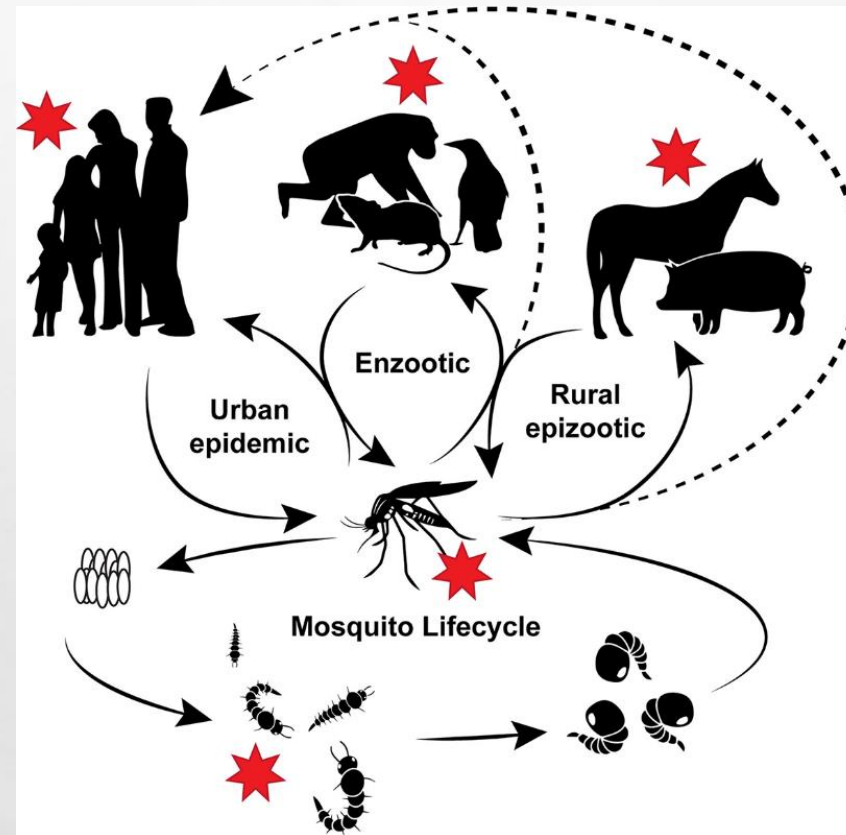


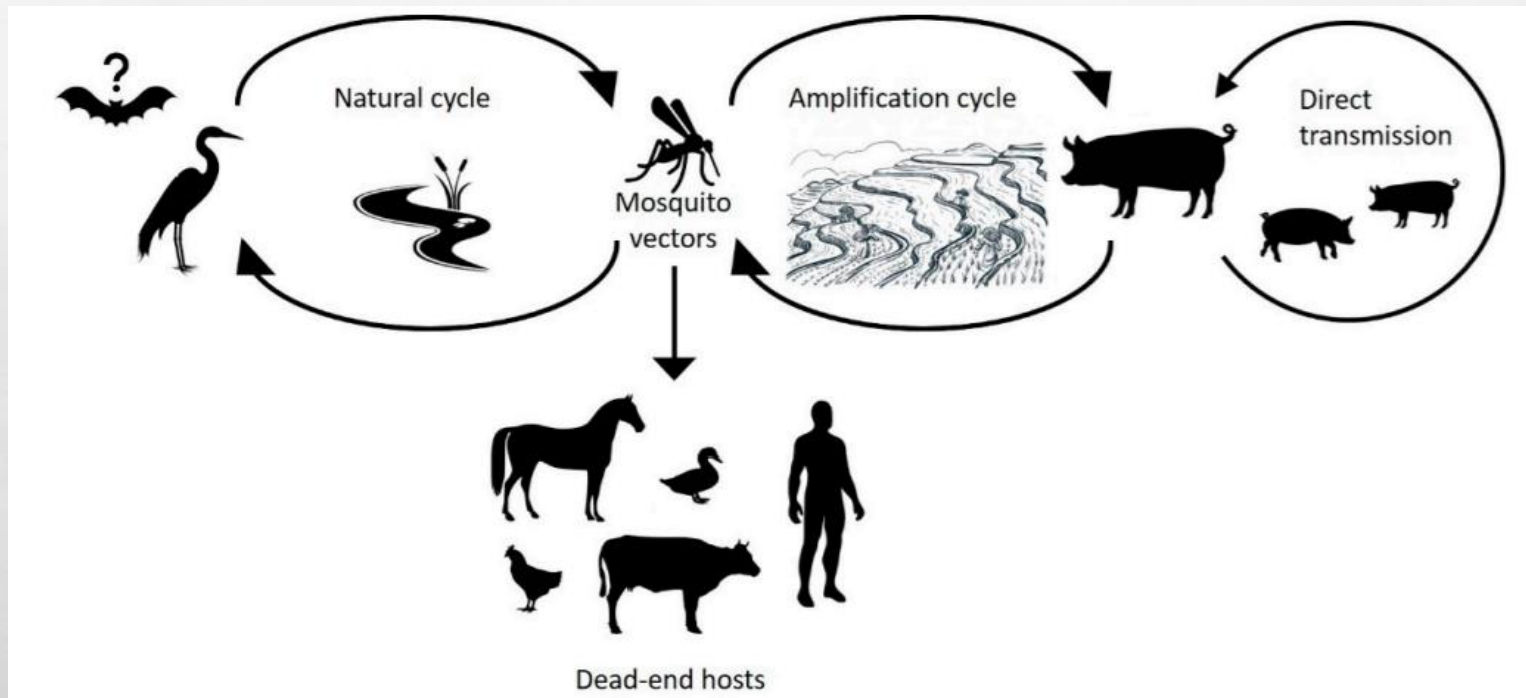
VECTOR-BORNE VIRUSES IN IRAN

DR. TARA VAT BAMDAD

TARBIAT MODARES UNIVERSITY







Arthropods in Iran

- Early detection of arboviruses in arthropods is a pre-requisite for designing and implementing adapted control measures and epidemiological studies.
- Once infected, mosquito females remain infected for all their life making virus detections possible at early steps before infections are reported in vertebrate hosts. Up to date, **64 mosquito species** are recorded in Iran and several cryptic species have been identified using molecular tools. Mosquitoes of the main genera, **Culex and Aedes** are incriminated as the most important vectors of arboviruses. The increasing volume of people displacements including movements of refugees, and the traffic of goods and animals between countries of the region, offer multiple opportunities for arbovirus introduction in Iran such as dengue virus (DENV), and West Nile virus (WNV).
- In total, **46 species of ticks** occur in Iran (10 Argasidae and 36 Ixodidae) from 10 genera.

Diversity of mosquito species in Iran (2017)

- A total of 1885 mosquitoes were collected, belonging to **10 species of genus Culex** including Cx. pipiens Complex, Cx. laticinctus, Cx. sinaiticus, and Cx. tritaeniorhynchus, one species of the genus Culiseta, Cs. longiareolata, and **five species of the genus Aedes**, Ae. caspius, Ae. vexans, Ae. detritus, Ae. albopictus, and Ae. unilineatus. Ae. vexans was the dominant species in the area (77.7%). During the study, seven Ae. unilineatus were collected in two villages near the city of Chabahar located in a coastal area; this is the first record for Iran, which has implications for public health such as dengue and Zika infections

- [M R Yaghoobi-Ershadi](#), 2017

Number of collected mosquito in Iran, 2015–2016

No	Mosquito taxon	Number of specimens (% of total number of specimens)
1	<i>Culex pipiens</i> s.l.	21 060 (56.429)
2	<i>Culex sitiens</i>	10 995 (29.461)
3	<i>Culex theileri</i>	3856 (10.332)
4	<i>Culex perexiguus</i>	486 (1.302)
5	<i>Culex pipiens pipiens</i> form <i>pipiens</i>	326 (0.874)
6	<i>Anopheles hyrcanus</i>	180 (0.482)
7	<i>Anopheles maculipennis</i> s.l.	117 (0.313)
8	<i>Anopheles superpictus</i>	109 (0.292)
9	<i>Culex tritaeniorhynchus</i>	42 (0.113)
10	<i>Anopheles stephensi</i>	16 (0.043)
11	<i>Anopheles claviger</i>	15 (0.040)
12	<i>Culex pipiens</i> form <i>pipiens</i> x <i>molestus</i>	15 (0.040)
13	<i>Culiseta longiareolata</i>	15 (0.040)
14	<i>Culex mimeticus</i>	14 (0.038)
15	<i>Culex hortensis</i>	11 (0.029)
16	<i>Aedes caspius</i>	8 (0.021)
17	<i>Anopheles pseudopictus</i>	8 (0.021)
18	<i>Culex pipiens</i> cf. <i>quinquefasciatus</i>	8 (0.021)
19	<i>Anopheles dthali</i>	6 (0.016)
20	<i>Anopheles fluviatilis</i> s.l.	6 (0.016)
21	<i>Culex pipiens pipiens</i> form <i>molestus</i>	5 (0.013)
22	<i>Anopheles apoci</i>	4 (0.011)
23	<i>Anopheles marteri</i>	4 (0.011)
24	<i>Anopheles plumbeus</i>	4 (0.011)
25	<i>Aedes vexans</i>	2 (0.005)

