidemiological characteristics:

Vaccine: Tularemia

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 3,075.

GenBank hits on 22/02/12: 2,703.

HealthMap feeds 2006-2011: 122.

ProMED feeds 1994-2011: 189.

BioCaster feeds 2006-2011: 265.

Approximate number of endemic countries: >46 [671].

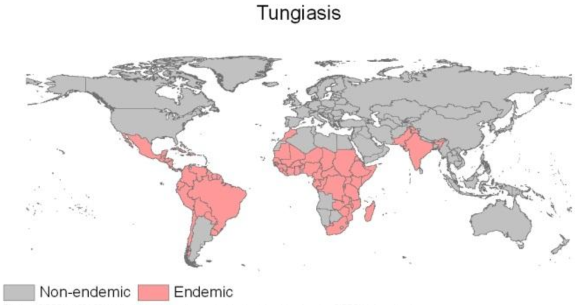
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	50	5	2	14	[859]
Disease	43	5	2	12	[860]
Disease	100	5.5	2	30	[861]
Disease	11	8	2	5	[862]
Disease	11	8.5	2	5	[863]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 67 occurrence points per country based on 3,075 results for “Tularemia” in PubMed and 46 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Tungiasis.

ICD-10 Code: B88.1.

Transmission category: Direct contact.

Agent: Parasite.

Taxonomy: Animalia, Arthropoda, Insecta, Siphonaptera, Tungidae,
Tunga penetrans, *T. trimamillata* [671, 672].

Natural history:

Mode of transmission: Direct contact [671].

Reservoir*: Pigs, dogs, cats, cattle, sheep, goats, horses, rodents, birds, elephants and monkeys [671] [864]

Incubation period: 10 days (range 8-12 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [864].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 192 for "Tungiasis," 122 for "*Tunga penetrans*," and 10 for "*Tunga trimamillata*".
- **GenBank hits on 22/02/12:** 66.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

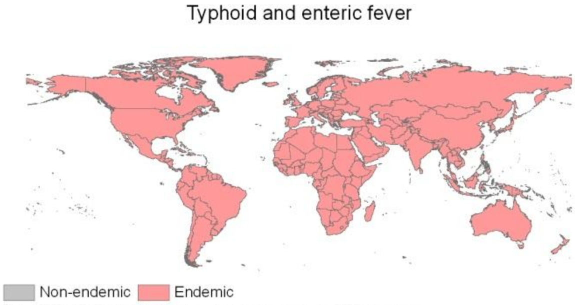
Approximate number of endemic countries: >88 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 2 occurrence points per country based on 192 results for “Tungiasis” in PubMed and 88 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Typhoid and enteric fever.

ICD-10 Code: A01.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Salmonella enterica* serotype Typhi [671, 672].

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated food and water; flies [671].

Reservoir*: Humans [671].

Incubation period: 18 days (range 15-21 days) [671].

Significant epidemiological characteristics:

Vaccine: Typhoid – injectible, Typhoid – oral.

Estimated R_0 value(s) from published literature:

Human: 0-2.4 [691, 865].

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 13,601 for "Typhoid" and 930 for "Enteric fever".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 959 for “Typhoid”.

ProMED feeds 1994-2011: 429 for “Typhoid”.

BioCaster feeds 2006-2011: 979 for “Typhoid” and 106 for “Paratyphoid”.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	4.5	2	N/A	[866]
Disease	100	4.5	2	N/A	[867]

Mapping recommendation: Option 1; do not map. Typhoid and enteric fever are endemic worldwide and vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

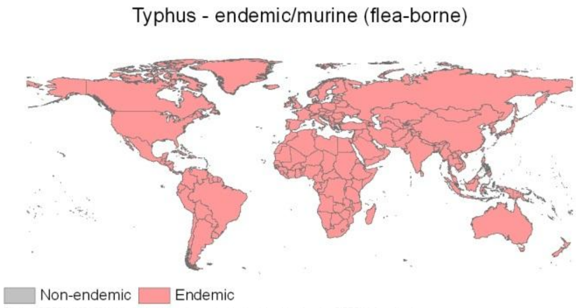
Disease: Typhus - endemic/murine (flea-borne).

