

## Genetic structure and invasion history of the oriental fruit fly, *Bactrocera dorsalis*: from mitochondrial barcodes to SNP markers

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### CONTEXT



Over the last decades, *Bactrocera dorsalis* (Diptera, Tephritidae), native to tropical and subtropical Asia, has emerged as a major pest of fruit and vegetable crops in sub-Saharan Africa and the Indian Ocean. *Bactrocera dorsalis* is a regulated pest in many countries and in the European Union, where it is frequently intercepted at points of entry.

Recently, it has also been caught outside the port of entry areas, under official EU monitoring schemes (e.g. Austria, France, Italy).

*B. dorsalis* (i) belongs to a complex of 88 species whose morphology is hard, if not impossible, to distinguish and (ii) is known to hybridize with two of them (*B. carambolae* and *B. kandiensis*).

### OBJECTIVE

Development of genome-wide SNP markers for *B. dorsalis* and first evaluation of the worldwide phylogeographic structure as well as of the mito-nuclear discordance.

### MATERIAL & METHODS

- Morphological identification of individuals

#### mtCOI

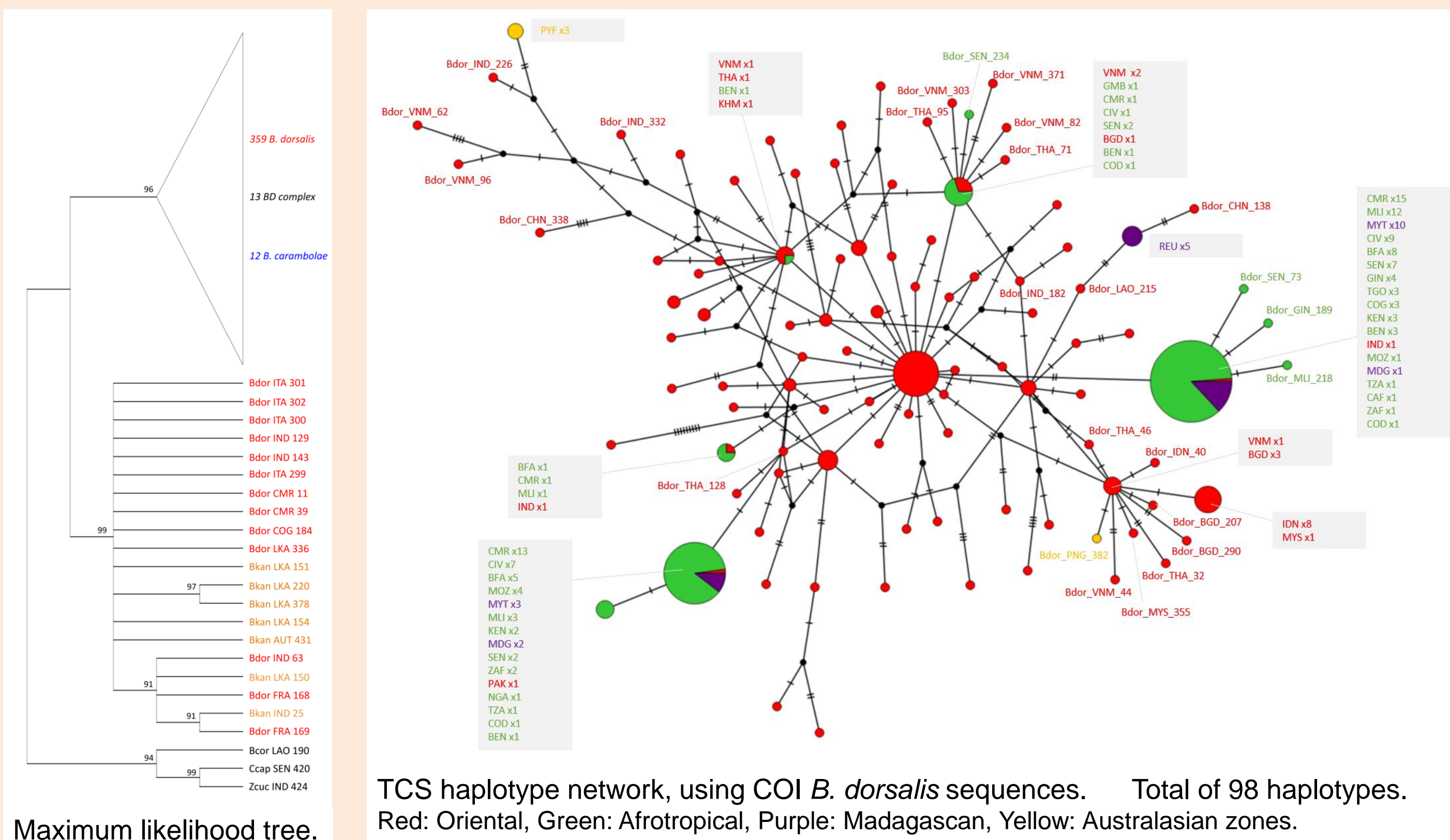
- 372 worldwide individuals identified as either *B. dorsalis*, *B. carambolae* or *B. kandiensis*, or poorly identified (BD complex)
- Sanger sequencing of the standard mitochondrial barcode (658bp)<sup>1</sup>
- Maximum Likelihood tree using MEGA<sup>2</sup>
- TCS haplotype network using POPART<sup>3</sup>