Shahhosseini, 2017, Tropical Medicine and International Health

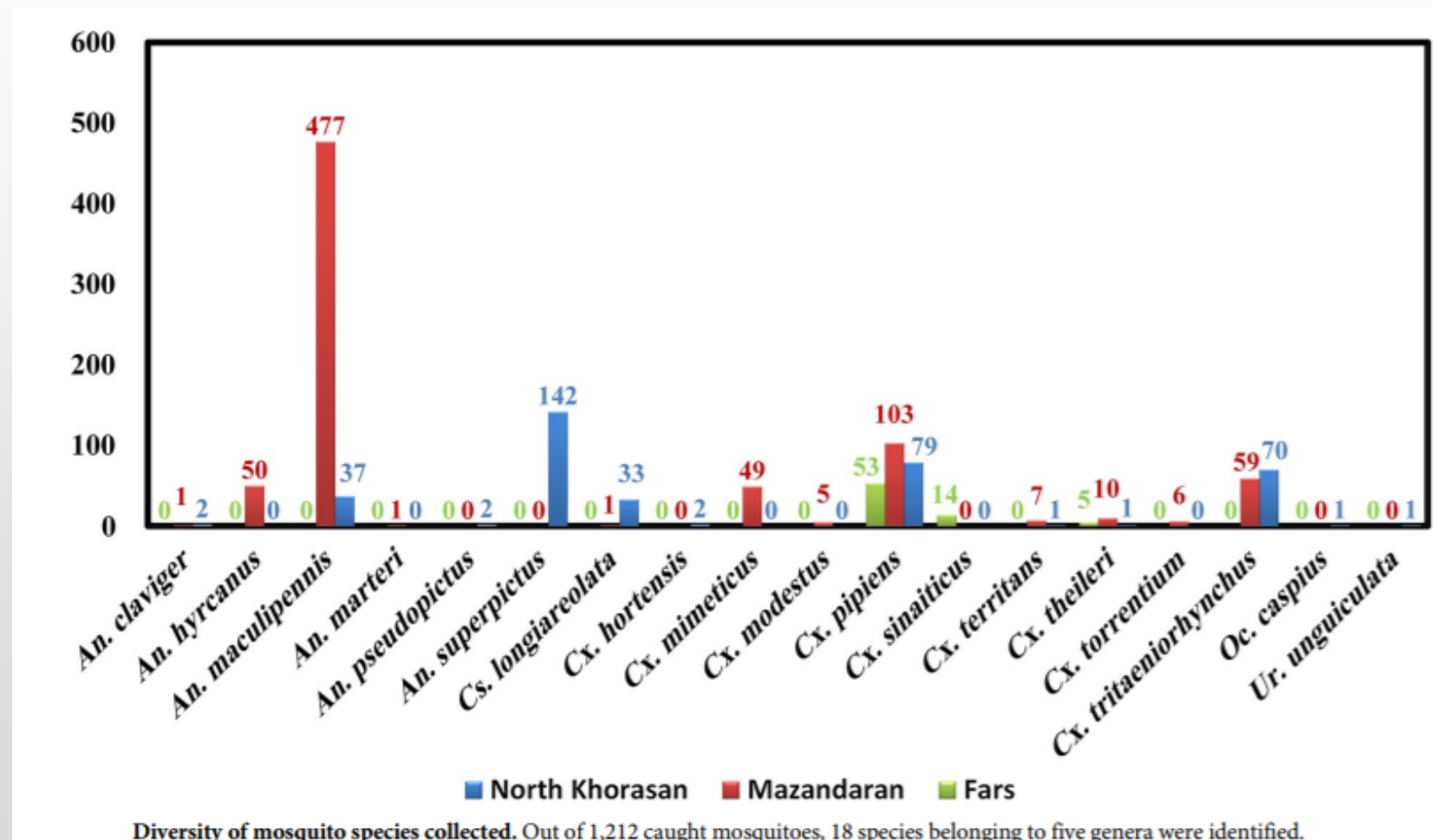
Diversity of mosquito species in Iran (2018)

- The source of blood meals for 580 blood-fed mosquito specimens of 20 different taxa were determined, resulting in the identification of 13 different host species (9 mammals including humans, 3 birds and 1 reptile), whereby no mixed blood meals were detected. Five mosquito species represented more than 85.8% of all collected blood-fed specimens: *Culex pipiens pipiens form pipiens* (305 specimens, 55.7% of all mosquito specimens), *Cx. theileri* (60, 10.9%), *Cx. sitiens* (51, 9.3%), *Cx. perexiguus* (29, 5.3%) and *Anopheles superpictus* (25, 4.6%). The most commonly detected hosts of the four most abundant mosquito species were humans (*Homo sapiens*; 224 mosquito specimens, 40.9% of all mosquito specimens), cattle (*Bos taurus*; 171, 31.2%) and ducks (*Anas* spp.; 75, 13.7%).

Diversity of mosquito species in Iran (2020)

- A total of 1,212 samples were processed: 371, 769, and 72 mosquito female samples from North Khorasan, Mazandaran, and Fars provinces respectively. Morphological identification revealed the presence of **18 species** belonging to **five genera** in the study area. The most prevalent species belonged to *Anopheles maculipennis* s.l. (42.41%), *Cx. pipiens* (19.39%), *An. superpictus* (11.72%), and *Cx. tritaeniorhynchus* (10.64%). *An. hyrcanus* (4.12%), *Cx. mimeticus* (4.04%), *Culiseta longiareolata* (2.8%), *Cx. theileri* (1.32%), *Cx. sinaiticus* (1.16%), *Cx. territans* (0.67%), *Cx. torrentium* (0.49%), *Cx. modestus* (0.41%), *An. claviger* (0.25%), *An. pseudopictus* (0.17%), *Cx. hortensis* (0.17%), *An. marteri* (0.08%), *Ochlerotatus caspius* (0.08%), and *Uranotaenia unguiculata* (0.08%) were also found .

Diversity of mosquito species in Iran (2020)



Diversity of Aedes species in Iran

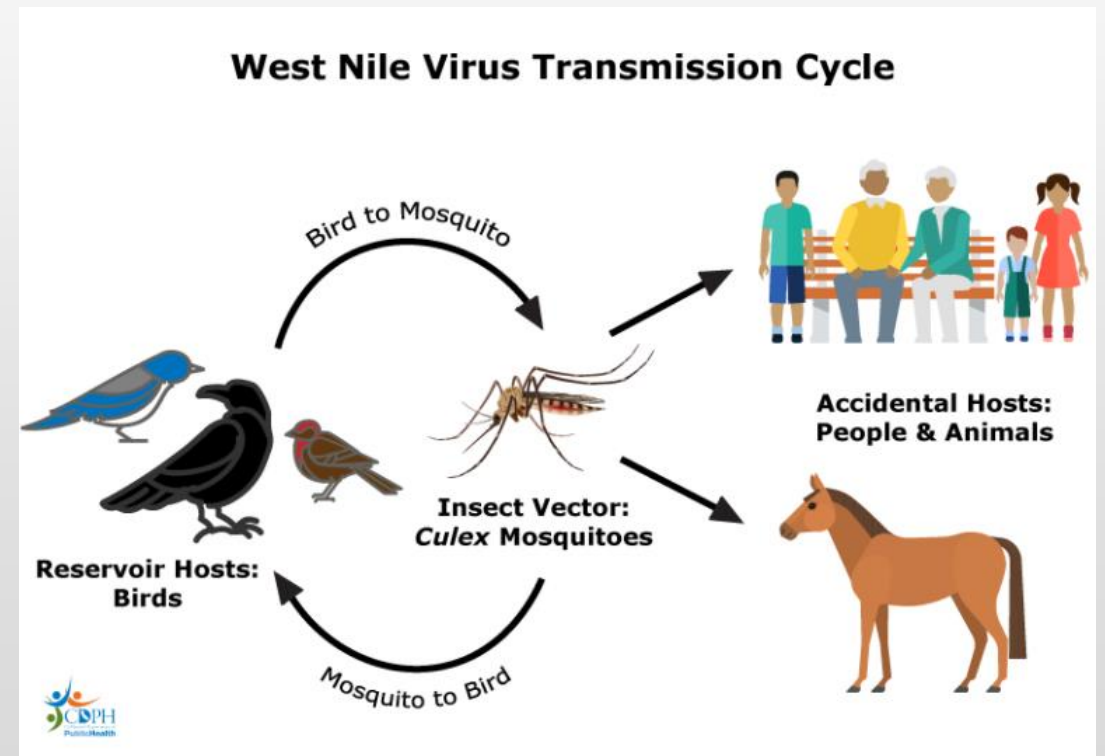
- In 2019, 694 larvae were collected from four counties, from which only 7.2% were *Aedes* larvae. Three species of *Aedes* were identified which include *Ae. caspius*, *Ae. vexans* and *Ae. flavescens*. *Aedes flavescens* is reported from Ardabil Province for the first time. *Aedes* species were a high density in borderline of Iran and Azerbaijan

