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ARTHROPOD-BORNE AND ARTHROPOD-RELATED VIRUSES IN IRAN AND NEIGHBORING COUNTRIES

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The present article is dedicated to my wife Elaheh and my son Arvin who have patiently supported me during my professional currier, especially providing this article
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Arthropods are very significant for human and veterinary medicine and health because of the burden of diseases caused by the pathogens they transmit. Databases, including the Web of Science, PubMed, Scopus, Google Scholar, CABI, Scientific Information Database, IranMedex and Magiran were searched to the end of December 2022 for publications concerning infections in Iran caused by arboviruses. Pertinent information was extracted and analyzed. Thirty-three viral infections occur in Iran, which are biologically or mechanically known or assumed to be transmitted by arthropods. Information about agents (viruses), distribution (in 31 Iranian provinces), hosts (human and animals) and known vectors in Iran was obtained for each disease. Also, a list of arboviruses was provided for the countries neighboring Iran, including Afghanistan, Armenia, Azerbaijan, Bahrain, Iraq, Kuwait, Oman, Pakistan, Qatar, Saudi Arabia, Turkey, Turkmenistan and the United Arab Emirates, as well as Djibouti, Somalia, Sudan, Syria and Yemen, which do not neighbor Iran but, like Iran, occur in the World Health Organization Eastern Mediterranean Region. This list includes 40 viruses which are not formally recorded in Iran. The viruses are members of 19 genera representing 14 families in which three, four, 20 and 29 viruses are sandfly-borne, biting midge-borne, mosquito-borne and tick-borne, respectively.

Keywords: arboviruses, biological transmission, mechanical transmission, mobovirus, reservoirs, vectors, zoonoses

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About 17% of the global burden of infectious and parasitic diseases is caused by vector-borne pathogens. After lower respiratory infections, diarrhoeal diseases, HIV/AIDS and tuberculosis, malaria displays the fifth highest burden among infectious and parasitic diseases (World Health Organization, 2008). Traditionally, malaria and leishmaniasis are major diseases in the World Health Organization (WHO) Eastern Mediterranean Region, caused by vector-borne malarial protozoa (mosquito-borne) and trypanosomes (sandfly-borne), respectively. Many other arthropod-borne viral (arboviral) infections, such as Crimean-Congo hemorrhagic fever, dengue fever, Japanese encephalitis, Rift Valley fever, sandfly fever, West Nile fever and yellow fever, are of lesser or more local importance (World Health Organization, 2004). While, the burden of malaria has decreased and the burden of leishmaniasis has not changed during recent years in the region (World Health Organization, 2004, 2008, 2017), some arboviral infections, such as Crimean-Congo hemorrhagic fever, Chikungunya fever, dengue fever, Rift Valley fever and West Nile fever, which are classified as neglected, emerging or reemerging infectious diseases (EIDs or RIDs), have been introduced into the region or Iran (World Health Organization, 2010; Parhizgari et al., 2017; Pouriayevali et al., 2019). It has been estimated that the majority of EIDs are zoonotic (60.3%) and 71.8% of these are caused by pathogens that originated from wildlife, such as Ebola virus, Nipah virus and severe acute respiraotory syndrome (SARS) virus. While 25.4% of EIDs are caused by viral and prion pathogens, 22.8% of EIDs are vector-borne (Jones et al., 2008). Some arthropod-borne viruses (arboviruses) are not pathogenic for humans but they are for domesticated animals; thus, they are very important in view of food production and/or have economical importance because of loss of eggs, milk or meat production, unhealthy offspring and loss of herds or fowl populations due to diseases such as African horse sickness (Dennis et al., 2019), African swine fever (Dixon et al., 2019), bluetongue (Maclachlan et al., 2015), bovine ephemeral fever (Walker, Klement, 2015), fowl pox (Della-Porta, 2001), rinderpest (Roeder et al., 2013) and Schmallenberg virus infection (Collins et al., 2019). Also, the possible use of some arthropods infected with certain arboviruses as weapons or bioterrorism is mentioned in published literature, such as mosquitoes infected with dengue, Rift Valley fever and yellow fever viruses and ticks infected with Colorado fever and Crimean-Congo hemorrhagic fever viruses (Lockwood, 2012). There are more than 600 known arboviruses (Conway et al., 2014) and about 100 of these infect humans and some 40 infect livestock (Hart, 2001). Fifty arboviruses are known to cause disease in homeotherm (endotherm) wild and domestic mammals and birds (Hubálek et al., 2014a).

Iran is located in the Middle East and southwestern Asia where the Afrotropical, Oriental and Palaearctic Regions converge. Iran is connected with Central Asia through Turkmenistan in the northeast, with southern Asia and the Oriental Region through Pakistan in the southeast and with the Afrotropical Region through the Arabian Peninsula in the south. For this reason, the region is interesting in view of biodiversity while at the same

time complicating interventions for vector control and integrated vector management (IVM) aimed at reducing the transmission of vector-borne pathogens and parasites and the burden of diseases. Iran also resides in the WHO Eastern Mediterranean Region along with 21 other countries: Afghanistan, Bahrain, Djibouti, Egypt, Iraq, Jordan, Kuwait, Lebanon, Lybia, Morocco, Oman, Pakistan, Palestine, Qatar, Saudi Arabia, Somalia, Sudan, Syria, Tunisia, the United Arab Emirates and Yemen (World Health Organization, 2004).

There are some recent and useful reviews of different arboviruses that occur in some of the aforementioned countries, such as Failloux et al. (2017) who reviewed arboviruses in the Mediterranean and Black Sea Regions, Atkinson and Hewson (2018) who reviewed arboviruses in Central Asia and Braack et al. (2018) who reviewed mosquito-borne viruses (moboviruses) in Africa. Also, there are some useful reviews on specific infections that occur in the region, such as African horse sickness (Dennis et al., 2019), African swine fever (Dixon et al., 2019), Akabane virus infection (Kirkland, 2015), Bhanja virus infection (Hubálek, 1987), bluetongue virus infection (Maclachlan et al., 2015), bovine ephemeral fever (Walker, Klement, 2015), bovine herpes (Chatterjee et al., 2016), Chikungunya virus infection (Silva et al., 2018), Crimean-Congo hemorrhagic fever (Nasirian, 2019), Hantaan virus infection (Bi et al., 2008), Rift Valley fever (Kenawy et al., 2018), rinderpest (Roeder et al., 2013), sandfly fever (Depaquit et al., 2010), Schmallenberg virus infection (Collins et al., 2019), West Nile fever (Eybpoosh et al., 2019) and Zika virus infection (Epelboin et al., 2017), as well as reviews for specific countries, such as Afghanistan (Wallace et al., 2002), Pakistan (Hayes, Burney, 1981), Sudan (Ahmed et al., 2020) and Turkey (Ergunay et al., 2011; Inci et al., 2013, 2016, 2018; Düzlü et al., 2020).

Recently, Azari-Hamidian et al. (2019) reviewed 14 mosquito-borne pathogens and parasites in Iran, including six viral infections (avian or fowl pox, bovine ephemeral fever, dengue, Rift Valley fever, Sindbis and West Nile fever), two bacterial infections (anthrax and tularemia), four helminthoses (*Deraiophoronema evansi* infection, dirofilariasis, lymphatic filariasis and setariasis) and two protozoal infections (avian and human malarias) and updated the checklist of Iranian mosquitoes. Also, Parhizgari et al. (2021) reviewed some selected diseases in Iran caused by vector-borne pathogens. They reviewed, for example, four arboviruses: Crimean-Congo hemorrhagic fever, dengue fever, sandfly fever and West Nile fever.

In the present article, we provide a comprehensive review of infections caused by arboviruses in Iran. We also provide a list of arboviruses in the countries neighboring Iran, as well as Djibouti, Somalia, Sudan, Syria and Yemen, which, like Iran, located in the WHO Eastern Mediterranean Region, and have not received much attention in recent reviews of arboviruses (Failloux et al., 2017; Braack et al., 2018). Thus, the present review includes 19 countries. Additionally, it includes some viruses that are not (true) arboviruses or are arthropod-related viruses which arthropods may mechanically transmit to humans and domestic animals, and were not included in the aforementioned reviews of arboviruses.

METHODS

Iran, with an area of approximately 1,648,195 km^2, is located between 25–40^o N latitude and 44–63^o E longitude and formally includes 31 provinces (Fig. 1). Iran is bordered by Armenia, Azerbaijan and Turkmenistan in the north, Afghanistan and Pakistan in the east, Iraq and Turkey in the west and the Persian Gulf and Oman Sea in the south, across which lie the countries of Bahrain, Kuwait, Oman, Qatar, Saudi Arabia and the United Arab Emirates. Hereafter, Iran, the aforementioned countries and five countries of the WHO Eastern Mediterranean Region, including Djibouti, Somalia, Sudan, Syria and Yemen, are referred to as "the region". Most parts of Iran and many countries in "the region" have arid climate based on different climate classifications. This investigation is based on publications listed in the Web of Science (Clarivate), PubMed, Scopus, Google Scholar, CABI, Scientific Information Database (SID), IranMedex and Magiran databases prior to December 2022. Firstly, principal textbooks on medical and veterinary entomology (for example Harwood, James, 1979; Lane, Crosskey, 1993; Mullen, Durden, 2019) were reviewed for information on diseases caused by arboviruses. Secondly, we searched the aforementioned databases using terms such as "arthropod-borne diseases", "arboviruses", "mosquito-borne viruses" and "moboviruses" to identify the names of viral infections associated with arthropods. Afterwards, the databases were searched to obtain literature reporting the occurrence of those diseases in animals and humans in Iran, Central Asia, the Middle East, southwestern Asia and the WHO Eastern Mediterranean Region (Harbach, 1988; World Health Organization, 2004). Finally, the searches were conducted using the keywords "extracted arthropod-borne viral disease names, Iran, Iranian" and "extracted arthropod-borne virus names, Iran, Iranian". Also, the searches were conducted with the names of the countries neighboring Iran and the five additional countries of the WHO Eastern Mediterranean Region. The names of diseases or infections comprised more than 73 keywords (names or terms) which were mentioned in the search results (Table 1, Fig. 2). It should be mentioned that there were more than one name or term for some infections or diseases. The generic names of arthropod-borne and arthropod-related viruses included *Alphavirus*, *Asfavirus*, *Avipoxvirus*, *Bandavirus*, *Capripoxvirus*, *Deltaretrovirus*, *Ephemerovirus*, *Flavivirus*, *Lentivirus*, *Morbillivirus*, *Orbivirus*, *Orthobunyavirus*, *Orthohantavirus*, *Orthonairovirus*, *Phlebovirus*, *Thogotovirus*, *Varicellovirus*, *Vesiculovirus* and *Zamolirhabdovirus*. Additionally, references cited in the retrieved publications were also reviewed to increase the coverage of the literature. Likewise, unpublished documents such as the Centers for Disease Control and Prevention (CDC) Arthropod-Borne Virus Information Exchange (available at https://stacks.cdc.gov) were used to increase the coverage. With few exceptions, only information obtained from books and peer-reviewed articles was used to prepare this review. Information about infectious agents (viruses), distribution (in 31 Iranian provinces) (Fig. 1), reservoirs or hosts (human and animals) and known vectors in Iran was obtained for each infection. Six mosquito-borne viral infections, which were recently reviewed by Azari-Hamidian et al. (2019), were mentioned only for

distributional records in the region or possible new data in Iran. Maes et al. (2018) was consulted for the latest classification of arboviruses of the order Bunyavirales. The capital letter abbreviations used for the names of viruses are based on the "International catalog of arboviruses including certain other viruses of vertebrates" (available at https://wwwn.cdc.gov/arbocat/VirusBrowser.aspx). There is one exception: all sandfly-borne phleboviruses were mentioned in one keyword "Sandfly fever". Those are abbreviated SFN-SV because the most common viruses among them are Naples (SFNV) and Sicilian (SFSV) viruses, and also to distinguish them from Semliki Forest virus (SFV). Also, sheep pox virus (SPV) and goat pox virus (GPV) were mentioned in one search result. Though they are different viruses, their clinical diseases are similar. The abbreviations of mosquito and sandfly genera and subgenera follow Reinert (2009) and Galati et al. (2017), respectively. For the valid species names of different arthropod taxa, the following references and webpages were consulted: biting midges (Borkent, Dominiak, 2020), horseflies (Moucha, 1976), mosquitoes (Azari-Hamidian et al., 2019, 2020; Harbach, 2023), sandflies (Secombe et al., 1993) and ticks (Gugliemone et al., 2010, 2014; Hosseni-Chegeni et al., 2019).

Figure 1. Map of Iran and its 31 provinces.

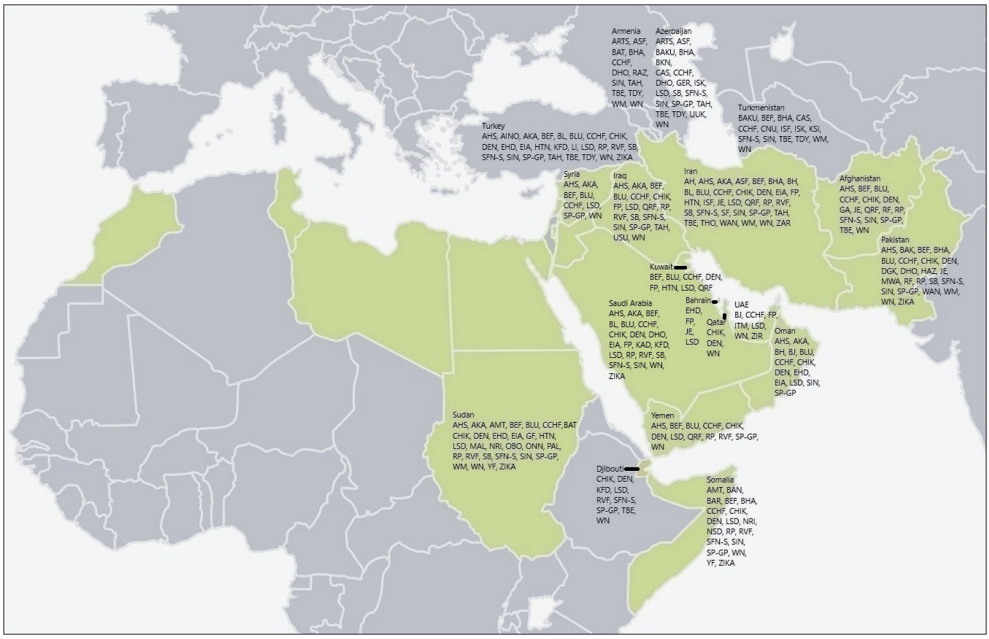

Figure 2. Map showing the arthropod-borne and arthropod-related viruses in the countries included in the present review and the highlighted countries of the World Health Organization Eastern Mediterranean Region. Abbreviations for viruses: AH = Abu Hammad, AHS = African horse sickness, AINO = Aino, AKA = Akabane, AMT = Arumowot, ARTS = Artashat, ASF = African swine fever, BAK = Bakau, BAKU = Baku, BAN = Banzi, BAR = Barur, BAT = Batai, BEF = Bovine ephemeral fever, BHA = Bhanja, BH = Bovine herpes, BJ = Barkedji, BKN = Batken, BL = Bovine leukemia, BLU = Bluetongue, CAS = Caspiy, CCHF = Crimean-Congo hemorrhagic fever, CHIK = Chikungunya, CNU = Chenuda, DEN = Dengue, DGK = Dera Ghazi Khan, DHO = Dhori, EHD = Epizootic haemorrhagic disease, EIA = Equine infectious anaemia, FP = Fowl pox, GA = Grand Arbaud, GF = Gabek Forest, GER = Geran, HAZ = Hazara, HTN = Hantaan, ISF = Isfahan, ISK = Issyk-Kul, ITM = Israel turkey meningoencephalitis, JE = Japanese encephalitis, KAD = Kadam, KFD = Kyasanur Forest disease, KSI = Karshi, LI = Louping ill, LSD = Lumpy skin disease, MAL = Malakal, MWA = Manawa, NRI = Ngari, NSD = Nairobi sheep disease, OBO = Obodhiang, ONN = O'nyong-nyong, PAL = Palyam, QRF = Quaranfil, RAZ = Razdan, RF = Royal farm, RP = Rinderpest, RVF = Rift Valley fever, SB = Schmallenberg, SFN-S = Sandfly fever, SF = Semliki Forest, SIN = Sindbis, SP-GP = Sheep pox-goat pox, TAH = Tahyna, TBE = Tick-borne encephalitis, TDY = Tamdy, THO = Thogoto, USU = Usutu, UUK = Uukuniemi, WAN = Wanowrie, WM = Wad Medani, WN = West Nile, YF = Yellow fever, ZAR = Zahedan rhabdovirus, ZIKA = Zika, ZIR = Zirqa.

