Change of clonal frequency in the second root sucker generation of hybrid aspen

Authors

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Abstract

Two hybrid aspen (*Populus tremula* L.× *P. tremuloides* Michx.) trials in southern Sweden were used for studies of clonal composition in the second of two root sucker regenerations. Trial 1 was established in 1998 and originally included eight clones randomly distributed in four plots, each having 10×10 positions. Trial 2 was planted in 1957, with 150 seedlings from each of 25 full sib families randomly planted. Genotyping, using six SSR markers, was performed on wood samples collected from the second root sucker generation in each trial.

Results from trial 1 clearly indicated a reduction in the genotypic diversity of the second sucker generation. All eight clones were still present, but at significantly different frequencies, with some close to zero. In trial 2, a total of 210 clones were found, genetically matched to 21 families, implying a rather marginal reduction in genetic variation. The clonal structure was mostly aggregated, but at the same time intermixing of ramets from different clones was quite common. The root suckers had, on average, spread 15m from the stumps of the previous sucker generation of the same clone and the maximum distance was 49 m.

The results indicate a change in clone frequencies over generations in root sucker stands of hybrid aspen. Hybrid aspen reforestation with seedlings originating from several unrelated families will retain genetic variation better in future sucker generations compared to clonal reforestations in which few clones are used. It is appropriate to use a higher number of clones than the normal five to eight used in Sweden today, in order to prevent future clone-specific damage as a result of reduction of clone diversity after several root sucker generations.

Keywords

Genetic variation, SSR-markers, Sweden