





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](#))