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Editorial: Insights in vector biology: 2021

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Editorial on the Research Topic
Insights in vector biology: 2021

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This editorial summarizes collections on the Research Topic "*Insights in Vector Biology*". Vectors of four major tropical diseases including malaria, Chagas, dengue and West Nile were considered. The editorial discusses vectors contributing to residual malaria transmission that reside mainly outdoors and not targeted by indoor vector control interventions, notably, long lasting insecticidal nets and indoor residual spraying; the concept of paratransgenesis- a parasite transmission blocking strategy which uses genetically-modified microbes made to produce antimalarial effectors inside the vector for malaria control; assessment of insecticide resistance in malaria vectors; insecticide resistance in Chagas disease vectors; reproductive biology of the dengue vector; and the importance of characterising blood host type in wild *Culex* species involved in the transmission of zoonotic flaviviruses such as West Nile virus (WNV).

In a Grand challenges paper on tropical infectious diseases, Torto and Tchouassi (2021) provided a synthesis of the progress made in the last three decades and future challenges. Therefore, the authors highlighted possible mitigation approaches for managing vectors associated with these diseases. The synthesis identified climate change, land use changes and urbanization as key drivers influencing the frequency of outbreaks of emerging and re-emerging infectious diseases, especially vectors of these diseases and their interactions with existing and novel pathogens. Some of the priority research areas recommended to researchers to consider included understanding physical cues, chemical ecology, transmission blocking, vector adaptation to environmental xenobiotics, and genetic control to help disrupt pathogen-vector-host interactions and to support disease control. Markedly, the other six contributions aligned with these recommendations.

Unplanned urbanization poses a risk to disease dynamics through changing vector adaptation. Over the past decade following urbanisation in Simbock neighborhood of Yaounde-city (Cameroon), Mbakop et al. documented significant shifts in the malaria vector composition: drastic reduction in the malaria species richness but increase in the abundance of three species *Anopheles gambiae*, *An. coluzzii* and *An. funestus s.s.* These findings are significant, indicating adaptation in response to land use by these species which are among the most efficient malaria vectors in sub-Saharan Africa (1). Over time, there was a reduction in malaria transmission estimated by parasite infection rates and entomological inoculation rates, perhaps linked to enhanced control measures. Nonetheless, *An. gambiae* populations exhibited different susceptibility levels to insecticides commonly used in public health. Such surveillance studies are critical for guiding malaria control toward elimination and align with the Global Technical Strategy for Malaria 2016–2030 (2).

Outdoor biting by anopheline mosquitoes has been identified as an important contributor to residual malaria transmission (3), yet most of the species remain poorly characterized in malaria endemic areas. Jones et al. (2021) report several undescribed anopheline mosquitoes among outdoor collections in northern Zambia. Mosquitoes were analysed by morphology and then sequencing of two genetic markers- mitochondrial cytochrome oxidase c subunit 1 (*COI*) and nuclear intergenic transcribed spacer 2 (ITS-2). The species if found to support malaria transmission can compromise the malaria vector surveillance and malaria control efforts. They recommended further characterisation of these species including taxonomic elucidation.

Resistance to insecticides remains a major impediment not only for effective control of malaria but also other vector-borne diseases. Chagas disease is a neglected tropical disease caused by the parasite *Trypanosoma cruzi* transmitted by the triatomine bug *Triatoma infestans*. Interventions against the disease rely on the use of residual pyrethroid spraying to control the vector. Dulbecco et al. (2022) detail how insecticide resistance may have led to failures in strategies to eliminate this vector in southern America. The mechanisms of resistance including increased insecticide detoxification, reduced affinity of the site of action, and reduced insecticide penetration through the cuticle, have all been documented in *T. infestans*. In the review paper, the authors emphasize the role played by P450 genes, a supergene family in metabolic resistance in triatomines. Metabolic resistance is significant as it produces many times more resistance than any other mechanism as observed in malaria vectors (4).

Newer approaches to vector control are being explored amongst them those that target the reproductive biology of disease vectors. Agudelo et al. (2022) explored the putative degradation of on non-stored sperm in the female reproductive tract of the dengue vector mosquito *Aedes aegypti*. By quantifying sperm after mating, the authors show that sperm storage in the spermatheca of females is influenced by ejaculate volume. The authors suggest that such physiological studies focused on understanding sperm transfer and storage in the female reproductive tract can help lay the groundwork for identifying sex-specific molecules mediating the process for disease vector control. Paratransgenesis is another strategy that uses genetically-modified microbe to produce antimalarial effectors inside the insect host for the control of malaria transmission. This strategy was reviewed by Fofana et al. (2022) who suggest that this strategy can contribute to curbing the spread of resistance to insecticides in mosquitoes and to drugs in parasites.

Knowledge of vector host-feeding behavior is essential to understanding the maintenance and emergence cycles of arboviral diseases. Reeves and Burkett-Cadena (2022) describe the blood feeding patterns through blood meal analysis of field collected *Culex* mosquitoes that are vectors of zoonotic Flaviviruses in North America. These viruses include WNV, St. Louis encephalitis virus and western equine encephalitis virus. Using DNA barcoding, they unexpectedly uncovered reptiles, particularly lizards in the feeding profile of four *Culex* species; *Culex nigripalpus*, *Culex tarsalis*, *Culex thriambus*, and *Culex stigmatosoma*, but not *Culex quinquefasciatus*. Evidently, host association varied among species belonging to the *Culex* subgenus. The authors recommended additional studies to elucidate the role of lizards in the epidemiology of zoonotic Flaviviruses.

Overall, the articles collated in this Research Topic illustrate that the risk patterns of vector-borne diseases are ever changing and require heightened surveillance employing a combination of tools including genetic/genomics analysis to identify new threats and how best to tackle them. As new threats become evident, novel approaches to contribute to the vector control toolbox are urgently required, which can be implemented through an integrated management strategy.

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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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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