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Reconstructing colonization routes of invasive species from molecular data: case studies in forest entomology

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The authors belong to a research consortium dealing with insect evolutionary biology and natural genetic structure at different scales. They were involved in various projects studying rangewide phylogeography of several species of forest pests (mainly seed chalcids, scolytids, processionary moths) in Europe and the Mediterranean Basin, and started to collaborate on host-parasitoid systems. In the recent years, they focused on the question of biological invasions, either involving geographic expansions of native species due to climate and landscape changes, or accidental introductions from different regions.

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Deciphering the colonization processes by which introduced pests invade new areas is essential to limit the risk of further expansion and/or multiple introductions by increasing vigilance against the identified key source populations. It also helps defining the ecological characteristics of introduced populations and predicting the potential extent of their distribution areas. In some cases, it can help choosing strains of potential auxiliary agents to develop biological control strategies. Yet, historical and observational data often provide incomplete, sparse or even misleading information on invasive populations' history.

In the last decade, population genetics has been used as an indirect tool to reconstruct routes of introduction, highlighting the complexity and the sometimes counterintuitive nature of the true story. The recent development of new model-based methods, such as approximate Bayesian computation (ABC), has allowed quantitative inferences in case of the complex evolutionary scenarios typically encountered during biological invasions. It specifically allows to compare alternative scenarios regarding the number and genetic composition of sources and to explore the number of successive introduction events from each source, the number of introduced individuals and the dynamics of demographic expansion after each introduction.

We describe the principles of the ABC analyses, here applied to microsatellite data and mitochondrial sequences of populations sampled within the native and the invasive range of a species. We will use three main examples in forest entomology, from which we obtained valuable information about the colonization routes and dispersal patterns, namely the cedar seed chalcid *Megastigmus schimitscheki*, the maritime pine bast scale *Matsucoccus feytaudi* and the Western conifer seed bug *Leptoglossus occidentalis*.