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► To cite this version:

Marion Javal, Alain Roques, Géraldine Roux. Thirteen years after the first record of the Asian Longhorned Beetle in Europe: a preliminary analysis of the invasion history.. *Sfécologie-2016*; International Conference of Ecological Sciences, Oct 2016, Marseille, France. 2016. hal-01603665

HAL Id: hal-01603665

<https://hal.science/hal-01603665v1>

Submitted on 3 Jun 2020

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Thirteen years after the first record of the Asian Longhorned Beetle in Europe : a preliminary analysis of the invasion history.

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Abstract

The Asian Longhorned Beetle (ALB) *Anoplophora glabripennis* is one of the insect species which benefited from the growing international trade from Asia. 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) it is crucial to understand this insect's invasion routes as well as its pathways of dispersal in the invaded areas. Such information is a prerequisite to anticipate and to contain ALB introductions.

In order to evaluate the genetic diversity in invasive populations compared to native ones we used sequences of mitochondrial *COI* gene as a preliminary approach. The objective was to determine if the European outbreaks resulted from multiple independent introductions or from the dispersal of a primary introduced population.

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. Among the ten haplotypes found in Europe, three of them are found in Asia and North America, two are shared with Asia only, and five have not been found elsewhere so far. 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 glabripennis*, mitochondrial markers, insect, ALB

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