ICD-10 Code: A75.2.

Transmission category: Vector-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia typhi* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Tick vector (*Xenopsylla* spp., *Nosopsyllus* spp.) [671].

Reservoir*: Rats [671].

Incubation period: 11 days (range 10-12 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [868].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 85 for "Endemic typhus," 499 for "Murine typhus" and 445 for "*Rickettsia typhi*".
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 127 for “Typhus”.
- **ProMED feeds 1994-2011:** 96 for “Typhus”.
- **BioCaster feeds 2006-2011:** 185 for “Typhus” and 5 for “Endemic typhus”.

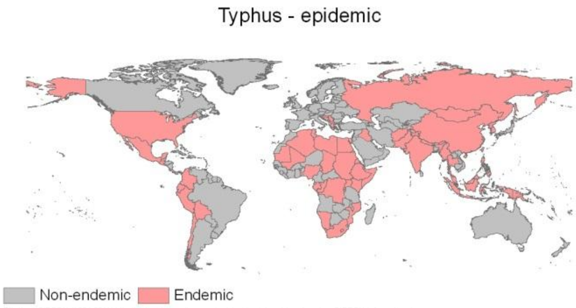
Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	5	8	2	N/A	[869]

Mapping recommendation: Option 1; do not map. Typhus – endemic/murine is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Disease</u>: Typhus - epidemic.

<u>ICD-10 Code:</u> A75.0.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Bacterium.

<u>Taxonomy:</u> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Rickettsia prowazekii* [671, 672].

<u>Natural history</u>:

Mode of transmission: Louse vector (*Pediculus* spp.); potential squirrel flea vector [671].

Reservoir*: Humans and possibly flying squirrels [671].

Incubation period: 12 days (range 10-14 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [870].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 251 for "Epidemic typhus" and 908 for "*Rickettsia prowazekii*".

GenBank hits on 22/02/12: 799.

HealthMap feeds 2006-2011: 127 for “Typhus”.

ProMED feeds 1994-2011: 96 for “Typhus”.

BioCaster feeds 2006-2011: 185 for “Typhus”.

Approximate number of endemic countries: >63 [671].

Previously published maps: Not found.

<u>Mapping recommendation:</u> Option 2; map observed occurrence.

There were approximately 4 occurrence points per country based on 908 results for “*Rickettsia prowazekii”* in PubMed and 63 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

<u>Future mapping potential</u>: Refine current global thumbnail map using systematic assembly of published occurrence data.

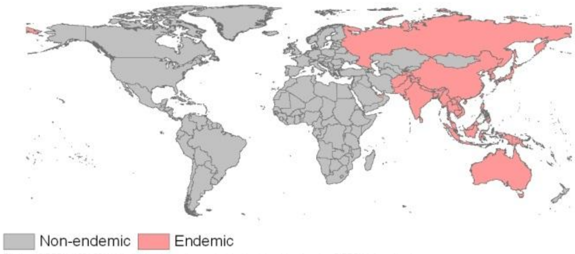
<ins>**Disease**</ins>**:** Typhus - scrub (mite-borne).

<ins>ICD-10 Code:</ins> A75.3.

<ins>Transmission category:</ins> Vector-borne.

<ins>Agent</ins>: Bacterium.

<ins>Taxonomy:</ins> Eubacteria, Proteobacteria, Alpha Proteobacteria, Rickettsiales, Rickettsiacae, *Orientia* [formerly *Rickettsia*] *tsutsugamushi* [671, 672].


Typhus - scrub (mite-borne)

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<ins>Natural history</ins>:

Mode of transmission: Mite vector (*Leptotrombidium deliense, L. fletcheri, L. akamushi, L. arenicola, L. Pallidum, L. scutellare*) [671].

Reservoir*: Rodents (*Rattus*, *Apodemus*, *Microtus*), mites and wild carnivores [671].

Incubation period: 10 days (range 8-12 days) [671].

<ins>Significant epidemiological characteristics</ins>:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [871, 872].

Reservoir: 0->5 (rodents) [872].

