Spatial genetic structure analyses of an invasive termite in France

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Introduction

Among social insects, termites are characterized as major pests which cause substantial economic damage to human-built structures. This is the case of ***Reticulitermes flavipes***, a subterranean species invasive in France and originated from Louisiana, probably introduced during the 18th century. This study aims at determining the extent to which this termite has spread within urban areas from one French region (Région Centre) by analyzing the spatial distribution of genetic variability at regional and local scales.

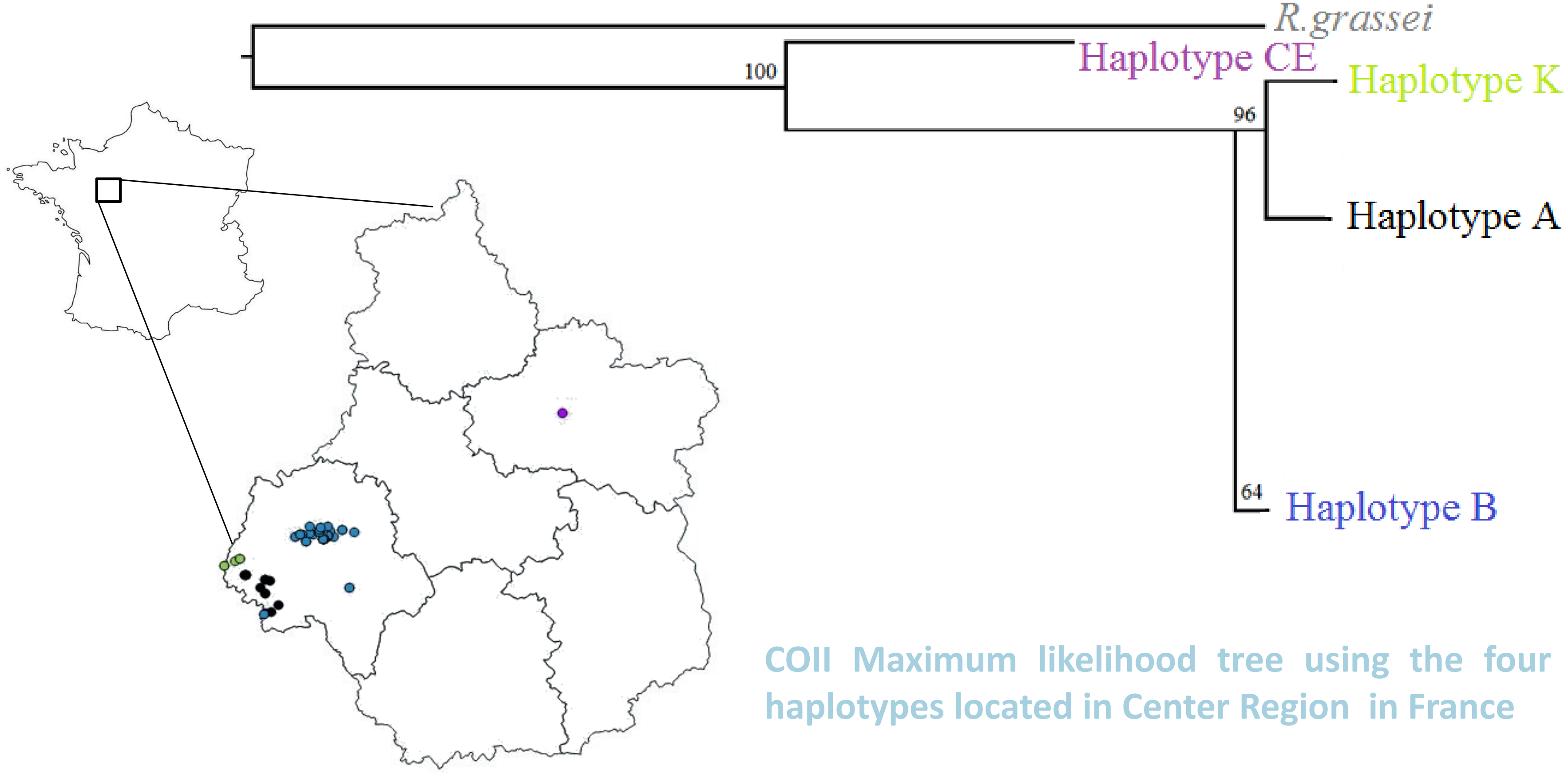
Regional scale

Methods → The genetic variability was determined using mitochondrial (COI and COII) and nuclear markers (12 loci microsatellites) on **92 samples localized in Région Centre**.