Virus Family	Viral Genus	Virus	Vector Species
Bunyaviridae	Orthobunyavirus	California serogroup viruses	Mosquito (Aedes sp.)
	Phlebovirus	Rift Valley Fever virus	Mosquito (various)
	Phlebovirus	Toscana virus	Sandfly (Phelbotomus sp.)
	Phlebovirus	Phlebotomus fever virus	Sandfly (phelbotomus)
	Phlebovirus	Sandfly Fever Naples virus	Sandfly (phelbotomus)
	Phlebovirus	Sandfly Fever Sicilian virus	Sandfly (phelbotomus)
	Phlebovirus	Heartland virus	Tick (A. americanum)
	Phlebovirus	Severe fever with thrombocytopenia syndrome virus	Tick (H. longicornis)
	Nairovirus	Crimean Hemorrhagic Fever virus	Tick (Hyalomma sp.)
Flaviviridae	Flavivirus	Dengue Virus	Mosquito (Aedes sp.)
	Flavivirus	Zika virus	Mosquito (Aedes sp.)
	Flavivirus	Yellow fever virus	Mosquito (Aedes sp.)
	Flavivirus	West Nile Virus	Mosquito (Culex sp.)
	Flavivirus	St. Louis Encephalitis virus	Mosquito (Culex sp.)
	Flavivirus	Japanese encephalitis virus	Mosquito (Culex sp.)
	Flavivirus	Murray Valley encephalitis virus	Mosquito (Culex sp.)
	Flavivirus	Usutu	Mosquito (various)
	Flavivirus	Omsk Hemorrhagic fever virus	Tick (dermacentor)
	Flavivirus	Kyasanur Forest Disease virus	Tick (Haemaphysalis sp.)
	Flavivirus	Tick-borne encephalitis virus	Tick (Ixodes and Haemaphysalis sp.)
	Flavivirus	Powassan virus	Tick (Ixodes sp.)
Orthomyxoviridae	Thogotovirus	Bourbon virus	Tick (A. americanum)
Reoviridae	Coltivirus	Colorado tick fever	Tick (dermacentor)
Rhabdoviridae	Vesiculovirus	Vesicular Stomatitis (New Jersey) virus	Sandflies (Lutz. Sp) Mosquitos (various)
	Vesiculovirus	Chandipura	Sandfly (Phlebotomus Sp.)
Togaviridae	Alphavirus	Barmah Forest Virus	Mosquito (Aedes and Culex sp.)
	Alphavirus	Chikungunya virus	Mosquito (Aedes sp.)
	Alphavirus	Venezuelan equine encephalitis virus	Mosquito (Culex sp.)
	Alphavirus	Sindbis virus	Mosquito (Culex sp.)
	Alphavirus	Equine encephalitis virus	Mosquito (Culex sp.)
	Alphavirus	Mayaro virus	Mosquito (Haemagogus sp.)

Virus families and common arthropod vectors of viral disease

West Nile Virus (VNW)

- West Nile virus is spread by the Culex species of mosquito. The main vector species are **Culex pipiens**, **Culex tarsalis**, and **Culex quinquefasciatus**, but **Aedes vexans**, **Aedes cinereus**, **Culex modestus**, **Culex theileri**, **Ochlerotatus caspius**, **Anopheles plumbeus**, **Coquillettidia richiardii**, **Ochlerotatus geniculatus**, and **Ochlerotatus cantans** have been reported in different regions.
- The symptoms of West Nile virus**
 - Fever.
 - Headache.
 - Body aches.
 - Skin rash on trunk of body.
 - Swollen lymph glands.
 - Encephalitis



WNV

- WNV is **the most prevalent Culex-transmitted virus** frequently reported in Iran. Humans and horses are common vertebrate hosts. **Migratory birds** play a critical role in introducing WNV; 15% were found serologically WNV-positive and among them, 54% concerned *Fulica atra* birds suggesting the potential role of common coots in WNV ecology in Iran.



Eurasian coot (*Fulica atra*)

چنگر یا پرلا

WNV

- The 32 317 mosquito specimens belonging to 25 species were morphologically distinguished and distributed into 1222 pools. *Culex pipiens* s.l. comprised 56.429%. One mosquito pool (0.08%), containing 46 unfed *Cx. pipiens* form *pipiens* (Cpp) captured in August 2015, was positive for flavivirus RNA. Subsequent sequencing and phylogenetic analyses revealed that the detected Iranian **WNV strain** belongs to lineage 2 and clusters with a strain recently detected in humans. **No flaviviruses other than WNV were detected in the mosquito pools.**

- The infection (IR), dissemination (DR), and transmission (TR) rates of *Cx. pipiens* s.l., collected from Iran, for West Nile virus (WNV) lineage 1a. *Cx. pipiens* s.l. mosquitoes in Iran are susceptible to WNV with **IR up to 89.7%, 93.6%, and 83.9% at 7, 14, and 21** days post-infection (dpi) respectively. In addition, DR and **TR** reached respectively 92.3% and **75.0%** at 21 dpi, and the number of viral particles delivered with saliva reached up to **1.33×10^5** particles. Therefore, an unexpected high risk of WNV dissemination in the region where *Cx. pipiens* s.l. mosquitoes are well established should be considered carefully and surveillance measures implemented accordingly

Epidemiology of WNV

- Chinikar et al., in 2012 and 2013, found that three patients developing encephalitis were positive for WNV by RT-qPCR assay and detected serologically positive sera in **1.3% of humans and 2.8% of equines in five geographic zones of north and central parts of Iran** between 2010 and 2012. All samples were tested for the immunoglobulin G (IgG) antibody to WNV by using an enzyme-linked immunosorbent assay (ELISA). WNV was also detected in mosquitoes: **Aedes caspius in the Northwest , and Culex pipiens in the North and the South**. Besides, the most critical mosquito-borne virus in the world is DENV mainly transmitted between humans by Aedes mosquitoes. Most human cases in Iran were reported in the southeast of the country near the border with Pakistan, though local transmission has not been confirmed yet. In addition, circulation of chikungunya virus (CHIKV) was suspected in Pakistan.
- **11% IgG seropositivity in Mashhad in 2015 for WNV**
-

WNV

- A total of 494 serum samples were tested for the presence of WNV and ZIKV IgG antibodies using ELISA assays. One hundred and two (20.6%) samples were reactive for WNV IgG antibodies. All serum samples were negative for ZIKV IgG antibodies. Using the multivariable logistic analysis, age (45+ vs. 1-25; OR = 3.4, 95% C.I.: 1.8-6.3), occupation (mostly outdoor vs. mostly indoor; OR = 2.4, 95% C.I.: 1.1-5.2), and skin type (type I/II vs. type III/IV and type V/VI; OR = 4.3, 95% C.I.: 1.7-10.8 and OR = 2.7, 95% C.I.: 1.3-5.5 respectively, skin types based on Fitzpatrick scale) showed significant association with WNV seroreactivity. We collected 2,015 mosquitoes in 136 pools belonging to 5 genera and 14 species. Three pools of **Culex pipiens complex were positive for WNV RNA** using real-time reverse transcription polymerase chain reaction (rtRT-PCR). ZIKV RNA was not detected in any of the pools. All WNV ELISA reactive serum samples were negative for WNV RNA. In conclusion, we provided evidence of the establishment of WNV in southern Iran and no proof of ZIKV in serum samples or in mosquito vectors.

Mazyar Ziyaeyan, Plos negl trop dis, 2018

- In 2019, total of 408 sera were taken from volunteers living in Khuzestan. The presence of specific immunoglobulin G (IgG) antibody against WNV was tested by the enzyme-linked immunosorbent assay (ELISA) method. Anti-WNV IgG antibody was detected in **97 (23.8%)** out of the 408 tested sera.

Dengue virus

Although there are several potential dengue vectors, the field isolation of viruses and epidemiological evidence clearly show that *Ae. aegypti* and *Ae. albopictus* are responsible for the majority of dengue transmission.

Dengue fever causes a high fever (40 C) and any of the following signs and symptoms:

Headache.

Muscle, bone or joint pain.

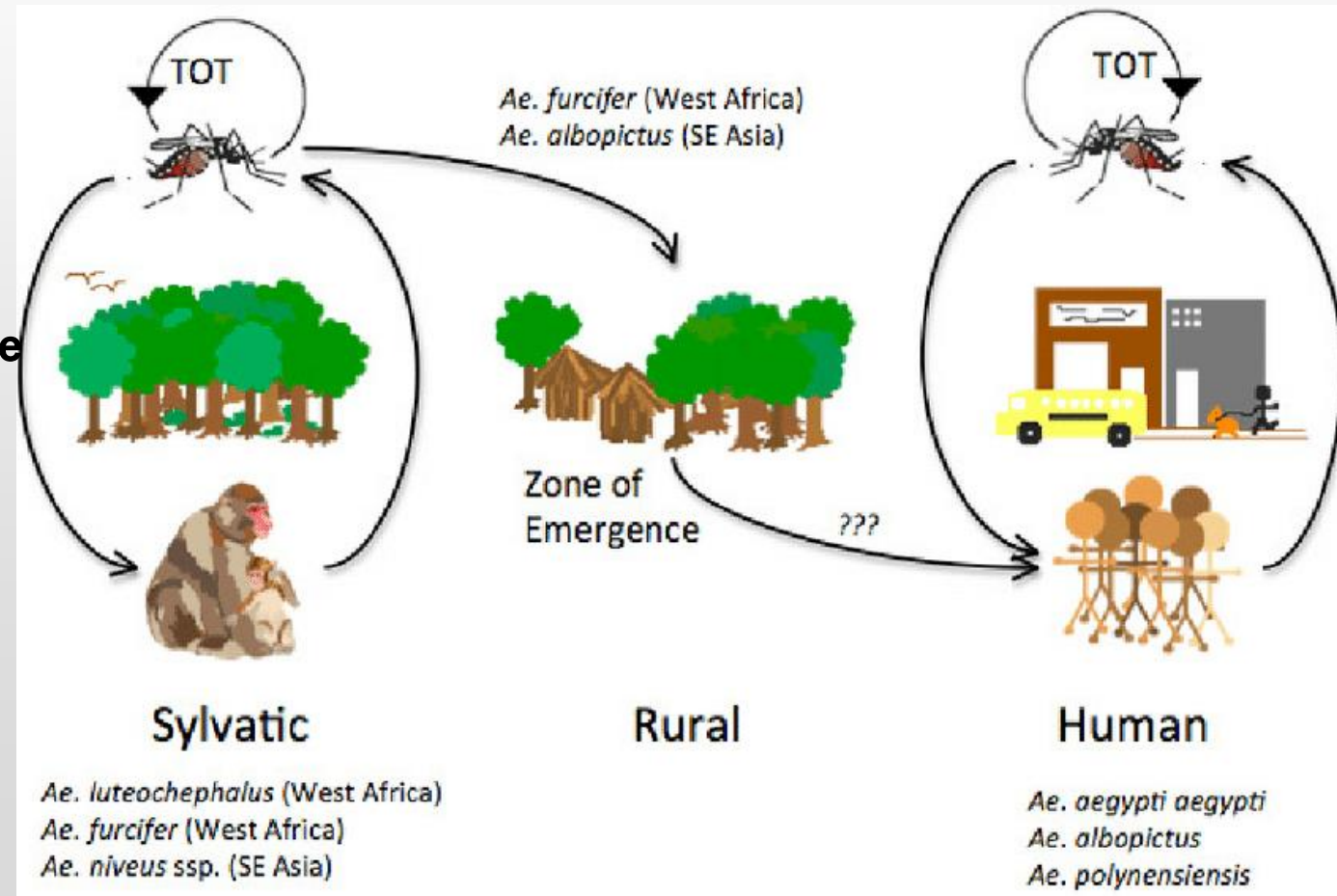
Nausea.

