RES-FOR HIGHLIGHT #12

February 2021

Single-step genomic evaluation of two RES-FOR populations

Overview

Particularly in open-pollinated (OP) tree populations, the inclusion of genomic information in quantitative genetics analyses has resulted in improving the estimated genetic parameters and accuracy of individuals' predicted breeding values (BV). Higher BV accuracy, through the Genomic Best Linear Unbiased Predictors (GBLUP) have been demonstrated empirically in genotyped forest trees. The GBLUP approach has recently been extended to the single-step GBLUP (ssGBLUP) method. The ssGBLUP method has proven its effectiveness in predicting the BVs of individual trees with (current generation) and without (next generation) phenotype data, through the simultaneous utility of all available information from the breeding program: phenotypes, genotypes, and pedigree.

Objectives

To estimate and compare variance components, theoretical accuracies and prediction ability of trees' BVs based on the spatial phenotypic adjustment of growth and disease traits from progeny trials of lodgepole pine and white spruce, using the conventional pedigree-based (ABLUP) and the combined pedigree and genomic-based (ssGBLUP) approaches.

Methods

Data from the RES-FOR populations consisting of 242 (lodgepole pine) and 150 (white spruce) OP families from 4 and 3 progeny trials, respectively, were used. Total height and diameter at breast height (1.3m) were measured at year 30 (HT30 & DBH30). Additionally, in the lodgepole pine population, the resistance to western gall rust trait was assessed at age 36 and transformed into normal score values (NSWGR36). To account for environmental variation within each site, the spatial phenotypic data was obtained by subtracting the estimated design, and autoregressive residual effects. For each population, two multiple-trait multiple-site individual-tree models were evaluated. Both models included a fixed effect of genetic group, random additive genetic effects (BV), and random errors. In the ABLUP model, the pedigree-based relationship matrix was used, while the genomic ssGBLUP model used a blend of pedigree and genomic relationship matrices (Figure 1). Genomic relationship matrices were calculated from a subset of SNP markers selected for their ability to infer ancestry (8K for lodgepole pine and 24K for white spruce). Predictive ability, determined as the Pearson correlation between the observed and predicted BV from the respective model, were calculated by 1 (lodgepole pine) or 5 (white spruce) replications of 10-fold cross-validation, and multiplied by the square root of the heritability of each trait-site.

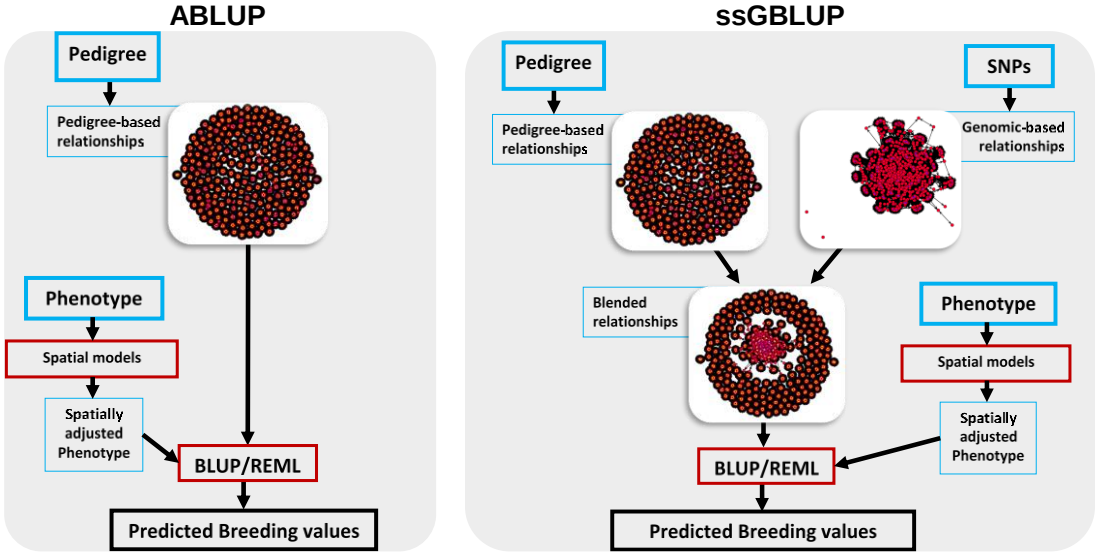

Figure 1. Graphical representation of the ABLUP and ssGBLUP approaches used for the RES-FOR genetic evaluation of the lodgepole pine and white spruce populations, using a network representation of the pedigree- and genomic-based relationships, and blended relationships among trees from the 242 open-pollinated lodgepole pine families.