Table 1. Distribution of arthropod-borne and arthropod-related viruses in the countries included in the present review

Viruses	Iran	Afghanistan	Armenia	Azerbaijan	Bahrain	Djibouti	Iraq	Kuwait	Oman	Pakistan	Qatar	Saudi Arabia	Somalia	Sudan	Syria	Turkey	Turkmenistan	UAE	Yemen	Main references for the country records
AH	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Hoogstraal (1985)
AHS	*	*	-	-	-	-	*	-	*	*	-	*	-	*	*	*	-	-	*	Rafyi (1961)
AINO	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	Contigiani et al. (2017)
AKA	*	-	-	-	-	-	*	-	*	-	-	*	-	*	*	*	-	-	-	Taylor, Mellor (1994)
AMT	-	-	-	-	-	-	-	-	-	-	-	-	*	*	-	-	-	-	-	Braak et al. (2018)
ARTS	-	-	*	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Lvov (1994)
ASF	*	-	*	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Beltrán-Alcrudo et al. (2017)
BAK	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Hoogstraal (1985)
BAKU	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Lvov (1994)
BAN	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	Henderson et al. (1968), Cahill (1971)
BAR	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	Butenko et al. (1981)
BAT	-	-	*	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Failloux et al. (2017)
BEF	*	*	-	-	-	-	*	*	-	*	-	*	*	*	*	*	*	-	*	Walker, Klement (2015)
BHA	*	-	*	*	-	-	-	-	-	*	-	-	*	-	-	-	*	-	-	Hubálek (1987)
BH	*	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	-	Hedger et al. (1980)
BJ	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	*	-	Camp et al. (2019)
BKN	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Lvov (1994)
BL	*	-	-	-	-	-	-	-	-	-	-	*	-	-	-	*	-	-	-	Hafez et al. (1990), Burgu et al. (2005)
BLU	*	*	-	-	-	-	*	*	*	*	-	*	-	*	*	*	-	-	*	Mellor et al. (2008, 2009)
CAS	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Lvov et al. (2014a)

Viruses	Iran	Afghanistan	Armenia	Azerbaijan	Bahrain	Djibouti	Iraq	Kuwait	Oman	Pakistan	Qatar	Saudi Arabia	Somalia	Sudan	Syria	Turkey	Turkmenistan	UAE	Yemen	Main references for the country records
CCHF	*	*	*	*	-	-	*	*	*	*	-	*	*	*	*	*	*	*	*	Blair et al. (2019), Nasirian (2019)
CHIK	*	*	-	-	-	*	*	-	*	*	*	*	*	*	-	*	-	-	*	Wahid et al. (2017)
CNU	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Lvov (1994)
DEN	*	*	-	-	-	*	-	*	*	*	*	*	*	*	-	*	-	-	*	WHO (2004)
DGK	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Darwish et al. (1983b)
DHO	-	-	*	*	-	-	-	-	-	*	-	*	-	-	-	-	-	-	-	Hoogstraal, Valdez (1980)
EHD	-	-	-	-	*	-	-	-	*	-	-	-	-	*	-	*	-	-	-	Mellor (2001e), Temizel et al.)2009)
EIA	*	-	-	-	-	-	-	-	*	-	-	*	-	*	-	*	-	-	-	Body et al. (2011)
FP	*	-	-	-	*	-	*	*	-	-	-	*	-	-	-	-	-	*	-	Tarello (2004, 2008)
GA	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Hoogstraal (1985)
GF	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Tesh et al. (1976 b), Tesh (1988)
GER	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Lvov et al. (2014c)
HAZ	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Darwish et al. (1983b)
HTN	*	-	-	-	-	-	-	*	-	-	-	-	-	*	-	*	-	-	-	Kassiri, Dehghani (2020)
ISF	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Atkinson, Hewson (2018)
ISK	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Lvov (1994)
ITM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	Camp et al. (2019)
JE	*	*	-	-	*	-	-	-	-	*	-	-	-	-	-	-	-	-	-	WHO (2004)
KAD	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	Al-Khalifa et al. (2007)
KFD	-	-	-	-	-	*	-	-	-	-	-	*	-	-	-	*	-	-	-	Hoffman et al. (2018)
KSI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	Atkinson, Hewson (2018)

Table 1. ***Continuation.*** Distribution of arthropod-borne and arthropod-related viruses in the countries included in the present review

Viruses	Iran	Afghanistan	Armenia	Azerbaijan	Bahrain	Djibouti	Iraq	Kuwait	Oman	Pakistan	Qatar	Saudi Arabia	Somalia	Sudan	Syria	Turkey	Turkmenistan	UAE	Yemen	Main references for the country records
LI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	Gao et al. (1997)
LSD	*	-	-	*	*	*	*	*	*	-	-	*	*	*	*	*	-	*	*	Tuppurainen et al. (2015)
MAL	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Blasdell et al. (2012b)
MWA	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Darwish et al. (1983b)
NRI	-	-	-	-	-	-	-	-	-	-	-	-	*	*	-	-	-	-	-	Braak et al. (2018)
NSD	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	Peiris (2001)
OBO	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Calisher et al. (1989)
ONN	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Ahmed et al. (2020)
PAL	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	Mohammad, Mellor (1990)
QRF	*	*	-	-	-	-	*	*	-	-	-	-	-	-	-	-	-	-	*	Converse, Moussa (1982)
RAZ	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Lvov (1994)
RF	-	*	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Hoogstraal (1985)
RP	*	*	-	-	-	-	*	-	-	*	-	*	*	*	-	*	-	-	*	Roeder et al. (2013)
RVF	*	-	-	-	-	*	*	-	-	-	-	*	*	*	-	*	-	-	*	Kenawy et al. (2018)
SB	*	-	-	*	-	-	*	-	-	*	-	*	-	*	-	*	-	-	-	Asadolahizoj et al. (2021)
SFN-S	*	*	-	*	-	*	*	-	-	*	-	*	*	*	-	*	*	-	-	Tesh et al. (1976b)
SF	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	The CDC Arthropod-Borne Virus Information Exchange (1962)
SIN	*	*	*	*	-	-	*	-	*	*	-	*	*	*	-	*	*	-	-	Hubálek et al. (2014a)
SP-GP	*	*	-	*	-	*	*	-	*	*	-	-	*	*	*	*	-	-	*	Tuppurainen et al. (2015)
TAH	*	-	*	*	-	-	*	-	-	-	-	-	-	-	-	*	-	-	-	Hubálek (2008), Barakat et al. (2016)

Viruses	Iran	Afghanistan	Armenia	Azerbaijan	Bahrain	Djibouti	Iraq	Kuwait	Oman	Pakistan	Qatar	Saudi Arabia	Somalia	Sudan	Syria	Turkey	Turkmenistan	UAE	Yemen	Main references for the country records
TBE	*	*	*	*	-	*	-	-	-	-	-	-	-	-	-	*	*	-	-	Im et al. (2020)
TDY	-	-	*	*	-	-	-	-	-	-	-	-	-	-	-	*	*	-	-	Lvov (1994)
THO	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Sureau et al. (1980)
USU	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	Barakat et al. (2016)
UUK	-	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Gromashevsky, Nikimorov (1973)
WAN	*	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-	-	Darwish et al. (1983b)
WM	*	-	*	-	-	-	-	-	-	*	-	-	-	*	-	-	*	-	-	Taylor et al. (1966a), Lvov (1994)
WN	*	*	*	*	-	*	*	-	-	*	*	*	*	*	*	*	*	*	*	Eybpoosh et al. (2019)
YF	-	-	-	-	-	-	-	-	-	-	-	-	*	*	-	-	-	-	-	Braak et al. (2018)
ZAR	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Dilcher et al. (2015)
ZIKA	-	-	-	-	-	-	-	-	-	*	-	*	*	*	-	*	-	-	-	Kindhauser et al. (2016)
ZIR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	Varma et al. (1973)

Abbreviations for viruses: AH = Abu Hammad, AHS = African horse sickness, AINO = Aino, AKA = Akabane, AMT = Arumowot, ARTS = Artashat, ASF = African swine fever, BAK = Bakau, BAKU = Baku, BAN = Banzi, BAR = Barur, BAT = Batai, BEF = Bovine ephemeral fever, BHA = Bhanja, BH = Bovine herpes, BJ = Barkedji, BKN = Batken, BL = Bovine leukemia, BLU = Bluetongue, CAS = Caspiy, CCHF = Crimean-Congo hemorrhagic fever, CHIK = Chikungunya, CNU = Chenuda, DEN = Dengue, DGK = Dera Ghazi Khan, DHO = Dhori, EHD = Epizootic haemorrhagic disease, EIA = Equine infectious anaemia, FP = Fowl pox, GA = Grand Arbaud, GF = Gabek Forest, GER = Geran, HAZ = Hazara, HTN = Hantaan, ISF = Isfahan, ISK = Issyk-Kul, ITM = Israel turkey meningoencephalitis, JE = Japanese encephalitis, KAD = Kadam, KFD = Kyasanur Forest disease, KSI = Karshi, LI = Louping ill, LSD = Lumpy skin disease, MAL = Malakal, MWA = Manawa, NRI = Ngari, NSD = Nairobi sheep disease, OBO = Obodhiang, ONN = O'nyong-nyong, PAL = Palyam, QRF = Quaranfil, RAZ = Razdan, RF = Royal farm, RP = Rinderpest, RVF = Rift Valley fever, SB = Schmallenberg, SFN-S = Sandfly fever, SF = Semliki Forest, SIN = Sindbis, SP-GP = Sheep pox-goat pox, TAH = Tahyna, TBE = Tick-borne encephalitis, TDY = Tamdy, THO = Thogoto, USU = Usutu, UUK = Uukuniemi, WAN = Wanowrie, WM = Wad Medani, WN = West Nile, YF = Yellow fever, ZAR = Zahedan rhabdovirus, ZIKA = Zika, ZIR = Zirqa

Infections in Iran caused by arthropod-borne viruses or the viruses which may be mechanically transmitted by arthropods

Asfaviridae

African swine fever

African swine fever is caused by the African swine fever virus (ASFV) (Asfaviridae: *Asfavirus*), the only DNA arbovirus that is pathogenic for animals. There are four antigenic types and 22 genotypes of ASFV. The disease occurs in Africa, America, Asia and Europe. Infections occur in Armenia and Azerbaijan. The virus infects all members of the pig family (Suidae). The disease is transmitted via direct route and also by the bite of soft ticks of the genus *Ornithodoros* (Parasitiformes: Argasidae) (Gibbs, 2001; Labuda, Nuttall, 2008; Hubálek, Rudolf, 2012; Vlasova et al., 2012; Hubálek et al., 2014a; Beltrán-Alcrudo et al., 2017; Dixon et al., 2019). The principal vectors are *O. erraticus* (Lucas), species of the *O. moubata* (Murray) complex (such as *O. moubata* and *O. porcinus* Walton), *O. savignyi* (Audouin) and *O. sonrai* Sautet et Witkowski in Africa, *O. erraticus* in Europe and *O. coriaceus* Koch, *O. puertoricensis* Fox and *O. turicata* (Dugès) in the Americas. Transovarial, transstadial and sexual (venereal) transmission of the virus occur throughout the life of the ticks (Plowright et al., 1970; Hoogstraal, 1985; Hess et al., 1987; Gibbs, 2001; Boinas et al., 2004, 2011; de la Fuente et al., 2008; Ravaomanana et al., 2010; Gallardo et al., 2011; Hubálek et al., 2014a; Beltrán-Alcrudo et al., 2017). There is some evidence that the stable fly *Stomoxys calcitrans* (Linnaeus) (Diptera: Muscidae) may be involved in mechanical transmission while feeding, or infection is due to ingestion of an infected fly by the host (Mellor et al., 1987; Baldacchino et al., 2013; Olsen et al., 2018a, b). The virus has been found in wild boars in East and West Azerbaijan Provinces of Iran (Rahimi et al., 2010; Beltrán-Alcrudo et al., 2017). At least 11 species of soft ticks, including four species of *Ornithodoros*, one being *O. erraticus*, occur in Iran (Hosseni-Chegeni et al., 2019; Hosseini-Chegeni, Tavakoli, 2020), however there is no information about the vector(s) of the virus in the country.

Flaviviridae

Dengue fever

Dengue fever, caused by the dengue fever virus (DENV) (Flaviviridae: *Flavivirus*), was reviewed by Azari-Hamidian et al. (2019). Some published documents which might be added to the Iranian literature are Baniasadi et al. (2016), Salehi-Vaziri et al. (2016), Heydari et al. (2018), Tavakoli et al. (2020) and Firooziyan et al. (2022). The virus has also been found in Afghanistan (Arsen'eva, 1982; Wallace et al., 2002; Elyan et al., 2014), Djibouti (World Health Organization, 2004; Andayi et al., 2014; Braak et al., 2018), Kuwait (Mustafa et al., 2001; Pacsa et al., 2003), Oman (Al-Abri et al., 2015), Pakistan (Hayes, Burney, 1981; World Health Organization, 2004; Afzal et al., 2015; Khan et al., 2016; Yaqub et al., 2017; Ahmad et al., 2020), Qatar (Humphrey et al., 2019), Saudi Arabia

(World Health Organization, 2004; Khan et al., 2008; Zaki et al., 2008; Memish et al., 2011; Shibl et al., 2012; Ahmed, 2015), Somalia (Oldfield et al., 1993; World Health Organization, 2004; Braak et al., 2018), Sudan (Watts et al., 1994; World Health Organization, 2004; Farnon et al., 2010; Braak et al., 2018; Ahmed et al., 2020), Turkey (Ergunay et al., 2011) and Yemen (World Health Organization, 2004; Shibl et al., 2012; Ciccozzi et al., 2014; Rezza et al., 2014; Alghazali et al., 2019; Al-Samadi, Ali, 2020; Abdul-Ghani et al., 2021). There are no recent reports of *Aedes aegypti* (Linnaeus) [*Stegomyia aegypti*] (Diptera: Culicidae), the main vector, in Iran (Azari-Hamidian et al., 2019). The other important vector, *Ae. albopictus* Skuse [*Stegomyia albopicta*], was recorded just one time in Iran based on five larvae and six adults found in Sistan and Baluchistan Province (Doosti et al., 2016). The species has not been recorded since and there is no evidence for indigenous transmission of DENV in the country.

Japanese encephalitis

Japanese encephalitis, caused by the Japanese encephalitis virus (JEV) (Flaviviridae: *Flavivirus*), is known from Asia and Australia. The virus has been isolated from different domesticated and wild mammals, such as bats, cattle, dogs, donkeys, monkeys, horses, pigs, rodents and water buffaloes, and also birds, including chickens, ducks, egrets, herons and water hens; however, important amplifying hosts in the epidemiology of the disease seem to be pigs and aquatic birds. The virus has been identified in different mosquito species of the genera *Aedes*, *Anopheles*, *Armigeres*, *Culex* and *Mansonia*, however the most important vector is *Culex tritaeniorhynchus* Giles, the rice field mosquito. Vertical (transovarial) transmission and sexual (venereal) transmission are also known for mosquito vectors (Barrett, 2001; Hubálek et al., 2014a; Gould et al., 2017). The virus has also been isolated from the biting midge *Forcipomyia* (*Lasiohelea*) *taiwana* Shiraki (Diptera: Ceratopogonidae) (Linley et al., 1983) and the hard ticks *Dermacentor marginatus* (Sulzer) (Parasitiformes: Ixodidae) and *Ixodes ricinus* (Linnaeus), as reported by Anastos (1957). Also, Hoogstraal (1966) listed a number of hard tick species of the genera *Dermacentor*, *Ixodes*, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus* which might serve as JEV hosts in nature. The virus is known in Pakistan and is suspected to be present in Afghanistan (Arsen'eva, 1982; Darwish et al., 1983a; Igarashi et al., 1994; Wallace et al., 2002; World Health Organization, 2004; Khan et al., 2016). Also, one febrile patient who entered China from Bahrain was positive for JEV-specific IgM antibody (Shi et al., 2016). Japanese encephalitis virus has been isolated from a number of mosquitoes, including *Aedes albopictus*, *Ae. curtipes* (Edwards) [*Cancraedes curtipes*], *Ae. vexans* (Meigen) [*Aedimorphus vexans*], *Anopheles barbirostris* van der Wulp, *An . sinensis* Wiedemann, *An. subpictus* Grassi s. l., *An. vagus* Dönitz, *Armigeres obturbans* (Walker), *Ar. subalbatus* (Coquillett), *Culex annulus* Theobald, *Cx. annulirostris* Skuse, *Cx. bitaeniorhynchus* Giles, *Cx. epidesmus* Theobald, *Cx. fuscocephala* Theobald, *Cx. gelidus* Theobald, *Cx. modestus* Ficalbi, *Cx. pipiens* Linnaeus, *Cx. pseudovishnui* Colless, *Cx. quinquefasciatus* Say,

Cx. sitiens Wiedemann, *Cx. theileri* Theobald, *Cx. vishnui* Theobald, *Cx. whitmorei* (Giles), *Mansonia annulifera* (Theobald), *Ma. bonneae* Edwards, *Ma. dives* (Schiner), *Ma. indiana* Edwards and *Ma. uniformis* (Theobald), according to Simpson et al. (1970, 1974), Peiris et al. (1994), Reuben et al. (1994), Dhanda et al. (1997), Barrett (2001) and Wang et al. (2007). According to unpublished data in Iran, the antibodies for the virus have been found in humans (3.4%) using the neutralization test (the CDC Arthropod-Borne Virus Information Exchange 1962, available at https://stacks.cdc.gov), however there is no verification or published documentation about the occurrence of the virus in the country. The main vector, *Culex tritaeniorhynchus*, has been found in at least 17 Iranian provinces (Zaim, 1987; Sofizadeh et al., 2018). The species is very abundant in three northern provinces, Golestan, Guilan and Mazandaran, with vast rice fields (Azari-Hamidian et al., 2018; Nikookar et al., 2018; Sofizadeh et al., 2018). Other mosquito species in Iran from which the virus has been isolated elsewhere include *Aedes albopictus*, *Culex bitaeniorhynchus*, *Cx. pipiens*, *Cx. pseudovishnui*, *Cx. quinquefasciatus*, *Cx. sitiens*, *Cx. theileri* and *Mansonia uniformis* (Reuben et al., 1994; Barrett, 2001; Wang et al., 2007; Azari-Hamidian et al., 2019, 2020). Also, the aforementioned hard ticks occur in Iran (Hosseni-Chegeni et al., 2019).