Vomiting.

Pain behind the eyes.

Swollen glands.

Rash.



First Iranian Imported Case of Dengue

- The patient was a 58-year-old Iranian woman with acute unexplained high-grade fever for 4 days, associated with skin rash, after returning from Southeast Asia. ELISA immunoglobulin M (IgM) antibodies to dengue and serum RT-PCR for dengue virus was positive. (Mardani, 2013, Int J Prev Med)
- Between 2000 and 2012. Serum samples from patients who were referred to the Arboviruses and Viral Haemorrhagic Fevers Laboratory of the Pasteur Institute of Iran and tested negative for Crimean-Congo Haemorrhagic Fever (CCHF) were tested for the presence of specific IgG and IgM and viral nucleic acid in blood. Of the 300 sera tested, 15 (5%) were seropositive, and 3 (1%) were both serologically and PCR positive. Of the 15 seropositive cases, 8 (53.3%) had travelled to endemic areas including Malaysia (5, 62.5%), India (2, 25%) and Thailand (1, 12.5%). In contrast, 7 (46.7%) of the cases had not reported travelling abroad. Of these, six cases were from the Sistan and Baluchistan province in southeast Iran and neighbouring Pakistan.

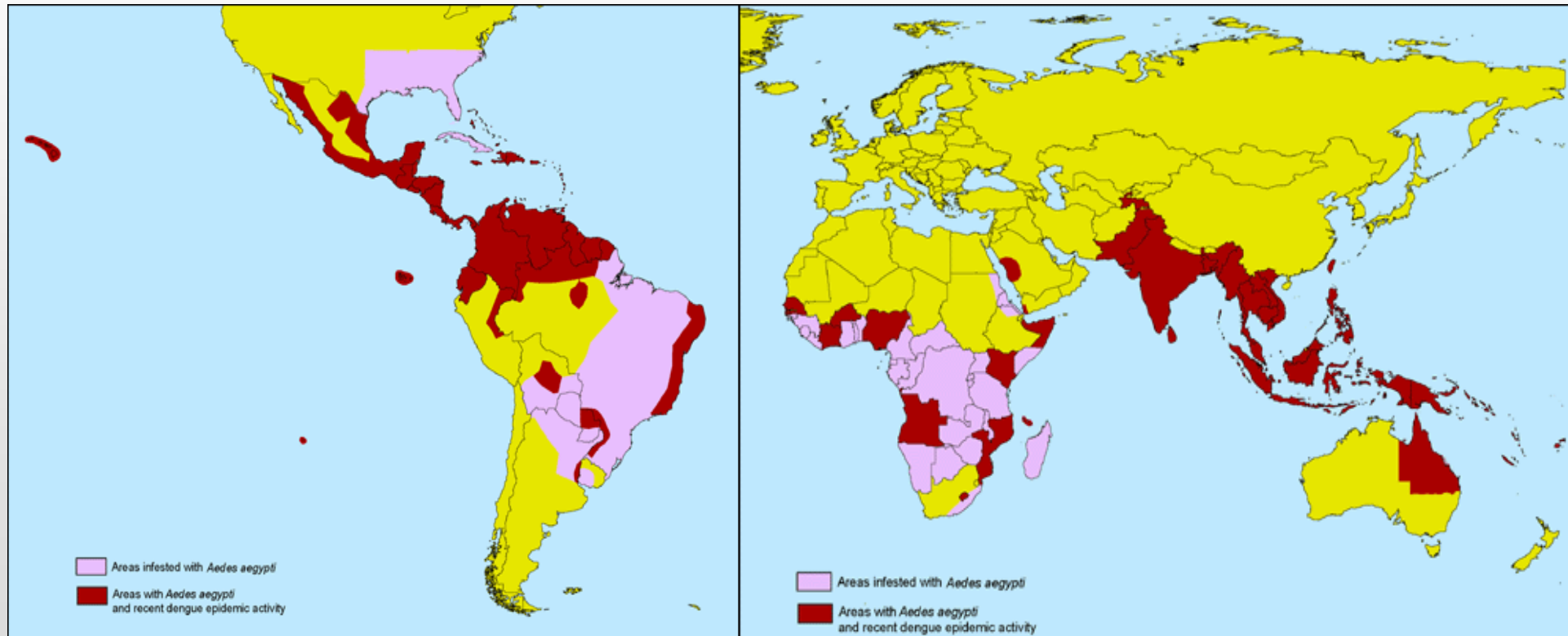
Dengue

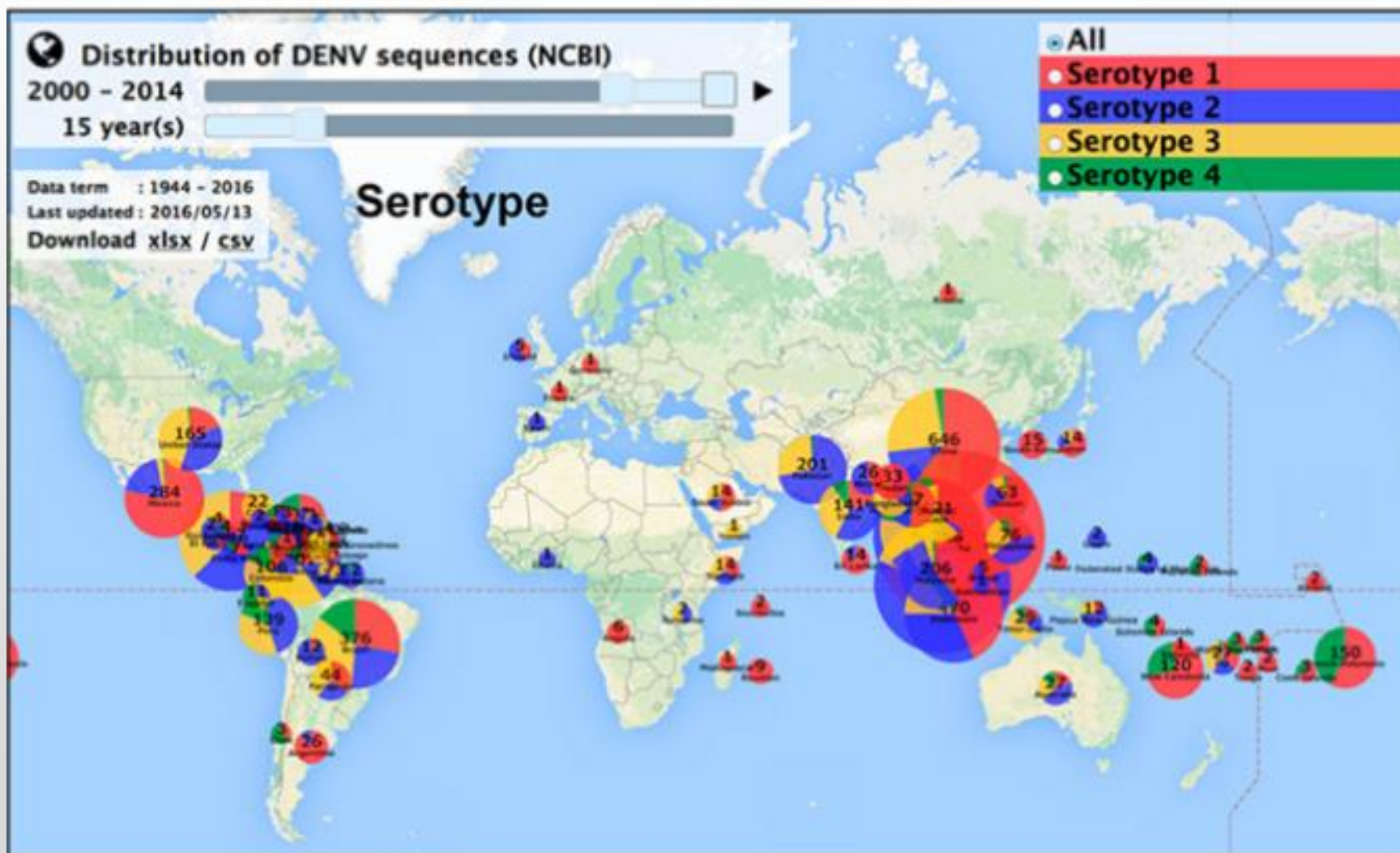
- Phylogenetic analysis showed that the origin of dengue virus among three Iranian travelers were in company with their travel history to **South-east of Asia (Malaysia)**. **It seems that travelers play an essential role in the epidemiology of dengue infections in Iran.** (chinikar 2016)

DENV

- A study (2008–2014) has identified *Aedes albopictus* in southern Iran. The species *A. albopictus* is most well-known for transmitting dengue and chikungunya viruses. In another study, *Aedes unilineatus* was also identified in the southeast of Iran (2012–2014). This mosquito species has been reported as a dengue vector in Karachi, Pakistan. These studies support establishment of DENV vectors in this area.
- Studies for finding other potential vector species, that is, *Aedes aegypti* mosquitos in this area can provide researchers with useful insights on DENV and its epidemiology in Iran.

