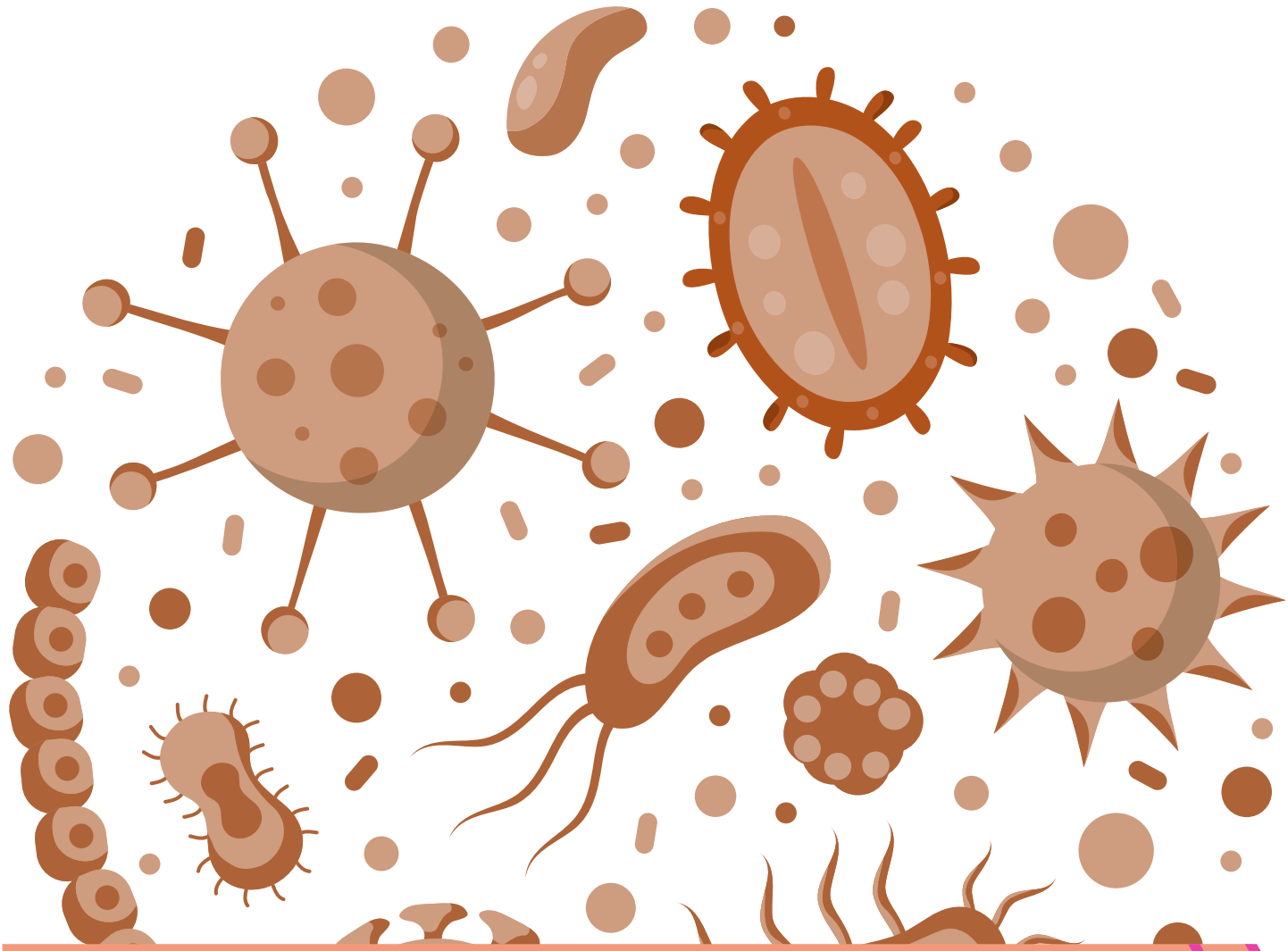
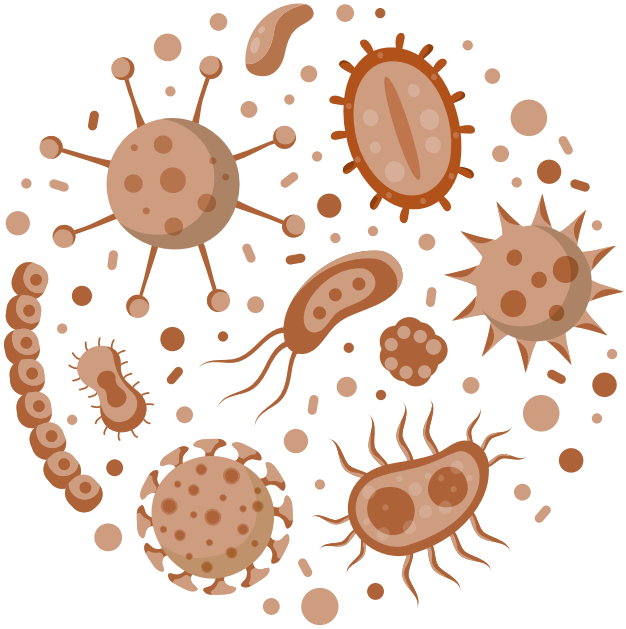
MediLabSecure

INSTITUT PASTEUR

PATHOGENS BOOKLET



www.medilabsecure.com

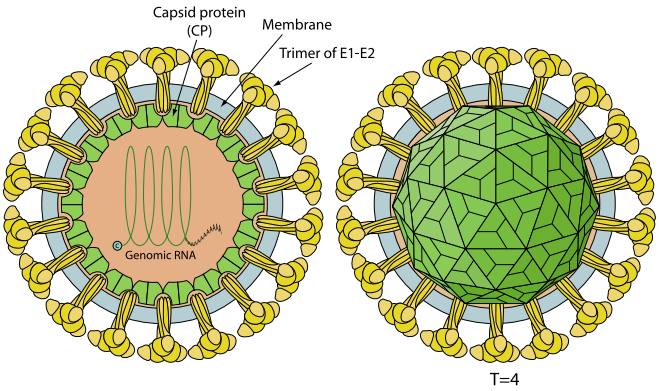


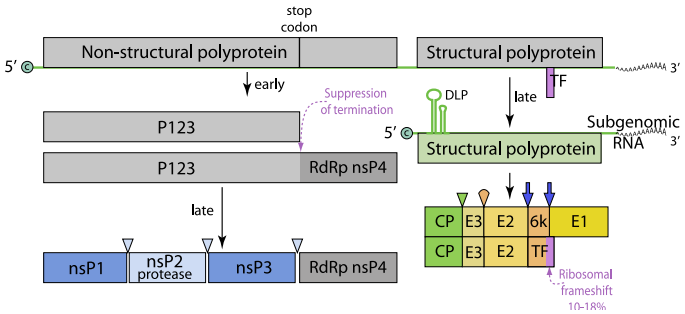
CONTENTS

CHIKUNGUNYA VIRUS

Family ***Togaviridae***
Genus ***Alphavirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,600 nt