<ins>Map(s) from published literature</ins>:

Total available literature:

PubMed hits on 04/11/11: 1,332 for "Scrub typhus" and 830 for "*Orientia tsutsugamushi*".

GenBank hits on 22/02/12: 871.

HealthMap feeds 2006-2011: 127 for "Typhus".

ProMED feeds 1994-2011: 96 for "Typhus".

BioCaster feeds 2006-2011: 185 for "Typhus" and 2 for "Scrub typhus".

Approximate number of endemic countries: >34 [671].

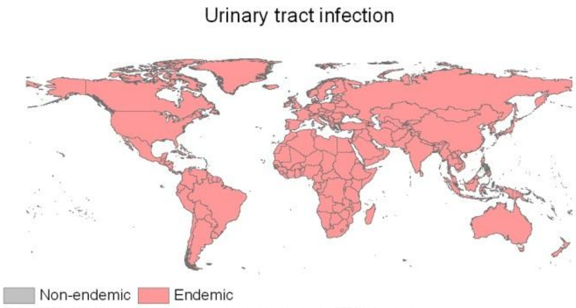
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	95	1.5	2	8	[747]
Vector	95	2.5	2	13	[747]
Disease	34	6	2	11	[873]
Disease	98	7	2	38	[874]
Disease	3	6	2	1	[875]

<ins>Mapping recommendation:</ins> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 39 occurrence points per country based on 1,332 results for “Scrub typhus” in PubMed and 34 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Urinary tract infection.

ICD-10 Code: N39.0.

Transmission category: Endogenous.

Agent: Bacterium or Fungus.

Taxonomy: EubacteriaProteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Escherichia coli*

Other facultative gram negative bacilli, enterococci, et al.

Various fungi [671, 672].

Natural history:

Mode of transmission: Endogenous [671].

Reservoir*: Humans [671].

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 13,575.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide.

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Urinary tract infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

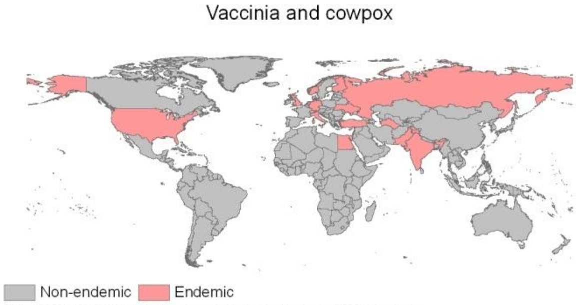
Disease: Vaccinia and cowpox.

ICD-10 Code: B08.0.

Transmission category: Animal contact.

Agent: Virus-DNA.

Taxonomy: Poxviridae, Chordopoxvirinae, Group I *Orthopoxvirus*, Vaccina virus [671, 672].



Vaccinia and cowpox

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with cattle and cats [671].

Reservoir*: Cattle, cats and rodents [671].

Incubation period: 3 days (range 2-4 days) [671].

Significant epidemiological characteristics:

Vaccine: Vaccinia immune globulin

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [876].

Reservoir: 0-19.15 (bank voles) [876].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 13,576 for "Vaccinia" and 896 for "Cowpox".

GenBank hits on 22/02/12: 1,395.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: 20 for “Cowpox”.

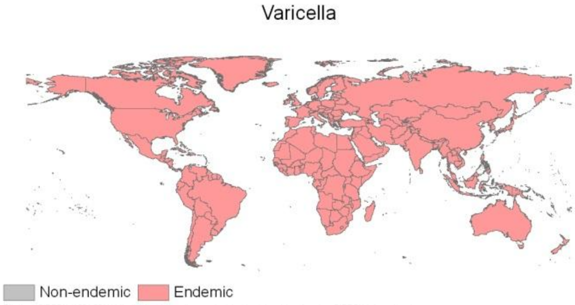
Approximate number of endemic countries: >14 [671].

Previously published maps: Not found.

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 970 occurrence points per country based on 13,576 results for “Vaccinia” in PubMed and 14 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Varicella.

ICD-10 Code: B01.

Transmission category: Direct contact.

Agent: Virus-DNA.

Taxonomy: Herpesviridae, Alphaherpesvirinae, Group I, *Varicellovirus*, Human Herpesvirus 3 (Varicella-zoster virus) [671, 672].