→ Phylogeographic analyses (TCS, Seaview), Bayesian clustering analyses and Principal Component Analyses (using or not spatial informations) allowed to define population genetic structure.

1) Phylogeographic analyses using mitochondrial data:

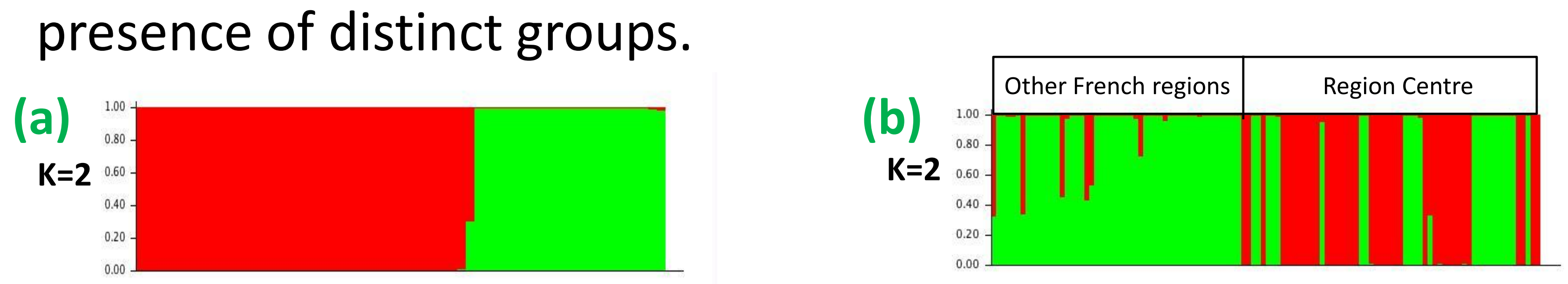
- 4 clades corresponding to 4 haplotypes suggest **4 distinct infestations.**



COII Maximum likelihood tree using the four haplotypes located in Center Region in France

2) Populations genetic analyses using microsatellite and mitochondrial markers:

- Bayesian clustering and multivariate analyses revealed the presence of distinct groups.



Assignment of individuals at each genetic cluster in Region Centre only (a) and with other French regions with STRUCTURE

- Geographic coordinates (PCAs) did not give supplementary informations on populations genetic structure.