Tick-borne encephalitis

Tick-borne encephalitis, caused by tick-borne encephalitis virus (TBEV) (Flaviviridae: *Flavivirus*), has been found in Asia and Europe. TBEV is the most important tick-borne pathogenic flavivirus in humans. The virus consists of three subtypes, also called clusters, including the western European subtype (formerly central European encephalitis virus – CEEV), the Siberian subtype (formerly West Siberian encephalitis virus – WSEV) and the far-eastern subtype (formerly Russian spring-summer encephalitis virus – RSSEV). The main reservoirs of the virus are small mammals, such as rodents and insectivores, and some wild carnivores, such as foxes, however the virus has also been isolated from chamois (*Rupicapra rupicapra*), dogs, horses and sheep. The main route of transmission is the bite of hard ticks; however, some local epidemics have been caused by consumption of unpasteurized milk or milk products. *Ixodes ricinus* is the main vector in Europe (the western European subtype) and *I. persulcatus* Schulze is the main vector in Asia (the Siberian and the far-eastern subtypes). Transovarial and transstadial transmission have been observed in both main vectors (Heinz, Holzmann, 2001; de la Fuente et al., 2008; Labuda, Nuttall, 2008; Wójcik-Fatla et al., 2011; Hubálek, Rudolf, 2012; Valarcher et al., 2015). According to Anastos (1957), TBEV [as (Russian) spring-summer encephalitis virus] has been isolated, in addition to *Ixodes ricinus* and *I. persulcatus*, from the following ticks (in the former USSR): *Dermacentor marginatus*, *D. nuttalli* Olenev, *D. silvarum* Olenev, *Haemaphysalis concinna* Koch, *H. japonica* Warburton, *Hyalomma dromedarii* Koch, *H. excavatum* Koch and *Ixodes trianguliceps* Birula. Additionally, the virus has been isolated from *Dermacentor reticulatus* (Fabricius) in Germany (Chitimia-Dobler et al., 2019),

Poland (Wójcik-Fatla et al., 2011) and Russia (Kislenko et al., 1987), *Ixodes hexagonus* Leach in the Czech Republic (Krivanec et al., 1988) and Croatia (Jemeršić et al., 2014), *Haemaphysalis punctata* Canstrini et Fanzago in the Czech Republic (Hubálek et al., 1989), *Ixodes ovatus* Neumann in Japan (Takeda et al., 1998), *Haemaphysalis flava* Neumann, *H. japonica*, *H. longicornis* Neumann and *I. nipponensis* Kitaoka et Saito in South Korea (Kim et al., 2009; Yun et al., 2012), *Hyalomma marginatum* Koch in Crimea (Hubálek, Rudolf, 2012), *Ixodes gibbosus* Nuttall in the Mediterranean (Hubálek, Rudolf, 2012), *Dermacentor silvarum*, *Ixodes pavlovskyi* Pomerantzev and *I. lividus* Koch (as *I. plumbeus* Leach) in Russia (Mikryukova et al., 2014; Pukhovskaya et al., 2018). Also, TBEV has been shown experimentally to be vectored by *Dermacentor marginatus*, *Haemaphysalis inermis* Birula and *Ixodes arboricola* Schulze et Schlottke (Lichard, Kozuch, 1967; Nosek et al., 1972; Nosek, Kožuch, 1985). The virus has also been isolated from fleas, including *Ceratophyllus indages* (Rothschild) (synonym: *Ceratophyllus tamias* Wagner) (Siphonaptera: Ceratophyllidae), *Palaeopsylla soricis* (Dale) (Siphonaptera: Hystrichopsyllidae), gamasid mites (Federov et al., 1959; Sotnikova, Soldatov, 1964; Naumov, Gutova, 1984), the horsefly *Hybomitra lundbecki* Lynborg (Diptera: Tabanidae) (Krinsky, 1976), the poultry red mite *Dermanyssus gallinae* (De Geer) (Mesostigmata: Dermanyssidae) (Sparagano et al., 2014) and the mosquito *Aedes vexans* (Pukhovskaya et al., 2018). The virus has been found in Afghanistan, Armenia, Azerbaijan, Djibouti, Turkey and Turkmenistan (Gromashevsky, Nikimorov, 1973; Heinz, Holzmann, 2001; de la Fuente et al., 2008; Ergunay et al., 2011; Inci et al., 2013, 2016; Elyan et al., 2014; Failloux et al., 2017; Atkinson, Hewson, 2018; Im et al., 2020). The disease was recently recorded in Mazandaran Province of northern Iran using ELISA. Among 448 serum samples, 3.6% were positive (Salehi-Vaziri et al., 2020). There is no information about the vector(s) in Iran, however *Ixodes ricinus*, the main vector, is a prevalent hard tick in northern areas of the country, especially the Caspian Sea littoral. *Dermacentor marginatus*, *Haemaphysalis concinna*, *H. inermis*, *H. punctata*, *Hyalomma dromedarii*, *H. excavatum* and *H. marginatum* also occur in Iran (Rahbari et al., 2007; Hosseni-Chegeni et al., 2019).

West Nile fever

West Nile fever, caused by West Nile fever virus (WNV) (Flaviviridae: *Flavivirus*) (synonyms or subtypes: Kunjin and Rabensburg viruses), was reviewed for Iran by Azari-Hamidian et al. (2019) and for the WHO Eastern Mediterranean Region by Eybpoosh et al. (2019). Information in the following publications might be added to those reviews: Shamsizadeh et al. (2015), Shahhosseini, Chinikar (2016), Ziyaeyan et al. (2018), Adham et al. (2019), Amini et al. (2019), Amini et al. (2020), Dehghani et al. (2020), Shahhosseini et al. (2020), Bakhshi et al. (2021) and Staji et al. (2021). The virus has also been found in Afghanistan (Arsen'eva, 1982; Wallace et al., 2002; Elyan et al., 2014), Armenia (Failloux et al., 2017), Azerbaijan (Gromashevsky, Nikimorov, 1973; Mirzoeva et al., 1974), Djibouti

(Andayi et al., 2014), Iraq (Barakat et al., 2016), Pakistan (Hayes, Burney, 1981; Hayes et al., 1982; Reisen et al., 1982; Darwish et al., 1983a; Sugamata, 1988; Sugamata et al., 1988; Igarashi et al., 1994; Bryan et al., 1996; Zohaib et al., 2015; Khan et al., 2016; Niazi et al., 2017; Yaqub et al., 2017), Qatar (DeCarlo et al., 2017; Dargham et al., 2021), Saudi Arabia (Al-Ghamdi, 2014; Hemida et al., 2019; Alqahtani, 2020), Somalia (Henderson et al., 1968; Cahill, 1971; Oldfield et al., 1993), Sudan (Salim, Porterfield, 1973; Watts et al., 1994; McCarthy et al., 1996; Depoortere et al., 2004; Farnon et al., 2010; Yousof et al., 2018; Ahmed et al., 2020), Syria (Azmi et al., 2017), Turkey (Inci et al., 2013; Failloux et al., 2017; Düzlü et al., 2020; Yildirim et al., 2021), Turkmenistan (Atkinson, Hewson, 2018), the United Arab Emirates (Wernery et al., 2007; Alfaresi, Elkoush, 2008) and Yemen (Qassem, Jaawal, 2014). Three mosquito species are known vectors of WNV in Iran: *Aedes caspius* (Pallas) s. l. [*Ochlerotatus caspius* s. l.] (Bagheri et al., 2015), *Culex pipiens* (Shahhosseini et al., 2017) and *Cx. theileri* (Shahhosseini et al., 2020). Other species which are known principal vectors in other countries that also occur in Iran include *Aedes albopictus*, *Coquillettidia richiardii* (Ficalbi), *Cx. modestus*, *Cx. perexiguus* Theobald, *Cx. pipiens*, *Cx. quinquesfasciatus*, *Cx. tritaeniorhynchus* and *Mansonia uniformis* (see Hubálek et al., 2014a; Azari-Hamidian et al., 2019, 2020).

Hantaviridae

Hantaan infection

Hantaviruses (Hantaviridae: *Orthohantavirus*), which cause haemorrhagic fever with renal syndrome (HFRS) in the Old World and hantavirus pulmonary syndrome (HPS) or hantavirus cardiopulmonary syndrome (HCPS) in the New World, are distributed worldwide. The main reservoirs of rural epidemiological pattern are the rodents of the genera *Apodemus* and *Clethrionomys* in Asia and Europe and *Microtus* and *Peromyscus* in the Americas, whereas in urban pattern domestic rodents (*Rattus* species) are reservoirs and in animal houses (vivaria) colonized experimental rats are reservoirs. The viruses that cause HFRS in the Old World include Dobrava (DOBV), Hantaan (HTNV), Puumala (PUUV), Saaremaa (SAAV) and Seoul (SEOV). Dobrava virus is found primarily in the Balkans. Haantan virus is widely distributed in eastern Asia, particularly in China, Russia and Korea. Puumala virus is found in Scandinavia, western Europe and western Russia. Saaremaa is found in central Europe and Scandinavia. Seoul virus is found worldwide. The virus is usually transmitted by contamination of wounds by the saliva, urine or faeces of rodents or by rodent bite (Xu, 2001; Bi et al., 2008; Zowghi et al., 2008; Kassiri, Dehghani, 2020). The virus has been found in Kuwait (Pacsa et al., 2002, 2003), Sudan (Ibrahim et al., 2017) and Turkey (Oncul et al., 2011; Gozalan et al., 2013). There is some evidence for transmission of the virus by the tropical rat mite *Ornithonyssus bacoti* (Hirst) (Mesostigmata: Macronyssidae), trombiculid mites (Prostigmata: Trombiculidae), such as *Eutrombicula splendens* (Ewing), *Leptotrombidium scutellare* (Nagayo, Miyagawa, Mitamura, Tamiya et Tenjin), *L. subpalpale* Vercammen-Grandjean et Langston, an unidentified ixodid tick (Houck et al., 2001; Xu,

2001) and the gamasid mites *Haemolaelaps glasgowi* (Ewing) and *Eulaelaps stabularis* (Koch) (Mesostigmata: Haemogamasidae) (Li, 1986). The first verified record of Hantaan virus in Iran was among street cleaners (4.5%) in Isfahan Province using ELISA and molecular tests as an EID (Chinikar et al., 2014). Later, positive sera were detected in 10 provinces of the country, East Azerbaijan, Fars, Ilam, Isfahan, Kerman, Mazandaran, Razavi Khorasan, South Khorasan, Tehran and Yazd, based on the results of ELISA (Salehi-Vaziri et al., 2019, 2021). Parhizgari et al. (2017) recognized the disease in Iran as an EID, and it was reviewed by Kassiri and Dehghani (2020). However, the aforementioned references mentioned that IgG to hantaviruses has been identified in Iran, which are genus-specific due to the close antigenic relationship of the Old World hantaviruses causing HFRS. In fact, HFRS is caused by various hantaviruses, not necessarily by Hantaan. The Hantaan virus itself circulates in the Far East and is unlikely to be detected in Iran. *Ornithonyssus bacoti* has been found on various rodents in different areas of Iran (Kamali et al., 2001) and at least 85 species of the mite family Trombiculidae are known to be present in the country (Stekolnikov et al., 2019), however there is no information about the possible role of mites in the transmission of Hantaan virus in Iran.

Herpesviridae

Bovine herpes

Bovine herpes, caused by the bovine herpes virus (BHV) (Herpesviridae: *Varicellovirus*), has a worldwide distribution. The virus has been found in different wild and domesticated ruminants, especially camels, cattle, goats and sheep. The disease generally displays two clinical syndromes, respiratory and genital. The disease causes significant financial losses because of a drop in milk production, abortion and deaths in cattle. The virus is mostly transmitted through respiratory infection and less importantly via genital tract infection (Wentink et al., 1993; Chatterjee et al., 2016). However, there is some evidence that the stable fly *Stomoxys calcitrans*, the face fly *Musca autumnalis* De Geer (Diptera: Muscidae) and the soft tick *Ornithodoros coriaceus* may be involved in mechanical transmission (Gibbs et al., 1972, 1973a, b; Taylor et al., 1982; Johnson et al., 1991; Baldacchino et al., 2013). Bovine herpes virus has been found in Oman (Hedger et al., 1980). The virus has been detected in bufalloes, camels, cattle, dogs, horses, humans, Indian gazelles and pigs, using serological and molecular tests, in the following provinces of Iran: Chaharmahal and Bakhtiari, Fars, Guilan, Hamedan, Isfahan, Kerman, Khorasan, Khuzistan, Kurdistan, Qazvin, Semnan, Tehran and Zanjan (Afshar, Tadjbakhsh, 1970; Hazrati et al., 1981; Kargar Moakhar et al., 2001, 2003; Sakhaee et al., 2009; Raoofi et al., 2012a; Sadri, 2012b; Shirvani et al., 2012; Bahari et al., 2013; Ezzi et al., 2013; Safarpoor Dehkordi et al., 2013; Nikbakht et al., 2015; Sharifzadeh et al., 2015; Hemmatzadeh et al., 2016; Seyfi Abad Shapouri et al., 2016; Adeli et al., 2017; Kaveh et al., 2017; Erfani et al., 2019; Noaman, Nabinejad, 2020; Hashemi et al., 2022). There is no information about possible transmission of the virus by arthropods in the country.

Nairoviridae

Abu Hammad virus

Abu Hammad virus (AHV) (Nairoviridae: *Orthonairovirus*) was first found in the soft tick *Argas hermanni* Audouin (Parasitiformes: Argasidae) in Egypt (Converse et al., 1974; Darwish et al., 1976; Casals, Tignor, 1980; Hoogstraal, 1985; Labuda, Nuttall, 2008; Kuhn et al., 2016). It has also been isolated from *A. hermanni* in Dormian Village of Isfahan Province in central Iran (Tesh, 1976, personal communication, cited by the CDC Arthropod-Borne Virus Information Exchange, available at https://stacks.cdc.gov; Hoogstraal, 1985). *Argas hermanni* is not mentioned in the most recent checklist of the soft ticks (10 species) in Iran (Hosseni-Chegeni et al., 2019). Although Hosseni-Chegeni and Tavakoli (2020) recently recorded the species in Lorestan Province in western Iran, there is no new information about AHV in Iran.

Crimean-Congo hemorrhagic fever

Crimean-Congo hemorrhagic fever (CCHF), caused by CCHF virus (CCHFV) (Nairoviridae: *Orthonairovirus*), occurs in Africa, Asia and Europe and is the most widely distributed medically important arboviral disease after dengue fever. The disease is the most significant tick-borne viral disease in humans. The virus has been found in different wild and domestic animals (birds and mammals). It has been isolated from more than 30 species of hard and soft ticks, however the main vector is *Hyalomma marginatum*. CCHFV is biologically transmitted to humans by the bite of an infected tick (horizontal transmission) or by direct contact with infected blood, body fluid, tissues and, possibly, crushed ticks (direct transmission). The virus can be transmitted via different routes in certain ticks, including transovarial, trans-stadial and sexual (venereal) transmission (Hoogstraal, 1979, 1981, 1985; Nuttall, 2001; Labuda, Nuttall, 2008; Chinikar et al., 2010b; Hubálek, Rudolf, 2012; Bente et al., 2013; Spengler et al., 2016; Al-Abri et al., 2017; Contigiani et al., 2017; Blair et al., 2019; Saleem et al., 2020). Also, as reported by Hoogstraal (1979) and Nuttall (2001), the virus has been isolated from species of *Culicoides* (Diptera: Ceratopogonidae). CCHFV occurs in Afghanistan (Hoogstraal, 1979; World Health Organization, 2004), Armenia (Karapetyan et al., 1974; Hoogstraal, 1979; Lvov, 1994; Failloux et al., 2017; Gevorgyan et al., 2019), Azerbaijan (Gromashevsky, Nikimorov, 1973; Semashko et al., 1974; Hoogstraal, 1979; Lvov, 1994), Iraq (Al-Tikriti et al., 1981; World Health Organization, 2004; Abul-Eis et al., 2012), Kuwait (Al-Nakib et al., 1984), Oman (Scrimgeour et al., 1996, 1999; Williams et al., 2000; Al-Zadjali et al., 2013; Body et al., 2016; Al-Abri et al., 2019), Pakistan (Begum et al., 1970a, d; Hoogstraal, 1979; Hayes, Burney, 1981; Darwish et al., 1983b; World Health Organization, 2004; Kasi et al., 2020), Saudi Arabia (El-Azazy, Scrimgeour, 1997; Hassanein et al., 1997; Memish et al., 2011), Somalia (Spengler et al., 2016), Sudan (Watts et al., 1994; Aradaib et al., 2011; Elata et al., 2011; Osman et al., 2013; Ibrahim et al., 2015; Spengler et al., 2016; Suliman et al., 2017; Ahmed et al., 2020), Syria (Blair et al., 2019), Turkey (Inci et al., 2013, 2016; Düzlü

et al., 2020), Tukmenistan (Aristova et al., 1973; Hoogstraal, 1979; Lvov, 1994; Atkinson, Hewson, 2018), the United Arab Emirates (Suleiman et al., 1980; Baskerville et al., 1981; Khan et al., 1997; Rodriguez et al., 1997; Schwarz et al., 1997; Al-Dabal et al., 2016; Aijazi et al., 2020; Camp et al., 2020; Khalafalla et al., 2021) and Yemen (Cecaro et al., 2013). Historically, Jorjani (Gorgani) (1042–1136 AD), in his monumental book "Treasure of the Khwarazm Shah" (Zakhireye Kharazmshahi), a Persian medical encyclopedia, described a hemorrhagic and arthropod caused disease about one thousand years ago that seemed to be CCHF (Hoogstraal, 1979; Jorjani, 2001). The first scientific reports of clinical signs of CCHF in humans in Iran date back to the 1960s (Aminol-Achrafi, Noraniyan, 1966a, b). The first records of antibodies to the virus in different domesticated and wild animals were identified in the early 1970s using the agar gel diffusion precipitation (AGDP) test (Chumakov et al., 1970; Chumakov, Smirnova, 1972; Saidi et al., 1975). Also, the first records of CCHFV antibodies in humans were identified in 4% of individuals tested in the Caspian Sea littoral provinces of Golestan, Guilan and Mazandaran using the hemagglutination inhibition (HI) test (Saidi, 1974) and 13% of people tested in six provinces of the country using the AGDP test (Saidi et al., 1975). Phylogenetic analysis showed that CCHFV in Iran includes at least five genomic variants (Senegalese, Pakistani, Iraqi, Afghani and Russian) and seven genotypes of six clades or lineages: clades I (Africa 3), III (Africa 1), IV (Asia 1 and 2), V (Europe 1), VI (Europe 2) and a new clade VII (Iran) (Chinikar et al., 2004, 2013b, 2016a, b; Morovvati et al., 2012; Kayedi et al., 2015; Al-Abri et al., 2017; Nasirian, 2020). Saidi et al. (1975), using the AGDP test, found positive antibodies in different domesticated and wild mammals in six provinces, East Azerbaijan, Golestan, Guilan, Razavi Khorasan, Isfahan and Tehran as follow: 38% of sheep, 36% of gaots, 18% of cattle and 3% of small mammals such as *Myotis blyti*, *Nyctalus noctula*, *Allactaga williamsoni*, *Mus musculus* and *Meriones crassus*. CCHFV was also serologically detected in a number of mammals and birds using ELISA, including goats (46%) and sheep (77.5%) in North Khorasan, Razavi Khorasan and South Khorasan Provinces (Bokaie et al., 2008; Chinikar et al., 2012b); in cattle (30%), goats (33.3%) and sheep (41.9%) in Ardebil Province (Telmadarraiy et al., 2010); in cattle (5.9%) in five Iranian provinces (Chaharmal and Bakhtiari, Razavi Khorasan, Semnan, Sistan and Baluchistan and South Khorasan) (Lotfollahzadeh et al., 2011); in sheep (15.5%) in East Azerbaijan Province (Rezazadeh et al., 2012, 2013); in cattle (25%), goats (24.8%) and sheep (58.7%) in differenet areas of Iran (Mostafavi et al., 2013a); in ostriches (20%) and sheep (54.2%) in Isfahan Province (Izadi et al., 2007; Mostafavi et al., 2013b); in sheep (0.8%) in Kohgiluyeh and Boyerahmad Province (Ghasemian et al., 2021); in sheep (3.7%) (Mostafavi et al., 2012) and (38.7%) (Faghihi et al., 2015) in Mazandaran Province; in cattle (9.6%) in Razavi Khorasan and South Khorasan Provinces (Lotfollahzade et al., 2009); and in camels (5.29%) in North Khorasan, Razavi Khorasan and South Khorasan Provinces (Champour et al., 2014). In general, infections of CCHFV in humans have been reported in at least 25 Iranian provinces (out of 31), with the highest rates in Sistan and

