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Editorial: 2022 in review: vector biology

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Editorial on the Research Topic
2022 in review: vector biology

This editorial summarizes collections on the Research Topic "*2022 in Review: Vector Biology*" that focus on entomologic surveillance insights related to mosquito-borne diseases such as dengue and malaria, and sandfly-borne leishmaniasis. Specifically, the editorial discusses the entomologic drivers of dengue virus transmission, host-feeding relationships among various mosquito vectors, sample efficiency of malaria vectors using a suite of trapping techniques and improving sandfly surveillance using odor-baited trapping strategies.

The research article by Kamau et al. assessed variation in the biological attributes of adult *Aedes aegypti* mosquitoes by estimating critical parameters of vectorial capacity (vectors abundance, human blood feeding rates, survival) that modulate the risk of transmission of dengue — the most prevalent human arboviral disease worldwide, which is expected to increase with projected population increase coupled with climate change and geographic expansion of the key vector (1). The study focused on *Ae. aegypti* populations in two settings in Kenya: peri-urban Rabai (coastal Region, dengue-endemic) and rural Kerio Valley (Rift Valley Region, no reported dengue outbreak). Correlations were then examined between each of these parameters and satellite-derived weather parameters, specifically temperature, rainfall, and relative humidity. The results found differential survival abilities between the Rabai and Kerio Valley populations. Both vector abundance and human blood-feeding rates were consistently lower in Kerio Valley, suggesting that the risk of dengue virus transmission may be strongly related to the degree of urbanization (1, 2). In both environments, there was a negative association between *Ae. aegypti* survival (estimated by parity) and abundance, which was modulated by weather conditions, notably temperature and relative humidity. These bionomic traits, together with appropriate ecological parameters, could be integrated into a modeling framework for risk prediction of dengue outbreak occurrence and spread trajectories.

In their research article Gonçalves et al. characterized the blood-feeding patterns of the malaria (*Anopheles arabiensis*) and arboviral [*Ae. aegypti*, and *Culex pipiens* sensu lato (s.l.)] vectors employing enzyme-linked immunosorbent assays. The specimens were collected in three municipalities on the island of Santiago, Cape Verde (Praia, Santa Cruz, and Santa Catarina). The results, mainly single-host blood meals, show high human blood feeding rates for *Ae. aegypti* consistent with the high anthropophagic tendency reported in the literature (3), with *An. arabiensis* exhibiting low levels of human feeding. *Culex pipiens* s.l. was more

random in its trophic outlook compared to the other mosquito species despite a high likelihood of human feeding. Interestingly, a strong negative association between *Cx. pipiens* s.l. feeding on dogs and goats was uncovered, similar to the relationship between *An. arabiensis* and the human host. Blood feeding patterns generally assessed by blood meal analysis, reflecting mosquito–host associations under the influence of biological and environmental factors (3, 4). Thus, quantifying the strength of such relationships should take into account the effects of genetics, habitat, and seasonal host abundance. As a conduit for pathogen transmission, knowledge of blood-feeding behavior should guide new vector control measures and provide potential insights into pathogen transmission.

Nwane et al., compared the performance of five trapping tools for the surveillance of anopheline mosquito species. These included human landing catches (HLCs), Clay Pots (CPs), Pyrethroid Spray Catches (PSCs), Window Exit Traps (WETs) and Centers for Disease Control-Light Traps (CDC-LTs). This was based on historical capture data from multi-year surveillance studies in two regions: Northern and Central Cameroon. HLC and CDC-LTs target adult host-seeking mosquitoes, while the others mainly target resting cohorts (PSC, CPs) or exiting mosquitoes (WETs). An assessment of the other methods as alternatives to HLC was made but it was suggested that caution should be exercised in the interpretation of results because of the likelihood of bias inherent in the different mosquito cohorts being targeted (host-seeking vs resting/exiting). Not all anopheline mosquitoes enter houses to allow for fair comparative assessments. A record of higher anopheline richness and abundance both indoors and outdoors in the HLC is not unexpected as it remains superior in trapping species that prefer humans (5). It remains the gold standard for incriminating anopheline species that can bite humans and thus associated with human malaria parasite transmission (5). Although inferior to HLC and targeting host-seeking mosquitoes, CDC-LTs are being considered as an alternative due to ethical issues with the former but efficiency can be improved by using olfactory cues such as carbon dioxide or other host-derived odors (6).

The article by Tchouassi et al. reported an evaluation of the enantiomeric forms [(R)-(-)- (R-form) and (S)-(+)- (S-form)] of the compound 1-octen-3-ol, as well as the racemic mixture for improved trapping of adult sandflies, vectors of *Leishmania* parasites that cause leishmaniasis in humans. The isomers have been found to elicit different behavioral responses in other blood-feeding insects such as mosquitoes. Because the isomers are commercially expensive, an elaborate procedure is described for synthesizing the individual isomers including enzymatic resolution of the enantiomeric mixtures incorporating a suite of chemical analytical techniques. These include coupled gas chromatography (GC) and nuclear magnetic resonance (NMR). Field trials using the individual compounds as baits in CDC light traps revealed a higher sensitivity for the R- form compared to the S-form only in *Phlebotomus martini*, the vector of the *Leishmania* parasites that cause visceral leishmaniasis, a neglected tropical disease that can be fatal if left untreated (7). This was evident in the significantly increased captures of this species but not in others dominated by *Sergentomyia* species. Sandflies of the latter genus are not known to be competent vectors of leishmaniasis. In practical terms, this

specific isomer can be incorporated into conventional traps to selectively increase the capture of this species. This would be beneficial for surveillance programs.

Overall, the collection of articles highlights the importance of active surveillance of vector populations, which is central to mapping the risk of vector-borne diseases and guiding appropriate control strategies. Vector range expansion is correlated with the emergence of pathogens in humans. Particular attention needs to be paid to data collection through active surveillance of key traits that modulate the risk of disease transmission and spread and provide insight into differential occurrence trends. Given the sporadic transmission foci (e.g., arboviruses) or low transmission (e.g. malaria) in some settings, the deployment of sensitive vector monitoring of adult populations is critical for the accurate assessment of disease epidemiology, taking into account pathogen infection, vector abundance and movement. Such sensitivity could be achieved by further exploring the olfactory cues that mediate chemical communication in different disease vectors (6).

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