#### SNPs

- 82 worldwide *B. dorsalis* individuals
- Library preparation using BestRAD<sup>4</sup> method and Illumina sequencing
- SNPs calling performed with in-house script using Stacks2<sup>5</sup> among others
- Clustering analysis using DAPC<sup>6</sup>

### RESULTS

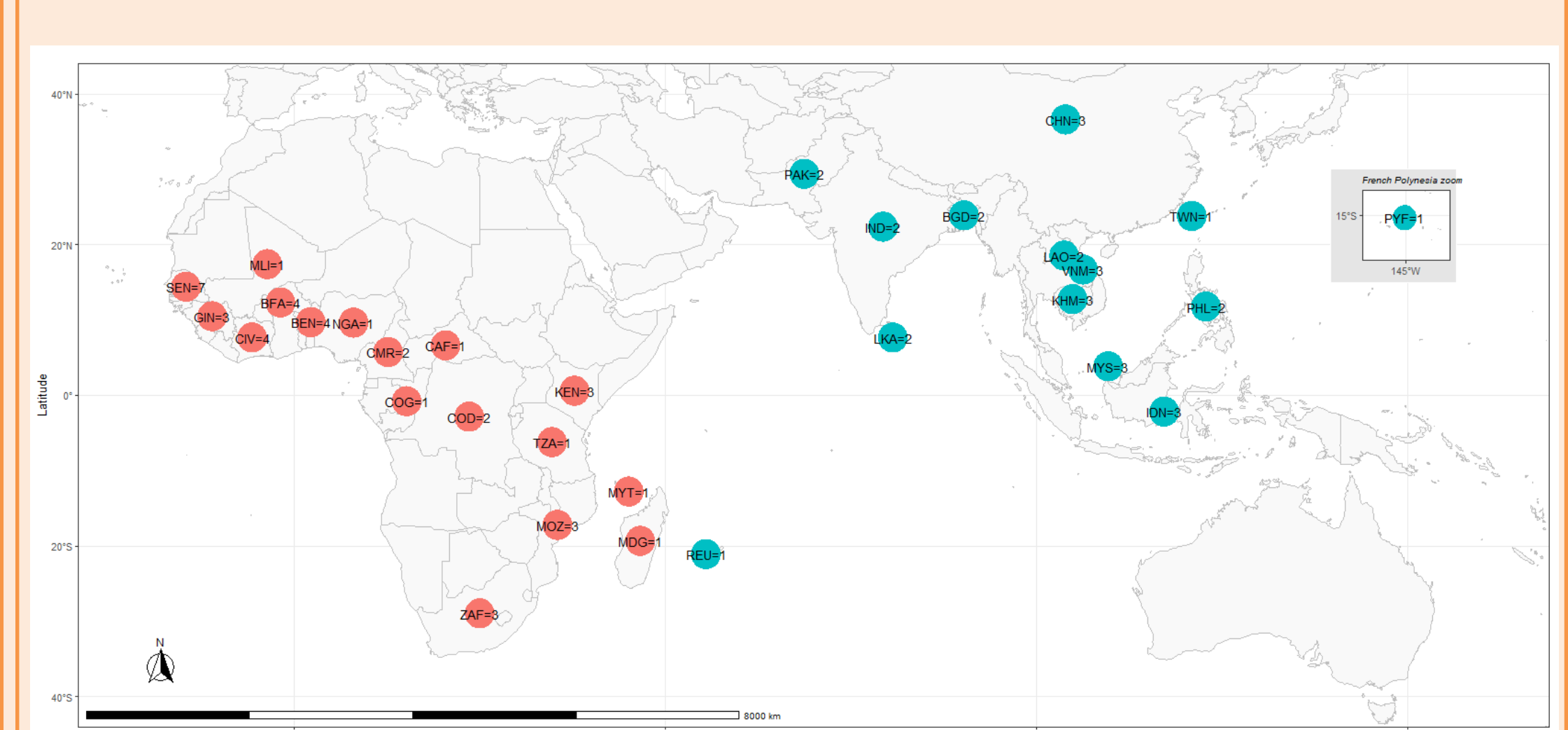
#### mtCOI



Mitochondrial DNA introgression from *B. kandiensis* to *B. dorsalis* observed in 13 specimens, either native, invasive or from EU incursions.

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.

#### SNPs



Two genetic clusters, corresponding to the native and invaded areas of *B. dorsalis* ( $F_{st} = 0.116$ ).

Higher level of genetic diversity in the native cluster (87% of polymorphic sites vs. 53%;  $H_e$  of 0,154 vs. 0,141).

Two invasive exceptions in the native cluster: samples from Réunion island and French Polynesia.

### CONCLUSION & PERSPECTIVES

Both mitochondrial and genome-wide SNP data on individual samples provide little information regarding the geographical structure within the native and invasive areas. 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).

<sup>1</sup> Herbert et al. 2003. <sup>2</sup> Tamura et al. 2021. <sup>3</sup> Leigh & Bryant D, 2015. <sup>4</sup> Ali et al. 2016. <sup>5</sup> Rochette et al. 2019. <sup>6</sup> Jombart et al. 2010.

COI\_Cytochrome c Oxidase I. SNP\_Single Nucleotide Polymorphism. TCS\_Templeton, Crandall and Sing method (1992). DAPC\_Discriminant analysis of principal components

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