Baluchistan, Isfahan and Fars Provinces (Chinikar, 2003; Chinikar et al., 2002, 2005, 2008, 2009, 2010a, c; Mostafavi et al., 2013a). Specific documents have been published about human cases of the disease in different provinces, including Ardebil (Asefi, 1974, 1977; Adham et al., 2021; Habibzadeh et al., 2021; Abazari et al., 2022), Chaharmahal and Bakhtiari (Mahzounieh et al., 2012), East Azerbaijan (Aminol-Achrafi, Noraniyan, 1966a, b; Asefi, 1974; Saidi et al., 1975; Ardoin, Karimi, 1982; Ardalan et al., 2006), Fars (Raoofi et al., 2012b; Rezaei et al., 2012), Golestan (Saidi, 1974; Saidi et al., 1975; Abbasi, Moradi, 2005); Guilan (Saidi, 1974; Saidi et al., 1975; Asefi, 1977), Hormozgan (Fazlalipour et al., 2019), Isfahan (Saidi et al., 1975; Chinikar et al., 2012a), Khuzistan (Sharififard et al., 2016), Kohgiluyeh and Boyerahmad (Hadinia et al., 2012), Kurdistan (Firouzmanesh et al., 2017; Shahbazi et al., 2019), Mazandaran (Saidi, 1974; Sadeghi et al., 2013), North Khorasan, Razavi Khorasan and South Khorasan (Saidi et al., 1975; Bokaie et al., 2008; Ebadiazar et al., 2011; Ziyaei et al., 2011; Chinikar et al., 2013a; Heydari, Movahed Danesh, 2013; Naderi et al., 2013; Shahhosseini et al., 2018); also co-infections of brucellosis and CCHF (Hashemian, Ebrahimi, 2010), Qazvin (Nikoonejad, Bijani, 2016), Qom (Saghafipour et al., 2012a, b; Farzinnia et al., 2013), Semnan (Arab-Ameree, Mirshafee, 2006), Sistan and Baluchistan (Izadi et al., 2003, 2004, 2006; Alavi-Naini et al., 2006; Sharifi Mod, Metanat, 2006; Owaysee Oskooei et al., 2008; Sharifi-Mood et al., 2014; Mostafavi et al., 2017; Nili et al., 2020); also co-infections of malaria and CCHF (Sharifi-Mood et al., 2011) and Tehran (Saidi et al., 1975). Some 53 to 154 human cases of CCHF were found in at least 24 provinces of Iran during 2006–2011, with highest number of cases in Sistan and Baluchistan, Isfahan, Razavi Khorasan, Khuzistan and Fars Provinces (Ramezankhani, Kaveh, 2014). Blair et al. (2019) reported that the total number of confirmed human cases of the virus in the country was 1256, with total deaths being 177 during 1999–2017 and cases per year ranging from 18 and 150. At least 47 species of ticks (11 species of soft ticks and 36 species of hard ticks) occur in Iran (Hosseni-Chegeni et al., 2019; Hosseini-Chegeni, Tavakoli, 2020). CCHFV has been isolated from different tick species using RT-PCR in various provinces, including Ardebil (28% of tested ticks were positive) (Telmadarraiy et al., 2010); East Azerbaijan (5.0%) (Shafei et al., 2016); Fars (4.5%) (Farhadpour et al., 2015); Golestan (5.3%) (Sedaghat et al., 2017); Hamedan (16.4%) (Telmadarraiy et al., 2008) (19.3%) (Tahmasebi et al., 2010); Ilam (6.6%) (Sharifinia et al., 2015); Kermanshah (3.8%) (Mohammadian et al., 2016); Kurdistan (5.6%) (Fakoorziba et al., 2012); Lorestan (6.7%) (Kayedi et al., 2015); Mazandaran (9.52%) (Faghihi et al., 2015); Qom (7.9%) (Telmadarraiy et al., 2012); Razavi Khorasan (3.8%) (Fakoorziba et al., 2015), (5%) (Maghsood et al., 2020); Semnan (4.3%) (Faghihi et al., 2018); Sistan and Baluchistan (4.3%) (Mehravaran et al., 2013); South Khorasan (15.9%) (Jafari et al., 2020); West Azerbaijan (8.33%) (Morovvati et al., 2012) and Yazd (5.71%) (Salim Abadi et al., 2011). The virus was isolated from the following species of ticks: *Alveonasus lahorensis* (Neumann), *Dermacentor marginatus*, *Haemaphysalis inermis*, *H. punctata*, *Hyalomma anatolicum* Koch, *H. asiaticum* Schulze et Schlottke, *H. scupense*

Schulze (synonym: *H. detritum* Schulze), *H. dromedarii*, *H. marginatum*, *H. schulzei* Olenev, *Rhipicephalus bursa* Canstrini et Fanzago, *Rh. sanguineus* (Latreille) and *Rh. turanicus* Pomerantsev, Matikashvili et Lotosky (Sureau, Klein, 1980; Sureau et al., 1980; Fakoorziba et al., 2015; Telmadarraiy et al., 2015). Fakoorziba et al. (2015) reported finding CCHFV in *Rhipicephalus appendiculatus* Neumann collected in Razavi Khorasan Province, however the record of this Afrotropical species in Iran is doubtful and the species is not mentioned in the checklist of Iranian ticks (Hosseni-Chegeni et al., 2019). Among the ticks from which the virus has been isolated in other countries, the following species occur in Iran: *Argas persicus* (Oken), *Dermacentor niveus* Neumann, *Ixodes ricinus*, *Rhipicephalus annulatus* (Say) and *Rh. rossicus* Yakimov et Kol-Yakimova (Hoogstraal, 1979; Hoogstraal, Valdez, 1980; Hosseni-Chegeni et al., 2019). A number of reviews of CCHF in Iran (Emadi-Kouchak et al., 2003; Chinikar et al., 2010b; Keshtkar-Jahromi et al., 2013; Keshtkar Jahromi, 2014; Mostafavi et al., 2014; Kouhpayeh, 2019; Mardani, 2019; Kassiri et al., 2020c), including two mata-analyses (Nasirian, 2019, 2020), have been published.

Orthomyxoviridae

Quaranfil virus

Quaranfil virus (QRFV) (Orthomyxoviridae: *Thogotovirus*) was first isolated from humans, the soft ticks *Argas arboreus* Kaiser, Hoogstraal et Kohls and *A. hermanni* and pigeon squabs in Egypt (Taylor et al., 1966b; Mourya et al., 2019). The virus has been found in several African and Asian countries. It has been isolated from the soft ticks *Argas arboreus*, *A. reflexus* (Fabricius), *A. hermanni*, *A. vulgaris* Filippova and the hard tick *Hyalomma dromedarii* (Hoogstraal, 1966, 1981, 1985; Taylor et al., 1966b; Williams et al., 1970; Converse, Moussa, 1982; Labuda, Nuttall, 2008; Presti et al., 2009). The virus has been found in Afghanistan, Iraq, Kuwait and Yemen (Williams et al., 1970; Converse, Moussa, 1982). One isolation of Quaranfil virus was obtained from *Argas vulgaris* collected near pigeon and sparrow nests in Razavi Khorasan Province of Iran (Klein et al., 1979; Sureau, Klein, 1980). Eleven species of soft ticks, including *A. hermanni* and 36 species of hard ticks, as well as *Hyalomma dromedarii*, are listed in the most recent checklist of Iranian ticks (Hosseni-Chegeni et al., 2019; Hosseini-Chegeni, Tavakoli, 2020), however there is no recent verification of *Argas vulgaris* in the country and it is not listed in the checklist. Nothing more is known about the virus in Iran.

Thogoto virus

Thogoto virus (THOV) (Orthomyxoviridae: *Thogotovirus*) is known to occur in Africa, Europe (Italy and Portugal) and Asia (Iran and Japan). The virus infects livestock (camels, cattle, goats and sheep), migratory birds and occasionally humans. The virus is transmitted by a number of species of hard ticks of the genera *Amblyomma*, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus* and can cause abortion in sheep (Haig et al., 1965; Albanese et al., 1972; Williams et al., 1973; Filipe, Calisher, 1984; Woodall, 2001c; Labuda, Nuttall, 2008;

Hubálek, Rudolf, 2012; Hubálek et al., 2014a; Yoshii et al., 2015). The virus has been isolated from *Amblyomma variegatum* (Fabricius), *Haemaphysalis longicornis*, *Hyalomma anatolicum*, *H. truncatum* Koch, *Rhipicephalus annulatus*, *Rh. appendiculatus*, *Rh. bursa*, *Rh. decoloratus* Koch, *Rh. evertsi* Neumann and *Rh. sanguineus* (see Haig et al., 1965; Albanese et al., 1972; Williams et al., 1973; Johnson et al., 1980; Filipe, Calisher, 1984; Jones et al., 1989; Woodall, 2001c; Hubálek et al., 2014a; Yoshii et al., 2015). There is just one record of Thogoto virus in Iran, which was found in *Hyalomma anatolicum* collected from cattle in Razavi Khorasan Province (Sureau, Klein, 1980; Sureau et al., 1980). Among other ticks from which the virus has been isolated, *Rhipicephalus annulatus*, *Rh. bursa* and *Rh. sanguineus* occur in Iran (Hosseni-Chegeni et al., 2019).

Paramyxoviridae

Rinderpest (cattle plague)

Rinderpest (cattle plague), caused by the rinderpest virus (RPV) (Paramyxoviridae: *Morbillivirus*), has sometimes been found in Africa, Asia, Australia, Europe and South America. The virus affected various mammals, including humans, but especially ruminants, primilarily buffaloes and cattle. The disease was economically very important. In the 1990s, Afghanistan, Iran, Iraq, Pakistan, Saudi Arabia, Somalia, Sudan, Turkey, Yemen and some other African and Asian countries were identified as the last active foci of rinderpest. Finally, after about 65 years and a global eradication program involving vaccinations and zoosanitory procedures, the disease was officially declared eradicated in 2011. Rinderpest is only the second disease to be eradicated and the greatest veterinary achievement of our time (Njeumi et al., 2012; Roeder et al., 2013). This disease is mentioned here as a historical example of successful international collaboration and acheivment, and the importance of a One Health approach. Rinderpest was not considered to be an arbovirus and was mainly transmitted via direct route, however there was some evidence, natural and experimental, for its mechanical transmission by horseflies, for example *Tabanus orientis* Walker (Krinsky, 1976; Foil, 1989). There is no historical information with regard to what the vector of virus may have been in Iran.

Peribunyaviridae

Akabane virus

Akabane virus (AKAV) (Peribunyaviridae: *Orthobunyavirus*) has been found in Africa, Asia and Australia. The virus infects various wild and domesticated mammals, including buffaloes, camels, cattle, elephants, giraffes, goats, horses, pigs and sheep. Infections in pregnant cattle, goats or sheep causes a variety of abnormalities in the fetus, principally arthrogryposis and hydranencephaly. Epizootics may cause a significant economical loss. Infections in adult animals are entirely subclinical. Certain species of *Culicoides* are the biological vectors of AKAV. The virus has also been isolated from a number of mosquitoes, for example *Aedes vexans*, *Anopheles funestus* Giles, *An. vagus*, *Culex tritaeniorhynchus*

and *Cx. vishnui*; however, they do not biologically transmit the virus and are of lesser importance as vectors (Oya et al., 1961; Wirth, Hubert, 1989; Mellor et al., 2000; Mellor, 2001c; Bryant et al., 2005; Hubálek et al., 2014a; Kirkland, 2015; Contigiani et al., 2017). The virus has been found in Iraq (Alsaad et al., 2017; Al-Salihi, Al-Dabhawi, 2019), Oman (Al-Busaidy, Mellor, 1991b), Saudi Arabia (Abu Elzein et al., 1998b), Sudan (Mohamed et al., 1996), Syria (Taylor, Mellor, 1994) and Turkey (Taylor, Mellor, 1994; Dagalp et al., 2021). The main vectors are *Culicoides brevitarsis* Kieffer and *C. wadai* Kitaoka in Australia, *C. oxystoma* Kieffer in Japan, *C. imicola* Kieffer and *C. milnei* Austen in Africa and *C. imicola* in Oman (St George et al., 1978; Kurogi et al., 1987; Al-Busaidy, Mellor, 1991b; Mellor, 2001c; Hubálek et al., 2014a). Also, *C. nubeculosus* (Meigen) and *C. variipennis* (Coquillett) have been shown to be capable of experimentally transmitting the virus (Jennings, Mellor, 1989). Serological tests, such as hemagglutination inhibition (HI) and enzyme-linked immunosorbent assay (ELISA), have been used to identify the virus in Iran: in Charmahal and Bakhtiari Province (15% in goats and 5.88% in sheep) (Kojouri et al., 2015), Golestan Province (10% in sheep, 80% in cattle) (Ahourai et al., 1992), Khuzistan Province (39.72% in sheep, 85.87% in cattle) (Ahi et al., 2015; Karami Boldaji et al., 2016), Semnan Province (23.3% in cattle) (Mohajer et al., 2019) and Tehran Province (56.52% in cattle) (Dehghan Rahimabadi et al., 2020). There are at least four genera of biting midges (Ceratopogonidae), *Atrichopogon* (three species), *Culicoides* (43 species), *Dasyhelea* (four species) and *Forcipomyia* (one species), with at least 51 species in Iran (Navai, 1974; Dominiak, Alwin, 2013; Pilvari et al., 2016), however there is no information about the vectors of the virus in the country. Among known possible vectors, *Culicoides nubeculosus* occurs in Iran (Jennings, Mellor, 1989; Abdigoudarzi, 2016). Two mosquito species, *Aedes vexans* and *Culex tritaeniorhynchus*, from which the virus was first isolated in Japan, also occur in Iran (Oya et al., 1961; Azari-Hamidian et al., 2019).

Schmallenberg virus

Schmallenberg virus (SBV) (Peribunyaviridae: *Orthobunyavirus*) occurs in Africa, Asia and Europe. SBV, as a newly emerging virus, was first detected in Germany (Schmallenberg City) and the Netherlands in 2011 (Gibbens, 2012; Hoffmann et al., 2012). The virus RNA or antibodies have been identified in a wide range of wild and domestic ruminants, including cattle, goats, sheep, buffaloes, camels, chamois, deer, llamas, moufflons and reindeer, and also non-ruminant species such as dogs, elephants, horses, pigs, wild boars and zebras. SBV infection is economically very important. Infections in adult cattle, goats and sheep are mild or subclinical or with clinical signs such as fever, drop in milk production and diarrhea; however, infections in pregnant cattle, goats or sheep may cause abortions or serious congenital malformation in offspring, such as arthrogryposis and hydranencephaly. Infection is not considered a zoonosis. The virus is biologically vectored by certain species of *Culicoides* biting midges (Gibbens, 2012; Hoffmann et al., 2012;

Nekoei et al., 2015b; Collins et al., 2019; Asadolahizoj et al., 2021). Infections have been found in Azerbaijan (Zeynalova et al., 2019), Iraq (Al-Barawary, 2018; Al-Baroodi, 2021), Pakistan (Wernery et al., 2013), Saudi Arabia (Taha et al., 2015), Sudan (Wernery et al., 2013) and Turkey (Azkur et al., 2013; Yilmaz et al., 2014; Tonbak et al., 2016). SBV has been isolated from *C. chiopterus* (Meigen), *C. dewulfi* Goetghebuer and *C. obsoletus* (Meigen) in Belgium (De Regge et al., 2012), from *C. chiopterus*, *C. obsoletus* and *C. scoticus* Downes et Kettle in the Netherlands (Elbers et al., 2013), from *C. obsoletus* and *C. punctatus* (Meigen) in Poland (Larska et al., 2013), from *C. imicola* (experimentally) and *C. obsoletus* in Spain (Pages et al., 2018) and from *C. chiopterus*, *C. deltus* Edwards (synonym: *C. lupicaris* Downes et Kettle), *C. dewulfi*, *C. imicola*, *C. newsteadi* Austen, *C. nubeculosus*, *C. obsoletus*, *C. pulicaris* (Linnaeus) and *C. scoticus* in France (Segard et al., 2018). Additionally, the Nearctic *C. sonorensis* Wirth et Jones has experimentally been shown to be an efficient vector (Veronesi et al., 2013). Transovarial transmission is also known for *Culicoides* vectors (Larska et al., 2013). Rasekh et al. (2018) detected SBV-specific antibodies in 5% of samples from horses using ELISA in North Khorasan and Razavi Khorasan Provinces. This was the first time that antibodies against SBV were detected in horses. However, the results should be verified using virus neutralization tests, PCR and SBV RNA isolation (Collins et al., 2019). Also, Rasekh et al. (2022) detected SBV-specific antibodies in 12.45% of samples from cattle using ELISA in Razavi Khorasan, South Khorasan and Sistan, Baluchistan Provinces. Among known vectors of the virus, *C. nubeculosus*, *C. pulicaris* and *C. punctatus* occur in Iran (Navai, 1974; Larska et al., 2013; Abdigoudarzi, 2016; Segard et al., 2018). Although at least 43 species of *Culicoides* are found in Iran (Navai, 1974), there is no information about the vector(s) of Schmallenberg virus in the country.