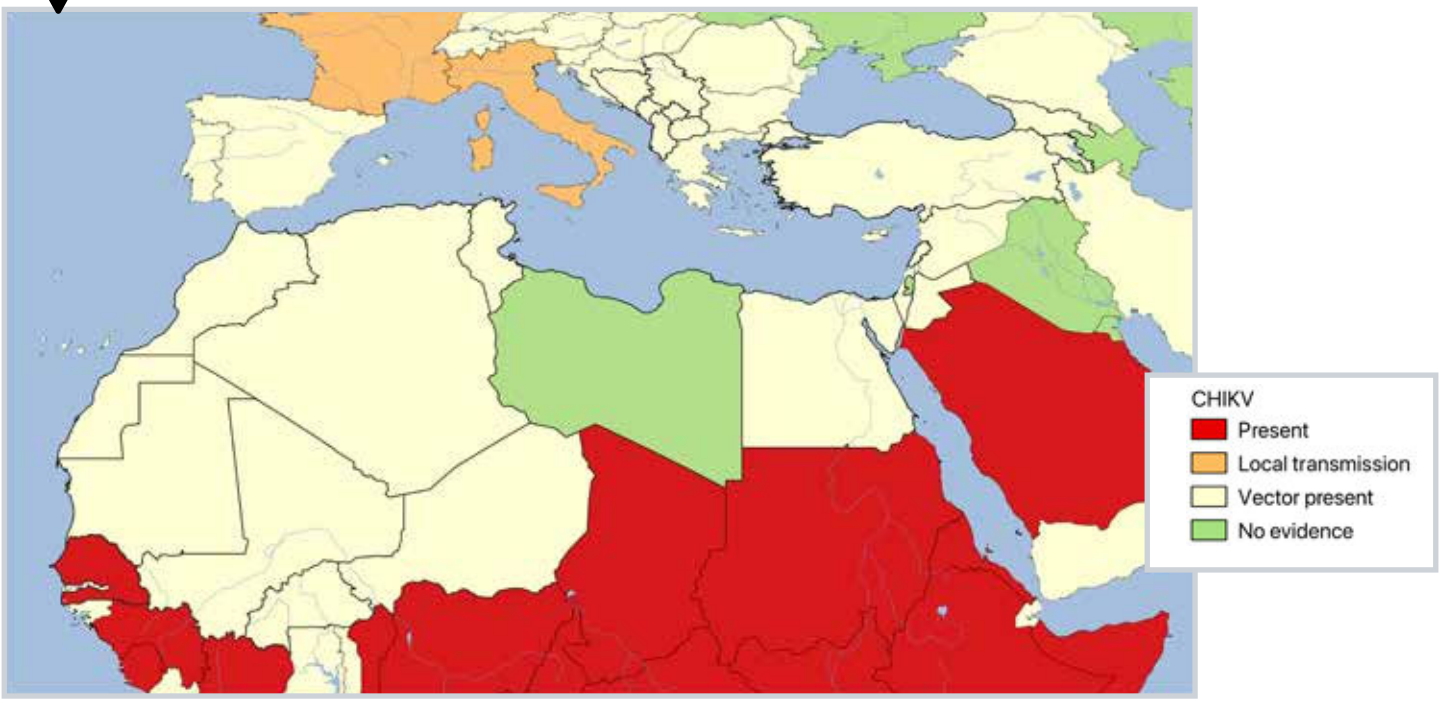


The genome is translated into one polyprotein.

Transmission

Vector	*Aedes* mosquitoes (*Ae. aegypti* & *Ae. albopictus*)
Reservoir host	Primates
Transmission	

Distribution



Geographical distribution	Mainly detected in Southern and Eastern Asia and in Central Africa. Present in America since 2013. Autochthonous cases detected in Europe (Italy, France) since 2007.
Emerging or Endemic?	Endemic in South-East Asia, Central Africa, South America and Indian Ocean. Emerging in Europe.

CHIKUNGUNYA VIRUS

Family ***Togaviridae***
Genus ***Alphavirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,600 nt

Clinical signs

Chikungunya virus causes severe, often debilitating joint pain in infected patients. Sometimes accompanied with headache, fever, severe muscle pain, rash, swelling in cervical lymph nodes and conjunctivitis.
Complicated forms of severe neuropathology are reported.

Incubation period	**2–10 days** after the bite from an infected mosquito
Mortality Rate	☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention
Mosquito bite prevention; surveillance and control of vector mosquitoes to reduce the transmission. Awareness and education activities for the general population.

Vaccine
In development, none commercialized yet.

Treatment
Treatment is supportive, based on pain medication and anti-inflammatory drugs.

Diagnostic tests

Type of Samples	Blood/serum
Human diagnostic tests	- 1 to 5 days after onset of symptoms: RT-qPCR and/or viral isolation - 5 to 7 days after onset of symptoms: RT-qPCR + Serology IgG/IgM - > 7 days after onset of symptoms: Serology IgG/IgM
Mosquitoes	RT-qPCR and/or viral isolation

Biosafety

Biosafety level 3

BSL3 for RT-PCR, viral culture and mosquito manipulations.

References • Tools • Useful links

https://www.who.int/news-room/fact-sheets/detail/chikungunya

https://www.pasteur.fr/en/medical-center/disease-sheets/chikungunya-0

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

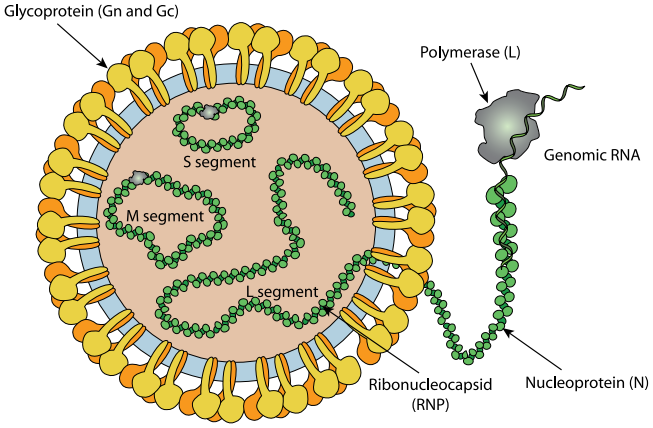
CRIMEAN-CONGO HAEMORRHAGIC FEVER

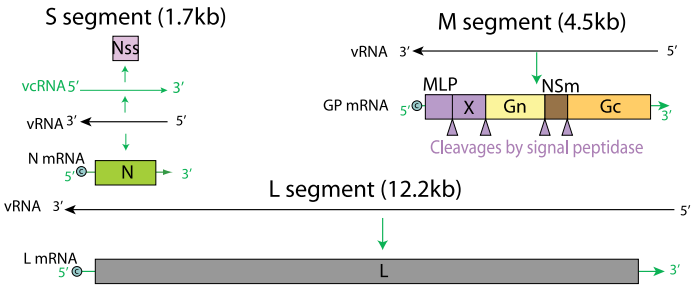
VIRUS

Family ***Nairoviridae***

Genus ***Orthonairovirus***

Linear genome
Negative sense single stranded RNA
Genome size: ~11-22,000 nt





The viral proteins are encoded by 3 genome segments.

Transmission

Vector Ticks (*Hyalomma ; Amblyomma ; Rhipicephalus*)

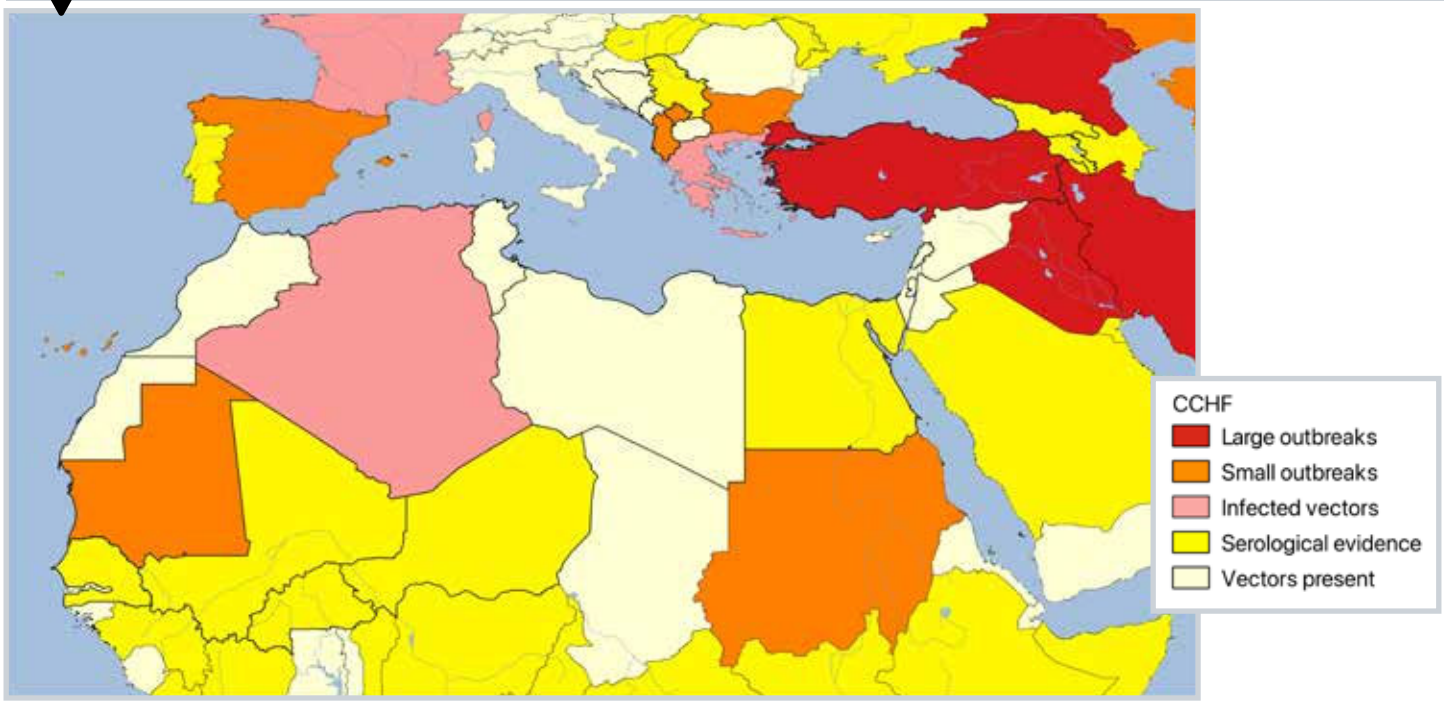
Reservoir host Cattle, hares, hedgehogs, rodents

