



MOLECULAR ASSAYS FOR IDENTIFYING MALARIA VECTORS IN ASIA: IMPORTANCE OF CORRECT SPECIES IDENTIFICATION.

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Malaria vector system in Southeast Asia is complex due to the number of species potentially involved in transmission. All Oriental malaria vectors belong to species complexes which cannot be distinguished on the sole basis of morphology. The follow-up and evaluation of preventive control measures are therefore hampered by the potential misidentification of vectors.

Efforts have been made to develop efficient alternative techniques to morphology. For decades, the gold standard for anopheline species identification was isozyme electrophoresis which requires fresh or frozen samples. The large development of PCR-based methods that constitute efficient and powerful identification tools changed drastically the panel of molecular identification assays without such conservation requirements.

This talk aimed at presenting the PCR-based assays available to identify the main Oriental malaria vectors with a special focus on the Culicifacies, Dirus, Fluvialilis, Maculatus, Minimus, and Sundaicus Complexes. Moreover, the importance of using PCR-based assays in entomological surveys will be highlighted through two examples. In central Vietnam, a RFLP-PCR assay showed that an unusual morphotype of *Anopheles minimus* was actually *An. varuna*, a non-vector species. Within the Minimus Complex, the use of an allele-specific PCR over large temporal and geographic surveys demonstrated the unreliability of two morphological characters considered as diagnostic.

Molecular identification assays have proven to be the most efficient tools to differentiate unambiguously malaria vectors versus non-vector species when morphology finds its limits. Proper species identification is essential and mandatory in any relevant study on malaria vectors for improving our knowledge on species distribution and biology, as well as for the application of successful vector control strategies.



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