Natural history:

Mode of transmission: Direct contact; inhalation [671].

Reservoir*: Humans [671].

Incubation period: 17.5 days (range 14-21 days) [671].

Significant epidemiological characteristics:

Vaccine: Varicella, Varicella-Zoster immune globulin, Herpes zoster.

Estimated R_0 value(s) from published literature:

- **Human:** 0-16.9 [691, 877, 878].
- **Reservoir:** There is no animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 9,988.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** 1,236 for “Chickenpox”.
- **ProMED feeds 1994-2011:** 142 for “Chickenpox”.
- **BioCaster feeds 2006-2011:** 1,710 for “Chickenpox”.

Approximate number of endemic countries: Worldwide.

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Varicella is endemic worldwide and is vaccine preventable.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Disease: Venezuelan equine encephalitis.

ICD-10 Code: A92.2.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Togaviridae, Group IV, *Alphavirus*, Venezuelan equine encephalitis (VEE) virus [671, 672].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Culex* [*Melanoconion*] spp., *Aedes taeniorhynchus*, *Mansonia* spp., *Psrophora confinnis*, *Sabethes* spp., *Deinocerites* spp., *Anopheles aquasalis*) [671].

Reservoir*: Rodents and horses [671].

Incubation period: 3.5 days (range 2-5 days) [671].

Significant epidemiological characteristics:

Vaccine: Venezuelan equine encephalitis (VEE for lab workers; commercially available vaccine for horses).

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [879, 880].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 647.

GenBank hits on 22/02/12: 342.

HealthMap feeds 2006-2011: 78.

ProMED feeds 1994-2011: 72.

BioCaster feeds 2006-2011: 5.

Approximate number of endemic countries: >21 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	70	1.5	2	6	[759]
Vector	100	2.5	2	14	[759]
Disease	98	5	2	27	[881]
Vector	4	7.5	2	1	[882]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 31 occurrence points per country based on 647 results for "Venezuelan equine encephalitis" in PubMed and 21 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Disease: Venezuelen haemorrhagic fever.

ICD-10 Code: A96.8.

Transmission category: Soil contact.

Agent: Virus-RNA.

Taxonomy: Arenaviridae, Group V, *Arenavirus*, Guanarito virus [671, 672].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Inhalation of infectious rodent secretions; contact with excretions [671].

Reservoir*: Rodents (cane mouse: *Zygodontomys brevicauda*) and potentiall other rodents (cotton rat: *Sigmodon alstoni*) [671].

Incubation period: 11.5 days (range 7-16 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 0 for "Venezuelen haemorrhagic fever" and 21 for "Guanarito virus".

GenBank hits on 22/02/12: 90.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [671]..

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	6.5	2	48	[883]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 21 occurrence points per country based on 21 results for “Guanarito virus” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its tick vectors. If occurrence data for these tick species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

Disease: *Vibrio parahaemolyticus* infection.

ICD-10 Code: A05.3.

Transmission category: Food/water-borne.

Agent: Bacterium .

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Vibrionales, Vibrionaceae, *Vibrio parahaemolyticus* [671, 672].

Vibrio parahaemolyticus infection

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Consumption of contaminated seafood [671].

Reservoir*: Fish and other seafood [671].

Incubation period: 0.6 days (range 0.4-0.8 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [884].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,087.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: 30.

ProMED feeds 1994-2011: 67.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	33	6.5	2	N/A	[885]

Mapping recommendation: Option 1; do not map. *Vibrio parahaemolyticus* infections are endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Viliuisk encephalomyelitis.

ICD-10 Code: G04.8.

Transmission category: Unknown.

Agent: Unknown.

Taxonomy: Picornavirales, Picornaviridae, Group IV, *Cardiovirus* (possibly), Theiler's murine encephalomyelitis-like virus [671, 672].

Natural history:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: There is no known animal reservoir for this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 11.

