

Realized Genomic Relationship and Genomic Selection in Loblolly Pine

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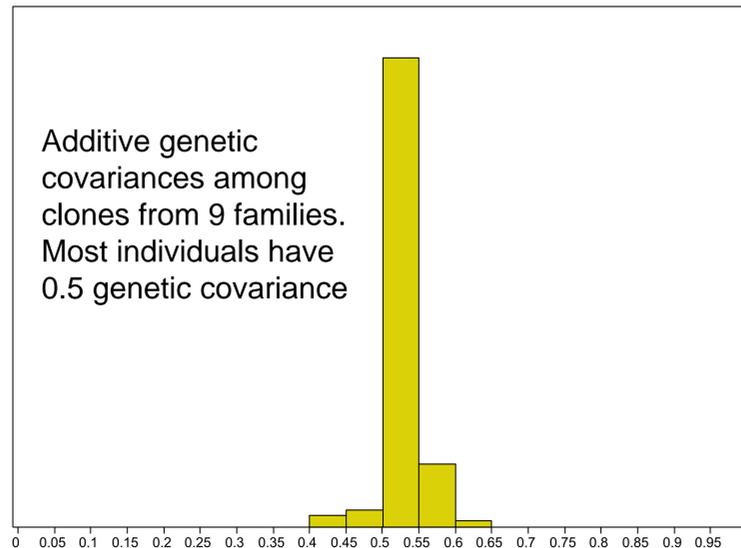
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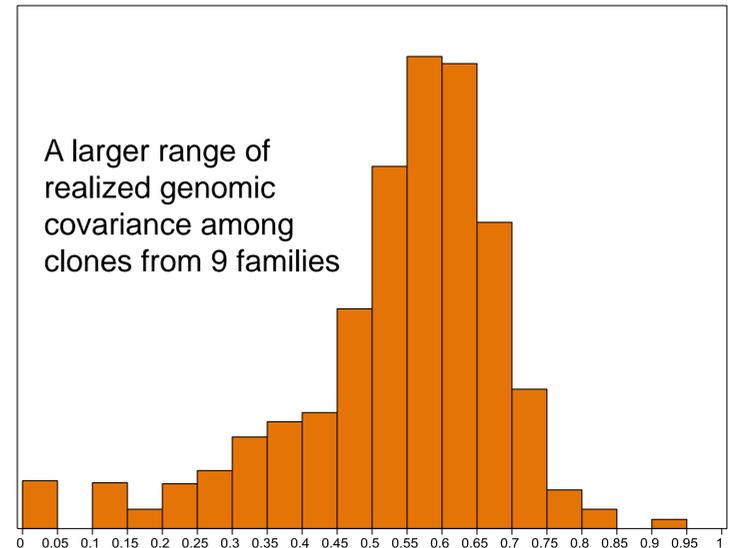
Hypothesis

- Using realized genomic relationships based on molecular markers could predict breeding values more accurately than using expected average genetic covariances derived from pedigrees (e.g., all pairs of full-sib offspring of a cross are assumed to share 50% of alleles in common)

Additive genetic covariances among clones from 9 families. Most individuals have 0.5 genetic covariance



A larger range of realized genomic covariance among clones from 9 families



Methods

- Population: 165 clones derived from 9 families were used. Breeding values (EBV1) were estimated using classical ABLUP with stem volume measurements made at age 5 years

- We used 3461 biallelic SNP markers to genotype all 165 clones

- To run GBLUP, realized genomic relationship matrix (**G**) was obtained using allele frequencies as follows:

