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Complexity of the vector system in South-East Asia: How to implement effective vector control?

The biodiversity of mosquito species involved in pathogen transmission throughout South-East Asia is particularly rich as compared to the other continents. Species belonging to the genera *Anopheles* and *Aedes*, respectively involved in the transmission of parasites (*Plasmodium* spp., *Wuchereria bancrofti*, *Brugia* spp.) and viruses (Dengue, Chikungunya) can occur in the same localities. In addition, the vector system is composite as each malaria vector in Asia belongs to a species complex in which sibling species are morphologically indistinguishable and may present different trophic behaviors and vectorial capacities ranging from non-vectors to major vector species.

Therefore, it is crucial to study appropriately the vector populations prior to apply any vector control program. Precise identification and bionomic studies allow targeting the correct vector species in control programs, and help to define the appropriate way to control them in relation to their specific behavior. Robust diagnostic tools have now been developed for improving knowledge on vectors and important information can be obtained on various aspects, such as species identification, vectorial capacity, behaviour, resistance/susceptibility level to insecticides, and seasonality along with environmental factors affecting the geographic distribution.

However, there is still a considerable lack of knowledge on the vectors. Do we know all the vectors, even secondary ones that may sporadically transmit and then maintain transmission? Can we prevent from an outbreak using a very early pathogen detection method? Can we assess the capacity of pathogen transmission by vectors harbouring a diverse microbiota? Can we develop simpler and cheaper diagnostic tools for vector characterization?

These are some of the questions we need to answer as part of a collaborative initiative for improving the control of vector borne diseases.

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