Dimensions and Scope of Vector-Borne Diseases in Domestic Livestock

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Abstract

Vector-borne diseases (VBDs) affect various domestic and wild animal species worldwide. Those affecting domestic livestock are of particular significance due to the diverse implications they have on the health and well-being of both animals and humans, the economy, and food availability. Under current conditions, global climate change, in addition to favoring the emergence of new, more resilient variants of pathogens, is being decisive in the expansion of the geographic range of distribution of vectors, the diversification of hosts and the incidence of diseases. In recent years, the increase in epizootics appears to be a constant, leading to the death or mass slaughter of animals, with the consequent economic losses and loss of animal protein availability. Official data on VBDs affecting different species of domestic livestock show the recurrence of previously eradicated diseases and the appearance of diseases in new locations and countries. The identification of new strains of pathogens, as well as the impact on unusual hosts, are increasing the impact on animal health around the world. In addition, the lack of monitoring and consistent information on these diseases, as well as the untimely notification of zoo sanitary events, outline a very complex panorama.

Keywords: Vector-borne diseases (VBDs), Etiological agents, Domestic livestock, Climatic conditions, Vectors, Arboviruses.

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Introduction

Domestic livestock provide countless benefits to humans. In addition to being a means of transport and cargo in many regions of the world, they provide natural fibers and other products. For the vast majority of rural communities, they represent an important source of income and subsistence, which contributes to the development of localities. Their most widespread contribution corresponds to their role in food security, through the production of meat and milk for human consumption (Vipham et al., 2020).

This last benefit, which is essential for survival, is at imminent risk due to the increased vulnerability of livestock health, extending to humans, since many of the diseases are zoonotic. One of the factors that is exacerbating this problem is climate change. Because of the increase in temperature, the physiological responses of animals to regulate body temperature lead to metabolic disorders and other alterations that affect their productive and reproductive performance. Increased rainfall increases flooding, as well as areas of stagnant water, prone to the reproduction and development of vectors such as mosquitoes. The convergence of these conditions is favoring the emergence of new, more resilient variants of pathogens, the expansion of the geographic range of distribution of vectors, the diversification of hosts and the increase in the incidence of diseases. The global change in climatic conditions, in addition to favoring the emergence of new, more resilient variants of pathogens, is being decisive in the expansion of the geographical range of distribution of vectors, the diversification of hosts and the incidence of diseases (Bernabucci, 2019; Ali et al., 2020; Sánchez et al., 2020).

Although climatic variations have a clear influence on the increase in diseases, the convergence of other factors exacerbates this problem. International trade, proximity to wild animals, air travel, as well as the import and export of livestock under poor surveillance measures, contribute to the geographic dispersion of vectors and the pathogens they carry (Semenza & Suk, 2018). Under these conditions, Vector-Borne Diseases (VBDs) appear as an important challenge for animal and public health. The pathogen-host-environment interaction plays a key role in the current behavior of these diseases. The increase in incidence, the recurrence of re-emerging diseases, and the registration of disease cases in new locations and countries appear as some of the indicators of the severity of problem faced. Likewise, the identification of new strains, unusual hosts and emerging and re-emerging diseases are decimating animal health. In addition, the close relationship between humans and domestic livestock, in addition to increasing the sources and risks of exposure, is facilitating the transmission of these diseases. The scope of the diseases, in addition to affecting economic security, due to the costs involved in vector control and medical care, has serious effects on public health. The high rates of morbidity and mortality, and the consequences of those that evolve with serious signs that can endanger the life of those who suffer from them, or reduce the ability to carry out daily and work activities, account for the complexity of this problem (Wilson et al., 2020; Chala & Hamde, 2021; Chakraborty et al., 2023).

Vector-borne Diseases of Domestic Livestock

A quarter of the diseases affecting domestic livestock of veterinary importance are VBDs (Abdullah et al., 2021). These diseases involve a significant number of vectors, mainly arthropods, of which mosquitoes and ticks stand out with around 300 and 116 species, respectively, identified worldwide. They also include other insects such as flies and bedbugs (Socha et al., 2022). Figure 1 integrates the most important VBDs of domestic livestock, associating them with their vectors. Based on the number of diseases in which each type of arthropod acts as the main vector, ticks are responsible for the transmission of 40.7%, followed by mosquitoes (37%), flies (18.6%) and triatomine bugs (3.7%). As mentioned in the figure, in the case of Anaplasmosis, the vectors are ticks, while flies and mosquitoes can transmit the disease secondarily by mechanical action (Railey & Marsh, 2021). Similarly, lumpy skin disease, although it can be transmitted by flies, its main vectors are mosquitoes (Sprygin et al., 2019).

