Phylogeographic structure of the oriental fruit fly, *Bactrocera dorsalis*: from the mitochondrial COI gene to nuclear SNPs

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Over the last decades, the oriental fruit fly, *Bactrocera dorsalis* (Diptera, Tephritidae), native to tropical and subtropical Asia, has invaded the sub-Saharan Africa, the Indian Ocean and Oceania. In invaded regions, *B. dorsalis* has emerged as a major pest of fruit and vegetables causing extensive damage and losses, and affecting the crop trade, especially mango. *Bactrocera dorsalis* is a regulated pest in many countries and in the European Union, where it has been recently caught outside the port of entry areas, during official EU monitoring programs (e.g. Austria, France, Italy).

Although this information is important for assessing the risk of introduction of the species into a new area, to date, the origins of these invasion events are not well identified. Previous studies used traditional genetic markers, such as the mitochondrial COI gene or a dozen of microsatellites, which failed to detect genetic differentiation at spatial scales fine enough to inform on the invasion history of *B. dorsalis*.

OBJECTIVES

- 1. Development and validation of thousands of genome-wide SNP markers.
- 2. Inform on the global spatial structure of *B. dorsalis* and address the possibility of mitonuclear discordance.

MATERIAL & METHODS

• B. dorsalis identification following the IPPC protocol¹

mtCOI

- Sanger sequencing of the standard mitochondrial barcode (658bp)²
- TCS haplotype network using POPART³ on 301 individuals

SNPs

- Library preparation using BestRAD⁴ method and Illumina sequencing
- SNPs calling performed with in-house script using Stacks2⁵ among others
- Structuring analysis using PCA⁶ on 76 individuals



In the native range: many unique haplotypes and a central haplotype distributed throughout the whole range. In the invasive range: two major haplotypes distributed throughout the whole range and minor in the native range. Three genetic clusters : continental Asia, Southeast Asian islands, and Africa.

Indications on the potential sources of the invaded islands. Higher level of genetic diversity in the continental Asian cluster.

PCA analysis of 39 258 SNPs.

One color per country.

CONCLUSION & PERSPECTIVES

While mitochondrial data provide little information regarding geographic structure within native and invasive areas, genome-wide SNP data on individual samples provide a more refined description of genetic structuring. Further genome-wide SNP analyses are ongoing using ~80 population samples of ~30 specimens representing 32 countries, in order to better inform on the invasion history and on the geographical origin of the many European incursions (e.g. >70 in France for the period 2021-2022, ~180 in Italy in 2022).

REFERENCES

¹FAO 2019. ²Herbert et al. 2003. ³Tamura et al. 2021. ⁴Ali et al. 2016. ⁵Rochette et al. 2019. ⁶Jombart et al. 2011. COI_Cytochrome c Oxidase I. SNP_Single Nucleotide Polymorphism. TCS_Templeton, Crandall and Sing method (1992). PCA_Principal Component Analysis.



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