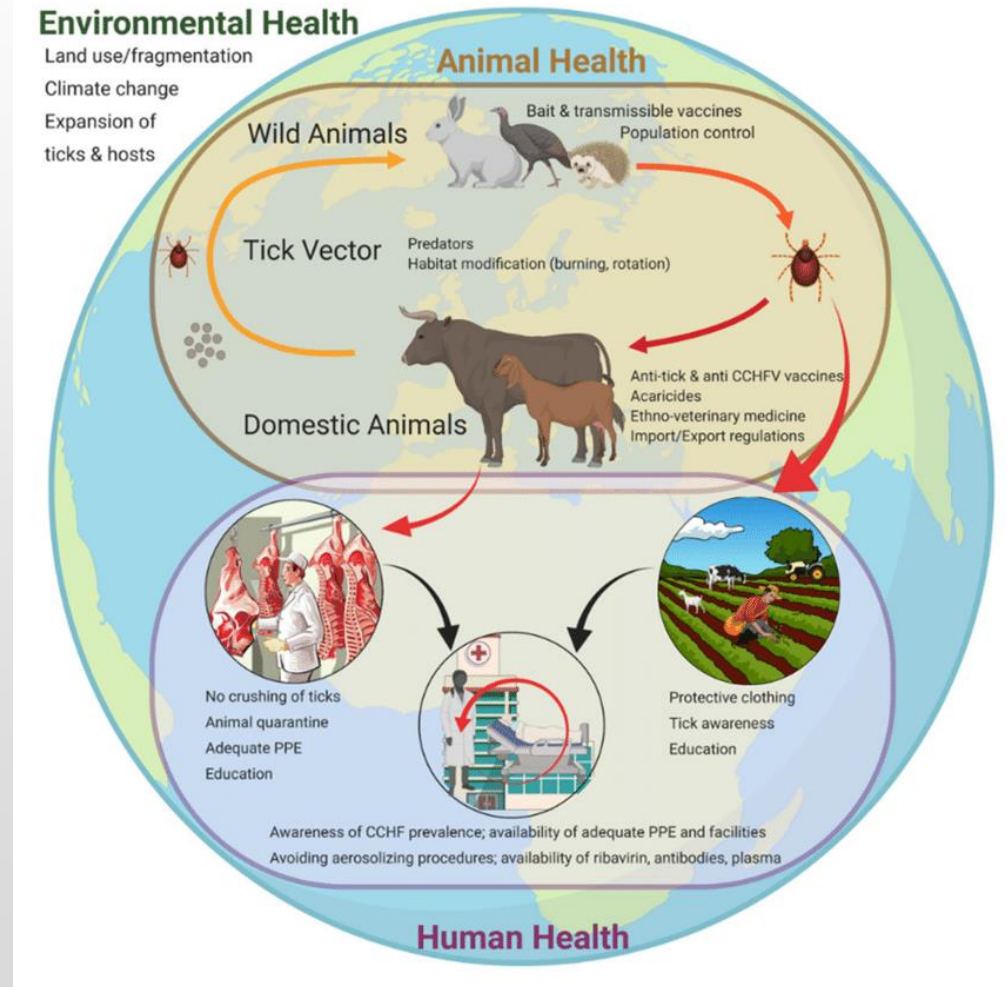
Pattern of *Aedes aegypti* and Dengue virus distribution over the world





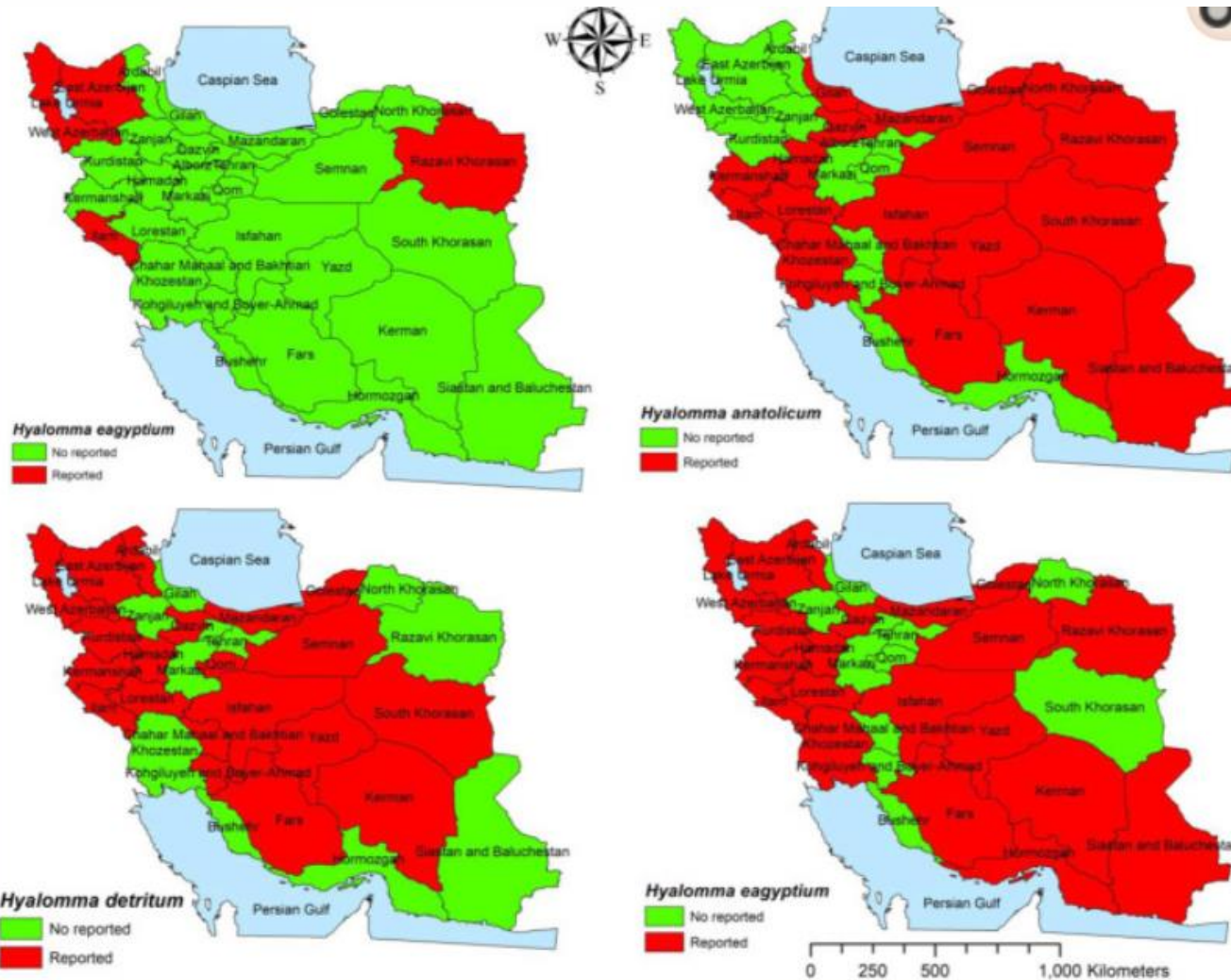
Crymian-Congo Hemorrhagic Fever (CCHF)

- During ten years study, 1054 tick specimens; including two species of Argasidae and 17 species of Ixodidae were examined for their infection to CCHF virus genome.
- The results show that *Rhipicephalus sanguineus*, *Hyalomma marginatum*, *H. anatolicum*, *H. asiaticum* and *H. dromedarii* were known as the most frequent species which were positive for CCHF virus.



CCHF

- Based on the results, nine genera and 37 species of soft and hard ticks were recorded in Iran. So far, **six genera and 16 species of hard and soft ticks were reported to be infected with the CCHF virus.** The infection to this virus was reported from **18 out of 31** provinces, with a high rate in Sistan and Baluchistan as well as Khuzestan provinces. The highest levels of CCHF infection belonged to *Hyalomma marginatum* and *H. anatolicum*.
- The main vectors of CCHF, *H. marginatum* and *H. anatolicum*, were reported in more than 38.7% of Iran's provinces, and these two species were identified as invasive species in Iran



J Arthropod-Borne Dis, March 2021, 15(1):
41–59

Presence of *Hyalomma egyptium*, *Hyalomma anatolicum*, (up) and *Hyalomma detritum* and *Hyalomma asiaticum* (down) report in Iran at the county

CCHF

- The presence of Crimean-Congo hemorrhagic fever virus (CCHFV) in Iran was first identified in studies of livestock sera and ticks in the 1970s, but the first human infection was not diagnosed until 1999. Since that time, the number of cases of CCHF in Iran has markedly increased.

