Breeding value prediction when trials are diverse in age and genetic structure

G.W.Dutkowski[1], K.A. Högberg[2], L.G. Stener[2] and B. Karlsson[2]

Breeding programs often have trials with genetic material of different pedigree type, parents with different selection histories, and sometimes clonal replication. Integrated analysis to select superior genotypes within such diverse genetic material is possible if the additive relationship matrix is used to link genotypes by their pedigree, selection history is taken into account, different ages of measurement are accounted for, and repeated measures for cloned genotypes are used. A seed orchard established in southern Sweden with phenotypic plus tree selections of Norway Spruce (*Picea abies* L. (Karst)) from stands of western European origin was used for ten test experiments. Initial tests used seedlings from open-pollinated (OP) families from the orchard and random control-pollinated (CP) crosses between the parents. Based on early age growth and form measurements new crosses were made between elite parents and the resulting offspring cloned. Early growth data from the clonal trials was combined with the early data and later growth measurements from the seedling trials. The data were adjusted using spatial analysis and standardised by an estimate of the additive standard deviation for each trait on each site, but the combined model allowed for different heritabilities on each site. Predictions of harvest age traits were based on an age:age correlation model for growth based on the Lambeth equation and a slight adverse correlation between growth and straightness. Of the best 100 genotypes on the index, two thirds came from the cloned genotypes, reflecting their selected parentage and higher breeding value accuracy, despite the lack of form and later age growth data. Only one selection came from the open-pollinated material, and the rest came from the control-pollinated, uncloned material. The accuracy of the breeding values was highest for the parents, closely followed by the cloned CP offspring. The uncloned CP genotypes were less accurate, but still well ahead of the uncloned OP offspring.

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[1] PlantPlan Genetics, c/- School of Plant Science, University of Tasmania, Locked Bag 55, Hobart 7001, Australia
 Greg.Dutkowski@plantplan.com
[2] Skogforsk (The Forestry Research Institute of Sweden), Ekebo 2250   S-268 90 Svalöv, Sweden