Transmission

Organs, blood

Secretions, blood, bodily fluids

Distribution



Geographical distribution Present in over 30 countries, including in Western, Central and South Africa, Central Asia, the Middle East, and Southeastern Europe.

Emerging or Endemic? Endemic in Africa, Türkiye, Balkan countries, Middle East and Asia. Emerging in Spain and some North African countries.

CRIMEAN-CONGO HAEMORRHAGIC FEVER

VIRUS

Family ***Nairoviridae***

Genus ***Orthonairovirus***

Linear genome
Negative sense single stranded RNA
Genome size: ~11-22,000 nt

Clinical signs

CCHF is characterized by a sudden onset of high fever, chills, severe headache, dizziness, back and abdominal pains. Additional symptoms include nausea, vomiting, diarrhea and neuropsychiatric and cardiovascular changes.
In severe cases, haemorrhagic manifestations, ranging from petechiae to large areas of ecchymosis, develop.

Incubation period	**3 days** after tick bite **6-13 days** after contact with infected body fluids
Mortality Rate	☒ HIGH ☒ MEDIUM ☐ LOW

Prevention and treatment

Prevention
Ticks surveillance, biosecurity measures in high risk occupations (slaughterhouse workers, veterinarians, shepherds, farmers, etc.).

Vaccine
None.

Treatment
None. For severe cases, supportive treatment for symptoms.

Diagnostic tests

Type of Samples	Blood, serum, tissue samples
Diagnostic tests	- RT-qPCR on tissues, blood or serum - Viral isolation - ELISA for antigen detection - Serology IgG/IgM (negative in the first days and in fatal disease) - Seroneutralization
Ticks	RT-qPCR and/or viral isolation

Biosafety

Biosafety level 3 - Biosafety level 4

BSL4 for all manipulations.
If not available, inactivation of samples in Glovebox or BSL3 conditions (+ full PPE) and diagnostic procedures under standard laboratory conditions (BSL2).

References • Tools • Useful links

https://www.who.int/news-room/fact-sheets/detail/crimean-congo-haemorrhagic-fever

http://www.sciencedirect.com/science/article/pii/S0166354204001639

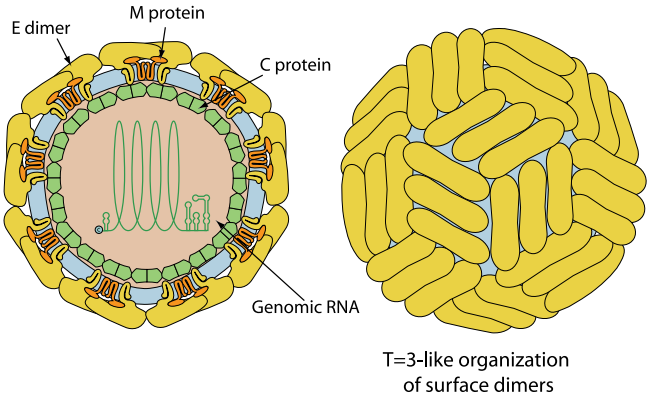
Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

DENGUE VIRUS

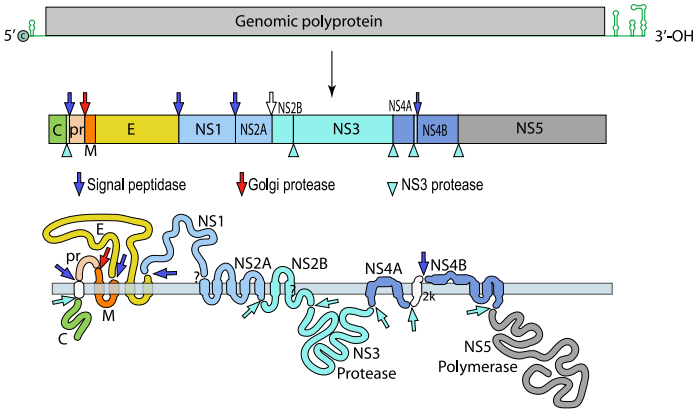
Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,000 nt
4 serotypes



T=3-like organization of surface dimers

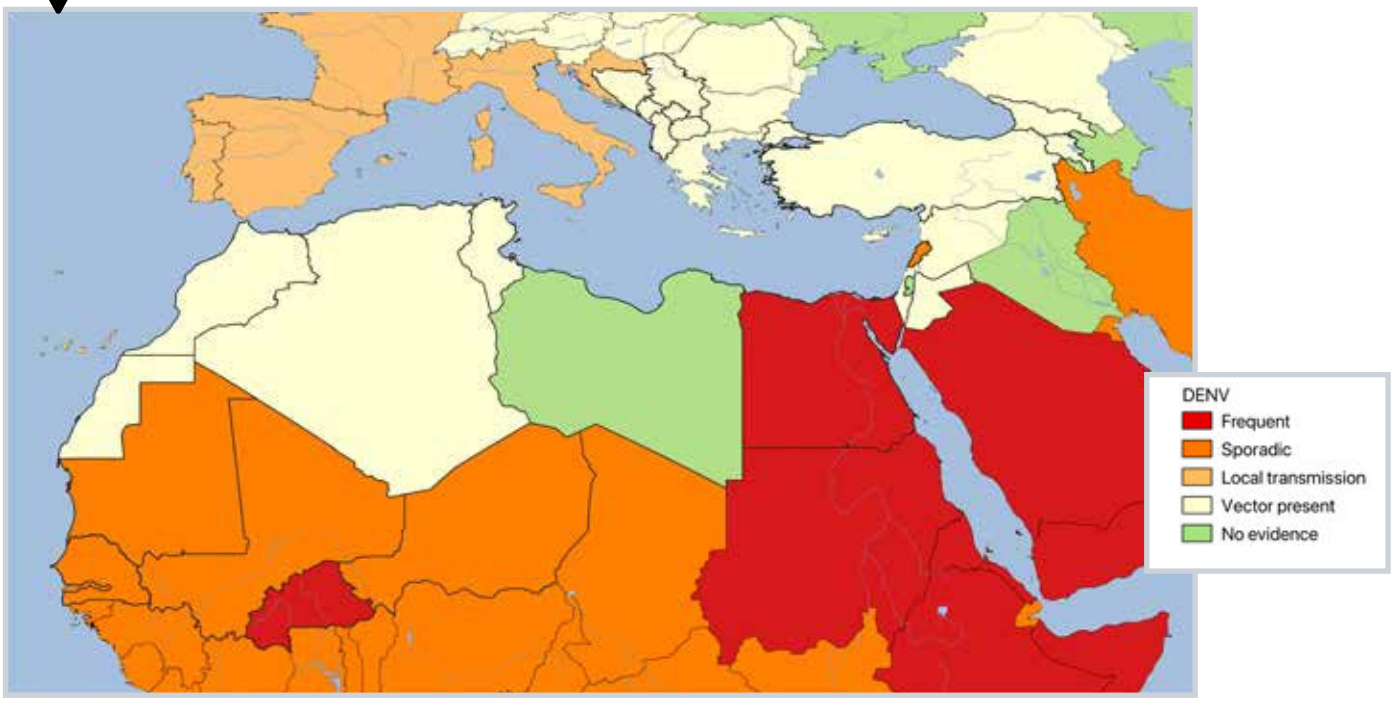


The genome is translated into one polyprotein.

