# Applicability of genomic selection on breeding of Turkish red pine

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**Abstract:** Populating the genome with dense marker coverage and predicting phenotypes from multi-locus genotypes for selection is called genomic selection (GS) or genome wide selection. GS jointly analyzes all markers in a population, attempting to explain the total genetic variance with dense genome-wide marker coverage through summing marker effects to predict breeding values of individuals. GS is the new frontier and a paradigm shift for plant and animal breeding programs. With advancement in DNA sequencing technologies and efficiency in genotyping, GS first has become a reality in animal breeding. Afterwards, it has been implemented for crop breeding. Genomic selection processes start from a training population or reference population. Candidates to establish a next cycle of breeding are selected through GS. Many GS programs routinely use single nucleotide polymorphisms (SNPs) markers to predict the genetic merit of offsprings. SNPs are primarily utilized association genetics and nucleotide differences occurring at specific locations in genome. With application GS, potential to increase genetic gain was estimated to be twofold and savings in logistical costs were estimated to be 92% in cattle breeding. Compared to crop and animal breeding programs, forest tree breeding is still as its infancy. The most advanced programs are in their third or fourth cycle of breeding. Forest trees in general, and conifers in particular take many years to breed (5-15 years) and progeny test (3-15 years). Because of large physical size of trees, it is difficult and expensive to cross trees. With application GS in forest trees, the breeding cycle time can drop almost in half, because selection decision could be made based on markers without phenotype as soon as seeds are available. This can increase genetic gain twofold per year. The tree breeding was started in 1960s in Turkey. A comprehensive Turkish red pine breeding program including progeny test and gene conservation was put into practice in 1994. Since then, totally, 90 ha progeny test was established with about 1850 plus tree/clone between 1998-2014 for each breeding zone. The progeny tests were open pollinated, the trees in the progeny tests were measured once in every four years. Genetic parameters from progeny tests (like heritability, genetic correlation and genotype environment interaction) were obtained. Genetic gains were satisfactory to carry out the Turkish red pine breeding. But, there is no study intending GS. In the light of last advancements, applicability of GS on the breeding of Turkish red pine is discussed in this paper.

**Keywords**: *Pinus brutia*, Marker assisted selection, Single nucleotide polymorphism, Tree breeding