

BREEDING WITHOUT BREEDING: CONFIRMATION OF THEORETICAL CONCEPT USING REAL-WORLD TREE IMPROVEMENT PROGRAM

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In traditional tree improvement programs, simple recurrent selection scheme has been adopted to capturing additive genetic variance through repeated cycles of controlled crosses, selection and testing. Traditionally, selection within breeding programs was based solely on phenotypic evaluation. Marker-based approaches have been proposed to speed up the delivery of genetic gain in forest tree breeding. While genomic selection is the robust and more promising alternative to MAS, it is associated with effective high-throughput genotyping technologies generating sufficiently high genome coverage. Since these strategies require whole genome scans, they are too expensive in operational forestry breeding programs under most circumstances. The Breeding without Breeding approach seems to be an appropriate alternative as it only requires a small set of neutral polymorphic marker loci (e.g., 10-20).

We demonstrate the practical utility of Breeding without Breeding strategy, which offers great opportunities for its wide application in many breeding or conservation programs worldwide. We demonstrate the application in breeding program of Scots pine in the Czech Republic. Two existing first-generation seed orchards and their corresponding half-sib progenies were used to demonstrate the concept. App. 10% superior offspring were genotyped. We tested two approaches of genetic analysis: (1) pedigree reconstruction (i.e. transformation of half-sib into full-sib progeny) when parental population is genotyped, and (2) selection based on relationship matrix when parental genotypes are unknown.

BwB allowed bypassing the most resource-demanding breeding activity, i.e. controlled pollination. Moreover, the estimated reduced contamination rate among superior offspring under prescribed effective population size confirmed our theoretical expectations.

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