



# Editorial: Biology, Systematics, Taxonomy, and Evolution of Insect Vectors

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## Editorial on the Research Topic

### Biology, Systematics, Taxonomy, and Evolution of Insect Vectors

Vector insects comprise several hematophagous invertebrate species grouped in the orders Diptera, Hemiptera, Anoplura, and Siphonaptera (Kuno and Chang, 2005). These species are responsible for the transmission of many infectious diseases such as dengue, chikungunya, Zika, yellow fever, malaria, lymphatic filariasis, leishmaniasis, Chagas disease, sleeping sickness, onchocerciasis, bubonic plague, Rift Valley fever, Japanese encephalitis, West Nile fever, tungiasis, typhus, louse-borne relapsing fever, sandfly fever, Crimean-Congo hemorrhagic fever, Lyme disease, relapsing fever, spotted fever, Q fever, and hence are of great importance to public health (World Health Organization, 2022). Vector-borne diseases account for more than 17% of all infectious diseases (caused by parasites, bacteria, or viruses), causing more than 700,000 deaths annually (World Health Organization, 2022). A better understanding of insect vector biology, systematics, taxonomy, and evolution can support more effective management and control strategies to mitigate the mortality and morbidity of these diseases. This is of great importance because, for the most part, vector control is the primary means by which incidences of vector-borne diseases in humans and animals are mitigated.

The studies presented in this Research Topic focused on two important orders of vector insects, namely, Diptera and Hemiptera. The genus *Aedes* Meigen, 1818 (Diptera, Culicidae) was discussed in several works: Martínez et al.; David et al.; Kelly et al.; Wang et al.; Virgínio et al., contributing to the taxonomic (Martínez et al.; Virgínio et al.), genetic/genomic (Martínez et al.; Kelly et al.), biological (David et al.) and entomo-epidemiological knowledge (Martínez et al.; Kelly et al.) of these vectors.

Martínez et al. presented important taxonomic, genetic (demonstrating that barcodes based on the COI gene fragment are successful method for identifying *Aedes* species) and entomo-epidemiological [diagnosing natural infection for dengue virus type 1 (DENV-1) and chikungunya virus (CHIKV)] for *Ae. aegypti* (Linnaeus, 1762) and *Ae. albopictus* (Skuse, 1894) from the eastern region of Colombia.

David et al. evaluated the development of *Ae. aegypti* in response to different variables of the physicochemical of water. They observed a positive relationship between factors such as the abundance of immatures and container volume and concentration of dissolved organic carbon (DOC), average dry weight of females and wing lengths of males and females, and temperature, as

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well as between male mean dry weight and water conductivity. Furthermore, Wang et al. evaluated biotic (bacterial diversity) and abiotic (physicochemical factors) issues that influence the larval density of mosquitoes of the genera *Aedes*, *Culex* Linnaeus, 1758, *Anopheles* Meigen, 1818, and *Mansonia* Blanchard, 1901 in Jiayang County, Shandong Province, China and concluded that the density and species can be jointly affected by these evaluated factors.

Kelly et al. performed population genomics studies of *Ae. aegypti* and suggested that populations from Exeter, California (CA), were reintroduced from the southern CA cluster following the elimination of the vector in 2015 by Delta Vector Control District (DVCD) activities. Demari-Silva et al. evaluated the genetic structure of *Anopheles cruzii* Dyar and Knab, 1908 from Ribeira Valley, southeastern Brazil, and verified whether the genetic structure was associated with forest cover, elevation, slope, and vegetation physiognomy. The authors observed two distinct lineages in the studied region associated with elevation and isolation by distance and proposed that differences in observed population structure found might be associated with the distribution of bromeliad species. Virgínio et al. presented the wing image database of mosquitoes (WingBank), developed from the geometric morphometry of the wings of these vectors. This image bank contains data referring to 77 species belonging to 15 genera of Culicidae.

Studies of Chagas disease vectors are related to the Rhodniini tribe (Hemiptera, Triatominae) (Marchant et al.; Filée et al.; de Paula et al.). Marchant et al. performed a transcriptomic study to evaluate the chemosensory gene expression of *Rhodnius robustus* Larrousse, 1927 and *R. prolixus* Stål, 1859. Among the 199 transcripts annotated in this study, 93% were conserved between *R. prolixus* and the sylvatic *R. robustus*; 12 novel takeout transcripts from the *R. prolixus* genome (Mesquita et al., 2015) were annotated; a large set of transcripts were found to be differentially expressed between males and females, with a majority of them overexpressed in males; 10 transcripts were specifically expressed in one sex and absent in another; three chemosensory transcripts were found to be expressed only in the reared *R. prolixus* and only one in sylvatic *R. robustus*; and 8,596 transcripts were differentially expressed, with most overexpressed in the sylvatic *R. robustus* samples.

de Paula et al. and Filée et al. performed phylogenetic [using mitochondrial rDNA (16S), nuclear ribosomal RNA (28S) and wingless (Wg) sequences] and phylogenomic studies [using 15

mitochondrial genes (13.3 kb), partial nuclear rDNA (5.2 kb) and 51 nuclear protein-coding genes (36.3 kb)], respectively, in the Rhodniini tribe. de Paula et al. presented dating related to the origin of the tribe Rhodniini (17.91 Mya ago), of the genus *Rhodnius* (9.13 Mya ago) and observed a close relationship between Rhodniini and Salyavatinae, highlighting that these vectors diverged from this subfamily 30.43 Mya. Furthermore, the authors highlighted that the colonization of bromeliads, palms trees, and bird nests represent important events for the speciation of *Rhodnius* spp. and discussed the evolution of hematophagy in a scenario where Rhodniini's ancestor could be pre-adapted for the invasion of these ecotopes that presented favorable factors such as water availability, thermal damping, and source of food (vertebrate inquilines) for the species of Rhodniini. Filée et al. discussed taxonomic and systematic issues of the Rhodniini tribe. They confirmed the specific status of *R. montenegrensis* Rosa et al., 2012 and *R. marabaensis* Souza et al., 2016 and the synonymy of *R. taquarussuensis* Rosa et al., 2017 with *R. neglectus* Lent, 1954, questioned the specific status of *R. milesi* Carcavallo et al., 2001 (that is more likely *R. nasutus* Stål, 1859) and suggested the generic reclassification of *Psammolestes tertius* Lent and Jurberg, 1965 to *R. tertius*. The authors observed a greater relationship between *pictipes* and *pallescens* groups than with the *prolixus* group and discussed which introgression events occurred in the three vector groups.

Finally, Wu et al. carried out studies on egg cannibalism of *Arma custos* (Fabricius, 1794) (Hemiptera: Asopinae) and observed that females exhibit a higher tendency for egg cannibalism than males and that cannibalism varies not only with the developmental stage of the eggs and nymphs but also with sex and reproductive status of females.

Thus, the Research Topic Biology, Systematics, Taxonomy, and Evolution of Insects Vectors addressed an important gap in the knowledge associated with biological, systematic, taxonomic, and evolutionary processes of insect vector species and helps further our understanding of issues related to the dynamics of vector-borne disease transmission, thus providing direction for activities related to vector control programs.

## AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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