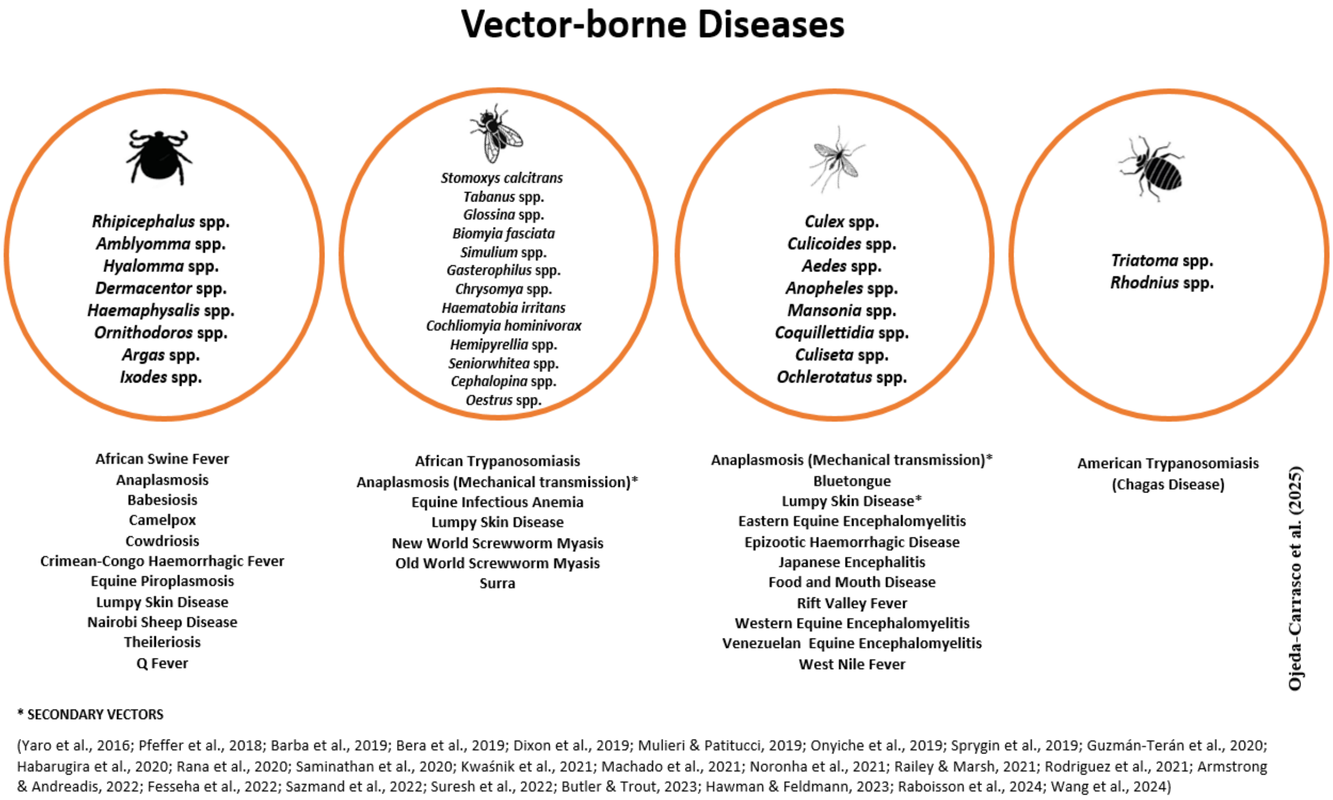

Fig. 1: Vector-borne diseases of domestic livestock

Regarding the etiological agents, Table 1 compiles information on the main VBDs affecting domestic livestock. Viruses (particularly arboviruses, transmitted by arthropods) are responsible for 55.6% of VBDs. They include 10 genera, with three that are common to different diseases (*Alphavirus*, *Flavivirus* and *Orbivirus*). In each case, although it is the same generic identification, there are differences at the genomic and antigenic level. The rest of the diseases include those caused by bacteria and protozoa (both with 18.5%), and insects (7.4%) (Laureti et al., 2018; Oliveira et al., 2020).