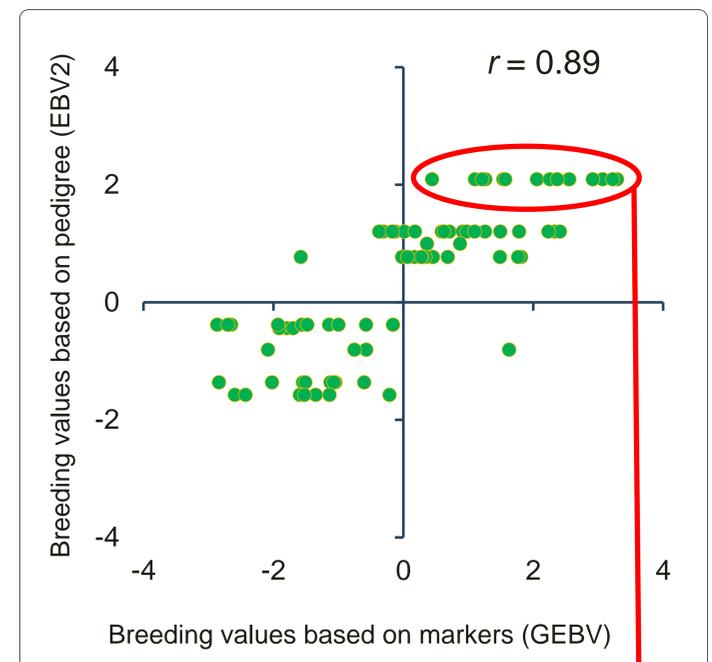
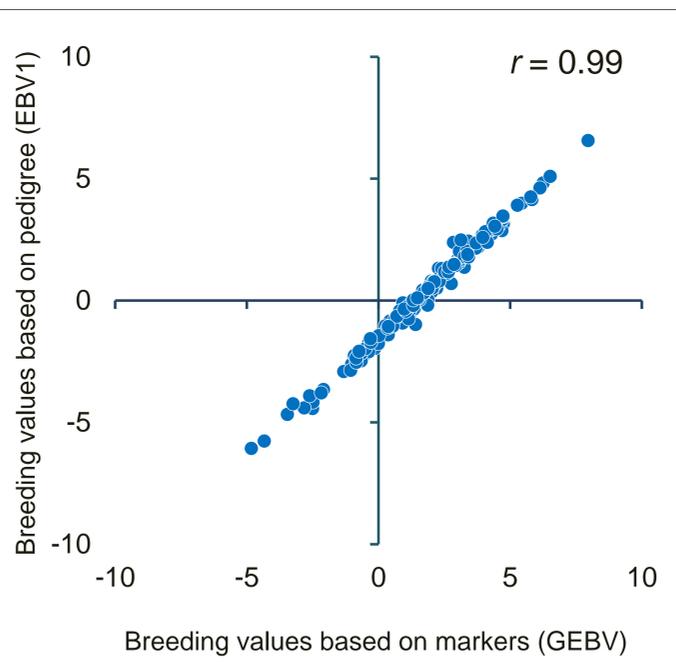
$\mathbf{G} = \mathbf{ZZ}' / [2 \sum_i p_i (1-p_i)]$, where **Z** is incidence matrix, p_i at locus i are observed minor allele frequencies of all genotyped subjects regardless of inbreeding and selection. This makes **G** analogous to **A** (average additive relationship matrix)

- Cross-validation methods:

- 10% within family: 148 clones (training), 17 clones (validation)

- 50% within family: 84 clones (training), 81 clones (validation)

- We obtained breeding values based on pedigree (EBV2) and based on genomic relationships (GEBV) for validation clones only



The predicted breeding values for all 165 clones based on pedigree (EBV1) were almost perfectly correlated with the predicted breeding values based on genomic relationships (GEBV)

These clones are from one full-sib family. They do not have phenotypic data. Using ABLUP, they all received the same (mid-parent mean) breeding value (EBV2). In contrast, using genomic relationships we see segregation within family (Mendelian sampling). We can rank these clones by GEBV and make selections within family, which is not possible using a breeding value based on average additive genetic relationship

Clones sampled for validation	Accuracy of predictions (r)	
	r (EBV2)	r (GEBV)
10% within family	0.61	0.76
50% within family	0.60	0.71

The accuracies of the predictions for GBLUP based on genomic relationships were higher than ABLUP based on pedigree

Conclusions

- GBLUP works in the same way as classical ABLUP: the model can include raw data, fixed effects of common environment, GxE interactions, spatial analysis, and other experimental or nuisance factors.

- Selection based on GBLUP should increase genetic gains in forest tree breeding. The major impact would be on reducing the need for expensive field testing, but it may also be possible to shorten the breeding cycle and thus increase genetic gain per unit time and cost

Acknowledgements

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