Transmission

Vector	*Aedes* mosquitoes (*Ae. aegypti* & *Ae. albopictus*)
Reservoir host	Primates
Transmission	

Distribution



Geographical distribution	Dengue is found in tropical and sub-tropical regions worldwide, mostly in urban and semi-urban areas.
Emerging or Endemic?	Endemic in more than 100 countries in Africa, America, Eastern Mediterranean, South-East Asia and the Western Pacific. Emerging in Europe.

DENGUE

VIRUS

Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,000 nt
4 serotypes

Clinical signs

Dengue is suspected with high fever (40°C) and 2 of the following symptoms: severe headache, pain behind the eyes, muscle and joint pains, nausea, vomiting, swollen glands or rash. Severe dengue is a potentially deadly complication due to plasma leaking, fluid accumulation, respiratory distress, severe bleeding or organ impairment.

Incubation period	**4–10 days** after the bite from an infected mosquito
Mortality Rate	☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention

Combat vector mosquitoes. Awareness and education activities for the general population.

Vaccine

Dengvaxia, registered for use on individuals who suffered a previous dengue infection.

Treatment

No treatment.
For severe forms, supportive treatment for symptoms.

Diagnostic tests

Type of Samples	Blood, serum, tissues
Human diagnostic tests	**1-5 days after onset of symptoms:** - Isolation of virus from blood, serum or tissues - Detection of nucleic acid (RT-PCR) in blood, serum, plasma or tissues - Antigen detection in serum **After 5 days:** - Dengue specific antibody response (IgM or IgG) in serum or plasma

Biosafety

Biosafety level 2

BSL2 for viral culture and nucleic acid/antigen detection.

References • Tools • Useful links

http://www.who.int/mediacentre/factsheets/fs117/en/

https://www.pasteur.fr/en/medical-center/disease-sheets/dengue

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

HUMAN CORONAVIRUSES

VIRUSES

Family ***Coronaviridae***

Genus & Subgenus

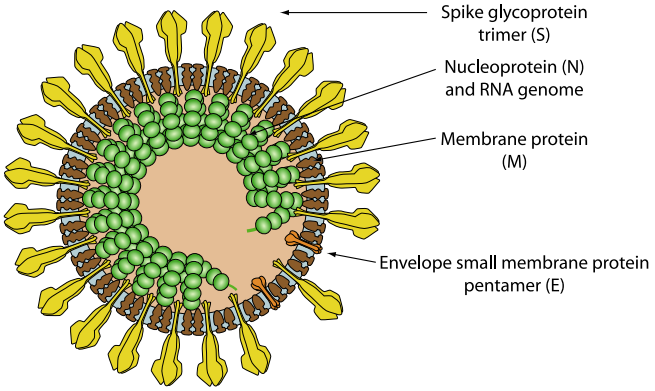
Linear positive sense single stranded RNA
Genome size: 27.000 to 32.000 nt

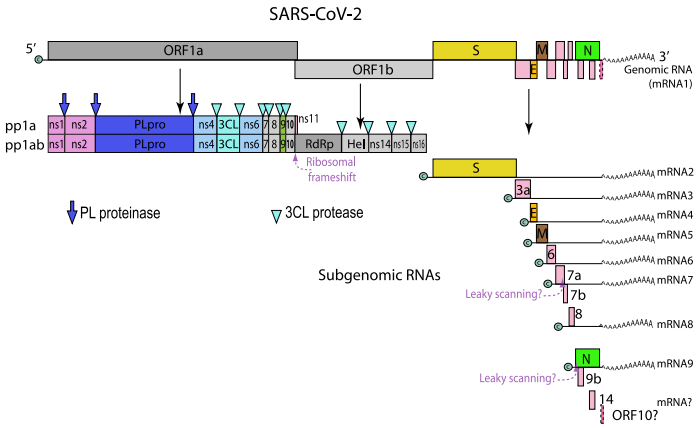
Alphacoronavirus
Species: *HCoV-229E; HCoV-NL63*

Betacoronavirus
Subgenus: *Embecovirus*
Species: *HCoV-HKU1; HCoV-OC43*

Subgenus : ***Sarbecovirus***
Species: *SARS-CoV; SARS-CoV-2*

Subgenus : ***Merbecovirus***
Species: *MERS-CoV*





Transmission

Vector	SARS-CoV / SARS-CoV-2 / MERS-CoV		
Reservoir host	MERS-CoV		
Transmission		Raw milk	Airborne

Distribution

Geographical distribution

SARS-CoV emerged in China in 2002. The virus spread in 29 countries carried by patients. The epidemic is thought to be extinct since 2004.

MERS-CoV emerged in Saudi-Arabia in 2012. The virus is endemic in the Middle-East. It spread in 27 countries carried by patients often infected during the pilgrimage to Mecca.

SARS-CoV-2 emerged in China in 2019 and caused a global pandemic. The virus is now endemic worldwide.

HUMAN CORONAVIRUSES

VIRUSES

Family ***Coronaviridae***

Genus & Subgenus

Linear positive sense single stranded RNA
Genome size: 27.000 to 32.000 nt

Alphacoronavirus	***Betacoronavirus***	Subgenus : ***Sarbecovirus***	Subgenus : ***Merbecovirus***
Species: *HCoV-229E; HCoV-NL63*	Subgenus: *Embecovirus* Species: *HCoV-HKU1; HCoV-OC43*	Species: *SARS-CoV; SARS-CoV-2*	Species: *MERS-CoV*

Clinical signs

229E, NL63, HKU1 and OC43 provoke mild respiratory diseases.
SARS and MERS provoke severe respiratory diseases sometimes associated with gastrointestinal symptoms.
COVID-19 (SARS-CoV-2) displays a large panel of symptoms, from asymptomatic cases to severe pneumonia accompanied by various symptoms (neurological, gastrointestinal, etc.)

Incubation period: Varies from **2–15 days** after exposition

Mortality Rate

SARS-CoV-2	☐ **HIGH**	☐ **MEDIUM**	☒ **LOW**
SARS-CoV	☐ **HIGH**	☒ **MEDIUM**	☒ **LOW**
MERS-CoV	☒ **HIGH**	☒ **MEDIUM**	☐ **LOW**

Prevention and treatment

Prevention
Respiratory protections, social distancing, hand sanitation, etc. Awareness and education activities for the general population.

Vaccine
No vaccine for SARS-CoV and MERS-CoV.
Numerous vaccines exist for SARS-CoV-2.

Treatment
Antiviral and monoclonal antibody treatments are available for COVID-19. Severe forms of COVID-19 and MERS necessitate hospitalization and supportive respiratory treatments.

Diagnostic tests

Type of Samples	Respiratory samples (sputum for MERS-CoV), blood/serum, saliva
Diagnostic tests	- RT-qPCR - Antigen detection (Rapid Diagnostic Tests) - Whole genome sequencing for SARS-CoV-2 variant identification - Viral isolation - Serology IgG/IgM for surveillance and epidemiology purposes

Biosafety

Biosafety level 2 - Biosafety level 3

BSL3 (including respiratory PPE) for manipulations and amplification of viruses. After inactivation of samples in glovebox or BSL3, diagnostic procedures can be performed under standard laboratory conditions (BSL2). SARS-CoV-2 diagnostic can be fully performed in BSL2.