Tahyna virus

Tahyna virus (TAHV) (Valtice fever) (Peribunyaviridae: *Orthobunyavirus*) (synonyms: *Lumbo*, *Trojica*) is known to occur in Africa, Asia and Europe (Labuda, 2001; Bennett et al., 2011). The virus has been found in Armenia (Failloux et al., 2017), Azerbaijan (Gromashevsky, Nikimorov, 1973; Lvov, 1994), Iraq (Barakat et al., 2016) and Turkey (Hubálek, 2008). It has been isolated from different domestic and wild mammals, such as rodents and insectivores, however it seems that the main reservoirs in Europe are hares and rabbits. Infection causes a non-fatal flu-like illness in humans. Infections in endemic areas, such as Central Asia, seem to be very frequent based on serological tests. The virus has been isolated from different mosquito species of the genera *Aedes*, *Anopheles*, *Culex* and *Culiseta*. Transovarial transmission has been documented (Labuda, 2001; Hubálek, 2008; Atkinson, Hewson, 2018). It seems *Aedes vexans* is the most important vector. Other known vectors are *Ae. cantans* (Meigen) [*Ochlerotatus cantans*], *Ae. caspius* s. l., *Ae. cinereus* Meigen, *Ae. communis* (De Geer) [*Ochlerotatus communis*], *Ae. excrucians* (Walker) [*Ochlerotatus excrucians*], *Ae. detritus* (Haliday) [*Ochlerotatus detritus*], *Ae. flavescens* (Muller) [*Ochlerotatus flavescens*], *Ae. punctor* (Kirby) [*Ochlerotatus punctor*], *Ae. sticticus*

(Meigen) [*Ochlerotatus sticticus*], *Anopheles hyrcanus* (Pallas), *Culex modestus*, *Cx. pallens* Coquillett, *Cx. pipiens* and *Culiseta annulata* (Schrank) (Labuda, 2001; Hubálek, 2008; Li et al., 2010; Hubalek et al., 2014b; Sonnleitner et al., 2014). According to Hannoun and Rau (1970), the virus has been experimentally transmitted in chickens by the soft tick *Argas reflexus*. Based on unpublished data, antibodies for the virus have been found in humans in Azerbaijan Province of Iran using the serological test (the CDC Arthropod-Borne Virus Information Exchange, 1976, available at https://stacks.cdc.gov), however there is no verified and published information about the occurrence of the virus in the country. Among known vectors of the virus, *Aedes caspius* s. l., *Ae. detritus*, *Ae. flavescens*, *Ae. vexans*, *Anopheles hyrcanus*, *Culex modestus*, *Cx. pipiens* and *Culiseta annulata* occur in Iran (Labuda, 2001; Hubálek, 2008; Li et al., 2010; Azari-Hamidian et al., 2019).

Phenuiviridae

Bhanja virus

Bhanja virus (BHAV) (Phenuiviridae: *Phlebovirus*) (synonym or subtype: Palma virus) occurs in Africa, Asia and Europe. Isolation of the virus from mammals is rare, however serological surveys indicate the highest prevalence of antibodies in domestic mammals, such as camels, cattle, dogs, goats, horses and sheep, and also antibodies have been detected in different wild mammals, birds and reptiles (Shah, Work, 1969; Hubálek et al., 1982, 2014a; Hubálek, 1987; Filipe et al., 1994; Labuda, Nuttall, 2008; Hubálek, Rudolf, 2012; Matsuno et al., 2013). The virus has been identified in Armenia, Azerbaijan, Pakistan, Somalia and Turkmenistan (Chunikhin, Karaseva, 1971; Semashko et al., 1973; Matevosyan et al., 1974; Hubálek et al., 1982, 2014a; Hubálek, 1987; Darwish et al., 1983b; Lvov, 1994; Hubálek, Rudolf, 2012; Failloux et al., 2017; Atkinson, Hewson, 2018). It has been isolated from at least 15 species of hard ticks of the genera *Amblyomma*, *Dermacentor*, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus* (Shah, Work, 1969; Hoogstraal, Valdez, 1980; Johnson et al., 1980; Hoogstraal, 1981; Hubálek et al., 1982, 2014a; Hubálek, 1987; Filipe et al., 1994; Hubálek, Rudolf, 2012). It seems that the only record of BHAV in Iran is based on a serological survey of 3000 humans and domestic and wild mammls. A “small proportion” showed antibodies to BHAV (Saidi, 1975). Also, Arata (1975) mentioned the presence of BHAV in Iran and listed it as a “representative rodent born [sic] disease”. There are at least 36 species of hard ticks representing five genera (*Dermacentor*, *Haemaphysalis*, *Hyalomma*, *Ixodes* and *Rhipicephalus*) in Iran (Hosseni-Chegeni et al., 2019), however there is no more recent information about the virus and its possible vector(s) in the country. The following 10 species, which are known vectors in other countries, occur in Iran: *Dermacentor marginatus*, *Haemaphysalis parva* (Neumann) (synonym: *H. intermedia* Nuttall et Warburton), *H. punctata*, *H. sulcata* Canstrini et Fanzago, *Hyalomma asiaticum*, *H. dromedarii*, *H. marginatum*, *H. scupense* (synonym: *H. detritum*), *Rhipicephalus annulatus*, *Rh. bursa* (Hoogstraal, Valdez, 1980; Hubálek et al., 1982, 2014a; Hubálek, 1987; Hubálek, Rudolf, 2012; Hosseni-Chegeni et al., 2019).

Rift Valley fever

Rift Valley fever, caused by the Rift Valley fever virus (RVFV) (Phenuiviridae: *Phlebovirus*) (synonym: Zinga virus), was reviewed by Azari-Hamidian et al. (2019) and Kassiri et al. (2020b). Information provided by Fakour et al. (2021) might be added to those reviews. In addition to Iran, the virus has also been recorded in Djibouti (Andayi et al., 2014), Iraq (Muhsen, 2012), Saudi Arabia (World Health Organization, 2004; Memish et al., 2011; Ahmed, 2015; Taha et al., 2015; Kenawy et al., 2018), Somalia (Oldfield et al., 1993; World Health Organization, 2004; Braak et al., 2018), Sudan (Watts et al., 1994; McCarthy et al., 1996; Braak et al., 2018; Ahmed et al., 2020), Turkey (Tezcan-Ulger et al., 2019) and Yemen (World Health Organization, 2004; Kenawy et al., 2018). Among known principal mosquito vectors, the following species (see Hubálek et al., 2014a and Azari-Hamidian et al., 2019, 2020) occur in Iran: *Aedes caspius* s. l., *Ae. vexans*, *Culex antennatus* (Becker), *Cx. perexiguus*, *Cx. pipiens*, *Cx. theileri*, *Cx. tritaeniorhynchus* and *Mansonia uniformis*, however there is no evidence for indigenous transmission of the virus in the country.

Sandfly fever (papatasi fever, *Phlebotomus* fever, three-day fever)

Sandfly fever, caused by different sandfly-borne phleboviruses (SFN-SV) (Phenuiviridae: *Phlebovirus*), which are transmitted in the Old World by species of the genus *Phlebotomus* (Diptera: Psychodidae, Phlebotominae), and probably also the genus *Sergentomyia* in the Mediterranean region, Africa, the Indian subcontinent, the Middle East and Central Asia, and in the New World by species of the genus *Lutzomyia*. Different vertebrates including bats, carnivora, insectivora, rodents and sheep, may serve as hosts in nature. Sandfly fever caused by most of the sandfly-borne phleboviruses is a self-limiting influenza-like disease without mortality, however acute meningitis or meningo-encephalitis has been reported for Toscana virus (TOSV) in several European countries (Adler, Theodor, 1957; Barnett, Suyemoto, 1961; Ashford, 2001; Depaquit et al., 2010; Ready, 2013; Dehghani et al., 2021). In addition to Iran, viruses that cause sandfly fever have also been found in Aghanistan, Azerbaijan, Djibouti, Iraq, Pakistan, Saudi Arabia, Somalia, Sudan, Turkey and Turkmenistan (Tesh et al., 1975, 1976b; Hayes, Burney, 1981; Arsen'eva, 1982; Darwish et al., 1983b; Tesh, 1989; Gaidamovich et al., 1990a, b; Nikolaev et al., 1991; Lvov, 1994; Watts et al., 1994; Bryan et al., 1996; McCarthy et al., 1996; Wallace et al., 2002; Riddle et al., 2008; Depaquit et al., 2010; Inci et al., 2013; Andayi et al., 2014; Alkan et al., 2015; Barakat et al., 2016; Failloux et al., 2017; Atkinson, Hewson, 2018; Ahmed et al., 2020). The main vector is *Phlebotomus papatasi* (Scopoli), the distribution of which coincides closely with the distribution of the disease. Dashli virus (DASHV), Karimabad virus (KARV), sandfly fever Naples virus (SFNV), sandfly fever Sicilian virus (SFSV) and Tehran virus (THEV) have been isolated from *Ph. papatasi* (Tesh et al., 1977; Ashford, 2001; Depaquit et al., 2010; Alkan et al., 2017). Also, SFSV was isolated from *Ph. ariasi* Tonnoir in Algeria (Izri et al., 2008). Corfou virus (CFUV), closely related to SFSV, was

isolated from *Ph. neglectus* Tonnoir (as *Ph. major* Annandale) in Greece (Rodhain et al., 1985). In Europe, Arbia virus (ARBV), closely related to Salehabad virus (SALV), SFNV and TOSV were isolated from *Ph. perfiliewi* Parrot (Ashford, 2001) and *Ph. perniciosus* Newstead (Verani et al., 1988; Ashford, 2001). TOSV has been isolated from *Sergentomyia minuta* Roundani (Charrel et al., 2006b) and Massilia virus (MASV), closely related to SFNV, has been isolated from *Phlebotomus perniciosus* (Charrel et al., 2009). Historically, the first reports of sandfly fever infection in Iran were by foreign investigators in the 1940s and 1950s (Hertig, Sabin, 1955; Barnett, Suyemoto, 1961; Hyams et al., 1995). Eight sandfly fever viruses have been found in Iran: DASHV, KARV, SFNV, SALV, SFSV, THEV, TOSV and sandfly fever Cyprus virus (SFCV). It seems that while Naples and Sicilian viruses are the most prevalent viruses in most studied areas, Karimabad virus is most abundant in Isfahan Province, in central Iran, and is also very common in Razavi Khorasan Province, in northeastern Iran, according to seroepidemiological studies (Saidi, 1974; Tesh et al., 1975, 1976a, b, 1977; Javadian et al., 1977; Saidi et al., 1977; Tesh, 1988, 1989; Mehrabi-Tavana, 1999, 2001; Mehrabi-Tavana et al., 2000; Alkan et al., 2017; Shiraly et al., 2017). There is doubt about the occurrence of SFCV and TOSV in Iran because of the rarity of cases and probable cross-reaction between viral serotypes (Shiraly et al., 2017). Saidi (1974) found seropositive antibodies for KARV in 3% of preschool children in the Caspian area using hemagglutination inhibition (HI) tests. Tesh et al. (1976a, b) reported positive neutralization tests for humans in different urban and rural areas of seven Iranian provinces: East Azerbaijan: SFSV (12%), SFNV (26%), KARV (1%); Guilan: SFSV (12.9%), SFNV (21.5%); Isfahan: SFSV (14.1–20%), SFNV (6.3–10%), KARV (50–75%); Kermanshah: SFSV (9.4%), SFNV (28.1%); Khorasan: SFSV (4.1–19%), SFNV (4.2–33.8%), KARV (1.0–31.1%); Khuzistan: SFSV (9.1–34.2%), SFNV (3.0–42.9%), KARV (0.8%); Tehran: SFSV (10.8–27.4%), SFNV (19.4–36.6%), KARV (5.9–11.8%). Tesh et al. (1977) isolated SFSV and KARV from *Phlebotomus papatasi* and possibly *Ph. caucasicus* Marzinowsky in Isfahan Province. Saidi et al. (1977) reported positive neutralization tests in Isfahan Province for humans: SFNV (17.2%), SFSV (25.4%) and KARV (66.4%); for sheep: SFSV (5.2%) and for the gerbil *Rhombomys opimus*: SFSV (34.2%) and KARV (31.6%). Mehrabi-Tavana (2001) reported positive HI tests for SFSV (60%) and SFNV (46%) in Ilam Province and SFSV (100%) and SFNV (33.3%) in Kermanshah Province in limited samples. Seroprevalence of indirect fluorescent antibody (IFA) tests in humans in Ilam Province gave positive results for SFSV (10.9%), SFNV (5%), SFCV (1.5%) and TOSV (1%) (Shiraly et al., 2017). Karimabad virus (KARV) and Salehabad virus (SALV) were found in *Phlebotomus* species and Tehran virus (THEV) was found in *Phlebotomus papatasi* for the first time in Iran in 1959 (International catalog of arboviruses including certain other viruses of vertebrates, available at https://wwwn.cdc.gov/arbocat/VirusBrowser.aspx). Dashli virus (DASHV) was first isolated and described from *Sergentomyia* species and *Ph. papatasi* collected in Dashliboroun of Golestan Provine, in northern Iran (Alkan et al., 2017). Additionally, there are many notes, letters and reviews on sandfly fever

in Iran (Mehrabi-Tavana, 2007, 2012, 2015, 2017a, b, c, d, e, f; Khoobdel et al., 2008; Azari-Hamidian et al., 2023). The most recent checklist of Iranian sandflies (Kasiri et al., 2000) includes 54 species, 31 species of the genus *Phlebotomus* and 23 species of the genus *Sergentomyia*. While at least 62 species of sandflies occur in Iran (Javadian, Mesghali, 1975; Artemiev, 1978; Secombe et al., 1993; Kasiri et al., 2000; Badakhshan et al., 2011; Akhoundi et al., 2012; Zahraei-Ramazani et al., 2013, 2015; Norouzi et al., 2020), the occurrence of some species and the number of species in Iran are controversial, with 44 to 50 species recorded by different investigators, for example Yaghoobi-Ershadi (2012), Karimi et al. (2014) and Moradi-Asl et al. (2019).

Poxviridae

Avian (fowl) pox

Avian (fowl or poultry) pox, caused by the avian (fowl) pox virus (FPV) (Poxviridae: *Avipoxvirus*), was reviewed by Azari-Hamidian et al. (2019). The papers by Ebrahimi et al. (2012), Khalesi et al. (2019), Sadat Mousavi et al. (2019), Zarifi et al. (2019), Khalili Gheidariy et al. (2020), Mehrabadi et al. (2020), Alemian et al. (2021), Mirzazadeh et al. (2021), Zamani et al. (2021) and Ghodsian et al. (2022) might be added to the Iranian literature pertaining to the virus. The virus has also been found in Bahrain (Samour et al., 1996), Iraq (Tantawi et al., 1981), Kuwait (Tarello, 2008), Saudi Arabia (Tarello, 2004) and the United Arab Emirates (Tarello, 2008), and has been isolated from the poultry red mite *Dermanyssus gallinae* in Iran (Eram et al., 2020).

Lumpy skin disease

Lumpy skin disease, caused by the lumpy skin disease virus (LSDV) (Poxviridae: *Capripoxvirus*), has been found in Africa, Asia and Europe. The virus infects cattle and water buffaloes. The infection causes huge economic losses in the livestock industry (Weiss, 1968; Hunter, Wallace, 2001; Tuppurainen, Oura, 2012; Al-Salihi, 2014; Tuppurainen et al., 2015; Namazi, Khodakaram Tafti, 2021). The disease is known in Azerbaijan, Bahrain, Djibouti, Iraq, Kuwait, Oman, Saudi Arabia, Somalia, Sudan, Syria, Turkey, the United Araba Emirates and Yemen (Kumar, 2011; Tuppurainen, Oura, 2012; Al-Salihi, 2014; Tageldin et al., 2014; Tuppurainen et al., 2015; Inci et al., 2016; Sevik, Dogan, 2017). To date, the main route of transmission of LSDV is mechanical, not biological, through the bites of haematophagous arthropods, therefore it has not been considered an arbovirus (Hunter, Wallace, 2001; Chihota et al., 2003; Tuppurainen, Oura, 2012; Al-Salihi, 2014; Sprygin et al., 2019). Recently, evidence was found for the biological transmission of LSDV by *Culicoides punctatus* in Turkey (Sevik, Dogan, 2017). Mechanical transmission of LSDV has been reported for different biting, or even non-biting, arthropods, including the stable fly *Stomoxys calcitrans* (Weiss, 1968; Baldacchino et al., 2013), the mosquito *Aedes aegypti* (Chihota et al., 2001), the hard ticks *Amblyomma hebraeum* Koch, *Rhipicephalus appendiculatus* and *Rh. decoloratus* (Lubinga et al., 2013a, b, 2014a, b; Tuppurainen

et al., 2013a, b), the horn fly *Haematobia irritans* Linnaeus (Diptera: Muscidae) (Kahana-Sutin et al., 2017), the house fly *Musca domestica* Linnaeus (Diptera: Muscidae) (Sprygin et al., 2018) and *Musca* (*Biomyia*) *confiscata* Speiser (junior homonym: *M. fasciata* Stein) (Diptera: Muscidae) (Weiss, 1968; as *Biomyia fasciata*). Also, transovarial and transtadial transmission of the virus in ticks has been reported (Lubinga et al., 2013b, 2014a). In Iran, the disease has been found in Alborz, East Azerbaijan, Fars, Guilan, Ilam, Kerman, Kermanshah, Khorasan, Khuzistan, Kurdistan, Mazandaran, Qom and West Azerbaijan Provinces (Norian et al., 2016; Jalili et al., 2017; Sameea Yousefi et al., 2017, 2018; Karimpour Somedel et al., 2019; Ghalyanchilangeroudi et al., 2021; Hedayati et al., 2021). There is no information about the possible role that arthropods may play in transmission in the country.

Sheep and goat pox

Sheep and goat pox is caused, respectively, by the sheep pox virus (SPV) and the goat pox virus (GPV) (Poxviridae: *Capripoxvirus*). While, sheep pox is clinically similar to goat pox, recent molecular findings have shown that these are two separate viruses. Most strains are host specific and cause severe clinical disease in either sheep or goats, while some strains have equal virulence in both of these animals. The disease occurs in Africa, Asia, Europe and the western USA. The virus infects ruminants (especially cattle, goats and sheep). The main route of transmission is close contact with infected animals (Rao, Bandyopadhyay, 2000; World Organisation for Animal Health, 2013; Mirzaei et al., 2015; Tuppurainen et al., 2015; Yune, Abdela, 2017). The stable fly *Stomoxys calcitrans* and the sheep head fly *Hydrotaea irritans* are assumed to play a role via mechanical transmission (Kitching, Mellor, 1986; Mellor et al., 1987). Infections have occurred in Afghanistan, Azerbaijan, Djibouti, Iraq, Oman, Pakistan, Somalia, Sudan, Syria, Turkey and Yemen (Hedger et al., 1980; Kitching, Mellor, 1986; Rao, Bandyopadhyay, 2000; World Organisation for Animal Health, 2013; Mirzaei et al., 2015; Tuppurainen et al., 2015). A disease control vaccination program has been ongoing for about 70 years in Iran (Rafyi, Mirchamsy, 1956; Rafyi, Ramyar, 1959; Ramyar et al., 1974; Sadri, Fallahi, 2010; Ghorani, Esmaeili, 2022). Despite this, some severe outbreaks still occur in the country with high morbidity and mortality. Sheep pox outbreaks mostly occur in the northwestern, northeastern and central provinces of Iran, including Azerbaijan, Hormozgan, Kermanshah, Qom, Fars, Bushehr, Kerman, Khorasan and Yazd Provinces, and goat pox outbreaks mostly occur in southern provinces, including Fars, Hormozgan, Kerman and Khorasan Provinces (Mirzaei et al., 2015; Karimpour Somedel et al., 2019). SPV pathology has been studied in Fars Province (Khoda Karam Tafti, Namdari, 2000). During a study in six Iranian provinces, including Azerbaijan, Fars, Hormozgan, Kerman, Khorasan and Khuzistan, 20.75% of goats were positive for GPV (Sadri, 2012c). A high rate of mortality due to a SPV outbreak was reported in Qom Province (Mirzaei et al., 2015). There is no information about the possible vector(s) of the viruses in the country.

