

GENETIC VARIATION IN THE FINNISH *QUERCUS ROBUR* POPULATIONS

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Populations of pedunculate oak, *Quercus robur*, are in Finland on the northern margin of the species' distribution in Europe. Populations north and east of Turku - Salo - Tammisaari -line are fairly isolated. The pattern is quite different from that in Central Europe, where the species' distribution is rather continuous and pollen flow between stands efficient. The effect of the fragmented distribution of the species' genetic structure has been studied using both neutral and quantitative characteristics.

Neutral genetic variability within and among oak populations was analysed using isozymes according to the standard procedures. Dormant winter buds were collected from 39 natural stands. In small populations all mature trees were sampled, otherwise 50 trees. Saplings were analysed in a smaller subset of 8 populations. Microsatellite variation was analysed within one population using primers published by other groups.

Field trials for the analysis of quantitative traits have been established using seeds sampled from 22 oak populations, 12-25 families/stand. Acorns were sown as 5 separate tests in the greenhouse using common con-

trols (single-tree plots, 16 replicates). Seedlings were measured for growth characteristics in 1998 and transplanted in the field in the spring of 1999.

Isozyme data indicates that the Finnish oak populations are more differentiated and less variable than the populations in Central Europe as expected due to the fragmented population structure. Estimates of population differentiation and expected heterozygosity for oak in Finland are between the extremes of silver birch (common, widespread) and white elm (uncommon, fragmented).

The genetic variability among populations for the initial growth characteristics is quite high and systematic spatial differences suggest the possibility of local selection. Among-families component of variance is very high in most populations, possibly as a consequence of non-random mating and spatial grouping of related trees. The mating structure within 2 stands will be analysed using microsatellites, which seem to be a very powerful tool due to the high variability even in small populations.