Current Dimensions of VBDs in Domestic Livestock

To dimension the current problem, two useful indicators are the geographic distribution and the prevalence. The distribution recorded in Table 1 allows identifying in a general way the coverage of VBDs. Each case reports the references considered for the integration of the registered distribution data. Until now, there is no updated monitoring system on changes in the distribution of diseases. To illustrate this situation, let us consider the case of African swine fever, originally endemic to sub-Saharan Africa. It subsequently spread its distribution to the Russian Federation, China, Mongolia and Vietnam (Brown & Bevins, 2018; Dixon et al., 2019). After these years, based on the records of the *World Animal Health Information System* (WAHIS), from 2019-2023, in addition to this African region and countries, 37 countries are added in the different regions. For Europe 18, Asia 16, two for the Americas and one for Oceania. Additionally, this disease, which is specific to wild and domestic pigs, reported 32 cases in cattle in Mozambique in 2019. Likewise, for this period, the highest prevalence in the African region was for the Democratic Republic of the Congo (25,383 cases), for Asia, Indonesia (404,737), for Europe, Romania (1,092,977), the Americas, the Dominican Republic (10,225) and Oceania, Papua New Guinea (500). These figures, in addition to the geographical expansion of the disease, show that based on the official data available, currently the greatest impacts do not necessarily correspond to the region where the disease originated. Table 2 integrates the prevalences for different domestic species for the period 2019-2023 (WHAIS, 2024).

Table 1: Main diseases transmitted to domestic livestock by vectors

Disease	Distribution	Etiologic agent	Vectors	References
African swine fever	Originally endemic to sub-Saharan Africa. Spread to Russian Federation, China, Mongolia and Vietnam.	Virus *Asfivirus,* Family Asfarviridae	Tick: *Ornithodoros moubata.*	(Brown & Bevins, 2018) (Dixon et al., 2019)
African trypanosomiasis	African continent, mainly sub-Saharan Africa.	Parasitic flagellated protozoa, *Trypanosoma* Subgenre (Subg.) *Nannomonas* (*T. congolense*), Subg. *Dutonella* (*T. Vivax*) and Subg. *Trypanozoon (T. brucei).* Sheep and goats: *Trypanosoma vivax, T. melophagium.*	Tsetse fly: *Glossina* spp., mainly *G. palpalis gambiensis, G. morsitans morsitans* and *G. fuscipes, G. Fusca.* Diptera: *Stomyx calcitrans* and *Haematobia irritans.*	(Yaro et al., 2016) (Betancur & Giraldo-Ríos, 2019)
American trypanosomiasis (Chagas disease)	Endemic to the American continent, from Mexico to Patagonia (Argentina).	Parasitic flagellated protozoan, *Trypanosoma cruzi*, Family Trypanosomatidae.	Triatomine bugs: *Rhodnius prolixus, Triatoma infestans* (main)*, T. sanguisuga, T. indictiva, T. lecticularia* and *T. rubida.*	(Rodríguez-Monguí et al., 2019) (Rodriguez et al., 2021)
Anaplasmosis	World.	Rickettsias (Bacteria) In cattle, *Anaplasma marginale, A. bovis, A. centrale, A. phagocytophylum, A. caudatum, A. phagocytophilum* Sheep: *A. ovis* Goats: *A capra*	Ticks: *Dermacentor marginatus*, *D. silvarum, D. andersoni, Rhipicephalus bursa*, *Ixodes* spp., *Hyalomma* spp., *Hamephysalis* spp. (*H. sulcata, H. longicornis, H. punctata, H. spinigera, H. sarva, H. arborensis*) and *Argas* spp. Mechanical transmission by insect bites: Flies (*Tabanus* spp.*, Stomoxys calcitrans* and *Haematobia irritans*) and gnats (*Culicoides* spp.).	(Jiménez et al., 2019) (Railey & Marsh, 2021)
Babesiosis	World, mainly in tropical and subtropical areas.	Intraerythrocytic apicomplexan protozoan *Babesia bovis, B. bigemina, B. divergens, B. major, B. ovata, B. occultans y B. jakimovi* Sheep and goats: *Babesia ovis* (more pathogenic) and *B. motasi.*	Ticks: By *B. bigemina*: *Rhipicephalus microplus* and *R. annulatus* (mainly), also *R. geigy* y *R. eversti.* By *B. bovis*: *R. microplus* and *R. annulatus*, also *R. geigy.* By *B. divergens*: *Ixodes ricinus* Sheep: *Rhipicephalus bursa, R. tiranices* and *R. revertis.*	(Ozubek et al., 2020) (Fesseha et al., 2022)
Bluetongue	World, including tropical and subtropical islands.	Virus *Orbivirus* Family Reoviridae	Mosquitoes: *Culicoides* spp. *C. varipennis var sonorensis* (main vector in United States), *C. brevitarsis* (Australia), *C. imicola* (Africa and the Middle East) and *C. dewlfi* (Europe).	(Belbis et al., 2017) (Saminathan et al., 2020)
Camelpox	Endemic to the Middle East, Africa and southern parts of the former USSR. South America (other camelids).	Virus *Orthopoxvirus*, Family Poxiviridae	Tick: *Hyalomma dromedari* (main) Secondarily: black flies *Simulium* spp. (*S. asakoae, S. yuphae, S. chiangdaoense, S. gombakense, S. phahompokense, S. fruticosum, S. maeaiense, S. fenestratum, S. equinum, S. erythrocephalum*); biting flies (*Stomyx calcitrans, Haematobia irritans, Pseudolynchia* spp., *Lutzomyia spp),* and gnats *(Culicoides* spp.*).*	(Balamurugan et al., 2013) (Bera et al., 2019)
Cowdriosis (Hydrocarditis)	Sub-Saharan Africa and coastal islands (mainly Madagascar, Mauritius, Sao Tome) and islands of the Caribbean.	Rickettsia (Bacteria) *Ehrlichia ruminantium*	Ticks: *Amblyomma hebraeum* (main) and *A. variegatum.*	(Esemu et al., 2018) (Matos et al., 2019)