GenBank hits on 22/02/12: 0.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >1 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	100	0	2	0	[886]
Disease	100	6.5	2	72	[886]
Disease	100	5.5	2	61	[887]
Disease	100	6.5	2	72	[888]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 11 occurrence points per country based on 11 results for “Viliuisk encephalomyelitis” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

Disease: Wesselsbron.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviridae, Group IV, *Flavivirus*, Wesselsbron virus [671, 672].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Aedes* spp., *Anopheles gambiae*, *An. pharoensis*, *Culex telesilla*, *Cx. univittatus*, *Mansonia uniformis*) [671].

Reservoir*: Sheep and cattle [671].

Incubation period: 3 days (range 2-4 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [889].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 75.
- **GenBank hits on 22/02/12:** N/A.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >31

Previously published maps: Not found.

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 2 occurrence points per country based on 75 results for "Wesselsbron" in PubMed and 31 endemic countries listed in the GIDEON database. With fewer than 25 hits per country it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its mosquito vectors. If occurrence data for these mosquito species are not available digitized versions of expert opinions of their ranges could usefully inform future mapping.

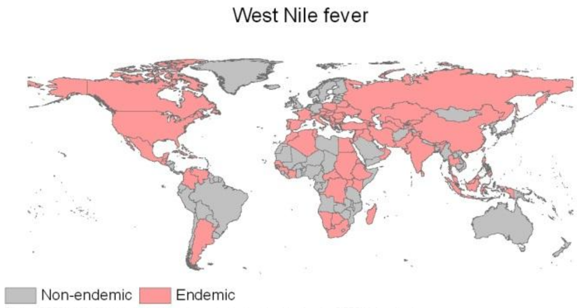
Disease: West Nile fever.

ICD-10 Code: A92.3.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviviridae, Group IV, *Flavivirus*, West Nile fever virus [671, 672].


West Nile fever

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Culex* spp., *Coquillettidia* spp., *Aedes* spp., *Anopheles* spp.); ticks also indicated as vector [671].

Reservoir*: Birds, horses, ticks, (possibly) bats [671].

Incubation period: 4.5 days (range 3-6 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [890-893].

Reservoir: 0-28 (birds), [782, 890-894].

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 2,562.

GenBank hits on 22/02/12: 18,334.

HealthMap feeds 2006-2011: 1,818.

ProMED feeds 1994-2011: 1,683.

BioCaster feeds 2006-2011: 2,068.

Approximate number of endemic countries: >84 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	69	3	2	11	[895]
Disease	71	3	2	12	[896]
Disease	89	4	2	20	[897]
Disease	21	7	2	8	[897]
Vector	95	4	2	21	[898]
Vector	100	9	4	100	[899]
Disease	1	8.5	3	0	[900]
Disease	6	7.5	3	4	[901]
Disease	6	7	3	3	[902]
Disease	6	7	2	2	[903]
Disease	0	8.5	2	0	[904]

Disease	6	7.5	2	2	[905]
Vector	6	8	3	4	[906]
Disease	6	7.5	2	2	[907]
Disease	1	7.5	3	0	[908]
Vector	6	7.5	4	5	[909]
Disease	1	8.5	2	1	[910]
Disease	6	8.5	2	3	[911]
Vector	6	8.5	3	4	[912]
Vector	6	7.5	4	5	[913]
Disease	7	7	2	3	PHAC
Disease	1	8.5	3	1	[914]
Disease	6	7.5	2	2	[760]
Disease	7	6	2	2	[915]
Disease	1	4	3	0	[915]
Vector	1	6	2	0	[916]
Disease	6	7.5	2	2	[917]
Disease	6	8.5	3	4	[918]
Disease	6	6	2	2	[898]
Disease	14	3	2	2	[919]
Disease	6	6.5	2	2	[920]
Disease	6	6.5	2	2	[921]
Disease	4	4	2	1	[922]
Disease	6	8	4	5	[923]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 31 occurrence points per country based on 2,562 results for “West Nile fever” in PubMed and 84 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

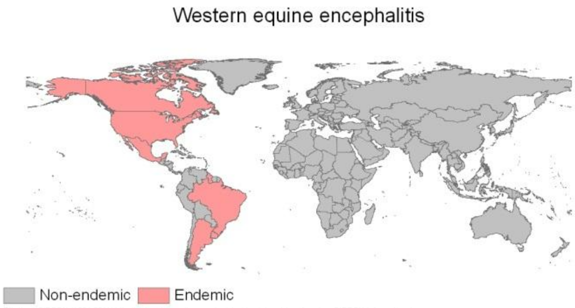
<u>Disease</u>: Western equine encephalitis.

