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Conference Abstract

Molecular origin tracing of *Bactrocera dorsalis* supports pathway analysis and surveillance in Belgium

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Abstract

Bactrocera dorsalis is one of the most important pests of commercial fruit crops worldwide and is regulated as a priority quarantine pest in the European Union. Between 2023 and 2025, adult males were detected for the first time in Belgium during national surveillance in public markets and community gardens. Together with earlier interceptions of larvae in imported fruit, especially mangoes, these findings raised key questions about the origin of the specimens and whether the Belgian detections reflected a single introduction event or repeated incursions through different pathways.

Trapped adult males were identified morphologically, while intercepted larvae were identified using molecular assays supported by morphology. All specimens were then analysed using whole-genome sequencing. Geographic assignment was investigated by comparing nuclear genomic variation with broad reference datasets, while mitochondrial genomes were analysed in parallel to assess whether mitochondrial patterns were consistent with nuclear-based inference.

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Both nuclear SNP variation and mitochondrial phylogeny supported differentiation between African and Asian reference populations. Within this framework, most trapped adults were assigned to Asian populations, whereas nearly all intercepted larvae grouped with African reference material. Formal origin assignment was achieved using a reduced diagnostic nuclear SNP panel and a standardized discriminant analysis of principal components (DAPC) based on COI barcodes. These methods produced largely consistent results, while also highlighting occasional cases of mitonuclear discordance.

Our analyses indicate that the adult males detected in Belgium do not represent a single introduction, but multiple independent incursions. The contrast between the inferred origin of trapped adults and that of larvae intercepted in fruit suggests that distinct introduction pathways may be involved, including intra-European trade and unauthorized fruit imports. The reduced nuclear SNP panel and the COI-based assignment framework provide scalable tools for plant protection agencies and diagnostic laboratories, supporting faster origin tracing, pathway analysis, and more targeted phytosanitary surveillance and response.

Keywords

Bactrocera dorsalis; origin tracing; SNP panel; COI barcoding; pathway analysis; phytosanitary surveillance

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Conflicts of interest

The authors have declared that no competing interests exist.