



Insecticide resistant *Anopheles* from Ethiopia but not Burkina Faso show a microbiota composition shift upon insecticide exposure

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Malaria remains a major public health challenge in Africa. However, the widespread emergence of insecticide resistance in *Anopheles* mosquitoes threatens the effectiveness of these vector control interventions. This study investigated the relationship between microbiota composition and insecticide resistance in *Anopheles gambiae*, *Anopheles coluzzii*, and *Anopheles arabiensis* populations collected from Ethiopia and Burkina Faso. Using 16S rRNA sequencing, the microbiota profiles of mosquitoes surviving and dying after deltamethrin exposure were compared. In addition, RNA sequencing was conducted on Ethiopian *An. arabiensis* populations to characterize transcriptomic changes associated with resistance. The findings revealed that microbiota composition did not significantly differ between resistant and susceptible mosquito populations from Burkina Faso, including laboratory colonies originating from the same region. In contrast, Ethiopian *An. arabiensis* exhibited distinct microbiota profiles between mosquitoes surviving and dying following insecticide exposure. Specific bacterial genera, including *Pantoea* and members of the *Erwiniaceae*, were significantly associated with mosquito survival after deltamethrin exposure. Transcriptomic analysis further demonstrated overexpression of multiple detoxification genes, including cytochrome P450s, GSTs, ABC transporters, and genes linked to respiration and ion transport pathways. Comparative analyses with other African *An. arabiensis* populations identified several consistently overexpressed detoxification genes across regions. Overall, the study demonstrates that microbiota composition may contribute to insecticide resistance in certain mosquito populations, alongside well-established genetic resistance mechanisms. These findings highlight the complexity of insecticide resistance and suggest that both microbial and transcriptomic factors should be considered in the development of future malaria vector control strategies.