<u>ICD-10 Code:</u> A83.1.

<u>Transmission category:</u> Vector-borne.

<u>Agent</u>: Virus-RNA.

<u>Taxonomy:</u> Togaviridae, Group IV, *Alphavirus*, Western equine encephalitis (WEE) virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

<u>Natural history</u>:

Mode of transmission: Mosquito vector (*Culex tarsalis*) [671].

Reservoir*: Birds, horses, amphians and reptiles [671].

Incubation period: 10 days (range 5-15 days) [671].

<u>Significant epidemiological characteristics</u>:

Vaccine: Western equine encephalitis.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [881].

Reservoir: Not found.

<u>Map(s) from published literature</u>:

Total available literature:

PubMed hits on 04/11/11: 326.

GenBank hits on 22/02/12: 118.

HealthMap feeds 2006-2011: 10.

ProMED feeds 1994-2011: 9.

BioCaster feeds 2006-2011: 181.

Approximate number of endemic countries: >7 [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	72	1.5	2	6	[759]
Vector	72	2.5	2	10	[759]

<u>Mapping recommendation:</u> Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 47 occurrence points per country based on 326 results for "Western equine encephalitis" in PubMed and 7 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Whipple's disease.

ICD-10 Code: K90.8.

Transmission category: Unknown.

Agent: Bacterium.

Taxonomy: Eubacteria, Actinobacteria, Actinobacteria, Actinomycetales, Cellulomonadaceae, *Tropheryma whipplei* [671, 672].

Natural history:

Mode of transmission: Unknown.

Reservoir*: Unknown.

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found

Reservoir: There is no known animal reservoir of this disease.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 1,342.

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps: Not found.

Mapping recommendation: Option 1; do not map. Whipple’s disease is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

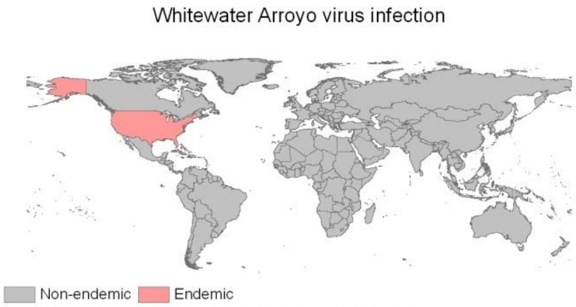
Disease: Whitewater Arroyo virus infection.

ICD-10 Code: A96.8.

Transmission category: Blood/body-fluid contact.

Agent: Virus-RNA.

Taxonomy: Arenaviridae, Group V, *Arenavirus*, Whitewater Arroyo virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Contact with infectious secretions [671].

Reservoir*: Rodents (woodrat: *Neotoma albigula*) [671].

Incubation period: Unknown.

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

- **Human:** <1; primarily a zoonotic disease [924].
- **Reservoir:** Not found.

Map(s) from published literature:

Total available literature:

- **PubMed hits on 04/11/11:** 23 for "Whitewater Arroyo".
- **GenBank hits on 22/02/12:** 50.
- **HealthMap feeds 2006-2011:** N/A.
- **ProMED feeds 1994-2011:** N/A.
- **BioCaster feeds 2006-2011:** N/A.

Approximate number of endemic countries: >1 [671].

Previously published maps: Not found.

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 23 occurrence points per country based on 23 results for “Whitewater Arroyo” in PubMed and 1 endemic country listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

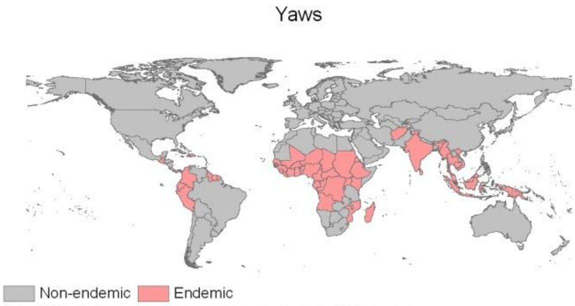
Disease: Yaws.