References • Tools • Useful links

https://www.who.int/news-room/fact-sheets/detail/middle-east-respiratory-syndrome-coronavirus-(mers-cov)

https://www.who.int/emergencies/diseases/novel-coronavirus-2019

https://covid19.who.int/

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

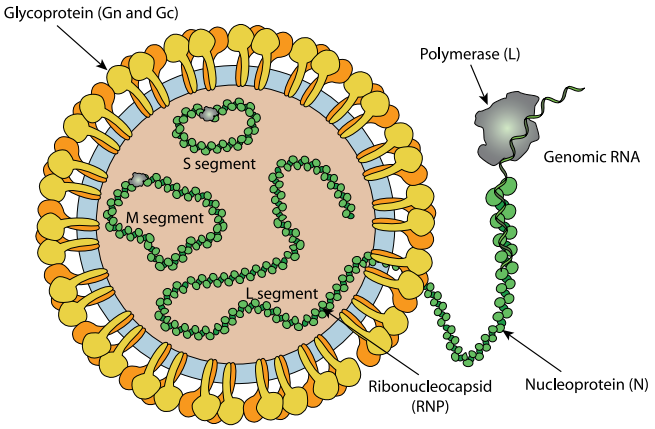
RIFT VALLEY FEVER

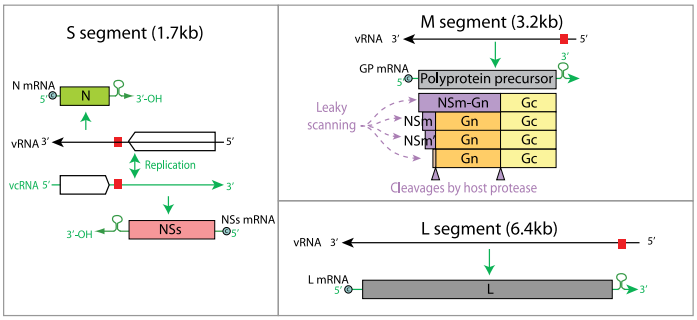
VIRUS

Family ***Phenuiviridae***

Genus ***Phlebovirus***

Linear genome
Negative sense single stranded RNA
Genome size: ~11,900 nt





The genome is organized in 3 segments S, M and L

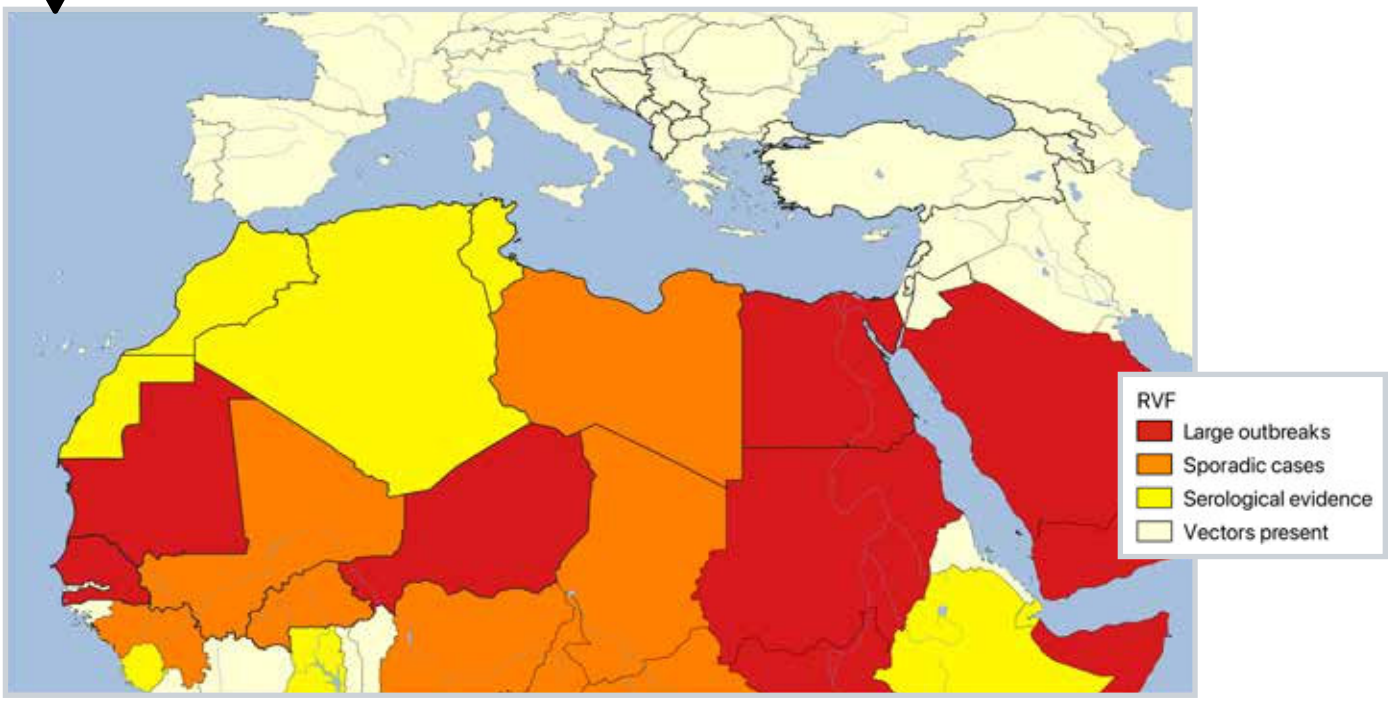
Transmission

Vector *Aedes* mosquitoes - *Culex* mosquitoes

Reservoir host Wild and domestic ruminants. Mosquitos can act as reservoirs, too.

Transmission Organs, blood, unpasteurized milk

Distribution



Geographical distribution Present in sub-Saharan, Western and South Africa. In 2010 the virus was detected for the first time outside Africa, in Arabian Peninsula. Recent outbreaks in Northern Africa.

Emerging or Endemic? Endemic in Eastern and Southern Africa. Emerging in Northern Africa.

RIFT VALLEY FEVER

VIRUS

Family ***Phenuiviridae***

Genus ***Phlebovirus***

Linear genome
Negative sense single stranded RNA
Genome size: ~11,900 nt

Clinical signs

Mild form is characterized by a feverish syndrome with sudden onset of flu-like fever, muscle pain, joint pain and headache. Sometimes neck stiffness, sensitivity to light, loss of appetite and vomiting. Severe form include ocular disease, meningoencephalitis or haemorrhagic fever.

Incubation period	**2–6 days** after the bite from an infected mosquito
Mortality Rate	☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention
Screening of blood donors and serological surveillance in sentinel animals. Surveillance and control of vector mosquitoes. Biosecurity measures in high risk occupations (slaughterhouse workers, veterinarians, shepherds, farmers, etc.). Awareness and education activities for at-risk groups.

Vaccine
No vaccines for humans. Live attenuated and inactivated vaccines available for animals.

Treatment
For severe forms, supportive treatment for s ymptoms.

Diagnostic tests

Type of Samples	Blood, serum, tissue samples
Diagnostic tests	- RT-qPCR on tissues, blood or serum - Viral isolation (Vero, BHK and AP61 mosquito cells) - ELISA for antigen detection - Serology IgG/IgM (cross reactivity with other Phleboviruses) - Seroneutralization
Mosquitoes	RT-qPCR and/or viral isolation

Biosafety

Biosafety level 3

BSL3 for diagnostic procedures, viral culture and mosquito manipulations.

Particular attention must be given to any aerosol production, as it is contagious.

