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Genomic Selection In *Eucalyptus*: Marker Assisted Selection Coming To Reality In Forest Trees

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Genomic selection (GS) involves selection decisions based on genomic breeding values estimated as the sum of the effects of genome-wide markers capturing most QTLs for the target trait(s). GS is revolutionizing breeding practice for complex trait in domestic animals. The same approach and concepts can be readily applied to forest tree breeding. Trees also have long generation times and late expressing traits. However the application of GS in forest trees has additional advantages: (1) large even-aged “discovery” populations can be quickly assembled and individuals accurately phenotyped at the clone mean level; (2) effective population sizes (N_e) can be tailored to specific breeding programs; (3) large full-sib families can be generated where abundant within-family variation can be exploited. From the breeding standpoint, GS and Association Genetics (AG) have common goals and use common tools. However differently from AG that aims at dissecting complex traits in their discrete components, GS precludes the discovery of individual marker-trait associations. Results from the first population in our proof-of-concept project are extremely encouraging. Deregressed breeding values for height and DBH and genotypes at 3,129 high quality DArT markers were collected for 1,000 randomly sampled *Eucalyptus* trees from 58 full sib-families involving 11 parents. Discovery and validation were carried out with 800 and 200 individuals respectively. Average realized selection accuracies of 67% for height and 69% for DBH were obtained. In this scenario, selection efficiency gain evaluated as the ratio of GS and phenotypic selection exceeds 350% by reducing breeding generation time from 8 to 2 years.