Crimean-Congo Haemorrhagic Fever	Asia, Africa and Europe.	Virus *Nairovirus*, Family Bunyaviridae	Ticks: *Hyalomma* spp. *H. marginatum,* the most important vector.	(Spengler et al., 2016) (Hawman & Feldmann, 2023)
Eastern Equine Encephalomyelitis	North America (United States and Canada), northern South America and the Caribbean.	Virus *Alphavirus*, Family Togaviridae	Mosquitoes (more than 25 species): *Culex* spp., *Aedes, Coquillettidia* spp., *Culiseta* spp. (mainly *C. melanura*).	(Vander Kelen et al., 2014) (Armstrong & Andreadis, 2022)
Epizootic Haemorrhagic Disease	North America, Africa, Asia and Oceania.	Virus *Orbivirus*, Family Reoviridae	Mosquitoes: *Culicoides* spp. (mainly) *C. imicola* , *C. sonorensis* , *C. obsoletus* , *C. brevitarsis* , *C. mohave* and *C. oxystoma*	(Noronha et al., 2021) (Jiménez-Cabello et al., 2023)
Equine Infectious Anemia	World, except in Japan and Iceland.	Virus *Lentivirus* Family Retroviridae	Flies: *Tabanus* spp. (main) *Stomoxys calcitrans.*	(Issel et al., 2014) (Machado et al., 2021
Equine Piroplasmosis	Asia, Central and South America, southern Europe and some parts of the southern of United States.	Apicomplexan intraerythrocytic protozoa *Babesia caballi* and *Theileria equi* (before *Babesia equi)*	Ticks: *Dermacentor* spp., *Hyalomma* and *Rhipicephalus* spp.	(Scoles & Ueti, 2015) (Onyiche et al., 2019)
Foot and Mouth Disease	Endemic in Africa, Asia, the Middle East and some South American countries.	Virus *Orbivirus*, Family Reoviridae	Mosquitoes: *Culicoides* spp.	(Knight-Jones & Rushton, 2013) (Brito et al., 2017)
Japanese Encephalitis	Asia, Oceania and parts of the western Pacific.	Virus *Flavivirus* Family Flaviviridae	Mosquitoes: *Culex* spp., mainly *C. tritaeniorhynchus*	Mansfield et al 2017 ; (Suresh et al., 2022)
Lumpy Skin Disease	Countries in the Middle East, Eastern Europe, Africa, especially in the Southern and Sub-Saharan regions.	Virus *Capripoxvirus* Family Poxviridae	Mosquitoes: *Aedes aegypti* (main). Probable: *Culex mirificens, Aedes natriounus* y *Culicoides punctatus* Moscas: *Stomoxys calcitrans* and *Biomyia fasciata*. Male ticks: *Riphicephalus appendiculatus* and *Amblyomma hebraeum*.	(Mulatu & Feyisa, 2018); (Sprygin et al., 2019)
Nairobi Sheep Disease	Central and Eastern Africa and some countries in Asia.	Virus *Ortonairovirus* Family Nairoviridae	Ticks: *Riphicephalus appendiculatus* (main), *Amblyomma variegatum* (main vector in Africa) *Haemaphysalis intermedia* (Asia) and *H. longicornis* (China)	(Rovid, 2022) (Wang et al., 2024)
New World screwworm Myiasis	North, Central and South America, Caribbean islands.	Parasitic insects Diptera Family Calliphoridae	Fly larvae: *Cochliomyia hominivorax.*	(Mulieri & Patitucci, 2019) (Pereira & Bricarello, 2020
Old World screwworm Myiasis	Southeast Asia, Indian Subcontinent, Tropical and Sub-Saharan Africa and some countries in the Middle East.	Parasitic insects Diptera Families Calliphoridae and Sarcophagidae	Fly larvae: *Chrysomya bezziana* (main), different animal species. Specific: Sheep and goats: *Oestrus ovis*. Only goats: *Hemipyrellia ligurriens*. Goats, buffaloes and cattle: *Seniorwhitea reciproca* Equines: *Gasterophilus* spp. Camels: *Cephalopina titillator*	(Sinha, 2012) (Rana et al., 2020)

