

## Global diversity and migration routes of Lecanosticta acicola

Lecanosticta acicola is an important needle pathogen for pine species causing brown spot needle blight, a disease that results in premature needle shedding and leads to growth reduction and potentially tree death. The pathogen originates from North America but it has been documented in Europe since the 20<sup>th</sup> century. Despite *L.* 

acicola being listed as a quarantine pathogen in Europe, the spread of the fungus has increased during recent decades, with new reports from many countries of Europe.

The BROWNSPOTRISK project aimed to broaden the knowledge about dispersal ability, genetic diversity, population structure and migration history of the pathogen. The characterization of aggressive strains that may represent an increased threat to pine species and the assessment of the potential of sexual recombination of *L. acicola* that could lead to a rise in diversity will enable more effective risk management of the pathogen.

During the project, a population study was conducted on isolates from America, Europe and Asia. Samples were analysed using microsatellite and mating type markers. *Lecanosticta acicola* has two mating types (*MAT1-1-1* and *MAT1-2*) that need to be present for the sexual reproduction of the fungus. From many of the newly described populations, only one mating type was found. The high proportion of clones and the ratio of mating types indicate that the pathogen mostly reproduces asexually and spreads via conidia in Europe, though sexual recombination could take place in some populations.

Results of the population study clearly highlight the human impact on the spread of the pathogen. In several instances, similar haplotypes were found in botanical gardens, arboreta and ornamental trees in city greeneries in different countries.





For the first time, the same haplotype was found to be present on two continents, in North America (Canada) and Europe (Germany). Older populations in Europe were characterized by a fragmented structure and several shared haplotypes between populations, which indicates a mixed population history with several introduction events not only from North America but also between European countries. This means that without proper quarantine measures there is a high risk of increasing the pathogen's genetic diversity by anthropogenic activities, when strains with different genetic origins and different mating types are mixed.

Project ID: *Lecanosticta* - Brown spot disease of pines - spread in European forest ecosystems: impact on pines, predisposing and contributing factors, control (BROWNSPOTRISK)