**Pollination patterns in Scots pine seed orchards**

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In Sweden most of the plants of Scots pine (*Pinus sylvestris*) originate from seed orchards. The percentage today is at least 85 % and this figure will increase. The full rotation genetic gains in production from the 2nd round of Swedish Scots pine seed orchards, established during the 1980s, are expected to be 10-15%, and plants from those now under establishment are expected to be around 25% . This percentage is however reduced by pollen contamination with pollen from outside the orchard. The contamination is difficult to avoid: Scots pine is a wide-spread species in Sweden, and even in areas where Norway spruce (*Picea abies*), the other major conifer in Sweden, dominate, non-bred natural Scots pines grow scattered among the spruces or in pure pine stands. The flight distance of pine pollen can also be quite long. As the seed orchards give more gain, the gain loss by pollen contamination becomes larger, and as the pine stands become genetically more disparate, the contaminating pollen cloud becomes more unpredictable. Although the contamination promotes the genetic diversity of the seed harvest, a general aim is thus to reduce it.

The first studies of pollen contamination in Scots pine seed orchards during the 1980s, used isozymes with limited precision. Today’s molecular marker techniques have higher precision and gives thus better estimates of the contamination, and can also be used for analyzing the pollination pattern within the seed orchard.

A study of the most advanced Scots pine seed orchard in production in Sweden, Västerhus, was performed the seed maturation year 2007 (Torimaru et al. 2009). All 28 clones in the seed orchard were genotyped based on nine microsatellite (SSR) loci. The nine SSR loci produced almost unique multilocus genotypes for each of the 28 clones, and paternal assignment of the studied seed was made with very high paternity exclusion probability. It was estimated that around 50% of the seeds produced in the seed orchard this year was seeds that had been contaminated with paternal genes from outside the orchard. Selfing frequency was very low. This contamination figure is compatible with similar old studies.

A clone-wise analyzes of the pollen contamination showed that the contamination varied considerably among clones. Furthermore, some clones contributed genetically around twice as much to the seed harvest, as compared to the number of grafts of the clone in the orchard, while other contributed genetically with only ca 1/10th of what their number of grafts indicated.

Further development of molecular markers will make it possible to evaluate the functions of seed orchards. Possible aspects are: *i)* appropriate maturity of the seed orchard for seed harvest, *ii)* the annual variation of the genetic quality of the seed harvest, *iii)* the genetic diversity of the seed harvest, *iv)* base information for genetic thinning of the seed orchard. In a longer perspective, molecular markers could possibly be used for e.g. evaluation of long-distance pollen transfer and identification of individual trees for forward selection in operational plantations from a certain seed orchard.