ICD-10 Code: A66.

Transmission category: Direct contact.

Agent: Bacterium.

Taxonomy: Eubacteria, Spirochaetes, Spirochaetes, Spirochaetes, Spirochaetaceae, *Treponema pallidum* ssp. *pertenue* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Direct contact; potentially through fomites or insect bites [671].

Reservoir*: Humans and possibly non-human primates [671].

Incubation period: 28 days (range 21-35 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 862.

GenBank hits on 22/02/12: 277.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >63.

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	93	3.5	2	36	[925]

Mapping recommendation: Option 2; map observed occurrence.

There were approximately 14 occurrence points per country based on 862 results for “Yaws” in PubMed and 63 endemic countries listed in the GIDEON database. With fewer than 25 hits per country, it is only possible to map recorded events of the disease.

Future mapping potential: Refine current global thumbnail map using systematic assembly of published occurrence data.

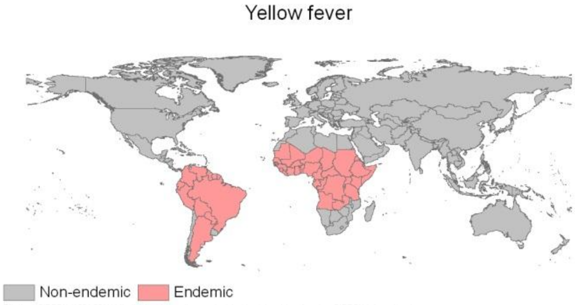
Disease: Yellow fever.

ICD-10 Code: A95.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviridae, Group IV, *Flavivirus*, Yellow fever virus [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Aedes* spp., *Haemagogus* spp., *Sabethes* spp.) [671].

Reservoir*: Humans, mosquitoes, monkeys and marsupials [671].

Incubation period: 4.5 days (range 3-6 days) [671].

Significant epidemiological characteristics:

Vaccine: Yellow fever

Estimated R_0 value(s) from published literature:

Human: 0-8.59 [926-928]

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 4,355.

GenBank hits on 22/02/12: 529.

HealthMap feeds 2006-2011: 1,473.

ProMED feeds 1994-2011: 956.

BioCaster feeds 2006-2011: 1,039.

Approximate number of endemic countries: >47.

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	18	4.5	3	7	[929]

Mapping recommendation: Option 4; niche mapping of risk using modelling techniques such as Boosted Regression Trees (BRT).

There were approximately 93 occurrence points per country based on 4,355 results for “Yellow fever” in PubMed and 47 endemic countries listed in the GIDEON database. With more than 25 hits per country, it is possible to apply modelling techniques such as BRT to map areas of potential risk.

Future mapping potential: Refine current maps using BRT modelling techniques and systematic searches of new occurrence data. Digitized expert opinion of known absence areas would also be useful to constrain the prediction extent for the BRT.

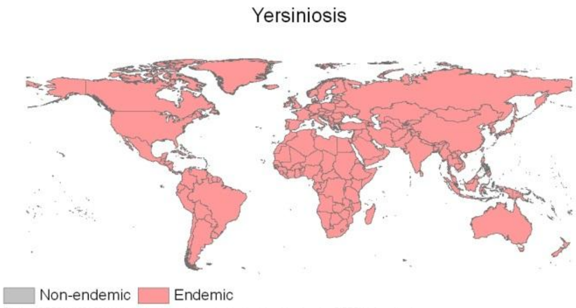
Disease: Yersiniosis.

ICD-10 Code: A04.6.

Transmission category: Food/water-borne.

Agent: Bacterium.

Taxonomy: Eubacteria, Proteobacteria, Gamma Proteobacteria, Enterobacteriales, Enterobacteriaceae, *Yersinia enterocolitica, Y. pseudotuberculosis* [671, 672].



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Faecal-oral route; consumption of contaminated food (e.g. meat, dairy products, vegetables) or water; contact with blood [671].