Reoviridae

African horse sickness

African horse sickness is a non-contagious infection caused by African horse sickness virus (AHSV) (Reoviridae: *Orbivirus*). Nine distinct serotypes of the virus are known (Sailleau et al., 2000; Mellor, 2001a; Mellor, Hamblin, 2004). Equids such as horses, mules, donkeys and zebras are the most important vertebrate hosts. Dogs may occasionally be infected, however they do not have an important role in the epidemiology of the disease and are considered dead-end hosts. The disease is not considered a zoonosis. Infections are widely distributed in Africa south of the Sahara, including Sudan, and are also enzootic in Yemen, both countries of the WHO Eastern Mediterranean Region (Mellor, 1994, 2001a; Mellor, Hamblin, 2004; Tkubet et al., 2016; Carpenter et al., 2017; Dennis et al., 2019). The mortality rates are 50–95, 50, 5–10% for horses, mules and Europran and Asian donkeys, respectively; however, mortality is rare in African donkeys and zebras (Tkubet et al., 2016). The disease is rarely seen as far northward as Algeria, Egypt, Libya, Morocco, Palestine, Portugal, Spain and Tunisia and eastward to Afghanistan, Cyprus, India, Iran, Iraq, Jordan, Oman, Pakistan, Saudi Arabia, Syria and Turkey (Rafyi, 1961; Hazrati, Taslimi, 1964; Hazrati, 1967; Mirchamcy, Hazrati, 1973; Hedger et al., 1980; Anderson et al., 1989; Mellor et al., 1990a; Mellor, 1994, 2001a). AHSV is biologically and exclusively vectored by certain species of *Culicoides* (Mellor et al., 2000), athough different haematophagous arthropods may be implicated in transmission, such as the mosquitoes *Aedes aegypti*, *Anopheles stephensi* Liston and *Culex pipiens*, the hard ticks *Hyalomma dromedarii* and *Rhipicephalus sanguineus* (Mellor, 1994) and the horsefly *Tabanus pluto* Walker (Krinsky, 1976). The only confirmed principal vector is *Culicoides imicola*, which is present in Africa, Asia and Europe (Mellor et al., 1990b, 2000; Mellor, 2001a). The species occurs in Bahrain, Iraq, Oman, Saudi Arabia, Turkey and the United Arab Emirates (Boorman, 1989), however it has not been reported in Iran (Navai, 1974). Also, *C. bolitinos* Meiswinkel is considered as a secondary vector and the North American *C. variipennis* has been experimentally found to be an efficient vector (Mellor et al., 1975, 2000; Mellor, 2001a). Two species, *C. obsoletus* and *C. pulicaris*, may be involved in transmission in Europe (Mellor et al., 1990b; Mellor, Hamblin, 2004). In summer 1959, infections were found in southern Iran following the outbreak in the Arabian Peninsula, which rapidly spread throughout the region, including Afghanistan, Cyprus, Iraq, Jordan, Libya, Pakistan, Syria, Turkey and India, over a period of three years (1959–1961). During the outbreak, the region lost more than 300,000 equines (Rafyi, 1961; Hazrati, Taslimi, 1964; Mirchamsy, Hazrati, 1973). The virus was isolated from horses (32.5%), mules (40.0%) and donkeys (20.0%) in Iran during the outbreak (Hazrati, Taslimi, 1964). After the outbreak, scientists in the Razi Institute of Iran studied the virus and produced a vaccine, as reviewed by Mirchamsy and Hazrati (1973). There is no recent record of the disease in Iran. At least 43 species of *Culicoides* are known to occur in Iran (Navai, 1974); However, there is no information about

the possible vector(s) of AHSV in Iran. Among known vectors, *C. pulicaris* occurs in the country (Navai, 1974; Mellor, Hamblin, 2004).

Bluetongue

Bluetongue virus (BLUV) (Reoviridae: *Orbivirus*) causes the disease of bluetongue, which has a worldwide distribution. Infections have been found in wild and domestic ruminants, especially sheep. The virus consists of 26, more likely 27, serotypes. The BLUV serotypes 1–24 are transmitted almost entirely and biologically by certain species of *Culicoides* biting midges, however there is not such certainty about the role of these midges in the transmission of BLUV-25 and BLUV-26 (Afshar et al., 1989; Wirth, Hubert, 1989; Afshar, 1994; Mellor, 2001d; Hubálek et al., 2014a; Maclachlan et al., 2015). Also, the sheep ked *Melophagus ovinus* (Linnaeus) (Diptera: Hippoboscidae) (Gray, Bannister, 1961; Luedke et al., 1965) and a number of mosquitoes, such as *Aedes lineatopennis* (Ludlow) [*Neomelaniconion lineatopenne*], *Ae. vigilax* (Skuse) [*Ochlerotatus vigilax*] and *Culex annulirostris*, are believed to be possible secondary or mechanical vectors (Weir et al., 1997; Hubálek et al., 2014a). In addition to biological transmission, BLUV may be occasionally and directly transmitted via semen and embryo transfer from infected countries to virus-free regions (Mellor, 2001d). Infections have been found in Aghanistan (Hassani, Madadgar, 2021), Iraq (Hafez et al., 1978), Kuwait (Maan et al., 2011a, b), Oman (Hedger et al., 1980; Al-Busaidy, Mellor, 1991a, b), Pakistan (Akhtar et al., 1997), Saudi Arabia (Hafez, Taylor, 1985; Abu Elzein et al., 1998a; Taha et al., 2015), Sudan (Abu Elzein, Tageldin, 1985; Abu Elzein, 1986; Mohammad, Taylor, 1987; Mohammad, Mellor, 1990), Syria (Mellor et al., 2008; Hubálek et al., 2014a), Turkey (Gür, 2008; Failloux et al., 2017) and Yemen (Stanley, 1990). The principal verified vectors are *Culicoides insignis* Lutz and species of the *C. variipennis* complex in the Americas, *C. imicola* in Africa and Europe and *C. actoni* Smith, *C. brevitarsis*, *C. fulvus* Sen et Das Gupta and *C. wadai* in Australasia and Indonesia (Mohammad, Mellor, 1990; Mellor et al., 2000, 2009). Additionally, the virus has been isolated from *C. milnei* and *C. tororoensis* Khamala et Kettle in Kenya (Walker, Davies, 1971), *C. pusillus* Lutz in Central America and the Caribbean (Mo et al., 1994), *C. peregrinus* Kieffer in Indonesia (Sendow et al., 1996) and *C. dewulfi*, *C. newsteadi*, *C. obsoletus*, *C. pulicaris*, *C. punctatus* and *C. scoticus* in Italy (Caracappa et al., 2003; Goffredo et al., 2015; Federici et al., 2019). Afshar and Kayvanfar (1974) identified precipitating antibodies to BLUV in sera of farm animals in Iran for the first time. Kargar Moakhar et al. (1988) found the international serotypes 3, 7, 20 and 22 in sheep in different areas of Iran using the agar gel immunodiffusion (AGID) and microneutralization tests. Serological surveys, using ELISA, found positive antibodies to BLUV in East Azerbaijan Province (in sheep, 67–76.44%) (Hasanpour et al., 2008; Imandar et al., 2014), Fars Province (in cattle, 19.77%, in goats, 55.70–85.3% and in sheep, 70.93–74.4%) (Mohammadi et al., 2012; Oryan et al., 2014; Manavian et al., 2017; Hashemi et al., 2018), Hamedan Province (in sheep, 46%) (Yavari et al., 2018),

Ilam Province (in sheep, 43.88%) (Khezri, Azimi, 2012b), Isfahan Province (in cattle, 2.69%, in goats, 49.19% and in sheep, 53.37%) (Noaman et al., 2008, 2013), Kerman Province (in camels, 100%, in cattle, 2.13%, in goats, 67.7% and in sheep 6.57%) (Mahdavi et al., 2006; Mozaffari, Khalili, 2012; Mozaffari et al., 2012, 2014), Khuzistan Province (in sheep, 55.9%) (Noroozikia et al., 2014), Kohgiluyeh and Boyerahmad Province (in sheep, 77.48%) (Sabaghan et al., 2014), Kurdistan Province (in sheep, 19.3–51.85%) (Khanbabaie et al., 2011; Khezri, 2012; Khezri, Azimi, 2012a, b; Khezri, Bakhshesh, 2014), Razavi Khorasan Province (in goats, 87.6% and in sheep, 90.0%) (Najarnezhad, Rajae, 2013), West Azerbaijan Province (in sheep, 34.7–55.9%) (Jafari-Shoorijeh et al., 2010; Sadri, 2012a; Hasanpour et al., 2014) and Yazd Province (in camels, 67.8%) (Mozaffari et al., 2013). In a study conducted in eight Iranian provinces, the total prevalence of BLUV antibodies found in sheep was 34.9%: the provinces included Ardebil (23.7%), East Azerbaijan (39.8%), Fars (25.3%), Ilam (42.6%), Khuzistan (15%), Kurdistan (41.7%), Qom (12.1%) and West Azerbaijan (64.8%) (Khezri, Azimi, 2013). In a study in seven provinces, Ardebil, East Azerbaijan, Fars, Ilam, Khuzistan, Kurdistan and Qom, the infection was investigated using RT-PCR for the first time in Iran and 10% of total samples were both seropositive and RT-PCR positive in sheep (Azimi et al., 2009). During another investigation in nine provinces, Ardebil, East Azerbaijan, Golestan, Isfahan, Markazi, Qazvin, Qom, West Azerbaijan and Yazd, 66.43% of all samples were serologically positive in sheep (Fallahi et al., 2013). In an investigation in three provinces of southeastern Iran, Hormozgan, Kerman and Sistan and Baluchistan, the total prevalence of BLUV antibodies was 92.67% in goats and 48.72% in sheep (Ezatkhah et al., 2014). In a study on wild ruminants in different areas of Iran, 12% of viral serological tests (ELISA) and 8% of PCR results were positive for BLUV in mouflon (*Ovis orientalis*) (Hemmatzadeh et al., 2016). Momtaz et al. (2011) compared the results of ELISA and RT-PCR for BLUV in sheep in Chaharmahal and Bakhtiari, Isfahan and Khuzistan Provinces. Another study in Chaharmahal and Bakhtiari Province indicated a significant relationship between seropositivity and topography (plains or mountains), sex (male or female) and abortion history (Noaman, Arzani, 2017). Bakhshesh et al. (2020) studied the large-scale seroprevalence and risk factors associated with the virus in the country. Khezri and Bakhshesh (2014), Oryan et al. (2014) and Hassani and Madadgar (2021) reviewed infections in Iran. Among known vectors of the virus, *Culicoides pulicaris* and *C. punctatus* occur in the country (Navai, 1974; Goffredo et al., 2015; Abdigoudarzi, 2016). Although at least 43 species of *Culicoides* are known to be present in Iran (Navai, 1974), there is no information about the vector(s) of bluetongue virus in the country.

Wad Medani virus

Wad Medani virus (WMV) (Reoviridae: *Orbivirus*) is distributed in Africa and Asia. The virus has been found in numerous species of hard ticks of the genera *Amblyomma*, *Dermacentor*, *Hyalomma* and *Rhipicephalus*. Serological tests have identified infections in cattle, camels, pigs, buffaloes and rodents (Taylor et al., 1966a; Hoogstraal, Valdez, 1980;

Labuda, Nuttall, 2008; Belaganahalli et al., 2015; Atkinson, Hewson, 2018; Dedkov et al., 2021). The virus has been found in Armenia, Pakistan, Sudan and Turkmenistan (Taylor et al., 1966a; Lvov et al., 1967; Begum et al., 1970a, d; Skvortsova et al., 1975; Hayes, Burney, 1981; Darwish et al., 1983b; Lvov, 1994; Alkhovsky et al., 2014c; Atkinson, Hewson, 2018). It has been isolated from the following ticks: *Amblyomma cajennense* (Fabricius) s. l., *Dermacentor nuttalli*, *Hyalomma anatolicum*, *H. asiaticum*, *Rhipicephalus guilhoni* Morel et Vassiliades, *Rh. microplus* (Canstrini), *Rh. sanguineus* and *Rh. turanicus* (see Taylor et al., 1966a; Lvov et al., 1967; Begum et al., 1970d; Hoogstraal, Valdez, 1980; Hayes, Burney, 1981; Voltsit, 1982; Alkhovsky et al., 2014c; Yadav et al., 2019; Dedkov et al., 2021). There is a unique record of Wad Medani virus in Iran, which was found in *Hyalomma anatolicum* collected from cattle in Razavi Khorasan Province (Sureau, Klein, 1980; Sureau et al., 1980). Among known vectors, *Hyalomma asiaticum*, *Rhipicephalus sanguineus* and *Rh. turanicus* occur in Iran (Taylor et al., 1966a; Hayes, Burney, 1981; Hoogstraal, Valdez, 1980; Hosseni-Chegeni et al., 2019).

Retroviridae

Bovine leukemia

Bovine leukemia, caused by the bovine leukemia virus (BLV) (Retroviridae: *Deltaretrovirus*), occurs worldwide. The virus consists of ten genotypes. The disease causes economical losses due to reduction in milk production, reproductive performance and length of life (Polat et al., 2017). The disease is mainly directly transmitted among cattle, however there is some evidence for mechanical transmission by horseflies (*Tabanus fuscicostatus* Hine, *T. nigrovittatus* Macquart, *T. nipponicus* Murdoch et Takahasi and *T. trigeminus* Coquillett), the stable fly *Stomoxys calcitrans* and the hard tick *Rhipicephalus microplus* (Foil, 1989; Foil et al., 1988; Foil, Issel, 1991; Baldacchino et al., 2013). Infections have been found in Saudi Arabia (Hafez et al., 1990) and Turkey (Burgu et al., 2005). The disease has been found in cattle in the following provinces of Iran based on ELISA and PCR tests: Alborz (45%) (Kazemimanesh et al., 2012), Ardebil (9.5%) (Kazemimanesh et al., 2012), Chaharmahal and Bakhtiari (18.4%) (Nekoei et al., 2015a), East Azerbaijan (50%) (Kazemimanesh et al., 2012), Guilan (100%) (Kazemimanesh et al., 2012), Isfahan (23.8–81.9%) (Morovati et al., 2012; Nekoei et al., 2015a), Kerman (15.5%) (Mohammadabadi et al., 2011), Markazi (53.3%) (Kazemimanesh et al., 2012), North Khorasan (1.5%) (Mousavi et al., 2014), Qom (57%) (Kazemimanesh et al., 2012), Razavi Khorasan (2.3–29.8%) (Kazemimanesh et al., 2012; Mousavi et al., 2014) and Tehran (17–88.8%) (Nikbakht Brujeni et al., 2010; Mohammadi et al., 2011; Kazemimanesh et al., 2012). The virus has also been found in sheep in Chaharmahal and Bakhtiari Province (2.7%) and Isfahan Province (6.7%) (Nekoei et al., 2015a). Recently, an investigation in Iran proposed the possible association between the human breast cancer and the BLV infection in cattle using the nested PCR technique (Khalilian et al., 2019). There is no information about possible transmission of the virus by arthropods in the country.

Equine infectious anaemia (swamp fever)

Equine infectious anaemia, caused by the equine infectious anaemia virus (EIAV) (Retroviridae: *Lentivirus*), has a worldwide distribution. The disease is the most important viral infection in horses. Although EIAV is not an arbovirus, it does not replicate in the vector and is not vectored biologically, haematophagous insects play an important role in its transmission and the epidemiology of infection (Issel, 2001; Issel, Foil, 2015). The virus has been found in Oman (Body et al., 2011), Saudi Arabia (Alnaeem, Hemida, 2019), Sudan (Wegdan et al., 2017) and Turkey (Marenzoni et al., 2013). Horseflies, such as *Chrysops flavidus* Wiedemann, *Hybomitra frontalis* (Walker), *H. lasiophthalma* (Macquart), *Tabanus fuscicostatus* and *T. sulcifrons* Macquart, and the stable fly *Stomoxys calcitrans* (less important), play an important role in mechanical transmission of the virus to horses, whereas mosquitoes, such as *Aedes aegypti* and *Psorophora columbiae* (Dyar et Knab), are linked to subclinical or inapparent infections (Hawkins et al., 1973; Krinsky, 1976; Foil et al., 1983; Foil, 1989; Foil, Issel, 1991; Green et al., 1996; Issel, 2001; Baldacchino et al., 2013). In Iran, the disease has been found in the provinces of Ardebil, East Azerbaijan, Isfahan, Kurdistan and Tehran (Hazrati et al., 1978; Momtaz, Nejat, 2010; Rezazadeh et al., 2016). There is no information about the possible role of arthropods in transmission of the virus in Iran.

Rhabdoiviridae

Bovine ephemeral fever

Bovine ephemeral fever, caused by the bovine ephemeral fever virus (BEFV) (Rhabdoviridae: *Ephemerovirus*), was reviewed by Azari-Hamidian et al. (2019). The papers by Bakhshesh et al. (2018), Pasandideh et al. (2018a, b, c, 2019a, b), Almasi, Bakhshesh (2019a, b), Mollazadeh et al. (2022) and Rezatofighi et al. (2022) might be added to the Iranian literature pertaining to the infection. The virus has also been found in Afghanistan (St George, 1988), Iraq, Kuwait, Pakistan, Saudi Arabia, Somalia, Sudan, Syria, Turkey, Turkmenistan and Yemen (St George, 1988; Lvov, 1994; Hubálek et al., 2014a; Walker, Klement, 2015), as well as Iran (Azari-Hamidian et al., 2019).

