

Which is the origin of the Estonian and Finnish *Dothistroma septosporum* populations?

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Dothistroma needle blight, also called red band needle blight, is one of the most important foliar diseases of *Pinus* spp. worldwide. This pathogen has been well known for causing severe outbreaks in pine plantations of the southern hemisphere but during two previous decades it has caused increasing damage on pines also in Europe and North America. Two pathogenic species have been recognized as causal agents of *Dothistroma* needle blight, *Dothistroma septosporum* (Dorog.) Morelet (teleomorph: *Mycosphaerella pini* Rostr.), and *Dothistroma pini* Hulbary (teleomorph unknown). They can infect 89 different hosts, 82 of which are *Pinus* species (Watt *et al.*, 2009). *D. septosporum* has a larger distribution area than *D. pini*, but both species are known to cause similar symptoms on needles. According to molecular studies, only *D. septosporum* has so far been detected in Czech Republic, Estonia and Finland, where the first records were made in 2000, 2006 and 2008, respectively. Appearance of *D. septosporum* in Estonia was detected from south to north during 2007-2008 (Drenkhan & Hanso, 2009). Today the fungus is present even in northern Finland.

We investigated 105 isolates of *D. septosporum* from Finland, Estonia and Czech Republic by determining their allele frequencies at 8 microsatellite loci (developed by Barnes *et al.* 2008). They originated from five different subpopulations: three from Estonia (incl. one population from a single tree), one from South-Central Finland and one from Czech Republic. Finnish and Estonian isolates were obtained from symptomatic needles of *P. sylvestris* but those from Czech Republic originated from seven various *Pinus* spp. and *Pseudotsuga menziesii*. All isolates originated from different tree individuals despite 19 isolates which were taken from one tree in Estonia.

All subpopulations showed to be highly diverse and a total of 92 different haplotypes were detected. The highest mean number of alleles was found from the Finnish population and lowest from the Estonian single tree population. Estonian, Finnish and Czech *D. septosporum* populations had similar high genetic diversities (0.693, 0.687, and 0.615, respectively). Calculation of Nei's genetic distance between the subpopulations showed that Finnish and Estonian populations were genetically closer to each other than to the Czech population. Differentiation between the subpopulations of *D. septosporum* in Estonia, Finland and Czech Republic was low but statistically significant. High genetic diversity of all investigated subpopulations

suggests occurrence of sexual proliferation. Moreover, high diversity also suggests recent introduction as a massive inoculum or a long time presence of *D. septosporum* in these areas.

References

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