

Highly clonal structure and abundance of one haplotype characterize the *Diplodia sapinea* populations in Europe and western Asia

Kalev Adamson¹, Marili Laas², Kathrin Blumenstein², Johanna Busskamp², Gitta Langer², Darta Klavina², Anu Kaur², Tiit Maaten², Martin Mullett², Michael Müller², Emilia Ondruskova², Allar Padari², Enn Pilt², Taavi Riit², Halvor Solheim², Liina Soonvald², Leho Tedersoo³, Eeva Terhonen², and Rein Drenkhan⁴

¹Eesti Maaulikool

²Affiliation not available

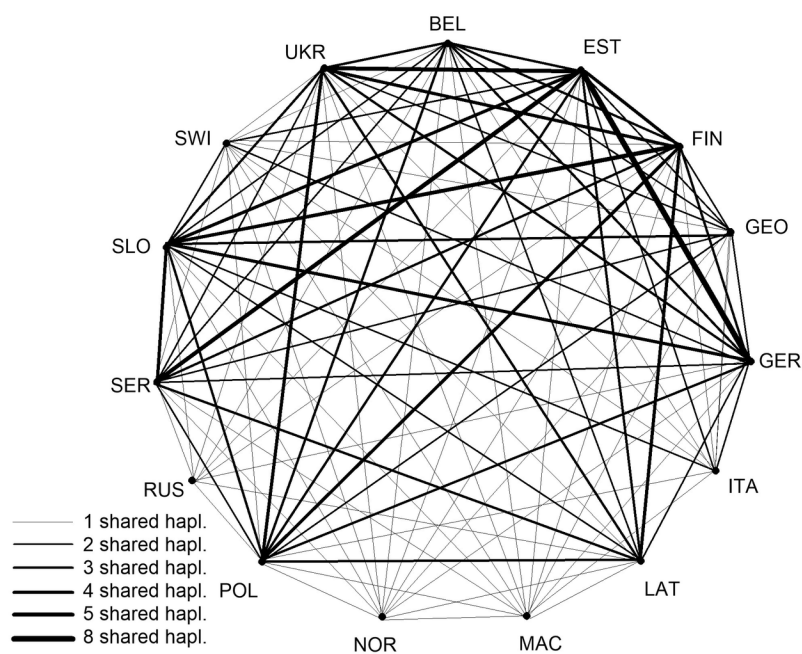
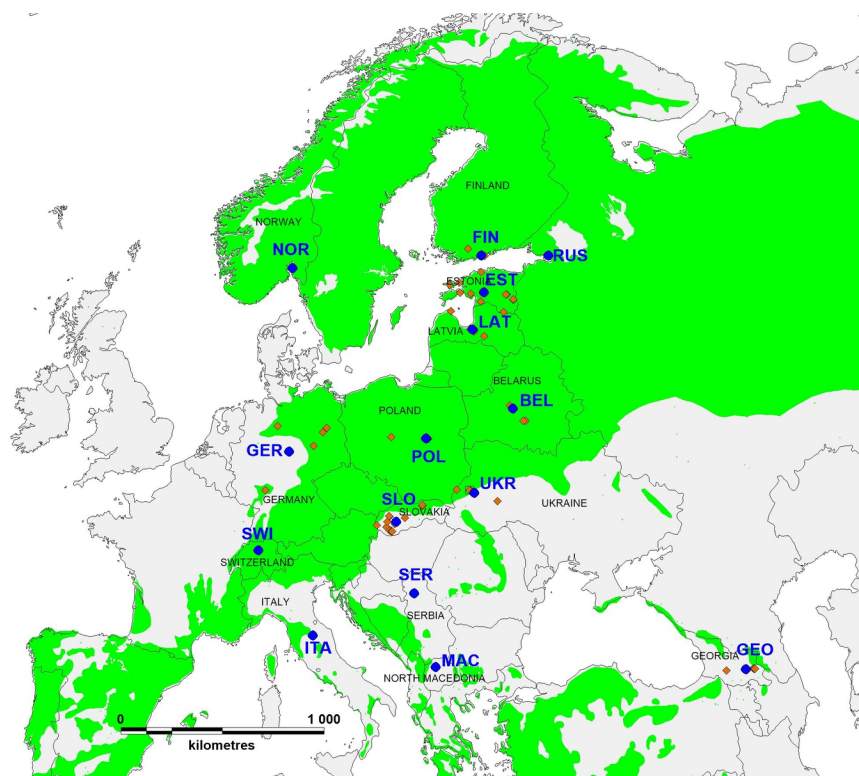
³University of Tartu

