Vector Hazard Report: Middle East

Part 2: Sand Flies, Ticks and Host Densities

Information gathered from products of The Walter Reed Biosystematics Unit (WRBU)

Catalog of Subfamily Phlebotominae

VectorMap

All material in this brief is provided for your information only and may not be construed as medical advice or instruction. No action or inaction should be taken based solely on the contents of this information; instead, readers should consult appropriate health professionals on any matter relating to their health and well-being.
# Table of Contents

## 1: Sand Fly-borne Diseases

- Cutaneous Leishmaniasis background
- Estimates of CL incidence
- Cutaneous (tropica) Leishmaniasis Endemic Areas
- Cutaneous (major) Leishmaniasis Endemic Areas, WHO 2012

- Visceral Leishmaniasis Background
- Estimates of VL Incidence
- Visceral Leishmaniasis Endemic Areas

- Sand Fly Vector Habitat Suitability Models
  - *Phlebotomus papatasi*
  - *Phlebotomus sergenti*
  - *Phlebotomus alexandri*

- Notes on Medically Important Sand Flies
  - *Phlebotomus papatasi*
  - *Phlebotomus sergenti*
  - *Phlebotomus alexandri*

## 2: Tick-borne Diseases

- Crimean-Congo Hemorrhagic Fever
- Relapsing Fever Borrelia

- Tick Vector Habitat Suitability Models
  - *Rhipicephalus annulatus*
  - *Amblyomma reflexus*
  - *Rhipicephalus microplus*
  - *Ornithodoros foleyi*

## 3: Host Densities

- Human population density
- Domestic animal population density
1: Sand Fly-borne Diseases

Cutaneous Leishmaniasis background
Estimates of CL incidence
Cutaneous (tropica) Leishmaniasis Endemic Areas
Cutaneous (major) Leishmaniasis Endemic Areas, WHO 2012

Visceral Leishmaniasis Background
Estimates of VL Incidence
Visceral Leishmaniasis Endemic Areas

Sand Fly Vector Habitat Suitability Models
*Phlebotomus papatasi*
*Phlebotomus sergenti*
*Phlebotomus alexandri*

Notes on Medically Important Sand Flies
*Phlebotomus papatasi*
*Phlebotomus sergenti*
*Phlebotomus alexandri*
Cutaneous Leishmaniasis (CL) is caused by an infection of protozoan parasites of the genus *Leishmania*. In the Middle East, the parasites are spread by the bite of sand flies of the genus *Phlebotomus*. (Dostalova and Volf, 2012)

CL can cause skin sores which range in size and appearance. Sores can develop into skin ulcers and can also cause swollen glands near the sores. The CDC estimates that world-wide there are approximately 0.7 to 1.2 million cases of cutaneous leishmaniasis annually. (CDC, 2014)

The World Health Organization estimates that approximately 95% of CL cases occur in the Americas, the Mediterranean basin, and the Middle East and Central Asia. (WHO, 2014)
Estimates of Cutaneous Leishmaniasis Incidence


Back to Table of Contents
Cutaneous (tropica) leishmaniasis endemic areas, WHO 2012
Cutaneous (major) leishmaniasis endemic areas, WHO 2012
Visceral Leishmaniasis

Visceral Leishmaniasis (VL) is also caused by an infection of protozoan parasites of the genus Leishmania. In the middle East, the parasites are spread by the bite of sand flies of the genus Phlebotomus. (Dostalova and Volf, 2012)

Unlike CL, Visceral leishmaniasis (VL) affects internal organs and many infected people may not show symptoms at all. According to the CDC, clinical evidence of visceral leishmaniasis includes swollen spleen and liver along with fever and weight loss. The CDC estimates that world-wide there are approximately 0.2 to 0.4 million cases of visceral leishmaniasis annually. (CDC, 2014)

The World Health Organization estimates that approximately 90% of new cases occur in six countries: Bangladesh, Brazil, Ethiopia, India, South Sudan, and Sudan. (WHO, 2014)
Estimates of Visceral Leishmaniasis Incidence, 2012
Visceral Leishmaniasis Endemic Areas, WHO 2010
Habitat suitability models: Sand Fly Vectors
Habitat suitability model: *Phlebotomus papatasi*
Habitat suitability model: *Phlebotomus sergenti*
Habitat suitability model: *Phlebotomus alexandri*
Medically Important Sand Flies

**Phlebotomus papatasi**

Often domestic, anthropophilic and abundant in (small) rodent burrows; proven vector of L. major to man and gerbils in U.S.S.R., Saudi Arabia, southern Morocco and central Tunisia (Killick-Kendrick, 1990; Killick-Kendrick et al., 1985; Lane & Fritz, 1986; Perffi’ev, 1966); suspected vector of L. arablea in Saudi Arabia (Killick-Kendrick, 1990). Of several Phlebovirus serotypes isolated from P. papatasi (in north Africa, southern Europe, Iran and central Asia), Naples and Sicilian were found infecting man only where this sandfly occurs (Tesh, 1988; Tesh et al., 1976).