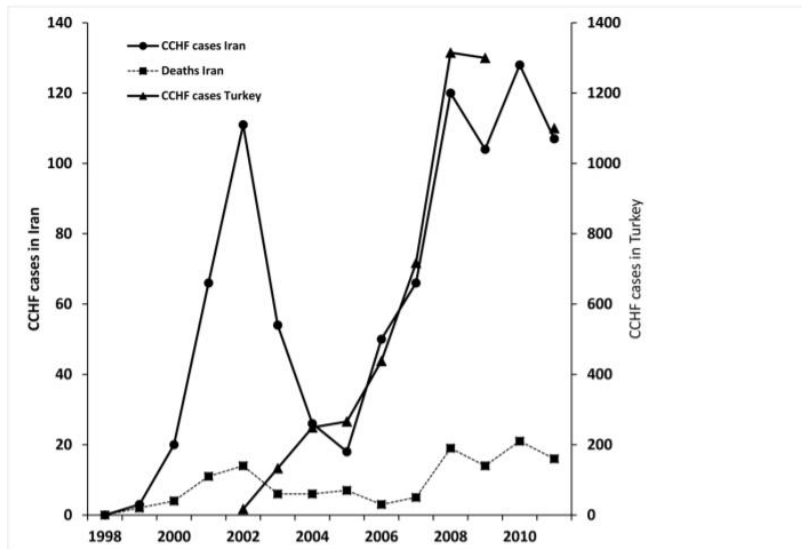
History of Crimean-congo hemorrhagic fever in Persia/ Iran.

Date	Description	Comment	Reference
1203 CE	Detailed description of hemorrhagic fever and its putative causative agent (vulture louse)	Description identical to Galen's, thus may not be specific to CCHF	(Jurjānī, 1203 CE)
1887–1888	Description of a fatal hemorrhagic disease among the nomadic Yomut Turkomen in northern Iran	Likely CCHF, but key details, such as fever and season, are missing	(Brown, 1893)
19 th century	Reports of a sometimes fatal disease though to be caused by <i>Argas persicus</i> in the Mianeh region in NW Iran	Unlikely to be CCHF, though some clinical features suggestive	(Nuttal, 1908)
1940's–1960's	Seasonal and sometimes fatal hemorrhagic fever known locally as <i>Gara Mikh</i> typhoid fever in East Azerbaijan, Iran.	Clinical and epidemiologic features consistent with CCHF.	(Aminolashrafi and Nooranian, 1966)
1966–69	Report of 41 cases of hemorrhagic fever from East Azerbaijan, Iran.	Possible CCHF outbreak	(Aminolashrafi, 1970)
1970–71	Sheep serum sent tested positive for CCHFV antibodies.	First documentation of CCHFV in livestock	(Chumakov, 1972)
1971–3	Report of 60 cases of hemorrhagic fever from East Azerbaijan, Iran.	First suspected cases of CCHF in humans.	(Asefi, 1973)
1970–1971	Sera of humans in northern Iran tested positive for anti-CCHFV antibodies	First documentation of CCHFV infection	(Saidi, 1974)
1974–1975	Hemorrhagic fever epidemic in northern Iran	Suspected CCHF, but not proven	(Ardoin and Karimi, 1982)
1999	Nosocomial transmission of CCHF	First confirmed cases of CCHF in Iran	(Mardani, 2001)

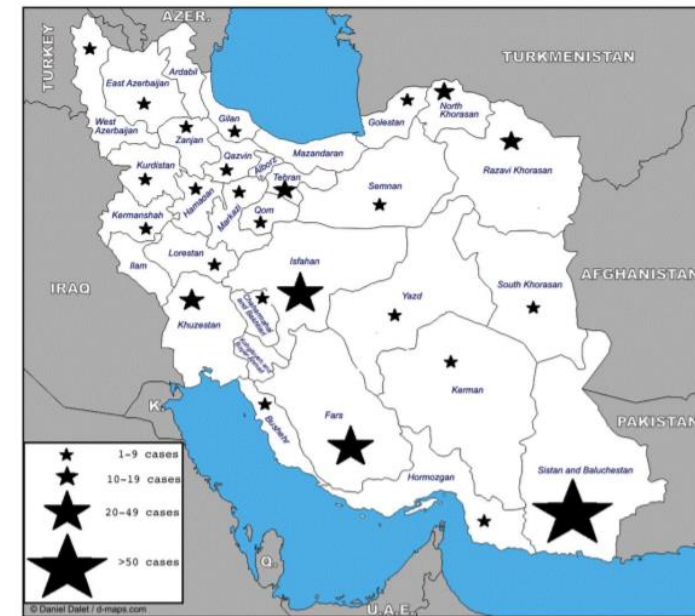
Published studies reporting cases of CCHF in Iran since 1999.

Years	Location	Number of cases	Summary	Possible mode of transmission	Reference
1999–2004	Sistan and Baluchestan	255 patients	Epidemiologic, laboratory and clinical description	Animal contact, nosocomial, tick bite, slaughtering	(Alavi-Naini, et al., 2006)
2001–2004	Fars, southern Iran	16 patients, 3 deaths	Epidemiologic, clinical and laboratory data are described.	Slaughtering, animal contact, tick bite	(Fakoorziba, et al., 2006)
1999–2007	Sistan and Baluchestan	123 patients, 19 fatalities		N/A	(Sharifi-Mood, et al., 2009)
1999–2001	Shahrekord (central Iran)	3 healthcare workers, 1 death		Nosocomial	(Mardani, et al., 2009)
2000–2009	All involved provinces	635 patients, 89 fatalities	Risk factors and geographic distribution	Slaughtering, animal contact, nosocomial	(Chinikar, et al., 2010)
2009	Mashhad (north-eastern Iran)	6 healthcare workers, 2 deaths		Nosocomial	(Naderi et al., 2011)
2011	Khorasan (north-eastern) Province	1 healthcare worker, fatal	A medical student who died within one week of exposure.	Nosocomial	(Naderi, et al., 2012)

Two Content Layout with SmartArt



Total number of confirmed CCHF cases in Iran and Turkey reported each year for the period 2000–12, with the total number of fatal cases in Iran. Data were obtained from the Pasteur Institute of Iran and from (Chinikar, et al., 2012; Yilmaz et al., 2008; Ergonul, 2009; Maltezos et al., 2010; Burki, 2012).



Total number of cases of CCHF reported by each province in Iran, over the period 2000–12. Data were obtained from the Pasteur Institute of Iran and from (Chinikar et al., 2012).

CCHF

- In 2016, The CCHFV RNA was detected in **5.2% of 492 ticks collected from livestock in different regions of Golpayegan**. The tick species that tested positive for the presence of CCHFV RNA included Hyalomma, Rhipicephalus and Haemaphysalis species. Phylogenetic analysis using the partial S-segment indicated that eight sequences clustered in clade IV (Asia-1) and three other sequences aligned within clade VI (Europe) with other CCHFV strains from Kosovo (Kosova1917) and Russia (Kashmanov).
- A molecular survey was conducted on hard ticks (Ixodidae) isolated from six counties in Golestan Province, north of Iran during 2014-15. The ticks were identified using morphological characteristics and presence of CCHFV RNA was detected using RT-PCR. Data revealed the presence of CCHFV in 5.3% of the ticks selected for screening. The infected ticks belonged to Hyalomma dromedarii, Hy. anatolicum, Hy. marginatum and Rhipicephalus sanguineus species.
- 2020, The CCHF virus genome was found in *Hyalomma marginatum* (5% male from Taibad and Sabzevar region and 1% female from Taibad).

CCHF

- Since the establishment of the Arboviruses and Viral Hemorrhagic Fevers Laboratory at Pasteur Institute of Iran in 2000, all probable human sera for CCHFV, DFV (mainly travelers) and WNV were tested serologically and molecularly. To conduct phylogenetic analyses, genomes obtained from Iranian patients were sequenced and analyzed by MEGA-6 software. Of 3104, 960 cases have been confirmed for CCHF and 135 deaths. **The highest rate of CCHF infection has been observed in Southeastern regions of Iran and slaughterers and farmers.** Phylogenetic studies have shown that clade IV (Asia 1 and 2), clade V (Europe-2) and clade VI (Europe-1) are circulating in Iran. DFV: Of 300, 3 (1%) were both serologically and RT-PCR positive. All three PCR positive samples had travel history to Malaysia. The phylogenetic tree demonstrated that all sequences fell into DENV-1 (genotype I and III).

- Between 2000 and 2016, a total of 908 CCHF suspected cases (in children less than 19 years old) were evaluated for CCHFV infection by CCHF IgM ELISA and RT-PCR. CCHFV infection was observed in 161 (17.73%) of subjects. Most CCHF positive children were male (70.8%) and >15 years of age (65.8%). Contact with livestock was the main risk factor (35.4%). Sistan and Baluchestan provinces had the highest frequency within the infected cohort (68.3%). The overall mortality rate was 11.8%.

Chikungunya virus (CHIKV)

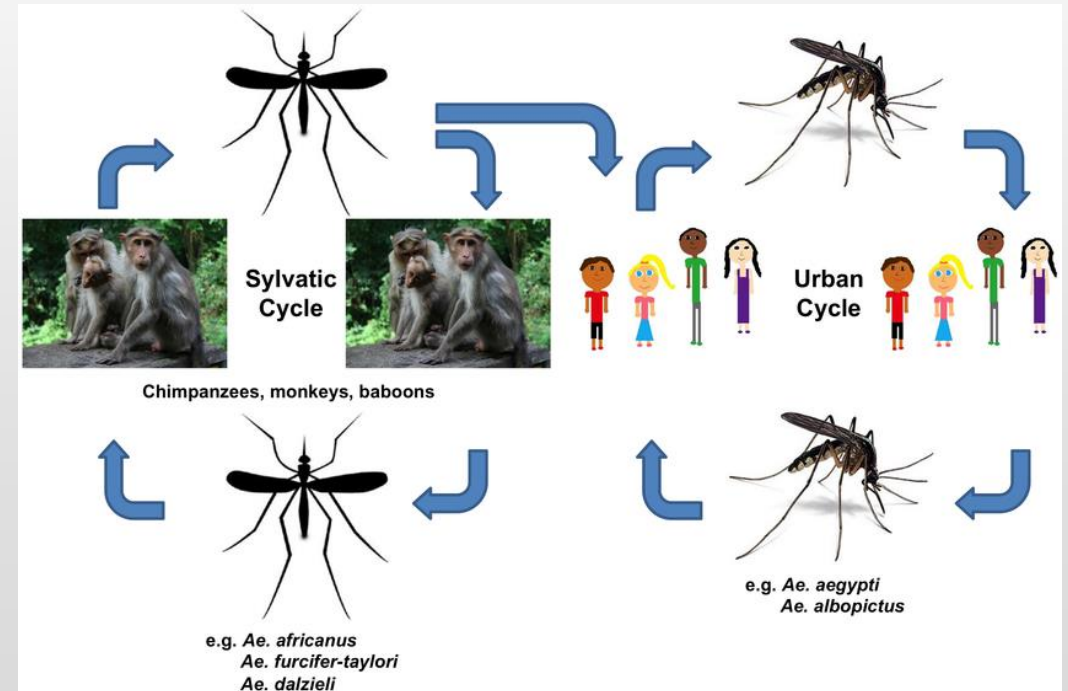
Chikungunya virus (CHIKV) is an arthropod-borne virus (family Togaviridae, genus Alphavirus) that was first isolated in Tanzania (Ross 1956, Mason and Haddow 1957). On the basis of its antigenic properties, CHIKV is placed within the Semliki Forest complex.

