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► To cite this version:

Solen Boivin, E. Lhuillier, Marie-Anne Auger-Rozenberg, Alain Chalon, Marie-Louise Cariou, et al.. A comparative approach in understanding biological invasions: What can be learnt from the analysis of DNA microsatellites in invasive *Megastigmus* seed chalcids?. 3. International Conference on Biological Invasions NEOBIOTA- From Ecology to Control, Sep 2004, Bern, Switzerland. 1 p. hal-02828230

HAL Id: hal-02828230

<https://hal.inrae.fr/hal-02828230>

Submitted on 7 Jun 2020

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A comparative approach in understanding biological invasions: What can be learnt from the analysis of DNA microsatellites in invasive *Megastigmus* seed chalcids?

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The large plantation of exotic conifers in Western Europe is likely to favour invasions of specific, exotic pest insects. There are numerous examples of insects introduction by humans in these new types of environments. Among them, exotic seed chalcids introduced along with host seeds constitute interesting models to understand these underlying biological processes. In this aim, three types of information are essential : the frequency of introduction of the insect species in the new environment, the size of the introduced populations and the subsequent pattern of expansion. However, tracking the history of such events is particularly difficult, and the assessment of the relative frequency of introductions or of the extent of long-distance dispersal remained for a long time an elusive goal of research on invasive species. Today, the routine use of highly variable molecular markers may provide an opportunity of assessing more easily these parameters.

Most invasive tree seed chalcids belong to the genus *Megastigmus* (Hymenoptera: Torymidae). We compared two insect-host systems differing by the duration passed since the first introduction. (i) The Douglas-fir seed chalcid *M. Spermotrophus* was probably introduced in the late 1800s along with seeds of its original host *Pseudotsuga menziesii* from Western North America to Europe and New-Zealand. The insect has virtually no competitors nor parasites in the introduction range. (ii) The Cedar seed chalcid *Megastigmus schimitscheki* was introduced around 1990-94 from Turkey to southern France. Originally a pest of Cedar-of-Lebanon and Cyprus cedar in the native range of Asia Minor and Cyprus, it shifted to seeds of Atlas cedar, *C. atlantica* at Mont Ventoux where two competitors in the genus *Megastigmus* were already present.

We used ten microsatellite loci in *M. spermotrophus* for the analysis of 7 native populations (USA and Canada) and 10 introduced populations (9 from Europe and one from New-Zealand). Five loci were used in *M. schimitscheki* to compare 9 native populations from Turkey and 1 from Cyprus with 7 invasive populations from France. The markers allowed to recounting the introduction events corresponding to these two systems. The invasion by *M. schimitscheki* proved to consist of only one insect introduction followed by a rapid expansion, this process resulting in a bottleneck and a loss of genetic variability in derived populations. The invasion by *M. spermotrophus* corresponded to the other extreme position with several introductions, a great number of founders insects and a weak expansion.