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Assessing potential expansion of the Pine Wood Nematode (*Bursaphelenchus xylophilus*) from the spatial genetic structure of the vector (*Monochamus galloprovincialis*)

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Monochamus galloprovincialis (Coleoptera, Cerambycidae) is the main factor involved in the natural spread of the Pine Wood Nematode (PWN), a serious pest for pine forests. Since its introduction in Portugal, the PWN has rapidly expanded its range to a large part of the country and will probably keep expanding to the rest of Europe. Estimation of dispersal abilities of *M. galloprovincialis* over various landscapes and across mountains is a key point to predict the invasion of the PWN in Europe, and will help to set up management for this pest.

Microsatellites are highly variable genetic markers. Their polymorphism provides information on genetic structure of organisms at a broad scale (phylogeography), but also at local scale (migration of individuals). We developed a set of 12 microsatellites loci specific to *M. galloprovincialis*. First assessments conducted on six populations along a European North-South transect reveal a reduction of the genetic diversity northward, with a maximum of allelic richness in Spain. This seems consistent with post glacial recolonization of Mediterranean species associated with Pines trees. We have also observed a significant differentiation between some Iberian populations.

Our perspectives are to use the microsatellites markers (i) to construct the European phylogeography of *M. galloprovincialis*, (ii) to estimate the effect of the Pyrenees and the landscape structure on dispersal abilities of this species, and finally, (iii) to look at the effect of PWN invasion on its genetic structure in Portugal.