A number of species of mosquitoes including: ***Aedes (Ae.) aegypti***, ***Ae. Albopictus***, ***Ae. africanus***, ***Ae. luteocephalus***, and ***Ae. furcifer-taylori***, and **wild primates** are involved in the cycle.

Chikungunya symptoms

The most common symptoms are fever and joint pain.

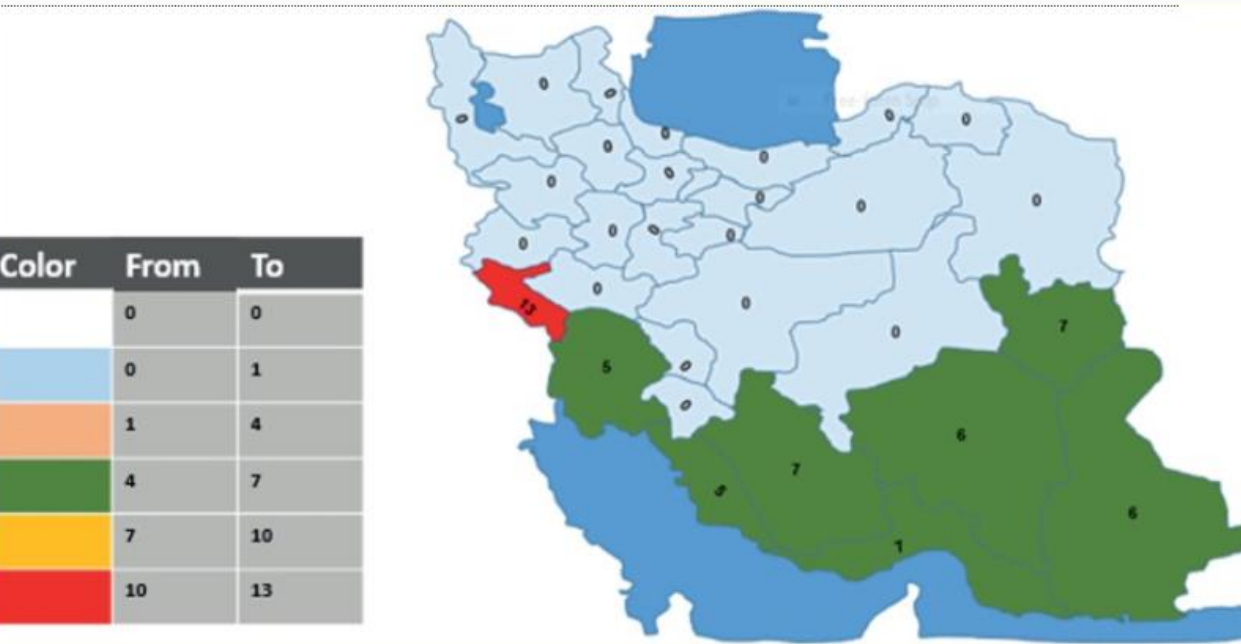
headache,
muscle pain,
joint swelling, or rash.



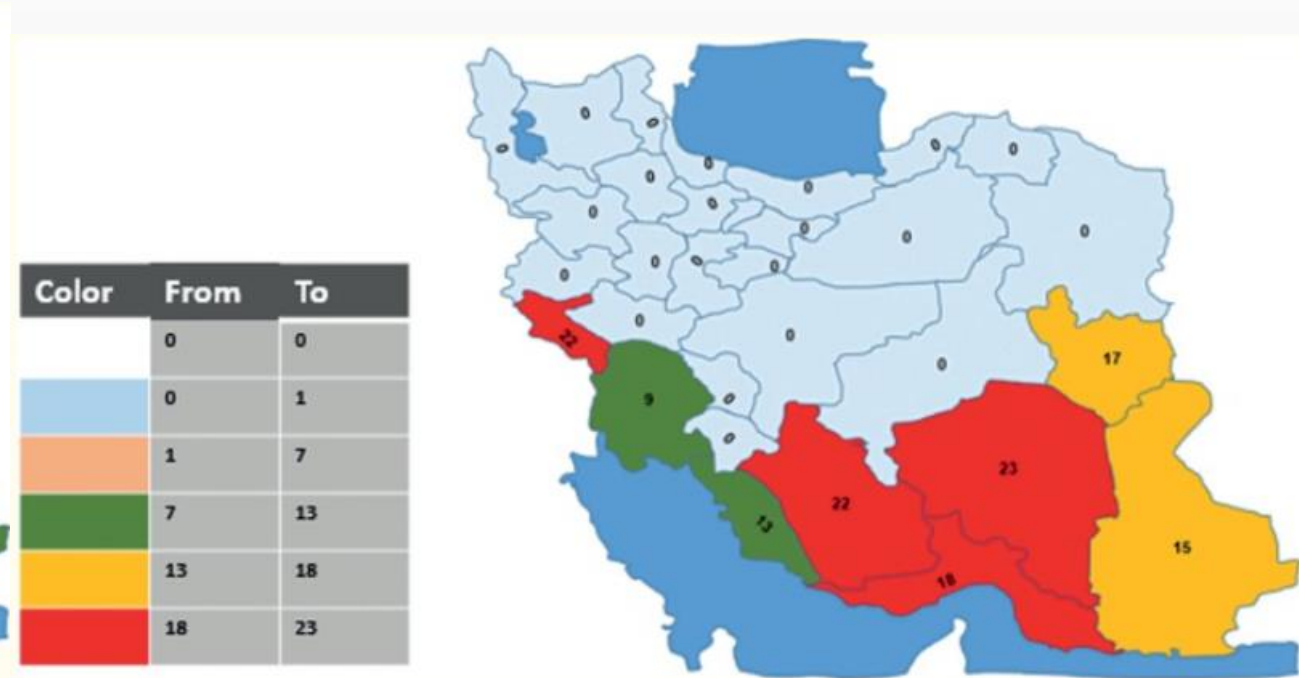
Chikungunya virus (CHIKV)

- Chikungunya virus (CHIKV) is a widespread mosquito-borne virus representing a serious challenge to public health. The largest outbreak in the Middle-East was recorded in 2016-2017 in Pakistan.
- Between April 2017 and June 2018, a total of 159 serum samples of CHIK suspected cases from 10 cities of Sistan and Baluchistan Province were tested by molecular and serological assays. In total, 40 (25.1%) of samples tested positive either by real time PCR or ELISA tests. Out of 151 samples serologically analyzed, **19 (12.6%) and 28 (18.6%) cases were positive for anti-CHIKV IgM and anti-CHIKV IgG antibodies, respectively.** Of 80 samples tested by real time PCR, CHIKV RNA was detected in 11 (**13.7%**) sera, all of them had recent travel history to Pakistan.

- Among measles and rubella IgM negative patients presenting with rash and fever from December 2016 to November 2017 . Of the 1306 sera tested, **210 were CHIKV seropositive and 82 were dengue seropositive.** Statistical analysis demonstrated a significant increase in the CHIKV IgM antibody seropositivity rate in Kerman.



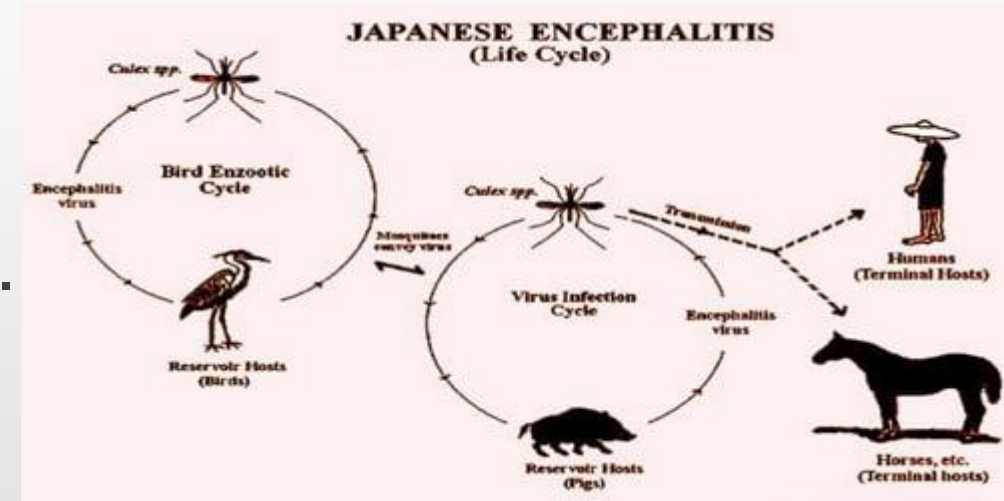
Map showing the DENV Seropositivity rate in study areas in Iran, 2017.