Q Fever	World, except New Zealand.	Bacteria *Coxiella burnetti*	Ticks: *Hyalomma dromedarii* and *H. anatolicum*. *Haemaphysalis cornupunctata, H. bispinosa* and *H. montgomeryi*. *Rhipicephalus haemaphysaloides, R. microplus* and *Argas persicus*.	(Ali et al., 2023) (Raboisson et al., 2024)
Rift Valley Fever	Africa and Arabian Peninsula.	Virus *Phlebovirus*, Family Bunyaviridae	Mosquitoes: *Aedes mcintoshi* (main), *A. vexans, A. albopictus, A. sudanensis, A. ochraceus* and *A. dentatus* (primary vectors). *Culex pipiens, C. poicilipes, C. univittatus, Anopheles* spp. and *Mansonia* spp. (secondary vectors).	(McMillen & Hartman, 2018) (Kwaśnik et al., 2021)
Surra	Africa, Asia, Middle East, Central America, South America and Canary Islands.	Parasitic flagellated protozoan *Trypanosoma evansi,* subgenre *Trypanozoon* Family Trypanosomatidae	Hematophagous flies: *Tabanus* spp. (mainly), *Haematopota* spp., *Chrysops* spp. Secondarily, *Haemotobia irritans, Stomoxys calcitrans, Musca* spp. and *Atylotus* spp. Vampires (Latin America): *Desmodus rotundus*	(Aregawi et al., 2019) (Sazmand et al., 2022)
Theileriosis	Worldwide, mainly in tropical and subtropical areas.	Obligate intracellular apicomplexan protozoans. *Theileria* spp. The two most pathogenic: *T. parva* (cattle and water buffalo) and *T. annulata* (tropical theileriosis, in cattle, yaks and water buffalo). Other species: *T. mutans, T. buffeli, T. velifera, T. taurotragi* and *T. sergenti*. Sheep and goats: *T. lestoquardi, T. luwnshuni* and *T. uilenbergi* *T. lestoquardi*, (before *T. hirci*) only species of economic importance in small ruminants.	Ticks: *Rhipicephalus* spp., (mainly *R. appendiculatus* by *T. parva)* *Hyalomma* spp., (*H. marginatum, H. rufipes, H. scupense* (predominantly by *T. annulata), H. truncatum, H. albiparmatum, H. impressum, H. nitidum, H. scupense* y *H. anatolicum*, dominant species in Africa. *Dermacentor* spp. mainly *D. nitens, D. albipictus* and *D. dissimilis* *Haemaphysalis longicornis,* mainly *H. sulcata, H. leporispalustris, H. spinigera*	(Gharbi et al., 2020) (Butler & Trout, 2023)
Venezuelan Equine Encephalomyelitis	Mexico, Central and South America	Virus *Alphavirus*, Family Togaviridae	Mosquito: *Culex melanoconium* the most important vector, also *C. taeniopus*	(Forrester et al., 2017) (Guzmán-Terán et al., 2020)
West Nile Fever	Africa, Europe, Middle East, Western Asia, North America and Australia	Virus *Flavivirus* Family Flaviviridae	Mosquitoes: *Culex* spp. mainly *C. pipiens*; also *Ochlerotatus triseriatus, O. japonicus japonicus* and *Aedes albopictus*. Mexico and Latin America: *Culex interrogator* and *C. nigripalpus* United States: *C. pipiens, C. tarsalis* and *C. quinquefasciato*. Europe: *C. pipiens, C. molestus* and *C. torrentium, Ochlerotatus caspius, Anopheles maculipennis* and *Coquillettidia richiardii*. Australia: *Culex annulirostris*	(Barba et al., 2019) (Habarugira et al., 2020)
Western Equine Encephalomyelitis	Alaska, United States, Colombia and Brazil.	Virus *Alphavirus*, Family Togaviridae	Mosquito: *Culex tarsalis* is the most important vector.	(Bergren et al., 2014) ; (Barba et al., 2019)

