

# Molecular methods to identify insects associated with sentinel trees

Short Term Scientific Mission (STSM), COST Action FP1401

Applicant: Marion Javal, INRA Orléans, France. [mjaval@orleans.inra.fr](mailto:mjaval@orleans.inra.fr)

Host: Dr Simone Prospero, WSL, Switzerland. [simone.prospiero@wsl.ch](mailto:simone.prospiero@wsl.ch)

Period: June-July 2016

## Summary

Sentinel trees are a new efficient method to identify insect species that may become invasive out of their native range. A number of xylophagous species is caught on such sentinel trees, including *Anoplophora glabripennis* (Coleoptera, Cerambycidae), the Asian Longhorned Beetle (ALB). ALB is invasive in Europe and outbreaks have been detected in several European countries including four in Switzerland, where the last outbreak has been detected in Berikon close to the city of Zurich in 2015. The objective of this Short Term Scientific Mission was to develop molecular tools to assign specimens found in the Swiss outbreaks to a source population, and above all to understand what the links between the different outbreaks are.

We genotyped 249 ALB specimens (eggs, larvae, pupae, adults) from the four known Swiss outbreak sites using 15 microsatellite loci and performed several distance and clustering analyses on the dataset. Results revealed that two of the four outbreaks (Berikon and Winterthur) were completely distinct from each other and from the other Swiss outbreaks. In addition, these outbreaks were genetically more homogeneous compared to the two other ones. This, and field observations, suggest that the outbreak in Marly is due to multiple and repeated introductions of beetles via wood packaging material. Moreover, it is highly probable that ALB invaded Brünisried thanks to human-mediated spread from Marly.

Genetic data still have to be linked to descriptors of the outbreak sites (e.g. host tree species, location of the tree, year of detection) in order to investigate more precisely which parameters may explain the current genetic structure of the outbreaks. However, our preliminary analyses revealed a complex invasion scenario in Switzerland, with probably distinct introduction events and also some human-mediated spread within the country.