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Exploring the invasion history of an exotic pest based on genetic markers: the case of the Asian long-horned beetle (Anoplophora glabripennis).

Marion Javal, Alain Roques, Géraldine Roux

INRA, UR0633 Zoologie forestière, Orléans, France

Insects are one of the most numerous groups of alien organisms introduced in Europe and as a result of globalization, the number of human-mediated introductions keeps growing. Among all the continents, Asia is so far considered as the region from which most of the newly-arrived alien species originate.

The Asian long-horned beetle (ALB) Anoplophora glabripennis is one of the insect species which benefited from international freight from Asia to Europe. It has been first detected in North America in 1996, then in Europe in 2003. This highly polyphagous species is able to infest a wide range of deciduous trees, especially in urban areas where its management results in significant economic costs.

In a context of recent European outbreaks (France 2013, Switzerland and Finland 2015), and in order to anticipate and to manage further ALB introductions, it is particularly important to uncover population's invasion routes as well as their pathways of dispersal in the invaded areas.

This work aims at evaluating the genetic structure of invasive populations in order to assess if the European outbreaks resulted from multiple independent introduction events or from the dispersal of a primary introduced population. We used sequences of mitochondrial COI gene as a preliminary approach. Our dataset covered most of the Europeans outbreaks, some populations in North America and some in the native Asian range.

So far, the analysis of 36 populations from China and Korea revealed 23 haplotypes, with a very blurred geographic structure, probably resulting of an historic arrangement faded by potentially more recent population translocations, as hypothesized in previous studies. Only ten haplotypes were yet observed in Europe, three of them being shared with Asia and North America, five being private haplotypes and two being shared with Asia only. The genetic structure observed in Europe suggests a complex invasion scenario which likely includes several introduction events as well as dispersal within the invaded areas.

Keywords: invasive species, genetic structure, Asian Longhorned Beetle, Anoplophora, mitochondrial markers, insect