Source: Prepared by the authors based on the cited references.

In the period 2019-2023, the number of animals affected by VBDs increased continuously until 2022, when it registered a significant increase, and decreased in 2023, with 751,768; 1,528; 4,507 and 1,279 cases (in thousands), respectively. Figure 2 shows the distribution by region (WAHIS, 2024).

On the Scope of VBDs

Without a doubt, from the above figures, it is possible to infer the multiple impacts generated by these diseases. Although many are not fatal, the damage they cause to the health of animals often affects both their productive and reproductive efficiency. Collaterally, death from disease and the slaughter of animals as control measures have important economic repercussions, which significantly undermine the livelihoods of many communities, especially in relation to food availability. In the area of human health, the increased risks posed by zoonotic VBDs impose serious challenges on health systems (Vipham et al., 2020; Chakraborty et al., 2023).

The magnitude of this scenario tends to become more acute when considering the causes underlying the reports of animal health events presented to the World Organization for Animal Health. The analysis of a sample of 355 randomly selected recent reports related to VBDs provides information on this matter. The highest percentages correspond to the recurrence of an eradicated disease (70.7%) and the appearance of a new strain in an area (12.4%). The rest of the events report the first appearance in an area (5.8%), the first appearance in the country (4.8%), a change or increase in incidence (3.6%), the recurrence of an eradicated strain (1.5%) and 1.2% the detection of an unusual host. In short, they reflect the reemergence of diseases, the increase in incidence and the expansion of hosts (WOAH, 2024).

A more detailed analysis of these reports allows us to identify areas of opportunity in the notification of events, with the consequent implications. Table 3 recovers some of these references. In the reports that mark the beginning and notification in 2024, only in three does less than a week pass. For the rest, the range is 1-3 months. In comparison, for the second group that begins with the report from Mauritania, the difference in times is longer (WOAH, 2024).

Table 2: Prevalence of VTE by domestic species (2019-2023).