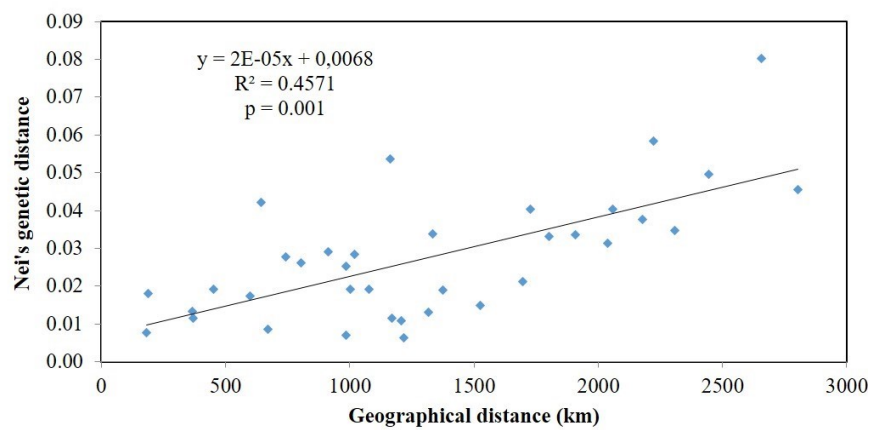
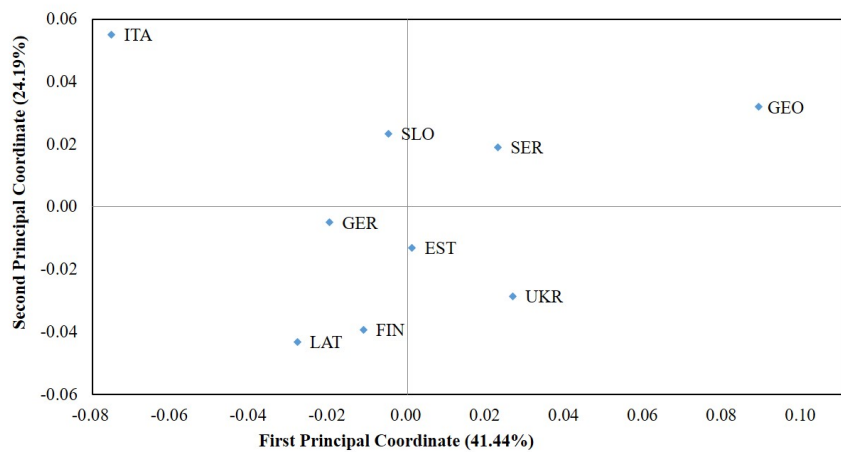
⁴Estonian University of Life Sciences

