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# The genetic bases of deltamethrin resistance in *Aedes albopictus* – A genomic travelling around the world

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## Résumé

Insect responses to chemical insecticides have been informative models of rapid adaptation to strong anthropogenic pressures and a great opportunity for studying molecular mechanisms underlying xenobiotic adaptation. The massive use of insecticides to limit arbovirus transmission led to the emergence and spread of resistance in *Aedes albopictus*. Until alternative vector control tools are widely implemented, understanding the diversity of resistance mechanisms and identifying their genetic basis is critical for developing durable pest control strategies and limit disease transmission.

In this frame, this study aimed at identifying genes involved in resistance to deltamethrin, the most widely-used insecticide against *Aedes* mosquitoes. Five regions were studied: southern Europe, the Indian Ocean, central Africa and South-East Asia.

To sample the genetic diversity of each studied region, one *Ae. albopictus* composite population per studied region was created by mixing several field populations. Composite populations from each region were then selected or not with the insecticide deltamethrin for several generations in order to purify resistance alleles.

Genomics and transcriptomics approaches were then combined to identify resistance alleles circulating in each region.

Distinct deltamethrin resistance mechanisms were identified in each region, including target site mutations, increased detoxification and cuticular alterations. The contrasted mechanisms observed across regions support the dynamic landscape of resistance in *Ae. albopictus* worldwide. From an applied perspective, such study paves the way for defining a set of molecular markers to track deltamethrin resistance in the field.

**Mots-Clés:** Insecticide resistance – Experimental evolution, *Ae. albopictus* – Genomics – Transcriptomics

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