	Cattle	Sheep	Goats	S-G*	Buffaloes	Camelids	Suidae	Equines	Poultry	Total
African swine fever	32						2,373,927			2,373,959
African trypanosomiasis	160,515	207	179	107	4,151	1,758	70	25		167,012
Anaplasmosis	83,222	23	36	156	3,329			34		86,800
Babesiosis	93,907	22	8	517	12,059			15		106,528
Bluetongue	46,711	159,633	1,461	16,489	42	5				224,341
Camelpox						2,431				2,431
Cowdriosis	20,851	1,624	5,979	369		485				29,308
Crimean-Congo haemorrhagic fever	37	28	49	96						210
Eastern equine encephalomyelitis								677		677
Epizootic haemorrhagic disease	3,333	69								3,402
Equine infectious anemia	6							57,771		57,777
Equine Piroplasmosis	1							1469		1,470
Foot and mouth disease	1,093,146	83,469	37,539	46,227	46,777	421	80,789			1,387,947
Japanese encephalitis							1,821			1,821
Lumpy skin disease	4,198,204	14	4	5	13,525					4,211,752
New World screwworm Myiasis	9,672	539	975	5	33	1	574	450	11	12,260
Old World screwworm Myiasis	1,837	1,264	81	573	21	7	2	9	2	3,796
Q fever	5,801	6,628	3,889	5,731		1,541				23,590
Rift Valley fever	4,042	322	2,623	187		112				7,286
Surra	1,097	10	6		1,317	8,532		1060		12,022
Theileriosis	133,218	304	88	200	7,097	12		19		140,938
Venezuelan equine encephalomyelitis								43		43
Western equine encephalomyelitis								4,413		4,413
West Nile fever		1						1,755		1,756
	5,855,632	254,157	52,917	70,662	88,351	15,305	2,457,183	67,740	13	8,861,960

* S-G= Mixed flocks of sheep and goats

Source: Prepared by the authors based on the processing of data available in WAHIS (2024).

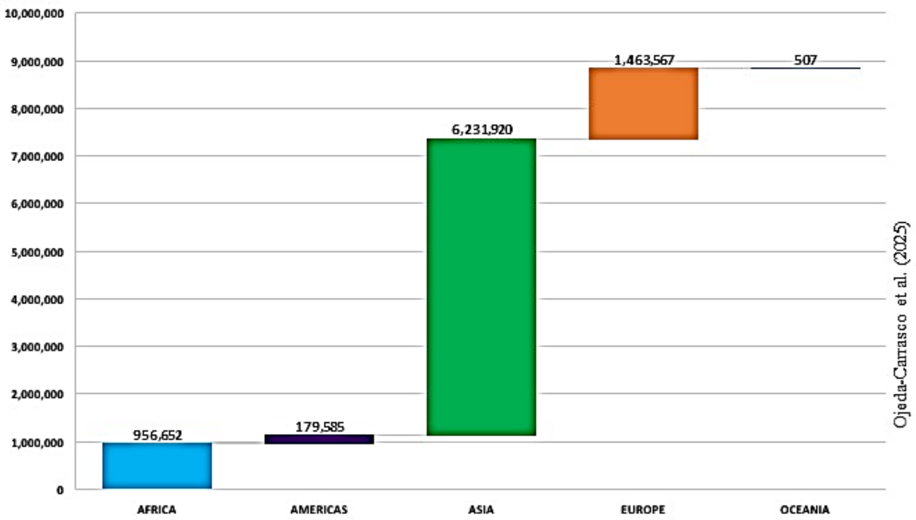

Fig. 2: Cumulative distribution of prevalence by region

As an example, two cases can show the significance of this information. In December 2024, Serbia reports (23 months later) on the «First occurrence in a zone or compartment» of African swine fever, identified in January 2023. From 2019-2023, this country records incidences for 35 zones. For the first half of 2024, the register includes 33 zones, of which only two (Kovin and Smederevo) coincide, which means that the report corresponds not only to one zone, but to 31 that did not appear in previous registers. In addition, the number of cases has significant increases. For the 5-year comparative, the highest incidences are recorded in 2023, for Braničevski (256 cases) and Južno-Banatski (156). In 2024, they correspond to Sremska Mitrovica (103) and Valjevo (414). The latter alone exceeds the two highest incidences of 2023 (WAHIS, 2024).