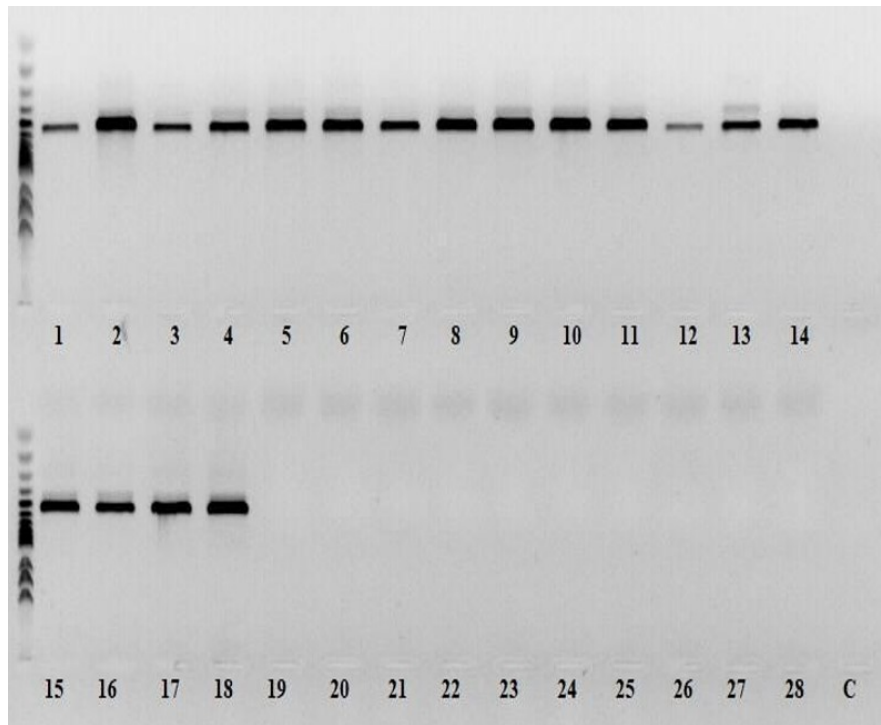
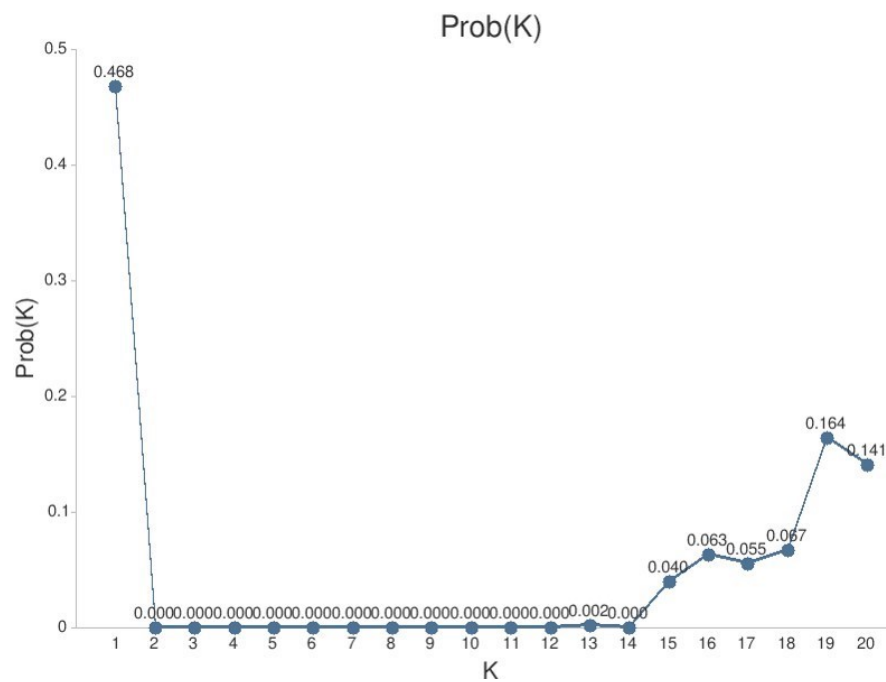
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Abstract

Diplodia sapinea is a cosmopolitan endophyte and opportunistic pathogen occurring on several conifer species in Europe for at least 200 years. In Europe, disease outbreaks have increased on several *Pinus* spp. in the last few decades. In this study, the genetic structure of the European *D. sapinea* population was investigated using thirteen microsatellite markers. In total, 425 isolates from 15 countries were analysed. A high clonal fraction and low genetic distance between most populations was found. One single haplotype dominates the European population, being represented by 44% of all isolates and found in nearly all investigated countries. Three genetically distinct subpopulations were found: Central/North European, Italian and Georgian. The recently detected populations of *D. sapinea* in northern Europe (Latvia, Estonia and Finland) share several haplotypes with the German population, suggesting introduction from Central Europe. The northern European populations show similar genetic diversity to those in Central Europe suggesting either that the fungus has existed in the North in an asymptomatic mode for a long time or that it has spread recently by multiple introductions. Although this fungus reproduces predominantly asexually, considerable genetic diversity was found even among isolates of a single tree. According to currently published allelic patterns, *D. sapinea* most likely originates from North America. In order to enable the detection of endophytic or latent infections of planting stock by *D. sapinea*, new species-specific PCR primers were designed. During the search for *Diplodia* isolates, we identified *D. africana* in California, USA, which is the first record of this species in North America.







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