

## GENOTYPIC DIVERSITY AND REPRODUCTIVE BIOLOGY OF *THEKOPSORA AREOLATA*, THE CAUSAL AGENT OF CHERRY SPRUCE RUST IN NORWAY SPRUCE SEED ORCHARDS

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Swedish forestry is sustained by planting about 200 million Norway spruce (*Picea abies*) seedlings every year. Most of these seedlings come from seed orchards, which have been established to transfer the genetic gain in growth and yield achieved through plant breeding since the 1940s. However, today there is a deficit of seeds coming from Swedish seed orchards mainly caused by irregular flowering, but also due to pest and pathogen infections such as *Thekopsora areolata*—the causal agent of cherry spruce rust, a fungus that significantly reduces seed production in Fennoscandia. Here, we aim to investigate the reproduction mode and population structure of the pathogen using a newly developed microsatellite marker and a hierarchical sampling strategy. Sampling was done at different locations: one in Norway, one in Finland and five in Sweden. For each location, one aecium per infected cone was analyzed. In addition, multiple aecia per scale and cone were sampled at two locations in Sweden. The results show an overall high genetic diversity in *T. areolata* at all hierarchical levels with no genetic structure, an indication of high gene flow and random mating. However, at the cone/scale level non-random mating was observed. These results suggest that *T. areolata* has long distance spore dispersal in Fennoscandia with common recombination events and vegetative spread in cones and scales.

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