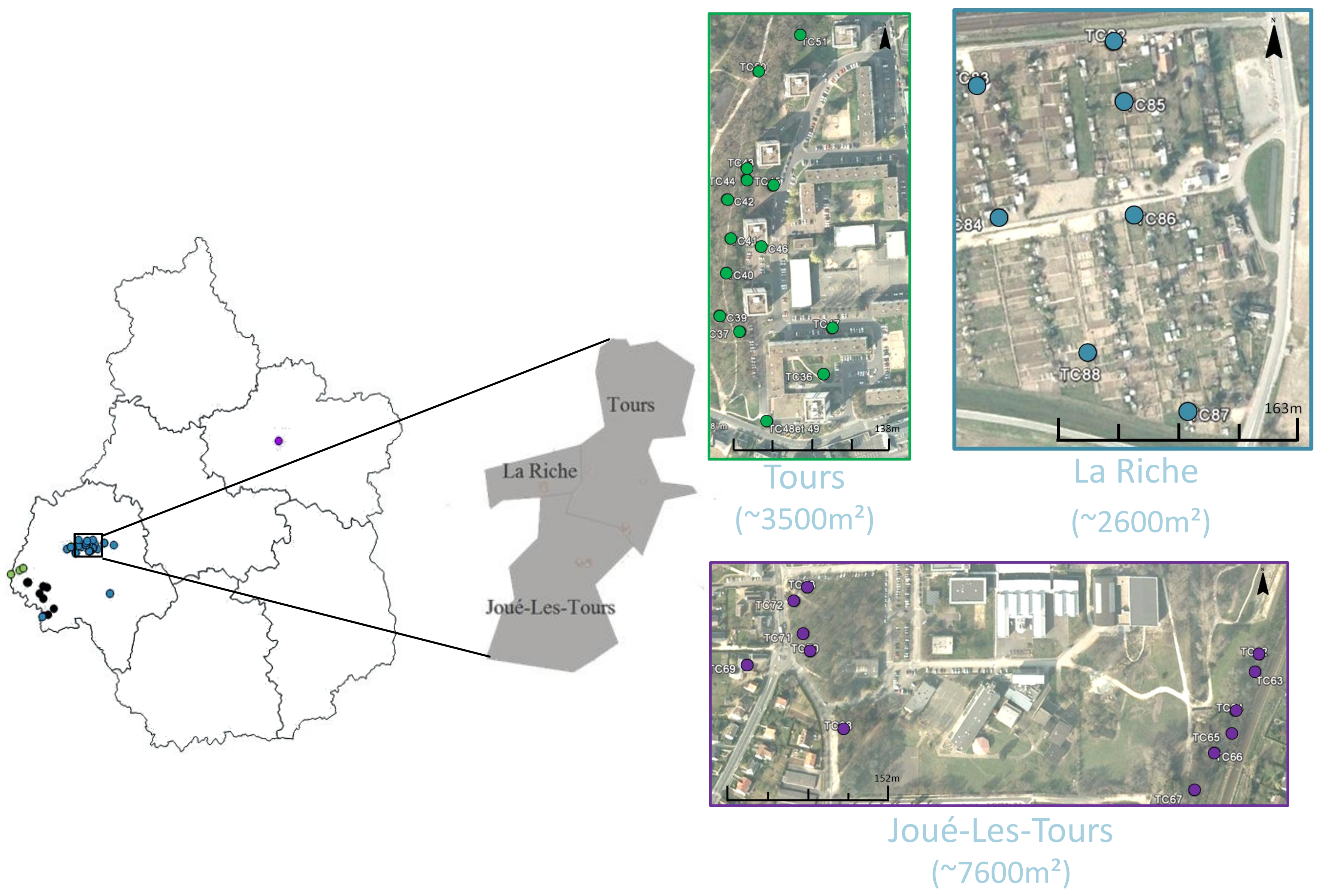
Local scale

Methods → **390 *R. flavipes* individuals** from 15, 11 and 7 collection points respectively from **three urban sites** (Tours, Joué-les-Tours, La Riche, in Center of France) were genotyped at 6 microsatellite loci.

→ Population genetic analyses (Genepop and *F*-stat) were used to determine colonies, their breeding system and their genetic diversity.

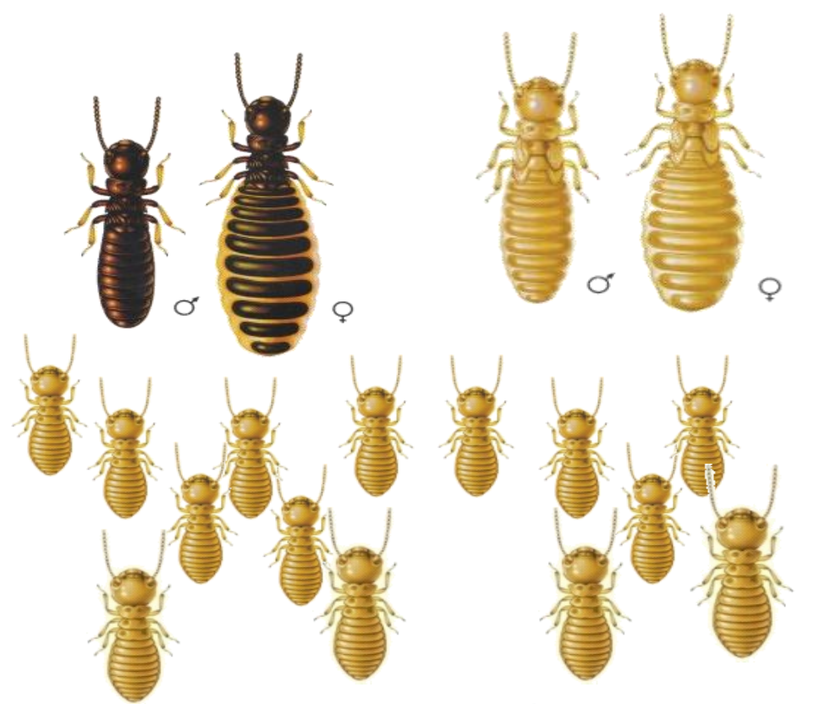
1) Delineation of colonies:

- For each urban site, individuals from all collection points belonged to a same, **large colony** (G-tests are significant between collect points, $p < 0.001$)



2) Social organization :

- The **3 colonies** were headed by both primary reproductives (kings and queens) and secondary reproductives (neotenics) to form **extended-family** colonies.



Extended family

Conclusion

- At regional scale, mtDNA analyses showed 4 main infestations centers in this region, originating from different zones of France and USA, showing another importation of *R. flavipes* different from Louisiana.

- At local scale, the analyses of population genetics show 3 colonies spatially extended which contained secondary reproductives. These 3 colonies were closed genetically suggesting a single introduction at the origin of the infested studied sites.

→ All results would allow to improve the termite management strategies of this invasive termite, particularly in Région Centre.

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