CONSTRUCTION OF REALIZED GENOMIC RELATIONSHIP MATRIX FOR BLUP OF BREEDING VALUES

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Genetic merit can be considered the finite sum of thousands of allelic effects, each physically located at some place on the genome, whose transmission can be traced through molecular markers. Traditionally, the BLUP of breeding values relies on average additive genetic covariances (the numerator relationship matrix **A**) derived from pedigrees to utilize information from relatives. For example, all the full-sib offspring of a cross are assumed to share 50% of genes inherited from parents. Such assumptions ignore Mendelian segregation of progeny within family. With vast advancements in marker genotyping technology and reduction in genotyping cost, it is now feasible to construct genetic covariances from markers. Dense markers are being used to trace identity by descent (IBD) at each locus and these IBD probabilities are being used to construct incidence matrices. Total genomic merit of candidates would be obtained by summing up many relevant marker effects.

Linear mixed models that utilize realized genomic relationships matrices could predict breeding values more accurately than those that use expected average genetic covariances derived from pedigrees. An approach that can be explored is the solving of mixed model equations by using the inverse of the genomic relationship matrix (**G**), in place of the **A** matrix. This may allow better estimation of individual allele effects, followed by summation across loci to obtain genomic estimated breeding values in a marker-only model.

The generation of the **G** matrix based on a set of biallelic SNP markers genotyped for a clonal population of loblolly pine and its application into calculation of accurate genomic estimated breeding values is discussed. The correlation between the genomic estimated breeding values and breeding values based on a pedigree-based model is used to determine the potential gain using markers in a forest tree breeding scenario.