[WRBU Species Page](#)

[Back to Table of Contents](#)
**Phlebotomus sergenti**

Extends further north than P. papatasi; considered a vector of *L. tropica* in Afghanistan, Crete, Iran, Iraq and India on the basis of distribution and ecology (Adler & Theodor, 1957; Lewis & Ward, 1987); susceptible to *L. major* and *L. tropica* and believed to transmit the latter in U.S.S.R. (Saf’janova, 1979)

WRBU Species Page
Medically Important Sand Flies

Phlebotomus alexandri

Proven vector of VL (L. donovani) in China (Killick-Kendrick, 1990; Lengo 1988); anthropophilic, montane species in Afghanistan (Artemiev, 1978a); suspected vector of CL (L. major) in Iran (Javadian et al., 1977), Mongolia and Turkmenistan (Dedet, 1979; Killick-Kendrick, 1990); and suspected vector of L. tropica killicki in Tunisia (Croset et al., 1978; Killick-Kendrick, 1990).
Tick-borne Diseases

1. **Crimean-Congo Hemorrhagic Fever**

2. **Relapsing Fever Borrelia**

3. **Tick Vector Habitat Suitability Models**
   - *Rhipicephalus annulatus*
   - *Amblyomma reflexus*
   - *Rhipicephalus microplus*
   - *Ornithodoros foleyi*
Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne disease caused by the virus *Nairovirus* in the family *Bunyaviridae*. Symptoms of CCHF include headache, fever, generalized pain, and vomiting. Symptoms can also include red eyes, a flushed face, a red throat, and petechiae. Severe bruising and bleeding can also occur. According to the CDC mortality rates for CCHF infection can range from 9% to 50% (CDC, 2014).

CCHF is spread by the bite of ticks in the family *Ixodid* and many wild and domestic animals can serve as a reservoir for the virus. The virus can also be spread from person to person through contact with blood and other bodily fluids (CDC, 2014).

According to the World Health Organization (WHO) CCHF is endemic in all of Africa, the Balkans, the Middle East and in South Asia (WHO, 2014).
Tick-borne relapsing fever (TBRF) is caused by a bacterial infection of certain species of the genus *Borrelia*. Infection is characterized by episodes of fever followed by an interval of no fever followed by a return of the fever. This cycle can occur 1 to 4 times and can also include generalized pain, nausea, vomiting, anorexia, dry cough, light sensitivity, rash, neck pain, eye pain, confusion, and dizziness (CDC, 2014).

TBRF is spread by the bite of infected ticks of the genus *Ornithodoros*. According to the CDC, humans most commonly come into contact with these ticks when sleeping in rodent infested structures (CDC, 2014).

TBRF has been reported from the Middle East, Africa, Europe and North America. TBRF is endemic in the north-west of the Islamic Republic of Iran (Mahram and Ghavami 2009).
Habitat suitability model: *Rhipicephalus annulatus*
Habitat suitability model: *Amblyomma reflexus*
Habitat suitability model: *Rhipicephalus microplus*
Habitat suitability model: *Ornithodoros foleyi*
Host Densities

Contents:

1. Human population density
2. Domestic animal population density

Back to Table of Contents
Human Density
People per sq. mile, LandScan 2011

Back to Table of Contents
References

Sand Flies
Maxent model for P. sergenti habitat suitability. GlobalUniqueIdentifier: USNM:SandflyModel:P_sergenti_Dornak_1
Maxent model for P. papatasi habitat suitability. GlobalUniqueIdentifier: USNM:SandflyModel:P_papatasi_Dornak_1
Maxent model for P. alexandri habitat suitability. GlobalUniqueIdentifier: USNM:SandflyModel:P_alexandri_Dornak_1

Ticks
Maxent model for Rhipicephalus annulatas habitat suitability. L. Dornak. GlobalUniqueIdentifier: USNM:TickModel:R_annulatus_Dornak_1
Maxent model for Amblyomma reflexus habitat suitability. L. Dornak. GlobalUniqueIdentifier: USNM:TickModel:A_reflexus_Dornak_1
Maxent model for Ornithodoros foleyi habitat suitability. L. Dornak. GlobalUniqueIdentifier: USNM:TickModel:O_foleyi_Dornak_1

Sand Fly and Tick Photos Courtesy of the AFPMB, Judith Stoffer (Waler Reed Biosystematics Unit) and Westbrook, Catherine. Identifying Southwest Asian Sand Flies: With Emphasis on Common Iraqi Phlebotomus Species.