Results

Overall, estimates of heritability averaged across sites using ssGBLUP were lower (lodgepole pine, except for HT30 at JUDY and SWAN sites, and NSWGR36 at TIME) or higher (white spruce, 3.16% for DBH30 and 1.47% for HT30, except for HT30 at the REDE site) than estimates using the ABLUP model (Table 1). In white spruce, the CARS site showed consistently lower heritability estimates for both growth traits relative to the CALL and REDE sites (results not shown).

Table 1. Averages of estimated narrow-sense heritability (± standard errors) using different models.

	Lodgepole Pine			White Spruce	
Model	**DBH30**	**HT30**	**NSWGR36**	**DBH30**	**HT30**
ABLUP	0.244 (0.016)	0.311 (0.023)	0.513 (0.030)	0.253 (0.031)	0.408 (0.047)
ssGBLUP	0.233 (0.029)	0.311 (0.044)	0.500 (0.056)	0.261 (0.032)	0.414 (0.047)

Theoretical accuracies of predicted BVs for offspring using ssGBLUP were slightly lower (lodgepole pine, from 0.53% to 2.80%, except for growth traits of genotyped trees) or consistently higher (white spruce, from 0.70% to 17.53%) than the ABLUP model (Table 2).

Table 2. Mean theoretical accuracies of predicted breeding values based in the ABLUP and ssGBLUP models.

	Lodgepole Pine			White Spruce		
Model	**Genotyped**	**Non-Genotyped**	**ALL**	**Genotyped**	**Non-Genotyped**	**ALL**
			DBH30			
ABLUP	0.598	0.598	0.598	0.550	0.601	0.592
ssGBLUP	0.601	0.585	0.588	0.625	0.611	0.612
			HT30			
ABLUP	0.644	0.654	0.653	0.607	0.709	0.690
ssGBLUP	0.646	0.642	0.643	0.714	0.714	0.714
			NSWGR36			
ABLUP	0.754	0.751	0.751	--	--	--
ssGBLUP	0.750	0.730	0.733	--	--	--

For the genotyped trees, the predictive ability values from the ssGBLUP model were higher (lodgepole pine, 3.07% for DBH30, 0.77% for HT30 and 7.85% for NSWGR36) or slightly lower (white spruce, 0.60% for DHB30 and 0.07% for HT30) than with the ABLUP model (Table 3). These results were consistent across the 4 lodgepole pine sites, while for white spruce slightly higher predictive ability values from the ssGBLUP model were obtained for the site with the lower heritability estimates, REDE (results not shown).

Table 3. Predictive ability (± standard errors) using the ABLUP and ssGBLUP models.

	Lodgepole Pine			White Spruce	
Model	**DBH30**	**HT30**	**NSWGR36**	**DBH30**	**HT30**
ABLUP	0.417 (0.009)	0.461 (0.013)	0.476 (0.022)	0.459 (0.012)	0.486 (0.010)
ssGBLUP	0.429 (0.008)	0.464 (0.012)	0.513 (0.021)	0.456 (0.012)	0.485 (0.011)

Conclusions

The multiple-trait multiple-site ssGBLUP approach based on spatial phenotypic adjustment has been successfully applied in the genetic evaluation of the two RES-FOR populations. The superiority of the ssGBLUP model was site-trait dependent. Estimated heritability did not provide a good indication of what one would expect for prediction of predictive ability. That is, when a lower (or higher) heritability was estimated, a higher (or lower) predictive ability was obtained.

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