References • Tools • Useful links

https://www.cdc.gov/vhf/rvf/index.html

http://www.who.int/mediacentre/factsheets/fs207/en/

https://www.woah.org/fileadmin/Home/eng/Animal_Health_in_the_World/docs/pdf/Disease_cards/RIFT_VALLEY_FEVER.pdf

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

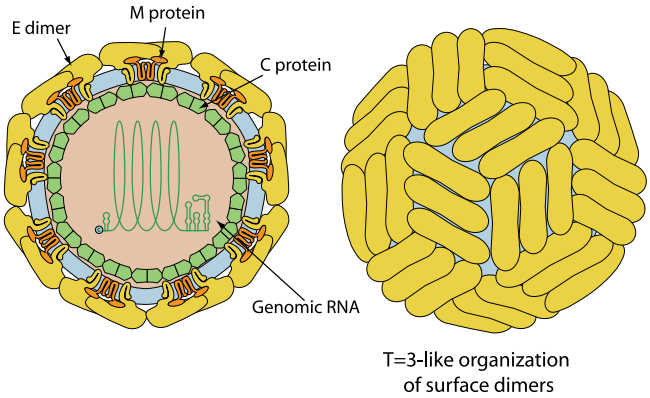
TICK-BORNE ENCEPHALITIS

VIRUS

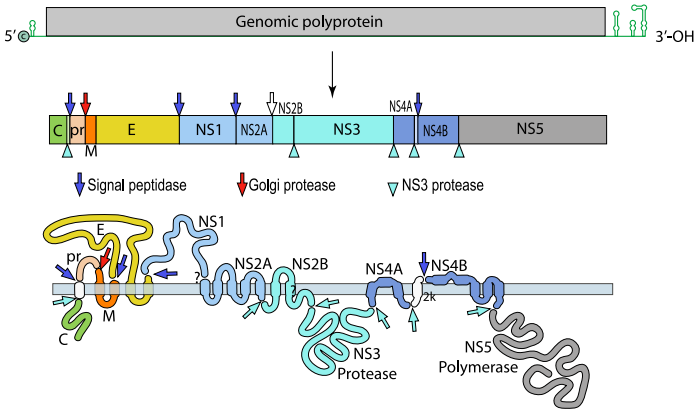
Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: 9.700 to 12.000 nt



T=3-like organization of surface dimers



The genome is translated into one polyprotein.

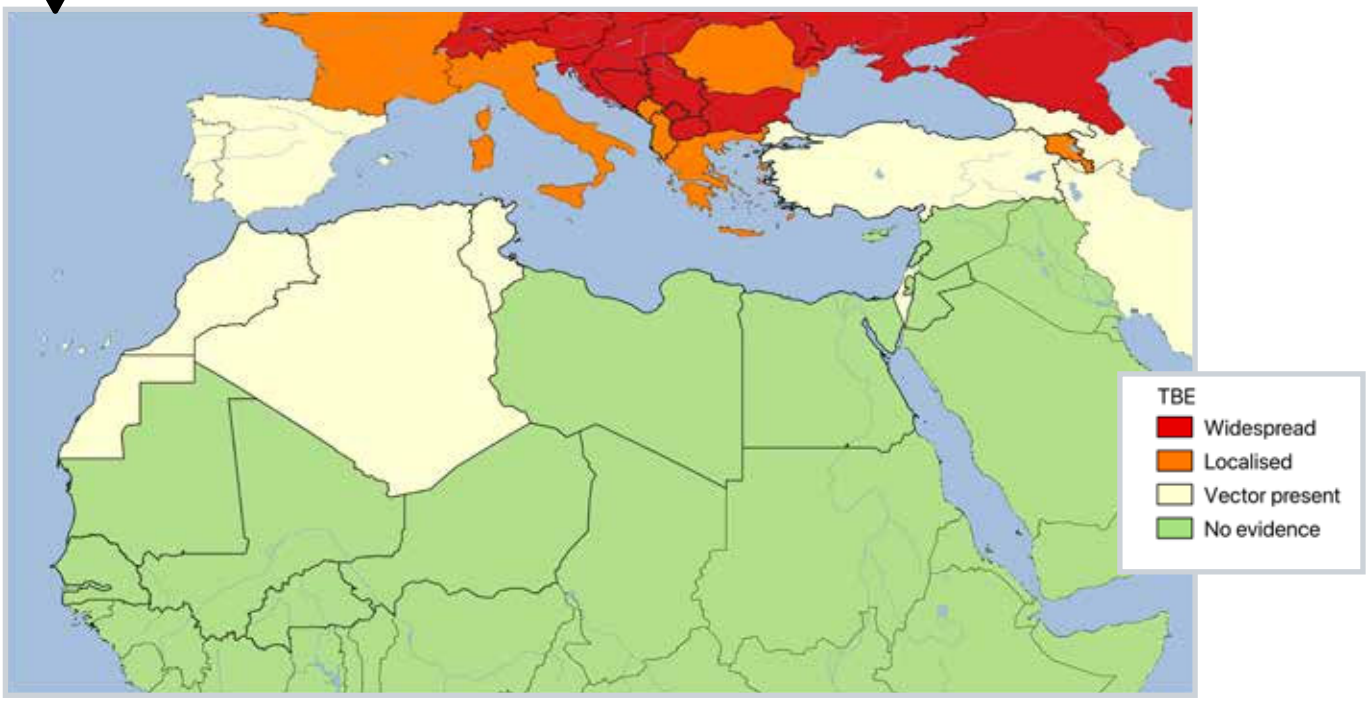
Transmission

Vector Ticks (*Ixodes*)

Reservoir host Rodents.
Cattle, hares and other wild mammals support virus circulation by enabling tick multiplication

Transmission Unpasteurized milk

Distribution



Geographical distribution Present in central, northern and increasingly western Europe, northern China, Mongolia and the Russian Federation, corresponding to the distribution of the ixodid tick reservoir.

Emerging or Endemic? Endemic in many countries in Europe and Asia.
Tends to occur focally even in endemic countries.

TICK-BORNE ENCEPHALITIS

VIRUS

Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: 9.700 to 12.000 nt

Clinical signs

Infection may induce an influenza-like illness followed, in about 30% of cases, by high fever and signs of central nervous involvement. Encephalitis developing during this second phase may result in paralysis, permanent sequelae or death. Severity of illness increases with age of the patient.

Incubation period **7–14 days** after the bite from an infected tick

Mortality Rate ☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention
Ticks surveillance and protection against tick bites.
Awareness and education activities for at-risk groups

Vaccine
One vaccine is available in endemic countries.

Treatment
No specific treatment, supportive treatment for symptoms.

Diagnostic tests

Type of Samples	Blood, cerebrospinal fluid (CSF)
Human Diagnostic tests	- Viral isolation from blood or CSF - IgM ELISA in serum or CSF
Animal Diagnostic tests	- RT-qPCR on tissues or blood - IgG or IgM ELISA - Seroneutralization
Ticks	RT-qPCR and/or viral isolation

Biosafety

Biosafety level 3

BSL3 for all manipulations.
After inactivation of samples in glovebox or BSL3, diagnostic procedures can be performed under standard laboratory conditions (BSL2).

References • Tools • Useful links

https://www.cdc.gov/vhf/tbe/exposure/index.html

https://www.who.int/health-topics/tick-borne-encephalitis#tab=tab_1

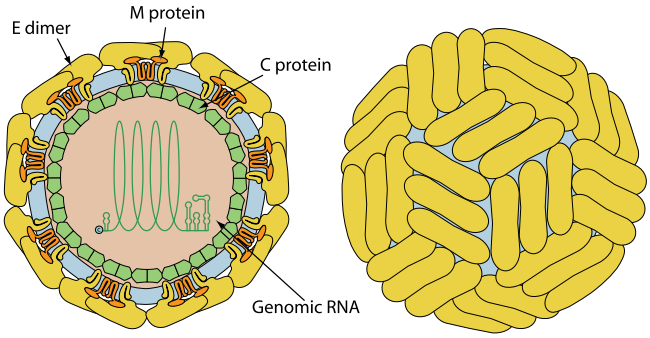
Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

WEST NILE VIRUS

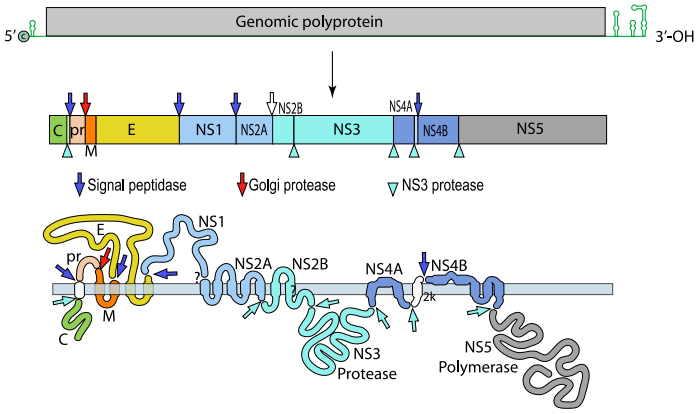
Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,000 nt



T=3-like organization of surface dimers



The genome is translated into one polyprotein.

