

1.4 Breeding by genomic selection: capturing the missing heritability of complex traits in forest trees

**DARIO GRATTAPAGLIA^{1,2}, MARCOS D. V. RESENDE^{3,4} MÁRCIO F. R. RESENDE JR.³,
CAROLINA P. SANSALONI^{1,5}, CESAR D. PETROLI^{1,5}, ALEXANDRE A. MISSIAGGIA⁶,
ELISABETE K. TAKAHASHI⁷, KARINA C. ZAMPROGNO⁸, ANDRZEJ KILIAN⁹**

⁴EMBRAPA Forestry Research, Colombo, PR, 83411-000, Brazil

⁶FIBRIA, Rod. Aracruz/Barra do Riacho, km 25, Aracruz, ES, 29197-900, Brazil

⁷CENIBRA Celulose Nipo Brasileira S.A, Belo Oriente, MG, 35196-000, Brazil

⁸VERACEL Celulose S.A., Eunápolis, BA, 45820-970, Brazil

Genomic selection (GS) involves selection decisions based on GEBV (Genome Estimated Breeding Values) estimated as the sum of the effects of genome-wide markers capturing most variation for the target trait(s). GS captures the "missing heritability" of complex traits in forest trees beyond the few effect variants that association genetics typically identifies. GS accuracies should match phenotypic BLUP-based-accuracies even with low-density marker panels (2-3 markers/centiMorgan) in populations with effective sizes $N_e \leq 60$. Genotypes at ~3,500 DArT markers and de-regressed phenotypes for Height (H), Diameter at Breast Height (DBH) and wood density (WD) were obtained in two Eucalyptus breeding populations (CEN and FIB) with contrasting effective sizes ($N_e=11$; $N_e=55$). Realized GEBV accuracies for H and DBH were 0.67 and 0.69 for CEN and 0.62 and 0.54 for FIB; 0.53 for WD in FIB. Not surprising GEBV accuracies were low (~0.18) across populations implying variable genotype-phenotype associations across backgrounds so that population-specific GS models will be necessary. GS-based reduction in breeding time by 50% should provide gains $\geq 100\%$ in selection efficiencies. With advances in genotyping-by-sequencing methods together with increasing numbers of independent GS studies in forest trees, the perspectives are that GS might soon cause a paradigm shift in forest tree breeding practice.