

## Population genetic structure of the invasive sycamore lace bug (*Corythucaciliata* Say, 1873)

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The sycamore lace bug (*Corythucaciliata* Say, 1873) has a North-American origin. The species have been introduced to Europe (Italy: 1964), Asia (China, Korea, Japan: 2001), Australia and South-America (Chile), followed by a rapid expansion. In the invaded areas the sycamore lace bug was found exclusively on *Platanus* species, however in its native distribution area it feeds on other plant species as well. Sycamore is a widely used ornamental tree species in the northern hemisphere. Insects sucking on the leaves cause aesthetical damage on the trees.

Our aim is to assess the genetic structure of the bug both in its native range (North-America) and in some of the introduced areas (Europe and Japan).

In order to answer this question we have collected *C. ciliata* populations from Europe, Japan and North-America (altogether 20 populations: N-America: 3, Europe: 14, Asia: 3). We have analyzed a 1200bp long fragment of the mitochondrial DNA (COI gene). At the moment we have sequence data for 20 individuals from 8 populations (Europe: 5, N-America: 1, Asia: 2). The sequences shows very high diversity, the 20 individuals represent 6 haplotypes with approx. 1% sequence divergence. Haplotypes found in Europe are present in some Asian populations, but none of the North-American is present in other continent.

Due to the high sequence divergence and haplotype diversity we are not able to describe any subdivision in the population structure now. To find an adequate answer to our original question we have to increase the number of the investigated populations (especially native ones) and apply other molecular genetic methods too.

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