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Use of molecular markers to identify cryptic species or complexes of sibling species in invasive or potentially invasive conifer pest insects

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Introduction: Molecular genetic approaches are powerful tools for studying evolutionary aspects of biological invasions, especially for the identification of cryptic species or divergent lineages which can hinder a clear biological characterization of invasive species. Phytophagous insects show several examples of complexes of sibling species as well as successful invasion histories. We will present two case studies of phytophagous invaders. The first case will consider species which have been extensively transported globally for decades along with the seed trade (*Megastigmus* spp. seed chalcids), and the second pine pitch weevil of unknown origin, *Hylobitelus xiaoi*, which is presently in outbreak and is expanding in southern China. We will present data showing tests of the efficiency of molecular techniques for assessing whether the insect species correspond to cryptic native species or invasive species.

Material and methods: We use a phylogeographic approach by sequencing mitochondrial DNA genes (COI and/or COII). Individuals from different localities and from different host species were sampled in both the invaded and the presumed native range of the species.

Results and discussion: The study revealed misidentifications in *Megastigmus* species which have been previously recorded either as invasive or native species. It validated the use of molecular tools to detect cryptic species in this genus. These results also highlighted the importance of studying genetics in native populations to confirm or invalidate species identification only based on morphological traits. It should allow both a clear identification of native lineages and the tracking of the source population for expansion in *Hylobitelus*.