Isfahan virus

Isfahan virus (ISFV) (Rhabdoviridae: *Vesiculovirus*) was isolated from pools of *Phlebotomus papatasi* for the first time in Isfahan Province of Iran (Tesh et al., 1977; Calisher et al., 1989). The virus has also been isolated from humans in the provinces of Isfahan (66.9%), Khuzistan (5.4%) and Tehran (3.3%), and from the rodents *Rhombomys opimus* in Isfahan Province (79%) and *Tatera indica* in Khuzistan Province (8.6%) using the neutralization test (Tesh et al., 1977). Additionally, the virus has been isolated from the mosquito *Aedes caspius* s. l. and the hard tick *Hyalomma asiaticum*, see Alkhutova et al. (1981), Alkhutova, Sadykov (1982), Labuda, Nuttall (2008) and Atkinson, Hewson (2018). *Aedes caspius* and *Hyalomma asiaticum* both occur in Iran (Azari-Hamidian et al.,

2019; Hosseni-Chegeni et al., 2019). Some isolations of the virus, or its antibodies, have been made in Central Asia (Tajikistan, Turkmenistan and Uzbekistan) (Gaidamovich et al., 1980; Lvov, 1994; Atkinson, Hewson, 2018).

Zahedan rhabdovirus

Zahedan rhabdovirus (ZARV) (Rhabdoviridae: *Zamolirhabdovirus*) was first recovered and described from the hard tick *Hyalomma anatolicum anatolicum* collected in Zahedan in Sistan and Baluchistan Province, southeastern Iran. The virus is lethal for mice and possibly pathogenic for other mammals. The mammalian host is not known (Dilcher et al., 2015).

Togaviridae

Chikungunya infection

Chikungunya infections caused by Chikungunya virus (CHIKV) (Togaviridae: *Alphavirus*) occur widely in sub-Saharan Africa and southern Asia. The virus has been isolated from different species of monkey, as well as bats and birds. It seems that non-human primates and humans are the main vertebrate hosts in Africa and Asia, respectively. The virus has been isolated from different mosquito species of the genera *Aedes*, *Anopheles*, *Coquillettidia*, *Culex* and *Mansonia*, as well as species of soft ticks (*Ornithodoros sonrai*) and hard ticks. It is probable that sylvan species of *Aedes* in Africa, for example *Aedes africanus* (Theobald) [*Stegomyia africana*] and *Ae. furcifer* (Edwards) [*Diceromyia furcifer*], and urban *Ae. aegypti* and *Ae. albopictus* in Asia are the main vectors (Hoogstraal, 1985; McCarthy et al., 1996; Diallo et al., 1999; Woodall, 2001a; Nsoesie et al., 2016; Failloux et al., 2017; Gould et al., 2017; Wahid et al., 2017; Silva et al., 2018; Simo et al., 2019). The virus may have been isolated from the tropical bed bug *Cimex hemipterus* (Fabricius) (Hemiptera: Cimicidae) (Rao, 1964). Other possible mosquito vectors, which were found naturally infected or are experimentally assumed to play a role in transmission, include *Aedes calceatus* (Edwards) [*Stegomyia calceata*], *Ae. cordellieri* (Huang) [*Diceromyia cordellieri*], *Ae. fulgens* (Edwards) [*Zavortinkius fulgens*], *Ae. luteocephalus* (Newstead) [*Stegomyia luteocephala*], *Ae. opok* (Corbet et van Someren) [*Stegomyia opok*], *Ae. taylori* (Edwards) [*Diceromyia taylori*], *Ae. vittatus* (Bigot) [*Fredwardsius vittatus*], *Coquillettidia fuscopennata* (Theobald), *Culex quinquefasciatus*, *Mansonia africana* (Theobald) and *Ma. uniformis* (Rao, 1964; Jupp et al., 1981; Jupp, McIntosh, 1990; Diallo et al., 1999, 2012; Woodall, 2001a; Silva et al., 2018). Chikungunya virus has been found in Afghanistan, Djibouti, Iraq, Pakistan, Qatar, Saudi Arabia, Somalia, Sudan and Yemen, and imported cases have been found in Oman and Turkey (Salim, Porterfield, 1973; Darwish et al., 1983a; Arsen'eva, 1982; Oldfield et al., 1993; Watts et al., 1994; Wallace et al., 2002; Farnon et al., 2010; Zayed et al., 2012; Andayi et al., 2014; Ciccozzi et al., 2014; Malik et al., 2014; Rezza et al., 2014; Afzal et al., 2015; Al-Abri et al., 2015; Barakat et al., 2016; Wahid et al., 2017; Yaqub et al., 2017; Humphrey et al., 2019; Ahmed et al., 2020; Sawal et al., 2021). Cases of CHIKV imported from Pakistan were recently found in Sistan and Baluchistan Province in southeastern Iran (Pouriayevali et al., 2019). More

recently, Bakhshi et al. (2020) detected the virus in *Anopheles maculipennis* Meigen s. l. in Mazandaran Province and in *A. maculipennis* s. l., *Culex tritaeniorhynchus* and *Culisetta longiareolata* (Macquart) in North Khorasan Province using primers designed for CHIKV Asian genotype, however they failed to isolate the virus and whole genome sequencing was not performed. Also, Tavakoli et al. (2020) detected CHIKV IgM seropositivity in 16.07% of samples in eight southern provinces of Iran. Among known vectors of Chikungunya virus, *Aedes albopictus*, *Ae. vittatus* and *Mansonia uniformis* occur in Iran (Diallo et al., 1999, 2012; Silva et al., 2018; Azari-Hamidian et al., 2019, 2020), however there is no information about the indigenous transmission of the virus in the country.

Semliki forest virus

Semliki forest virus (SFV) (Togaviridae: *Alphavirus*) (synonym or subtype: Me Tri virus) occurs mostly in Africa south of the Sahara, but the virus has been found in eastern Russia and Vietnam and antibodies have been detected in Borneo, India, Indonesia, Malaysia, the Philippines and Thailand. It seems that the main reservoirs are domesticated mammals, such as cattle, horses and pigs. However, the virus has also been isolated from monkeys, wild birds, rodents and insectivores. Among arthropods, the virus has been isolated from species of the mosquito genera *Aedes*, *Culex* and *Eretmapodites* and the hard tick *Rhipicephalus guilhoni* (Ha et al., 1995; Pfeffer, 2001; Tan et al., 2008; Hubálek et al., 2014a). The virus was first isolated from *Aedes abnormalis* (Theobald) [*Aedimorphus abnormalis*], but it seems the main vector in Africa is *Ae. africanus*. It has been detected in *Ae. vexans* and *Culex pipiens* in eastern Russia and *Cx. tritaeniorhynchus* in Vietnam, and has been found in many species in Africa, including *Aedes aegypti*, *Ae. argenteopunctatus* (Theobald) [*Catageiomyia argenteopunctata*], *Ae. fuscinervis* (Edwards) [*Neomelaniconion fuscinerve*], *Ae. jamoti* (Hamon et Rickenbach) [*Neomelaniconion jamoti*], *Ae. opok*, *Ae. palpalis* (Newstead) [*Neomelaniconion palpale*], *Ae. punctocostalis* (Theobald) [*Neomelaniconion punctocostale*], *Ae. togoi* (Theobald) [*Tanakaius togoi*], *Ae. vittatus*, *Eretmapodites chrysogaster* Graham, *Er. grahami* Edwards, *Culex quinquefasciatus* and *Mansonia africana* (Lee et al., 1974; Gaidamovich et al., 1975; Ha et al., 1995; Pfeffer, 2001; Hubálek et al., 2014a). According to unpublished data in Iran, antibodies for the virus were found in humans (3%) using the neutralization test (the CDC Arthropod-Borne Virus Information Exchange, 1962, available at https://stacks.cdc.gov). Among known vectors of the virus, *Aedes vexans*, *Ae. vittatus*, *Culex pipiens*, *Cx. quinquefasciatus* and *Cx. tritaeniorhynchus* occur in Iran (Pfeffer, 2001; Hubálek et al., 2014a; Azari-Hamidian et al., 2019). There is no recently verified and published information about the occurrence of the virus in the country.

Sindbis fever

Sindbis fever, caused by Sindbis fever virus (SINV) (Togaviridae: *Alphavirus*) [synonyms or subtypes: Babanki, Karelian, Kyzylagach (KYZV), Ockelbo, Pogosta and Whataroa],

was reviewed by Azari-Hamidian et al. (2019). In addition to Iran, the virus has also been found in Afghanistan (Arsen'eva, 1982; Wallace et al., 2002), Armenia (Failloux et al., 2017), Azerbaijan (Lvov, 1994; Lundström, Pfeffer, 2010; Storm et al., 2013; Alkhovsky et al., 2014d), Iraq (Riddle et al., 2008; Barakat et al., 2016), Oman (Camp et al., 2019), Pakistan (Darwish et al., 1983a), Saudi Arabia (Wills et al., 1985; Al-Khalifa et al., 2007; Lundström, Pfeffer, 2010; Storm et al., 2013), Somalia (Oldfield et al., 1993), Sudan (Hoogstraal, 1966; Farnon et al., 2010), Turkey (Hubálek et al., 2014a) and Turkmenistan (Atkinson, Hewson, 2018). Recently, Hanafi-Bojd et al. (2021) detected Sindbis fever virus in the pools of *Culex pipiens* and *Cx. theileri* in West Azerbaijan Province of Iran. Bakhshi et al. (2022) reviewed the virus in Iran and adjacent countries. Principal vectors of the virus in other countries that also occur in Iran include *Cx. torrentium* Martini and *Culiseta morsitans* (Theobald) (Hubálek et al., 2014a; Azari-Hamidian et al., 2019).

Unclassified virus

Wanowrie virus

Wanowrie virus (WANV) (unclassified) was first isolated from *Hyalomma marginatum* in India (Dandawate et al., 1970; Labuda, Nuttall, 2008). The virus was later found in *Hyalomma impeltatum* Schulzae et Schlottke collected from camels in Egypt (Williams et al., 1973) and identified in the brain of a human in Sri Lanka who died from an infection (Pavri et al., 1976). Antibodies against WANV have been detected in sera of domestic abunaks and humans in Pakistan (Darwish et al., 1983b). There is just one record of Wanorie virus in Iran, isolated from *Hyalomma asiaticum* collected from goats in Razavi Khorasan Province (Sureau, Klein, 1980; Sureau et al., 1980). Two other ticks from which the virus has been isolated, *H. impeltatum* and *H. marginatum*, also occur in Iran (Hosseni-Chegeni et al., 2019).

Other viruses in the countries neighboring Iran

There are other diseases and infections caused by arboviruses or viruses which may be mechanically transmitted by arthropods in the countries neighboring Iran and in the WHO Eastern Mediterranean Region that need to be considered. Although these viruses have not been formally reported in Iran, their eventual occurrence in the country is very possible, especially in view of tourism, immigration and the presence and/or importation of possible vectors, hosts, reservoirs and migratory birds. The names of infections, viruses and country records are as follow:

Flaviviridae

Banzi virus (BANV) (Flaviviridae: *Flavivirus*), transmitted by mosquitoes, known in Somalia (Henderson et al., 1968; Cahill, 1971).

Barkedji virus (BJV) (Flaviviridae: *Flavivirus*), transmitted by mosquitoes, known in Oman and the United Arab Emirates (Camp et al., 2019).

Israel turkey meningoencephalitis virus (ITMV) [synonym or subtype: Bagaza virus (BAGV)] (Flaviviridae: *Flavivirus*), transmitted by mosquitoes and possibly biting midges, known in the United Arab Emirates (Hubálek et al., 2014a; Camp et al., 2019).

Kadam virus (KADV) (Flaviviridae: *Flavivirus*), transmitted by ticks, known in Saudi Arabia (Wood et al., 1982; Al-Khalifa et al., 2007; Labuda, Nuttall, 2008).

Karshi virus (KSIV) (Flaviviridae: *Flavivirus*), transmitted by ticks, known in Turkmenistan (Hoogstraal, 1985; Labuda, Nuttall, 2008; Atkinson, Hewson, 2018).

Kyasanur Forest disease virus (KFDV) (Flaviviridae: *Flavivirus*) [synonyms or subtypes: Alkhurma virus, Aka Alkhumra virus or Alkhurma hemorrhagic fever virus (ALKV or AHFV)], transmitted by ticks and possibly mosquitoes, known in Djibouti, Saudi Arabia and Turkey (Hoogstraal, 1985; Zaki, 1997; Charrel et al., 2005, 2006a, 2007; Madani, 2005; Labuda, Nuttall, 2008; Alzahrani et al., 2010; Carletti et al., 2010; Memish et al., 2010, 2011; Mahdi et al., 2011; Shibl et al., 2012; Ahmed, 2015; Horton et al., 2016; Atkinson, Hewson, 2018; Hoffman et al., 2018; Shah et al., 2018).

Louping ill virus (LIV) (Flaviviridae: *Flavivirus*) (synonym: Negishi virus) (Hubálek et al., 2014a), transmitted by ticks, known in Turkey [as LI-like virus or Turkish sheep encephalomyelitis virus (TSEV)] (Hartley et al., 1969; Gao et al., 1997; Gould, 2001; de la Fuente et al., 2008; Hubálek, Rudolf, 2012; Inci et al., 2016; Düzlü et al., 2020).

Royal farm virus (RFV) (Flaviviridae: *Flavivirus*), transmitted by ticks, known in Afganistan and Pakistan (Williams et al., 1972; Darwish et al., 1983a; Hoogstraal, 1985; Labuda, Nuttall, 2008).

Usutu virus (USUV) (Flaviviridae: *Flavivirus*), transmitted by mosquitoes, known in Iraq (Barakat et al., 2016).

Yellow fever virus (YFV) (Flaviviridae: *Flavivirus*), transmitted by mosquitoes, known in Somalia and Sudan (Henderson et al., 1968; Cahill, 1971; Salim, Porterfield, 1973; Oldfield et al., 1993; Watts et al., 1994; Monath, 2001; World Health Organization, 2004; Farnon et al., 2010; Gould et al., 2017; Braak et al., 2018; Ahmed et al., 2020).

Zika virus (ZIKAV) (Flaviviridae: *Flavivirus*), transmitted by mosquitoes, known in Pakistan, Saudi Arabia, Somalia, Sudan and Turkey (Henderson et al., 1968; Cahill, 1971; Darwish et al., 1983a; Tomori, 2001; Evans et al., 2017; Kindhauser et al., 2016; Benelli, Romano, 2017; Dehghani, Amiri, 2017; Epelboin et al., 2017; Gould et al., 2017; Alayed et al., 2018; Sezen et al., 2018; Tavakoli et al., 2018; Noorbakhsh et al., 2019; Ahmed et al., 2020; Nikookar et al., 2020; Kassiri et al., 2020a; Saleem et al., 2022).

Nairoviridae

Artashat virus (ARTSV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Armenia and Azerbaijan (Hoogstraal, 1985; Lvov, 1994; Alkhovsky et al., 2014b, 2017).

Caspiy virus (CASV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Azerbaijan and Turkmenistan (Hoogstraal, 1985; Lvov, 1994; Labuda, Nuttall, 2008; Lvov et al., 2014a; Alkhovsky et al., 2017).

Dera Ghazi Khan virus (DGKV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Pakistan (Begum et al., 1970a, c; Hayes, Burney, 1981; Darwish et al., 1983b; Labuda, Nuttall, 2008; Kuhn et al., 2016).

Geran virus (GERV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Azerbaijan (Lvov et al., 2014c; Alkhovsky et al., 2017).

Hazara virus (HAZV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Pakistan (Begum et al., 1970a, b; Hayes, Burney, 1981; Darwish et al., 1983b; Labuda, Nuttall, 2008; Hartlaub et al., 2020).

Issyk-Kul virus (ISKV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks and mosquitoes, known in Azerbaijan and Turkmenistan (Lvov, 1994; Gavrilovskaya, 2001; de la Fuente et al., 2008; Labuda, Nuttall, 2008; Atkinson et al., 2015; Atkinson, Hewson, 2018). Gavrilovskaya (2001) noted the possible occurrence of this virus in Iran, Afghanistan and Pakistan.

Nairobi sheep disease virus (NSDV) (Nairoviridae: *Orthonairovirus*) [synonym or Indian subtype: Ganjam virus (GANV)], transmitted by ticks, known in Africa (including Somalia) and Asia (India and Sri Lanka) (Johnson et al., 1980; Davis, 1997; Peiris, 2001; de la Fuente et al., 2008; Hubálek et al., 2014a). Hoogstraal and Valdez (1980) considered the virus as "a prime candidate for investigation in Iran".

Tamdy virus (TDYV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known in Armenia, Azerbaijan, Turkey and Turkmenistan (Lvov, 1994; Labuda, Nuttall, 2008; Lvov et al., 2014b; Failloux et al., 2017; Atkinson, Hewson, 2018).

Zirqa virus (ZIRV) (Nairoviridae: *Orthonairovirus*), transmitted by ticks, known on Zirqa Island in the Persian Gulf (the United Arab Emirates) (Hoogstraal et al., 1970; Varma et al., 1973; Labuda, Nuttall, 2008; Kuhn et al., 2016). The name of the virus was misspelled as Zirga in the original paper (Varma et al., 1973).

Orthomyxoviridae

Batken virus (BKNV) (Orthomyxoviridae: *Thogotovirus*), transmitted by mosquitoes and ticks, known in Azerbaijan (Lvov et al., 1974; Lvov, 1994; Hoogstraal, Valdez, 1980; Frese et al., 1997; Labuda, Nuttall, 2008; Alkhovsky et al., 2014a). Hoogstraal and Valdez (1980) considered this virus as "a candidate for investigation in Iranian sheep and goats".

Dhori virus (DHOV) (Orthomyxoviridae: *Thogotovirus*), transmitted by ticks, known in Armenia, Azerbaijan, Pakistan and Saudi Arabia (Williams et al., 1973; Semashko et al., 1974; Hoogstraal, Valdez, 1980; Darwish et al., 1983b; Jones et al., 1989; Al-Khalifa et al., 2007; Labuda, Nuttall, 2008; Hubálek, Rudolf, 2012; Failloux et al., 2017).

Peribunyaviridae

Aino virus (AINOV) (Peribunyaviridae: *Orthobunyavirus*) (synonyms: Kaikalur and Samford viruses), transmitted by biting midges and mosquitoes, known in Turkey (Mellor, 2001b; Hubálek et al., 2014a; Contigiani et al., 2017).