Back to Table of Contents
**References con’t**

**Host Densities:**

- People/1 Sq Km. This Product Was Made Utilizing The Landscan (2011)™ High Resolution Global Population Data Set Copyrighted By UT-Battelle, LLC, Operator Of Oak Ridge National Laboratory Under Contract No. DE-AC05-00OR22725 With The United States Department Of Energy. The United States Government Has Certain Rights In This Data Set. Neither Ut-Battelle, Llc Nor The United States Department Of Energy, Nor Any Of Their Employees, Makes Any Warranty, Express Or Implied, Or Assumes Any Legal Liability Or Responsibility For The Accuracy, Completeness, Or Usefulness Of The Data Set. Available At Http://Www.Ornl.Gov/Sci/Landscan/

- Global Cattle density (2005): The Gridded Livestock of the World FAO (2007). This dataset forms part of a global livestock mapping project by the Food and Agriculture Organization’s Animal Production and Health Division (FAO-AGA). Predicted global cattle density (2005), corrected for unsuitability, adjusted to match FAOSTAT totals for the year 2005. Number per square km, spatial resolution of 3 arc minutes (approx. 5km). These data are freely available through the GLW website, through an interactive web application known as the Global Livestock Production and Health Atlas (GLiPHA), and through the FAO GeoNetwork data repository (see http://www.fao.org/AG/AGAInfo/resources/en/glw/GLW_dens.html)

- Global Sheep density (2005): The Gridded Livestock of the World FAO (2007). This dataset forms part of a global livestock mapping project by the Food and Agriculture Organization’s Animal Production and Health Division (FAO-AGA). Predicted global sheep density (2005), corrected for unsuitability, adjusted to match FAOSTAT totals for the year 2005. Number per square km, spatial resolution of 3 arc minutes (approx. 5km). These data are freely available through the GLW website, through an interactive web application known as the Global Livestock Production and Health Atlas (GLiPHA), and through the FAO GeoNetwork data repository (see http://www.fao.org/AG/AGAInfo/resources/en/glw/GLW_dens.html)

- Global Poultry density (2005): The Gridded Livestock of the World FAO (2007). This dataset forms part of a global livestock mapping project by the Food and Agriculture Organization’s Animal Production and Health Division (FAO-AGA). Predicted global poultry density (2005), corrected for unsuitability, adjusted to match FAOSTAT totals for the year 2005. Number per square km, spatial resolution of 3 arc minutes (approx. 5km). These data are freely available through the GLW website, through an interactive web application known as the Global Livestock Production and Health Atlas (GLiPHA), and through the FAO GeoNetwork data repository (see http://www.fao.org/AG/AGAInfo/resources/en/glw/GLW_dens.html)

- Global Goat density (2005): The Gridded Livestock of the World FAO (2007). This dataset forms part of a global livestock mapping project by the Food and Agriculture Organization’s Animal Production and Health Division (FAO-AGA). Predicted global goat density (2005), corrected for unsuitability, adjusted to match FAOSTAT totals for the year 2005. Number per square km, spatial resolution of 3 arc minutes (approx. 5km). These data are freely available through the GLW website, through an interactive web application known as the Global Livestock Production and Health Atlas (GLiPHA), and through the FAO GeoNetwork data repository (see http://www.fao.org/AG/AGAInfo/resources/en/glw/GLW_dens.html)
The Walter Reed Biosystematics Unit is part of the Walter Reed Army Institute of Research and is based at the Smithsonian Institution Museum Support Center. To access taxonomic keys, the Systematic Catalog of Culicidae or to learn more about WRBU visit www.wrbu.org.

VectorMap is only as good as the data you provide. If you have collection records, models or pathogen testing results please contact the VectorMap team to learn how to contribute data at mosquitomap@si.edu.


The published material reflects the views of the authors and should not be construed to represent those of the Department of the Army or the Department of Defense.