

were retained for analysis as they met quality and minor allele frequency criteria. Association studies were carried out using a mixed linear model approach on single and multiple SNPs. Results of SNP-by-SNP analyses showed that between 325 and 600 SNPs were significantly associated ($P \leq 0.05$) with single traits related to earlywood, latewood or total wood before correction for false-discovery rate. The variation explained by most significant SNPs for each trait varied between 1.1 and 3.3%. Multilocus Bayesian mixed models analyses were also tested and the results indicated that about 20 to 25% of the phenotypic variation could be explained using 40 to 60 SNPs per trait.

Prediction of genetic effects was also tested with models that included 1) pedigree information, 2) genomic information, and 3) both pedigree and genomic information. The predictive value of the models was estimated by cross-validation with within-family samples. Estimates of accuracy (correlation between individual genetic values and their estimates) were weak to moderate, in agreement with expectations for this population in low linkage disequilibrium. Nevertheless, their amplitude suggests that economically useful gains could be obtained if selection delays are reduced.

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THE RE-DISCOVERY OF THE DOMINANCE VARIATION BY USING THE OBSERVED RELATIONSHIP MATRIX AND ITS IMPLICATIONS IN BREEDING

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Dominance effects have been neglected in animal and plant breeding, mainly because the variance estimates are usually small and non-significant compared to the additive effect. Consequently, many breeding programs rely only on breeding values to make progress. It is well known that the partition of the genetic variance into additive, dominance and epistasis is not perfect and estimations are confounded with each other. The Objective of this study is to test the use of a relationship matrix derived from molecular markers (O) to separate the genetic variance components. For the complex trait tree height we compare different BLUP models under additive and full (additive plus non-additive) assumptions with the use of either the pedigree relationship matrix (A) or the O matrix in a clonal breeding population of *Pinus taeda*. Our results show that the additive-BLUP model with the O matrix (add-O) increased the accuracy and heritability by 10% compared to additive-BLUP with the A matrix (add-A). A full-BLUP model with A matrix (full-A) could not partition the variance components, leading to the conclusion that almost all the genetic variation is additive (80%). However, a full-BLUP with O matrix (full-O) partitioned the genetic components, changing the conclusions about the proportion of additive (40%) and dominance (41%) components. With ten-time cross validation on all models, add-A (0.64), add-O (0.67) and full-A (0.65) have similar BV-predictive ability, but the full-O model (0.84) showed a predictive ability 26% greater than add-O. The increase in prediction capacity is not only due to the use of the O matrix but also to the correction for non-additive effects. We show that the use of the O matrix in a BLUP context (GBLUP) efficiently partitions the genetic variance components, changing from the purely additive conclusions to a scenario where dominance and additive effects are equally important.

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MULTIPLE RISK FACTORS FOR HUMAN CARDIOVASCULAR DISEASE AND OBESITY ARE HERITABLE IN A SINGLE, EXTENDED PEDIGREE OF RHESUS MACAQUES

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Large, managed populations of rhesus macaques are a powerful resource for dissecting the genetic