Table 3: Notification of zoosanitary events to the WOAH

Disease	Reason for notification	Country	Start of the event	Notification
African swine fever	RED	Albania	25/12/2024	28/12/2024
Myiasis by *Cochliomyia hominivorax*	RED	Guatemala	25/10/2024	29/10/2024
Equine infectious anemia	FAZC	Bulgaria	06/08/2024	12/08/2024
Foot and mouth disease	NSC	Palestine	07/11/2024	03/12/2024
African swine fever	FAZC	Bhutan	16/07/2024	03/09/2024
Babesiosis	RED	Ecuador	07/11/2024	27/12/2024
Bluetongue	NSC	Denmark	27/07/2024	16/09/2024
Lumpy skin disease	FAC	Japan	05/11/2024	27/12/2024
Bluetongue	NSC	North Macedonia	14/10/2024	19/12/2024
Foot and mouth disease	RED	China	15/10/2024	30/12/2024
Eastern equine encephalomyelitis	RED	Ecuador	01/05/2024	18/07/2024
West Nile fever	FAC	Poland	26/07/2024	25/10/2024
Bluetongue	NSC	Greece	18/09/2024	16/12/2024
Q fever	FAC	Philippines	13/02/2024	01/07/2024
Rift Valley fever	RED	Mauritania	29/09/2021	30/12/2024
Crimean-Congo haemorrhagic fever	RED	Mauritania	04/02/2022	30/12/2024
Camelpox	RED	Iran	05/03/2022	28/08/2024
Myiasis by *Cochliomyia hominivorax*	RED	Panama	16/08/2022	30/07/2024
African swine fever	FAZC	Serbia	03/01/2023	23/12/2024
Lumpy skin disease	FAC	Libya	08/04/2023	30/12/2024
African swine fever	RED	Russia	10/05/2023	18/07/2024
Myiasis by *Cochliomyia hominivorax*	RED	Costa Rica	14/07/2023	18/11/2024
Epizootic haemorrhagic disease	FAC	Portugal	13/07/2023	29/11/2024
Q fever	FAC	Estonia	23/10/2023	05/09/2024

RED=Recurrence of eradicated disease; FAC=First appearance in the country; FAZC=First appearance in zone or compartment; NSC=New strain in the country.

Source: Prepared by the authors based on information on animal health events (WHAIS, 2024)

The second corresponds to myiasis caused by *C. hominivorax*. In July 2024 (23 months later), Panama reports the «Recurrence of an eradicated disease», identified in August 2022. Prior to the event, from 2005-2021 this country reported 335 cases, 88.9% in cattle, and in lower percentages for horses, pigs and dogs. As of 2022 with the notified identification, the numbers have increased alarmingly. In 2022, 1,000 cases, 2023 (5,812) and for the first half of 2024 (9,201). The affected species include birds, sheep, goats, buffalo and cats. This implies that, between the identification of the event and the notification, this disease affected 16,013 animals. The 2019-2023 period records 12,511 cases. Present in nine countries, Bolivia, Costa Rica, Cuba, Ecuador, Guyana, Panama, Paraguay, Peru and Venezuela. The highest prevalences for Panama (6,986) and Cuba (2,180). For the first half of 2024, the number of affected countries increases by integrating Nicaragua (791 cases), Honduras (23), Mexico (2) and Guatemala (1). It is noteworthy that this disease, considered endemic in the Americas, reports 1,780 cases (2019) in Eritrea, Africa (WAHIS, 2024).

It is clear that the effects caused by these late reports do not only affect the locality of origin. The lack of timely information prevents the implementation of control strategies that prevent the spread of diseases. These conditions lead to reactive rather than proactive responses, which undoubtedly implies that each locality faces its own challenges.

Conclusions

The VBDs are a reference to show the magnitude and scope that diseases can have today. The interrelation between climate change and the adaptations of pathogens and vectors outlines a panorama of dizzying changes. The recurrence of diseases, the appearance of new strains and the emergence of diseases increase the number of epizootic outbreaks, incidences and prevalences throughout the world, a situation aggravated by the impact on new hosts. Likewise, some originally endemic diseases expand their geographic distribution not only to adjacent localities, but also to other regions and continents, because of the commercial exchange of livestock and international travel, favoring the dispersion of vectors and pathogens. The implications are not predictive, but real. Millions of affected animals see their health compromised, as well as their productive and reproductive capacities. The risks to human health are increasing, with the consequent economic losses. In an increasingly demanding scenario, there is a strong impact on food availability. Taken together, this reflects the fact that, while efforts to control these diseases are not in vain, they are so far insufficient. Given this complexity, it is essential to redouble our efforts to find strategies that can at least mitigate the effects of these diseases.

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