Reservoir*: Pigs, rodents, rabbits, sheep, goats, cattle, horses, dogs, cats and bats [671].

Incubation period: 5.5 days (range 4-7 days) [671].

Significant epidemiological characteristics:

Vaccine: None.

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [930].

Reservoir: Not found

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 503 for "Yersiniosis," 4,983 for "*Yersinia enterocolitica*," 503 for "Yersiniosis" and 2,017 for "*Yersinia pseudotuberculosis*".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide [671].

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	1	7	2	N/A	[931]

Mapping recommendation: Option 1; do not map. Yersiniosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of "global" distribution shown on thumbnail maps.

Disease: Zika.

ICD-10 Code: A92.8.

Transmission category: Vector-borne.

Agent: Virus-RNA.

Taxonomy: Flaviridae, Group IV, Flavivirus, Zika virus [671, 672].

Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Natural history:

Mode of transmission: Mosquito vector (*Stegomyia* (*Aedes*) spp.) [671].

Reservoir*: Humans, mosquitoes and monkeys [671].

Incubation period: 6.5 days (range 5-8 days) [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: <1; primarily a zoonotic disease [889].

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 68.

GenBank hits on 22/02/12: 14.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: >12.

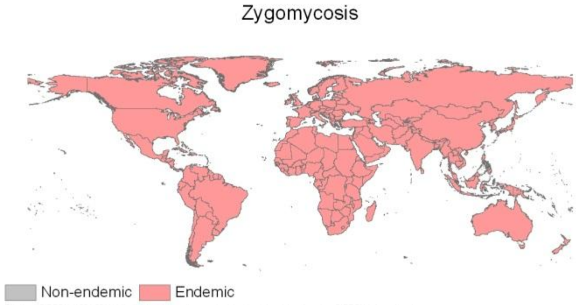
Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	0	7.5	2	0	[932]
Disease	100	4.5	2	33	[933]

Mapping recommendation: Option 3; map maximum potential range based on vector and reservoir species.

There were approximately 6 occurrence points per country based on 68 results for “Zika” in PubMed and 12 endemic countries listed in the GIDEON database. With fewer than 25 hits per it is possible to map the maximum potential range of this disease through use of vector distribution data.

Future mapping potential: Generate known distribution map using systematic searches of occurrence data for the disease and its *Aedes* vector. If occurrence data for this mosquito species is not available digitized versions of expert opinions of their ranges could usefully inform future mapping.



Citation: GIDEON (1994-2011) http://web.gideononline.com/web/epidemiology/. Los Angeles: GIDEON Informatics, Inc.

Disease: Zygomycosis.

ICD-10 Code: B46

Transmission category: Direct contact

Agent: Fungus

Taxonomy: Fungi

Zygomycota, Zygomycetes, Mucorales, Mucoraceae,
Mucor spp.
Rhizopus spp. (*R. arrhizus* is most common)
Absidia spp.
Saksenaeaceae,
Saksenaea spp. [671, 672].

Natural history:

Mode of transmission: Inhalation; direct contact; fomites (bandages) [671].

Reservoir*: Saprophytes

Incubation period: Variable [671].

Significant epidemiological characteristics:

Vaccine: None

Estimated R_0 value(s) from published literature:

Human: Not found.

Reservoir: Not found.

Map(s) from published literature:

Total available literature:

PubMed hits on 04/11/11: 947 for "Zygomycosis," 2,181 for "*Mucor*," 2,607 for "*Rhizopus*," 442 for "*Absidia*" and 53 for "*Saksenaea*".

GenBank hits on 22/02/12: N/A.

HealthMap feeds 2006-2011: N/A.

ProMED feeds 1994-2011: N/A.

BioCaster feeds 2006-2011: N/A.

Approximate number of endemic countries: Worldwide.

Previously published maps:

D/V/H	Geographic scope	Data quality score	Mapping option used	Metascore	Reference
Disease	34	6.5	2	N/A	[934]

Mapping recommendation: Option 1; do not map. Zygomycosis is endemic worldwide.

Future mapping potential: None. However, human population density maps may be useful to help identify high infection potential areas and to give a more realistic depiction of “global” distribution shown on thumbnail maps.

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