Transmission

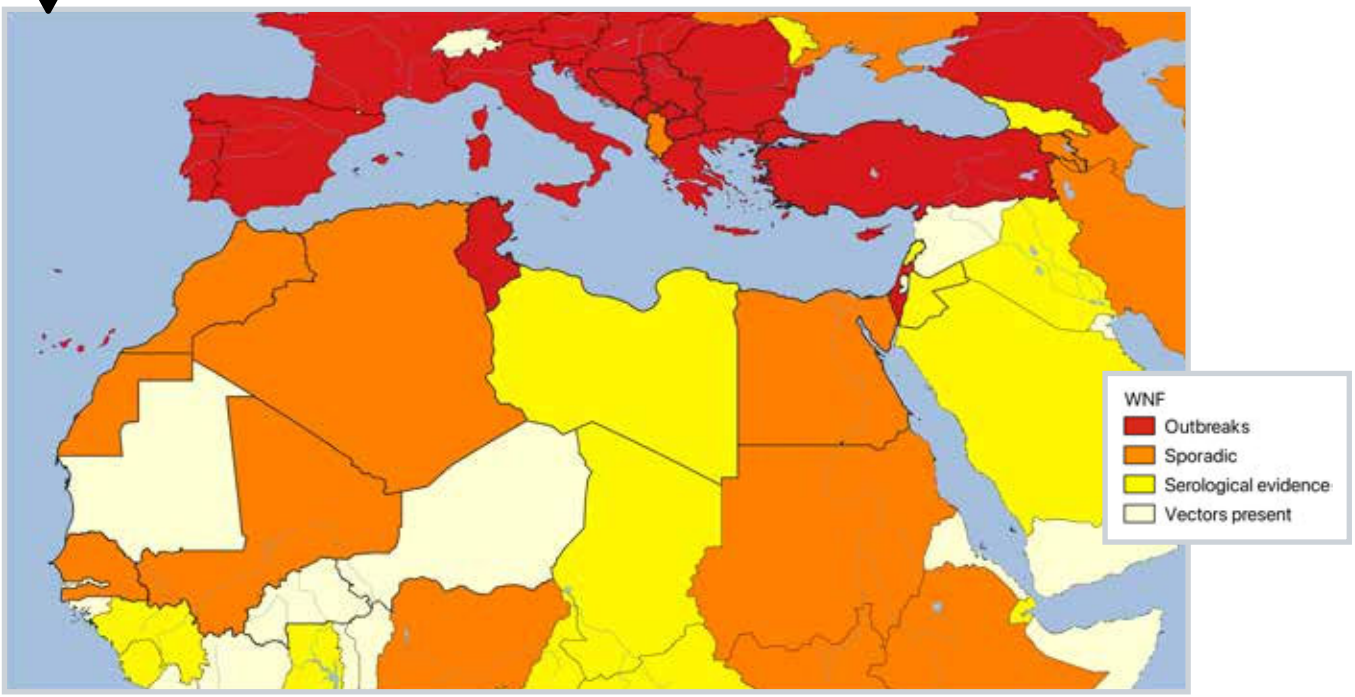
Vector Main: *Culex* pipiens, although other *Culex* species can also transmit the virus depending on the region (*Cx. univittatus, Cx perexiguus, Cx quinquefasciatus,* etc.)

Reservoir host Wild birds (Horses suffer the infection but are dead-end hosts)

Transmission

Transplant, maternal, blood transfusion

Distribution



Geographical distribution WNV is present in all continents except Antarctica.

Emerging or Endemic? Endemic in Africa, America, South-East Asia, Southern Europe, Middle East and the Western Pacific. Emerging in Northern Europe.

WEST NILE VIRUS

Family ***Flaviviridae***
Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~11,000 nt

Clinical signs

Asymptomatic in most cases (70-80%).
Symptoms: include fever, headache, tiredness and body ache, nausea, vomiting, occasionally with a skin rash (on the trunk of the body) and swollen lymph glands.
1 in 150 infected people develop a severe illness that affects the central nervous system and can be lethal

Incubation period **3–14 days** after the bite from an infected mosquito

Mortality Rate ☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention
Surveillance and control of vector mosquitoes to reduce transmission. WNV surveillance programs in birds and mosquitos are essential for early warning.

Vaccine
No vaccine is available for humans, but several have been developed for horses.

Treatment
Treatment is supportive, based on pain medication and anti-inflammatory drugs.

Diagnostic tests

Type of Samples	**Human:** Cerebrospinal fluid (CSF), blood/ serum, urine **Animals:** blood, saerum, organs (central nervous system, spleen, heart, kidney), growing feathers, oral swabs. CSF and urine in horses
Human Diagnostic tests	- Isolation of WNV from blood, urine or CSF - Detection of WNV nucleic acid (RT-PCR) in blood, urine or CSF - WNV specific antibody response (IgM) from CSF or IgG+IgM+seroneutralization in blood
Animal Diagnostic tests	- Isolation of WNV from blood, organs, feathers or CSF - Detection of WNV nucleic acid (RT-PCR) in blood, organs, feathers or CSF - Horses: WNV specific antibody response (IgM) from serum + neurological symptoms

Biosafety

Biosafety level 2 - Biosafety level 3

BSL2 for diagnostic procedures and mosquito manipulations.
BSL3 for viral culture and seroneutralization.

References • Tools • Useful links

http://www.who.int/mediacentre/factsheets/fs354/en/

https://www.cdc.gov/westnile/index.html

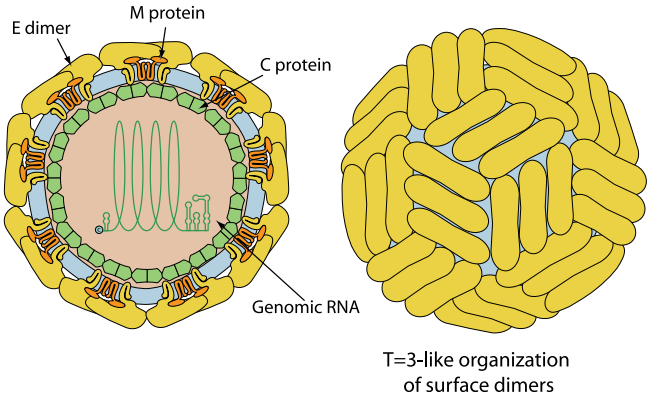
http://www.oie.int/fileadmin/Home/eng/Health_standards/tahc/current/chapitre_wnf.pdf

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS

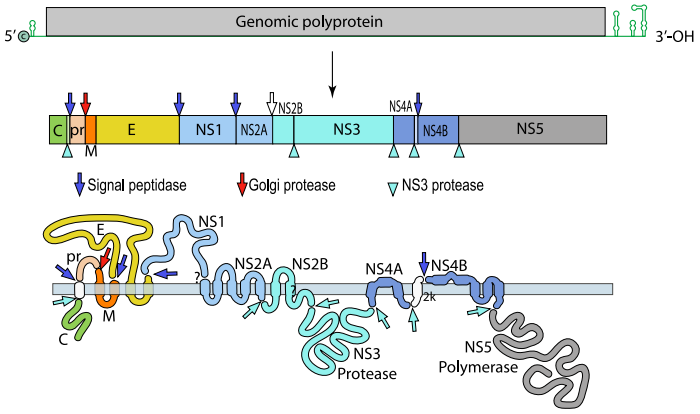
ZIKA VIRUS

Family ***Flaviviridae***
Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~10,000 nt



T=3-like organization of surface dimers



The genome is translated into one polyprotein.