Map showing the CHIKV Seropositivity rate in study areas in Iran, 2017.

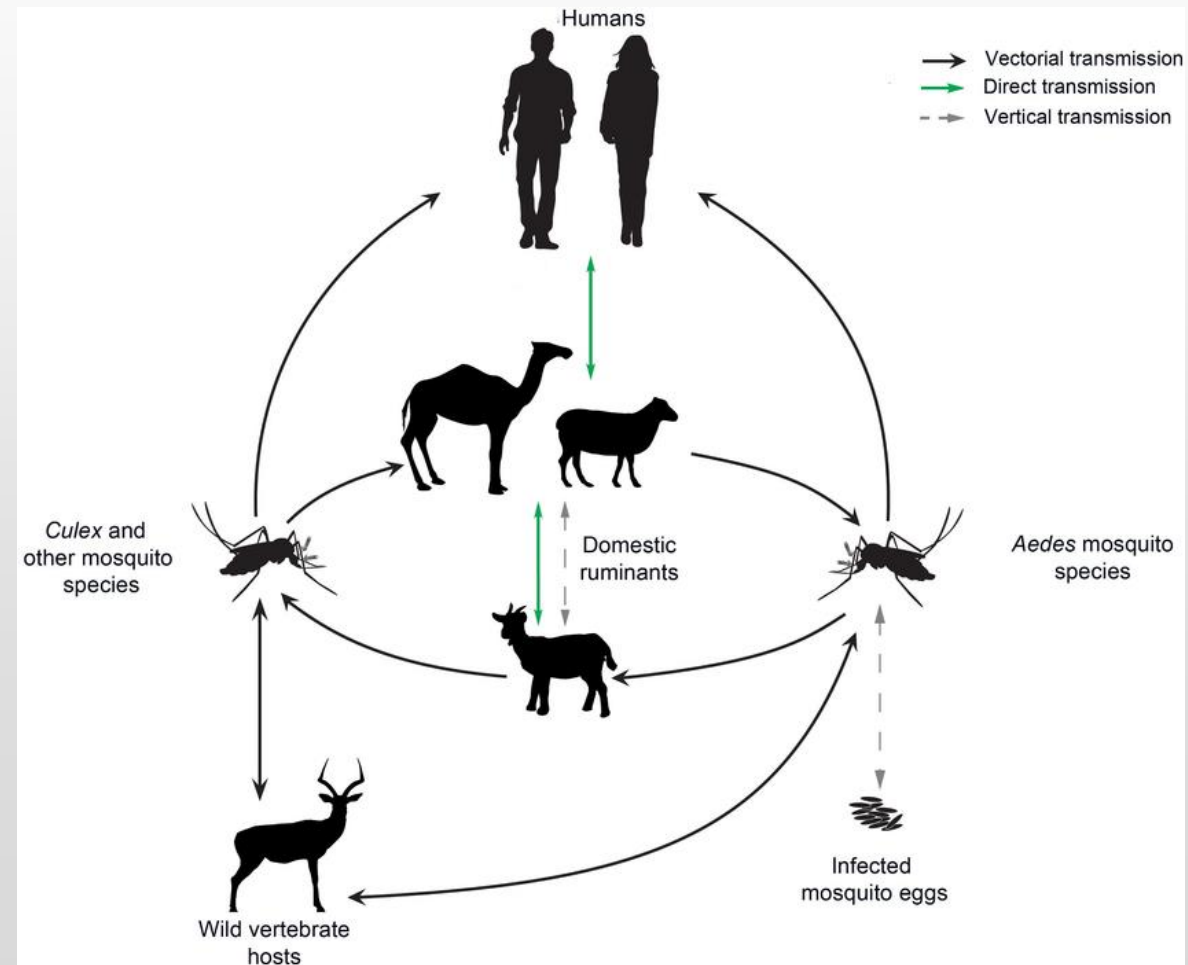
Japanese Encephalitis Virus

- At least 14 mosquito species have been confirmed as JEV vectors, and experimental vector competence has been demonstrated in a further 11 species. However, the major vectors of the virus are from the *Culex* vishnui subgroup, particularly *Cx. tritaeniorhynchus*. Other *Culex* species including *Cx. bitaeniorhynchus*, *Cx. fuscocephala*, *Cx. gelidus*, *Cx. annulirostris*, and *Cx. quinquefasciatus* are important secondary JEV vectors that may also be primary vectors in some regions. The distribution of *Cx. tritaeniorhynchus* extends from Pakistan in the West to Japan in the East, and from China/Korea in the North to Indonesia in the South. It has also been found in Greece and Turkey, suggesting a possible continuum from Pakistan to Turkey via an unconfirmed presence in Iran.



Rift Valley fever (RVF)

- Rift Valley fever (RVF) is a zoonotic vector-borne disease that primarily affects domestic animals but can also infect humans. transmitted by a broad spectrum of mosquito species, especially *Aedes* and *Culex* genus, to animals (domestic and wild ruminants and camels) and humans. Rift Valley fever is endemic in sub-Saharan Africa and in the Arabian Peninsula, with periodic epidemics characterised by 5–15 years of inter-epizootic periods. **Humans** can become infected by the **RVF virus (RVFV)**, through the bites of **vectors**, by contact with infected animals and animal materials

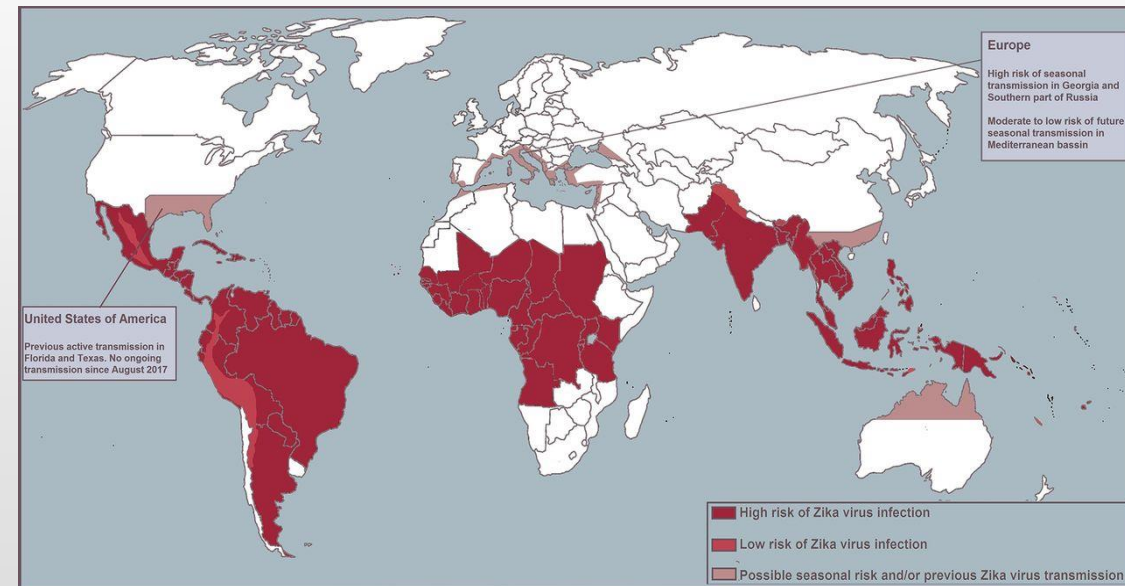


Rift Valley fever (RVF)

- In Iran, from January 2016 to December 2016, blood samples were collected from 288 ruminants (118 cattle, 142 sheep and 28 goats) of both sexes in the Kurdistan Province of western Iran. Clinical symptoms and history of abortions were recorded. The presence of RVFV-specific antibodies was investigated by c-ELISA and indirect immunofluorescence assay (IIFA). The results of both tests were positive for five (1.7%) out of a total of 288 animals, The results of the study revealed the presence of low-level RVFV circulation among the ruminants of Kurdistan Province in Iran indicating that they are at risk of exposure to the virus during their lifetime. . No human cases have been reported up to now from Iran.

Is Iran Threatened By Zika Virus?

Zika virus is an Arbovirus identified first time in 1947 in Uganda. Zika epidemic is a threat far greater than the Ebola outbreak. The World Health Organization has urged Asian countries to be vigilant about the risk of spreading Zika virus and preventive measures to control it. In Iran, 64 species of mosquitoes from Culicidea family have been reported three of which belong to the Aedes genus, and one of which is Aedes albopictus. Iran also has suitable climate for endemic transmission of Zika virus. Immigrants from neighboring countries for economic reasons, could increase the risk of disease transmission in Iran. The destination countries of Iranian passengers, especially in East Asia, are at risk or have been reported to have cases of Zika. So, traveling to areas where active Zika virus exists and its transmission is common, could potentially increase the risk of transmission of Zika. Close supervision alongside the borders is necessary when foreign people arrive in the country.



Practical Neurology 2018;18:271-277.

Hantavirus

- From April 2014 to June 2016, 113 cases from 25 different provinces of Iran were analyzed for Hantavirus infection by IgM/IgG ELISA and pan-Hantavirus RT-PCR tests.
- Although, viral genome was detected in none of the subjects, IgM and IgG antibodies were detected in 19 and 4 cases, respectively.

- [Mostafa Salehi-Vaziri](#) ,J Med Virol, 2019

FIGURE 26.2. Global distribution of flaviviruses. The global distribution of flaviviruses with significant impact on global health.

