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Editorial

Diversity, Distribution and Phylogeny of Vector Insects

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Mosquitoes (Fam. Culicidae), sand flies (Subfam. Phlebotominae), biting midges (Fam. Ceratopogonidae), black flies (Fam. Simuliidae) and stable flies (Fam. Muscidae) are groups of insects capable to transmit pathogens of public health and veterinary importance [1–5]. These pathogens include viruses, bacteria, protozoans and helminths that affect humans (e.g., Zika and dengue viruses), domestic and wild animals (e.g., Bluetongue and Equine infectious anemia virus), and agents that cause zoonotic diseases such as West Nile, Leishmaniasis and Onchocerciasis [6–10]. These insects not only transmit pathogens, but also are responsible for human and domestic livestock nuisances and allergies [3,4].

More than 700,000 humans die every year due to pathogens transmitted by vector insects worldwide, such as malaria and dengue [11–13]. Outbreaks have nowadays become increasingly frequent in certain regions. For example, in Europe, viruses such as West Nile and bluetongue occur in several countries, and leishmaniasis cases have increased during the last decade [2,7,14]. Control measures against these diseases are usually focused on the vector insect since, in most cases, vaccines are not available [15]. Knowing the distribution of the different vectors and understanding their biology, behaviors and genetic relationships could help humans to manage the control of vector diseases transmitted by them; therefore, the study of the diversity and phylogeny of vector insects in determined areas is crucial to understand the relationships between its hosts and the pathogens that can be transmitted, including aspects related to their epidemiology.

In this Special Issue, we included studies about the identification, diversity, distribution and population dynamics of mosquitoes, sand flies, biting midges and black flies in different countries, including a review of stable flies. In this context, this Special Issue includes 12 articles, of which 11 are research papers and one is a review. The group with the highest number of publications is mosquitoes, with six papers. Ruiz-Arrondo et al. (contribution 1) studied the species composition and population dynamics of Culicidae in three aquatic ecosystems located in a peri-urban area of a city in northern Spain. They observed that the different hydrological management practices of each environment could play a key role in determining the abundance of mosquito genera. In the same line, Rosa-Silva et al. (contribution 2) studied the effect of rain on the spatial distribution and abundance of container-breeding mosquitoes in Brazil, demonstrating that human occupation and rainfall impact interactions between invasive urban species such as *Aedes albopictus* and *Aedes aegypti*. and sylvatic species. Continuing with studies on the distribution of mosquitoes, this time in the state of Queretaro in Mexico, Ortega Morales et al. (contribution 3) identified 33 new records of mosquito species for this state, including two undescribed species. They morphologically and molecularly described one of them as *Shannoniana huasteca* n. sp. In turn, the study conducted by Ibáñez-Justicia et al. (contribution 4) includes novel information regarding malaria vector species from the *Anopheles maculipennis* complex in 161 locations (including overwintering sites) during the National Surveillance program in the Netherlands, with the first record of *Anopheles daciae* in the country. The study of Vanderheyden et al. (contribution 5) reported the distribution of *Culex pipiens* s.s and

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Cx. torrentium in Belgium, using the COI and ACE2 loci. In the only study of this Special Issue carried out in Africa, phylogenetic analyses were conducted by Montalvo-Sabino et al. (contribution 6) on 65 mosquito species collected in South Africa, Mozambique and Angola, with new records for Afrotropical fauna. In addition, male genitalia were morphologically identified and associated with phylogenetic analysis.

Culicoides and black flies constitute the group of insect vectors with the second highest number of papers published in this Special Issue, with each having two publications. On the one hand, there is an ecological study of two of the main vector species of bluetongue in Europe, *Culicoides obsoletus* s.l. and *Culicoides imicola*, in which Barceló et al. (contribution 7) determined its nocturnal activity, showing different activity patterns according to the month and the time after the sunset. On the other hand, there is a molecular study in which Dähn et al. (contribution 8) designed PCR primers based on the COI gene to identify 21 biting midge species from the subgenus *Culicoides* in the Paleartic region. In addition, PCR assays were performed for the first time on recently described species of the Pulicaris group. Regarding the studies about black flies, Adler and Reeves (contribution 9) identified a pattern of north–south differentiation in the genus *Prosimulium* of western North America, and described a new species, *Prosimulium supernum*. Meanwhile, Kúdelová et al. (contribution 10) carried out the DNA barcoding of 25 black fly species from Slovakia, finding hidden diversity as well as shared barcode sequences among the studied species. A study on sandflies has also been published in this Special Issue. A new sand fly record for Spain, *Phlebotomus perfiliewi* s.l., was morphologically and phylogenetically described in González et al. (contribution 11), including a discussion about potential confusion with *Phlebotomus perniciousus*. Finally, Duvallet and Hogsette (contribution 12) reviewed several aspects of the genus *Stomoxys* sp., including worldwide diversity, distribution and genetic approaches to identify the origin and population dynamics of this genus.

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List of Contributions

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