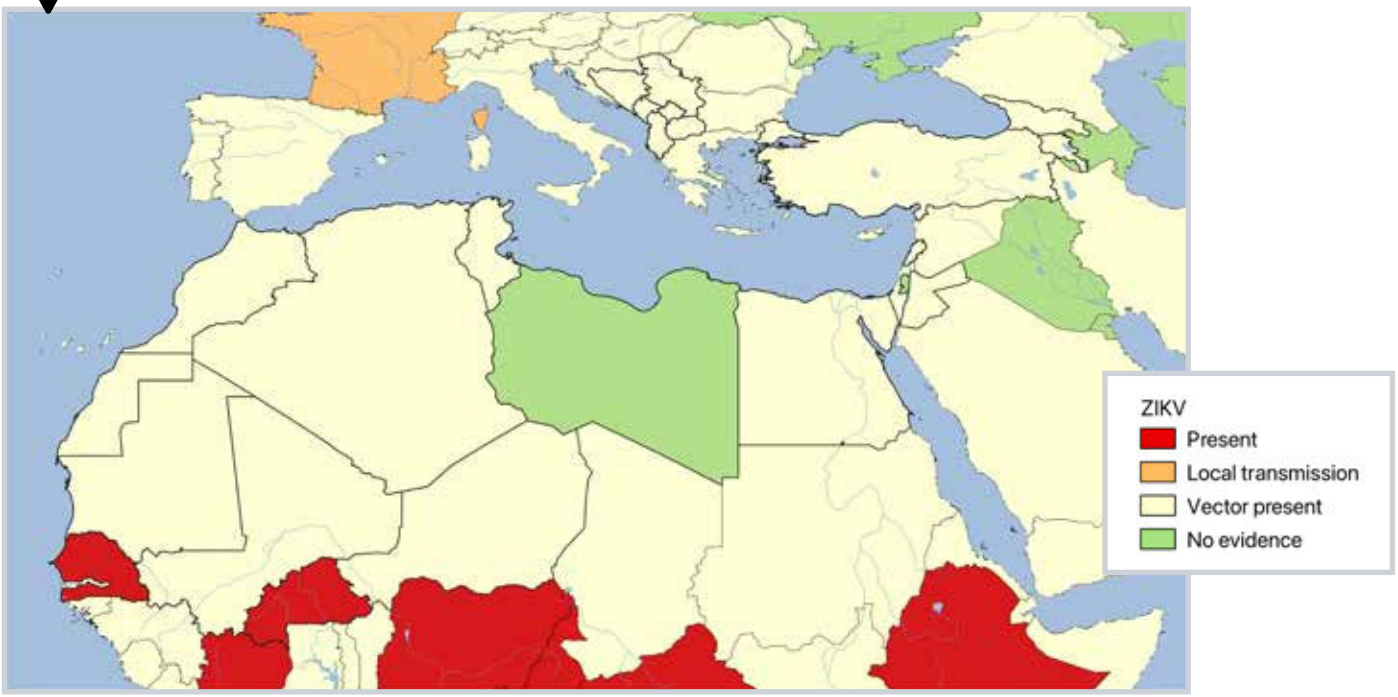
Transmission

Vector *Aedes* mosquitoes (*Ae. aegypti* & *Ae. albopictus*)

Reservoir host Primates

Transmission Maternal, sex, blood

Distribution



Geographical distribution 89 countries and territories in Africa, America, the Caribbean, Asia and the Pacific have reported Zika infection.

Emerging or Endemic? Endemic in Central and West Africa and South America.
Five locally-acquired cases were reported in Europe in 2019.

ZIKA

VIRUS

Family ***Flaviviridae***

Genus ***Orthoflavivirus***

Linear genome
Positive sense single stranded RNA
Genome size: ~10,000 nt

Clinical signs

Mostly asymptomatic. Symptoms include fever, rash, headache, joint pain, conjunctivitis, muscle pain. Complications: Zika virus infection during pregnancy is cause of congenital brain abnormalities, including microcephaly; Zika virus can also trigger Guillain-Barré syndrome.

Incubation period **3–12 days** after the bite from an infected mosquito

Mortality Rate ☐ HIGH ☐ MEDIUM ☒ LOW

Prevention and treatment

Prevention
Mosquito bite prevention; surveillance and control of vector mosquitoes to reduce transmission. Awareness and education activities for the general population.

Vaccine
None.

Treatment
No specific treatment available.

Diagnostic tests

Type of Samples	Blood, serum, urine, saliva, semen
Human Diagnostic tests	**1-5 days after onset of symptoms:** - RT-PCR assays - Serological tests (IgM and neutralizing antibodies)
Animal Diagnostic tests	- IgG and IgM ELISA - Seroneutralization

Biosafety

Biosafety level 2

BSL2 for diagnostic procedures and mosquito manipulations.

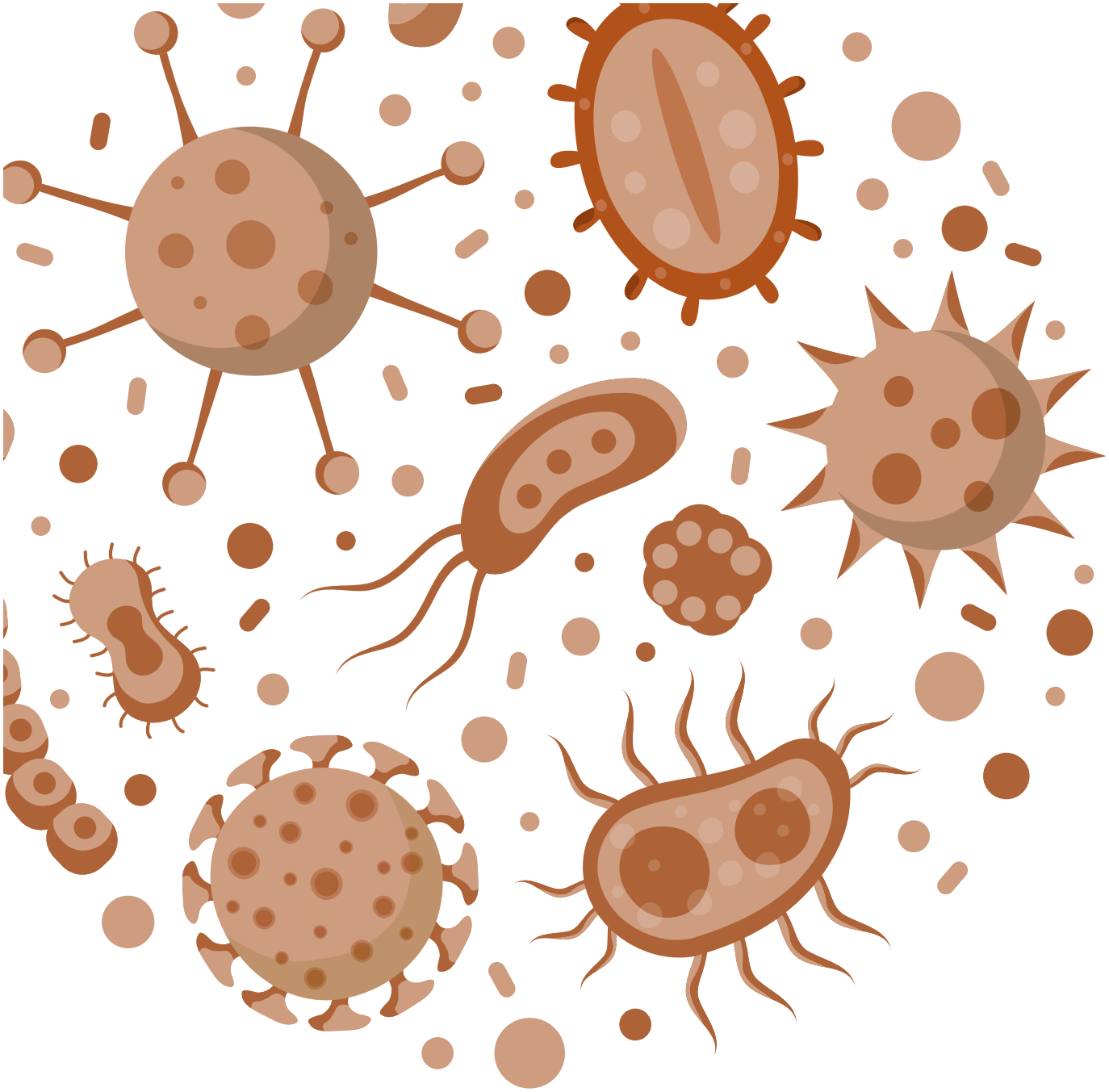
References • Tools • Useful links

https://www.pasteur.fr/en/medical-center/disease-sheets/zika

https://www.cdc.gov/zika/

http://www.who.int/mediacentre/factsheets/zika/en/

Virus schematic adapted from http://viralzone.expasy.org
Map produced by Avia-GIS



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