ARPHA Conference Abstracts 9: e204106
doi: 10.3897/aca.9.e204106

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Conference Abstract

Improving surveillance of *Dacus frontalis* through DNA barcoding and ortholog-based phylogenomics

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Received: 15 Jun 2026 | Published: 15 Jun 2026

Citation: Kratz F, Esselens L, Vanderheyden A, Vanden Abeele S, Abir H, Delatte H, Addison P, Cugala D, Mwatawala M, Barech G, Khaldi M, Smitz N, De Meyer M, Bonte J, Dermauw W, Virgilio M (2026) Improving surveillance of *Dacus frontalis* through DNA barcoding and ortholog-based phylogenomics. ARPHA Conference Abstracts 9: e204106. https://doi.org/10.3897/aca.9.e204106

Abstract

Dacus frontalis is an economically important fruit fly widely distributed across Africa and already intercepted in the European Union, making reliable diagnostics essential for trade and phytosanitary surveillance. Recent coordinated sampling with African partner institutions revealed unusually high mitochondrial divergence in the cytochrome c oxidase subunit I (COI) barcode region, with approximately 4% divergence between North African and sub-Saharan populations. This level of intraspecific variation complicates routine identification and highlights the need for a geographically broader molecular reference framework, as well as complementary genomic tools able to resolve lineage structure and support future origin tracing.

To improve diagnostic robustness, we are expanding continental COI coverage by generating new Sanger barcodes and by recovering mitochondrial barcode sequences from short-read genomic datasets. In parallel, we are developing an ortholog-based

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genomic workflow that combines OMA standalone for ortholog detection with Read2Tree for phylogenomic reconstruction. This framework is intended to move beyond single-locus inference and provide genome-wide resolution of differentiation patterns within *D. frontalis*.

Current analyses based on COI consistently recover two well-differentiated mitochondrial lineages, broadly corresponding to northern and sub-Saharan sampling regions. Increasing barcode coverage is improving the representation of African populations and refining our interpretation of this divergence. The ortholog-based component is still under development, but it is expected to test whether the same structure is supported across the nuclear genome and to identify markers useful for future origin-tracing applications.

Building an integrated molecular framework combining expanded COI coverage with an emerging ortholog-based genomic approach will strengthen diagnostic capacity for *D. frontalis*. By enabling more robust identification and providing a foundation for future origin tracing, this work supports early detection, surveillance, and phytosanitary preparedness in Africa and in regions at risk of introduction, including the European Union, where *D. frontalis* has already been detected in France and a single intercepted specimen was recorded in Belgium.

Keywords

Molecular diagnostics; DNA barcoding; phylogenomics; origin tracing; phytosanitary surveillance; Dacus frontalis

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Presented at

Neobiota 2026, the 14th International Conference on Biological Invasions

Funding program

Contract RT26/06 DAFROSTOP

Conflicts of interest

The authors have declared that no competing interests exist.