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I am PhD student at INRA, URZF. My research interest focus on macro and micro evolution of phytophagous beetles in relation with their environment.

My previous projects at Natural History Museum (UK) aimed at reconstructing the deep phylogeny of weevils based on mitogenome sequences, and to relate diversification of lineages to host plants and larval lifestyle.

*I am now working at a different evolutionary scale. My PhD deals with dispersal of the beetle *Monochamus galloprovincialis*, the vector of the pine wood nematode in Europe. I try to identify the landscape features affecting dispersal behavior of this species to uncover potentials pathways to the spread of the nematode. *M. galloprovincialis* being a native species, we also explore the micro evolutionary processes involved in its intra-specific diversification.*

Landscape Genetics of *Monochamus galloprovincialis*, vector of the pine wood nematode in Europe.

Julien HARAN, Alain ROQUES, Christelle ROBINET & Géraldine ROUX-MORABITO

The pine wood nematode (PWN), *Bursaphelenchus xylophilus* (Steiner & Burher) Nickle (Nematoda, Aphelenchoididae) is the causal agent of the pine wilt disease (PWD), a virulent syndrome killing susceptible pines trees within few months. From its native area in North America, it has been introduced in several Asian and European countries causing considerable damages to native pine forests. The PWN was detected for the first time in Europe in Portugal 15 years ago. From its introduction site, it rapidly expanded its range to a large part of the country and entered into Spain. In Europe, the native longhorn beetle *Monochamus galloprovincialis* (Olivier, Coleoptera, Cerambycidae) is the only known vector for this nematode. This beetle performs its larval development in the wood of declining pine trees and spread the PWN when it emerges from infected wood. Thus, the natural dispersion of the PWN is highly depending on dispersal abilities of the beetle. Given the rapid range expansion of this pest and the threat to forests involved, it is crucial to identify potential barriers to dispersal of *M. galloprovincialis* to define suitable pest management strategies.

Based on 1043 individuals from Iberian Peninsula, genotyped at 13 microsatellites loci, we conducted a landscape genetics analysis to uncover the landscape features affecting dispersal of *M. galloprovincialis*. To avoid confounding effect of evolutionary history of this species in the area of study, we used a nested sampling design and assessed population genetic structure in order to select the appropriate populations and the optimal scale for correlation analysis.

Our results show that mountain ranges represent a break to dispersal of *M. galloprovincialis*, and subsequently potential barriers to the spread of the PWN. We also show that the experimental design (scale and populations selected) strongly influence the results of landscape genetics approach.