GENERAL PREDICTION MODEL FOR AGE-AGE GENETIC CORRELATIONS IN *PINUS TAEDA*

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Abstract:--In long rotation crops such as forest trees, traits are rarely measured at all ages up to harvest age. Therefore, modelling of age-age genetic correlations is essential for predicting optimum selection age. Using data from four progeny tests of Pinus taeda planted in Zimbabwe assessed up to rotation age for height at 1.5, 9.5, 13.5, and 22.5 years, a tropical prediction model for age-age genetic correlations was derived (Gwaze et al. 1996, rg = 0.98 + 0.065 $\log_e$ (younger age/older age)). This model was significantly different from phenotypic models such as Lambeth's (Lambeth 1980). The tropical model was tested using data from twenty genetic tests of P. taeda from south eastern USA, assessed at 3, 5, 8, 10, 15, 17, 20 and 25 years (Table 1). The tests were located in Arkansas, Georgia, Louisiana and Texas. Possibilities of developing a general prediction model for P. taeda based on age-age genetic correlations were explored.

Table 1. Details of P. taeda genetic tests used in analyses.

Set	Organization	Sites	Parents	Reps/site	Trees	Assessments ages
1	International Paper Company	2	222	3	4251	3, 5, 10, 15, 17, 25
2a	Texas Forest Service	12	129	3-16	9647	5, 10, 15, 20
2b	Georgia-Pacific	5	61	3-9	14033	10, 15, 20, 25
2c	Crown Zellerbach	1	11	4	1475	3, 5, 8, 10, 15

Age-age genetic correlations were estimated using individual tree model ASREML (Gilmour et al. 1997). Genetic correlations were higher than family mean correlations. Strong linear relationships between age-age genetic correlations and log of age ratios were obtained (Table 2). The slopes of the regression models of the USA datasets were significantly higher than that of the tropical model. The main reason for the differences between these models is that genetic correlations involving very young ages were much higher in Zimbabwe tests than in the USA. The slopes of the western and eastern datasets were not significantly different. Thus, a pooled regression for all USA datasets was

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appropriate. The USA model for combined datasets was not significantly different from the Lambeth model despite that the former was based on phenotypic correlations.

Table 2. Parameter estimates for fitted models and fit statistics.

Model	ß0 (Se)	P_i (Se)	RMS	df	R2
Tropical	0.98 (0.044)	0.065 (0.026)	0.0032	4	0.61
Set 1	1.03 (0.015)	0.294 (0.013)	0.0009	13	0.97
Set 2a	1.02 (0.044)	0.204 (0.052)	0.0023	4	0.80
Set 2b	1.04 (0.022)	0.218 (0.039)	0.0005	4	0.89
Set 2c	0.97 (0.047)	0.253 (0.053)	0.0047	8	0.74
USA combined	1.04 (0.019)	0.284 (0.020)	0.0035	35	0.85

The study suggests that a general predictive model for both the tropical and temperate regions may not be appropriate. Therefore, two separate prediction models for P. taeda in the tropical and temperate areas should be derived, with the one derived here using USA data being appropriate for temperate areas. However, with high gentic quality seed and better site management in the advanced generation tests, genetic control of height at very young ages might be higher, and genetic correlations between very young ages and mature ages might increase. Under this hypothesis, the general model involving advanced generation USA tests and the tropical model might agree more closely.

ACKNOWLEDGEMENTS

This study was funded by USDA Forest Service and Roslin Institute. We thank the members of the Western Gulf Forest Tree Improvement Program for the data.

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Keywords: Age-age genetic correlation, modelling, selection age, Pinus taeda.