Bakau virus (BAKV) (Peribunyaviridae: *Orthobunyavirus*), transmitted by mosquitoes and ticks, known in Pakistan (Hayes, Burney, 1981; Darwish et al., 1983b; Hoogstraal, 1985).

Batai virus (BATV) (Peribunyaviridae: *Orthobunyavirus*) (synonyms: Calovo, Chitoor, Olkya, Olyka and UgMP-6830), transmitted by mosquitoes, known in Armenia and Sudan (Nashed et al., 1993; Failloux et al., 2017).

Ngari virus (NRIV) (Peribunyaviridae: *Orthobunyavirus*) (synonym: Garissa virus), transmitted by mosquitoes, known in Somalia and Sudan (Bowen et al., 2001; Braak et al., 2018).

Phenuiviridae

Arumowot virus (AMTV) (Phenuiviridae: *Phlebovirus*), transmitted by mosquitoes, known in Somalia and Sudan (Tesh, 1988; Braak et al., 2018; Ahmed et al., 2020).

Gabek Forest virus (GFV) (Phenuiviridae: *Phlebovirus*), transmitted by sandflies, known in Sudan (Tesh et al., 1976b; Tesh, 1988).

Grand Arbaud virus (GAV) (strain Art 363) (Phenuiviridae: *Phlebovirus*), transmitted by ticks, known in Afghanistan (Hannoun, Rau, 1970; Williams et al., 1972; Hoogstraal, 1985; Hubálek, Rudolf, 2012; Palacios et al., 2013).

Manawa virus (MWAV) (Phenuiviridae: *Phlebovirus*), transmitted by ticks, known in Pakistan (Hayes, Burney, 1981; Darwish et al., 1983b; Hoogstraal, 1985; Labuda, Nuttall, 2008).

Razdan virus (RAZV) (Phenuiviridae: *Bandavirus*), transmitted by ticks, known in Armenia (Lvov, 1994; Labuda, Nuttall, 2008; Alkhovsky et al., 2013).

Uukuniemi virus (UUKV) (Phenuiviridae: *Phlebovirus*), transmitted by mosquitoes and ticks, known in Azerbaijan (Gromashevsky, Nikimorov, 1973; Labuda, Nuttall, 2008; Hubálek, Rudolf, 2012).

Reoviridae

Baku virus (BAKUV) (Reoviridae: *Orbivirus*), transmitted by ticks, known in Azerbaijan and Turkmenistan (Lvov et al., 1971; Andreev et al., 1973; Gromashevsky, Nikimorov, 1973; Lvov, 1994; Labuda, Nuttall, 2008; Atkinson, Hewson, 2018).

Chenuda virus (CNUV) (Reoviridae: *Orbivirus*), transmitted by ticks, known in Turkmenistan (Taylor et al., 1966b; Hoogstraal, 1985; Lvov, 1994; Belaganahalli et al., 2015; Atkinson, Hewson, 2018).

Epizootic haemorrhagic disease virus (EHDV) (Reoviridae: *Orbivirus*), transmitted by biting midges and possibly mosquitoes, known in Bahrain, Oman, Sudan and Turkey (Al-Busaidy, Mellor, 1991a; Mellor et al., 2000; Mellor, 2001e; Temizel et al., 2009; Wernery et al., 2013; Hubálek et al., 2014a).

Palyam virus (PALV) (Reoviridae: *Orbivirus*), transmitted by mosquitoes, known in Sudan (Mohammad, Mellor, 1990; Mellor et al., 2000).

Rhabdoviridae

Barur virus (BARV) (Rhabdoviridae: *Vesiculovirus*), transmitted by ticks, known in Somalia (Butenko et al., 1981; Labuda, Nuttall, 2008).

Malakal (MALV) (Rhabdoviridae: *Ephemerovirus*), transmitted by mosquitoes, known in Sudan (Calisher et al., 1989; Blasdell et al., 2012b).

Obodhiang virus (OBOV) (Rhabdoviridae: *Ephemerovirus*), transmitted by mosquitoes, known in Sudan (Calisher et al., 1989; Blasdell et al., 2012a).

Togaviridae

O'nyong-nyong virus (ONNV) (Togaviridae: *Alphavirus*), transmitted by mosquitoes, known in Sudan (Salim, Porterfield, 1973; Woodall, 2001b; Ahmed et al., 2020).

Disscusion

The viruses which are associated with arthropods may be arranged in four ecological groups: (1) Arthropod-borne viruses (arboviruses), (2) arthropod-transmitted animal viruses, (3) arthropod viruses and (4) arthropod-transmitted plant viruses. The first two groups include the viruses of medical and/or veterinary importance (Turell, 2019). Arboviruses are the viruses which are biologically transmitted from one vertebrate host to another via the bite of haematophagous arthropods, including biting midges, mosquitoes, sandflies or ticks. These viruses replicate in both arthropod vectors and vertebrate hosts. Thus, the viruses which are not transmitted by bite or merely mechanically transmitted by bite are not among (true) arboviruses. The term “arbovirus” has no taxonomic importance, it is a vernacular term that signifies a virus transmitted by an arthropod. Nearly all arboviral infections are zoonotic (World Health Organization, 1967; Hart, 2001; Turell, 2019). The World Health Organization (1967) provided nine criteria for considering a virus as an arbovirus (five relating to the transmission cycle and four unrelated to the transmission cycle). It seems that, based on the aforementioned definition of an arbovirus and the nine criteria, different viruses may be grouped into four categories: (1) True arboviruses, (2) probable arboviruses, (3) possible arboviruses and (4) most probably or definitely not true arboviruses (World Health Organization, 1967; Hart, 2001). The World Health Organization (1967) also mentioned four criteria for the recognition of a vector of an arbovirus and classified them as suspected, probable and confirmed vectors based on those criteria. Arboviruses are generally divided into two groups based on their pathogenicity to humans: (1) Arthropod-borne viruses pathogenic to humans and (2) arboviruses not pathogenic to humans (Hubálek, 2008).

Arthropod-transmitted animal viruses do not replicate in the arthropod vectors but do so in vertebrate hosts and are mechanically transmitted (Turell, 2019). There are a few important viral infections which arthropods mechanically play an important role in their transmission and epidemiology, such as equine infectious anaemia, caused by the equine infectious anaemia virus vectored by horseflies, stable flies and mosquitoes (Foil, Issel,

1991; Issel, Foil, 2015), lumpy skin disease, caused by the poxvirus lumpy skin disease virus transmitted by stable flies, mosquitoes, ticks and *Culicoides* biting midges (Chihota et al., 2003; Sprygin et al., 2019) and myxomatosis, caused by the Myxoma virus (Poxviridae: *Leporipoxvirus*) transmitted by mosquitoes, fleas and horseflies (Jellison, 1959; Krinsky, 1976; Fenner, 2001; Brugman et al., 2015).

Arthropod viruses replicate only in arthropods. They cannot cause disease in vertebrates because they do not replicate in vertebrates, though they may be pathogenic to the infected arthropod (Turell, 2019). These viruses are isolated only from arthropods, including mosquito-only (mosquito-specific) flaviviruses (Cella et al., 2019) or those that are pathogenic only to arthropods (Tinsley, 1979; Beckage et al., 1993). However, there is no evidence for whether they are pathogenic to humans or domesticated animals and biologically or mechanically transmitted to vertebrate hosts. Thus, they are not arboviruses and are not of medical and veterinary significance, however they are important in view of being a potential agent for biological control (Tinsley, 1979; Beckage et al., 1993) or because of their impact on the biology of infected arthropods such as flight activity or reproductivity, and their impact on the circulation of their related vector-borne pathogens (Goenaga et al., 2015; Cella et al., 2019).

Finally, arthropod-transmitted plant viruses can be transmitted mechanically or biologically to plants by some arthropods, including certain species of aphids, leafhoppers, plant bugs and plant mites (Turell, 2019).

With the exception of one unclassified virus, the viruses treated in the present review are members of 19 genera belonging to 14 families. The taxonomic placements of the viruses are as follow. (1) Asfaviridae: *Asfavirus* – ASFV; (2) Flaviviridae: *Flavivirus* – BANV, BJV, DENV, ITMV, JEV, KADV, KFDV, KSIV, LIV, RFV, TBEV, USUV, WNV, YFV, ZIKAV; (3) Hantaviridae: *Orthohantavirus* – HTNV; (4) Herpesviridae: *Varicellovirus* – BHV; (5) Nairoviridae: *Orthonairovirus* – AHV, ARTSV, CASV, CCHFV, DGKV, GERV, HAZV, ISKV, NSDV, TDYN, ZIRV; (6) Orthomyxoviridae: *Thogotovirus* – BKNV, DHOV, QRFV, THOV; (7) Paramyxoviridae: *Morbillivirus* – RPV; (8) Peribunyaviridae: *Orthobunyavirus* – AINOV, AKAV, BAKV, BATV, NRIV, TAHV, SBV; (9) Phenuiviridae: *Bandavirus* – RAZV, *Phlebovirus* – AMTV, BHAV, GAV, GFV, MWAV, RVFV, SFN-SV, UUKV; (10) Poxviridae: *Avipoxvirus* – FPV, *Capripoxvirus* - LSDV, GPV, SPV; (11) Reoviridae: *Orbivirus* – AHSV, BAKUV, BLUV, CNUV, EHDV, WMWV, PALV; (12) Retroviridae: *Deltaretrovirus* – BLV, *Lentivirus* – EIAV; (13) Rhabdoviridae: *Ephemerovirus* – BEFV, MALV, OBOV, *Vesiculovirus* – BARV, ISFV, *Zamolirhabdovirus* – ZARV; (14) Togaviridae: *Alphavirus* – CHIKV, ONNV, SFV, SINV; unclassified virus: WANV.

In addition to various nonspecific signs and symptoms, such as fever, main clinical syndromes associated with the arboviruses treated herein that are pathogenic to humans and animals include: (1) Neurological maladies (meningitis, encephalitis, encephalomyelitis): BHAV, JEV, SINV, TBEV, WNV (Hubálek et al., 2014a), (2) hemorrhagic disease: AHSV, ASFV, CCHFV, DENV, RVFV (Hubálek et al., 2014a), (3) abortion and congenital disorders

such as arthrogryposis and hydranencephaly: AKAV, SBV (Hubálek et al., 2014a; Collins et al., 2019; Asadolahizoj et al., 2021), (4) vesicular stomatitis: ISFV (Atkinson, Hewson, 2018) and (5) microcephaly: ZIKAV (Kassiri et al., 2020a).

The viral infections treated in the present review may be classified into four categories based on their main vectors: (1) Biting midge-borne – AHSV, AKAV, BLUV, SBV, (2) mosquito-borne – AMTV, BANV, BATV, BJV, CHIKV, DENV, JEV, MALV, NRIV, OBOV, ONNV, PALV, RVFV, SFV, SINV, TAHV, USUV, WNV, YFV, ZIKAV, (3) sandfly-borne – GFV, ISFV, SFS-NV and (4) tick-borne – AHV, ASFV, ARTSV, BAKUV, BARV, BHAV, CCHFV, CASV, CNUV, DGKV, DHOV, GAV, GERV, HAZV, KADV, KSIV, LIV, MWAV, NSDV, QRFV, RAZV, RFV, TDYV, THOV, TBEV, WMV, WANV, ZARV, ZIRV. It is noteworthy that some other arthropods are involved or assumed to be involved in the transmission of some viruses, including blackflies (Diptera: Simuliidae) – RVFV (Bouloy, 2001), fleas – FPV, TBE (Federov et al., 1959; Sotnikova, Soldatov, 1964; Naumov, Gutova, 1984; Della-Porta, 2001), horseflies – AHSV, BLV, EIAV, RPV, TBE (Krinsky, 1976; Foil, 1989), mites – FPV, HTNV, TBE (Naumov, Gutova, 1984; Della-Porta, 2001; Houck et al., 2001; Xu, 2001; Sparagano et al., 2014), sheep head fly (*Hydrotaea irritans*) – GPV, SPV (Kitching, Mellor, 1986), horn fly (*Haematobia irritans*) – LSDV (Kahana-Sutin et al., 2017), face fly (*Musca autumnalis*) – BHV (Johnson et al., 1991) , house fly (*Musca domestica*) – LSDV (Sprygin et al., 2018), sheep ked (*Melophagus ovinus*) – BLUV (Gray, Bannister, 1961; Luedke et al., 1965), *Musca* (*Biomyia*) *confiscata* – LSDV (Weiss, 1968), stable fly (*Stomoxys calcitrans*) – ASFV, BHV, BLV, EIAV, FPV, LSDV, GPV, SPV (Kitching, Mellor, 1986; Mellor et al., 1987; Della-Porta, 2001; Baldacchino et al., 2013) and tropical bed bug (*Cimex hemipterus*) – CHIKV (Rao, 1964).

The role of arthropods in the transmission of different viruses and the epidemiology of their infections is very disportionate and complicated, summarized as follows: (1) Some arboviruses are mostly and biologically transmitted by certain arthropods. Other ways of infection (generally defined as direct route or transmission) such as direct contact with an infected person (or animal), contact with infected blood, body fluid and tissues, or via the respiratory route and alimentary tract, do not have an important role in the epidemiology of infection or their roles are uncertain. AHS is an example of these types of infections (Mellor, 2001a). (2) While some arboviruses are mostly and biologically transmitted by certain arthropods, other ways of direct transmission are also important in the epidemiology of infection in animals or transmission to humans, such as CCHF (Saleem et al., 2020). (3) There are a few arboviruses which are biologically transmitted by arthropods, but it seems that the direct route of transmission is more significant in the epidemiology of the disease, such as ASF (Beltrán-Alcrudo et al., 2017). (4) Exceptionally, some arthropods mechanically have an important role in the transmission and epidemiology of a few viruses, such as horseflies, mosquitoes and fleas in relation to myxomatosis (Krinsky, 1976; Bibikova, 1977), stable flies, mosquitoes, ticks and *Culicoides* biting midges in the case of lumpy skin disease (Tuppurainen et al., 2015) and horseflies and the stable fly in EIAV infection

(Issel, 2001). (5) There are some viruses for which their major transmission route is direct. Certain arthropods may be mechanically involved in transmission, although their role in the epidemiology of disease is not important or uncertain such as horseflies in relation to foot and mouth disease virus (Picornaviridae: *Aphtovirus*) and rinderpest virus (Krinsky, 1976). It is noteworthy that the late Professor M.P. Chumakov (1909–1993), a famous Russian virologist, placed more emphasis on other possible ways of transmission (direct route), even for well-defined and biologically transmitted viral infections (true arboviruses) (World Health Organization, 1967), which shows the complex and complicated epidemiology of viral (arboviral) infections. Moreover, the interrupted blood feeding of haematophagous arthropods and their potential role in the mechanical transmission of infections should not be neglected, even for the diseases caused by viruses for which biological transmission is well and undoubtedly defined. That may explain some of the explosive outbreaks of arboviral infections among vertebrate hosts that occur in just a few weeks (World Health Organization, 1967). Finally, the role of each of the aforementioned factors (biological or mechanical transmission via arthropods and/or direct route) associated with every disease may be different in various foci; thus, the epidemiology of every infection and the role of possible vectors should be extensively investigated in each focus. In view of the lack of a specific vaccine or treatment for many viral infections, this basic knowledge will foster better decisions about how and whether to control diseases by means of vector control programs, sanitary procedures and/or health education.

Conclusion

The background, definitions and criteria presented herein clearly show that there is not enough information about many viral (arboviral) infections in the region and available information is very disportionate when considering countries or different epidemiological aspects of infections. Even infections that are endemic and widespread in the region, for which there is relatively more information, such as BEF, CCHF, SFN-S, SIN and WNF, much more investigation is required, for example, there is little information about the vectors of BEF in the region. On the other hand, there is little or no information about the epidemiology of many viral infections and their vectors in the region, including BLU and many RIDs and EIDs. Additionally, information on viruses in wildlife, which cause many RIDs and EIDs, is very poor in comparison to information for humans and domesticated animals. Last but not least, the records of many viral infections are based merely on serological tests, which have their own limitations such as cross reactions; therefore, isolation and genetic analysis of those viruses is necessary. The studies of the ecology of vectors, as well as the epidemiology of related infections are necessary to provide basic knowledge for vector control programs. This has been a very significant part of integrated vector control in the One Health approach to decrease the burden of infections in humans and domestic animals in concert with wildlife conservation. Moreover, expanding interdisciplinary and international collaborations is necessary for fast detection, monitoring

and surveillance of viral infections and the vectors that cause them, in order to conduct appropriate integrated vector and infection control programs.

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DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

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ВИРУСЫ, ПРЯМО ИЛИ КОСВЕННО ПЕРЕДАВАЕМЫЕ ЧЛЕНИСТОНОГИМИ, В ИРАНЕ И СОСЕДНИХ СТРАНАХ

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Ключевые слова: арбовирусы, биологическая передача патогена, механическая передача патогена, мобовирусы, очаги, переносчики, зоонозы

РЕЗЮМЕ

Членистоногие являются очень важной группой для медицины и ветеринарной медицины из-за огромного количества переносимых ими патогенов. В данной работе были проанализированы базы данных, включающие Web of Science, PubMed, Scopus, Google Scholar, CABI, Scientific Information Database, IranMedex и Magiran, на период конца декабря 2002 г. в отношении арбовирусных инфекций, выявленных в Иране. В Иране были обнаружены тридцать три инфекции, прямо или косвенно переносимые членистоногими. Для каждого заболевания приводятся данные об агентах (вирусах), распространении (в 31 иранской провинции), хозяевах (людях и животных) и известных переносчиках в Иране. В дополнение приведен список арбовирусов для соседних стран, включающих Афганистан, Армению, Азербайджан, Бахрейн, Ирак, Кувейт, Оман, Пакистан, Катар, Саудовская Аравия, Турция, Туркменистан и Объединенные Арабские Эмираты, а также Джибути, Сомали, Судан, Сирию и Йемен, которые, хотя и не граничат с Ираном, но, подобно Ирану, входят в Восточно-средиземноморский регион, выделенный Всемирной Организацией Здравоохранения (ВОЗ). Список включает 40 вирусов, формально не зарегистрированных в Иране. Эти вирусы относятся к 19 родам 14 семейств, из которых 3 вируса переносятся москитами, четыре – мокрецами, 20 – комарами, и 29 – иксодовыми клещами.