

***Bactrocera dorsalis* in the Indian Ocean: a tale of two invasions**

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Background: *Bactrocera dorsalis* (Hendel) is among the most widespread tephritid species, including established populations on islands in the Indian Ocean. This region is of great phytosanitary concern as it connects Asia, Africa and Europe through economic, cultural and political ties. Although the invasion history may be estimated by dates of first recordings, a genomic approach has not been adopted yet. We aim to genetically analyse the islands' populations and reconstruct the invasion routes into and within the region. The obtained results may provide novel insights, useful for phytosanitary policymaking.

Methods: Genomic DNA sequence data were collected from 230 *B. dorsalis* specimens by PE Illumina Novaseq 6000 Whole-Genome Sequencing (12x coverage, read size 150bp). The resulting reads were mapped to a *B. dorsalis* reference genome followed by SNP calling and filtering. Invasion history was reconstructed by assessing genetic parameters such as genomic diversity and differentiation metrics. A population level maximum-likelihood tree reconstruction, principal component analysis, ancestry analysis, kinship networks, and runs of homozygosity (ROH) were performed to render a robust image of dispersal patterns within the study area.

Results: A western invasion pathway involved stepping-stone dispersal of *B. dorsalis* from the east African coast into the Comoros, Mayotte and Madagascar with a decreasing genetic diversity. The Mascarenes (R  union and Mauritius) on the other hand were colonized directly from Asia and form a distinct cluster. The low nucleotide diversity suggests that only a few genotypes invaded the Mascarenes. The presence of many long ROH in the introduced populations are indicative for population bottlenecks, with a more severe bottleneck effect for populations along the western migration pathway than on the Mascarenes.

Conclusion: The western and eastern *B. dorsalis* populations in the Indian Ocean are genetically very distinct and likely originate from different sources. Our data shows that direction of dispersal of an invasive species might be more complex than initially assumed when looking at proximity between populations alone. We show that a genomics approach can assist in assessing the status of upcoming pest species and might help policymakers in improving phytosanitary protocols.

Keywords: phylogeography, dispersal, gene flow, whole-genome sequencing, population genetics