Analysis and Selection of the CFGRP 4th Cycle Slash Pine Tree Improvement

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Melbourne, Florida

OBJECTIVES

- Report details of the statistical analyses conducted to estimate breeding values (BV) from all parents and offspring tested of the 4th-generation of genotypes in slash pine. .
- Perform new selections to advance breeding and testing of the 4th-generation of genotypes in slash pine.

OVERVIEW OF DATA

- **Traits Assessed**
  - Cumulative rust (CRust): presence of rust at any time of measurement.
  - Annual increment of stem volume (ivol).

- **2nd and 3rd generation data included in analysis**
  - Data: PMX1 (8), PMX2 (8), and FS1 (8) series.
  - Different models for PMX1, PMX2 and FS trials.
  - Pedigree information for ALL generations.

DATA ANALYSIS: GOALS

- **Single-site Analysis**
  - Evaluate genetic worth of each site and trait.
  - Estimate: Heritability (h^2), Dominance (d^2), etc.

- **Multi-Environmental Trial (MET) Analysis**
  - Obtain Volume, R50 predictions for 'paper selections'.
  - Calculate MET heritability, site-to-site genetic correlations.
  - Estimate *genetic gain* of new (and old) selections.

DATA ANALYSIS: OVERVIEW

Summary Statistics

Series	Test	Age	Surv	CRust	HT	DBH
PMX1	BE766	8	81.4	51.4	33.5	5.6
PMX1	CE762	8	95.1	**7.3**	31.9	5.1
PMX1	EE764	5	89.0	-	18.5	3.4
PMX1	EE764	8	88.0	60.7	-	-
PMX1	FE765	8	65.6	**16.8**	32.8	5.8
PMX1	HE761	8	76.7	31.5	28.1	4.8
PMX1	IE760	8	74.6	51.5	30.1	5.2
PMX1	LE763	8	75.6	53.7	31.7	5.6
PMX1	SE767	8	88.4	46.9	23.9	4.9
PMX2	BE775	6	79.8	57.4	22.7	4.3
PMX2	EE769	6	63.8	57.1	23.6	4.6
PMX2	FE773	6	94.4	**3.0**	20.8	3.7
PMX2	HE768	6	88.5	**18.8**	22.5	3.9
PMX2	IE772	6	82.9	46.0	21.2	4.2
PMX2	ME774	6	89.2	**18.8**	22.4	4.0
PMX2	SE770	6	87.2	54.6	22.4	4.9
PMX2	WE771	6	73.8	55.6	15.8	3.2
FS	AE830	5	89.1	56.1	24.0	4.5
FS	BE832	5	92.0	35.6	22.5	4.3
FS	FE831	5	95.9	31.1	17.1	3.0
FS	HE835	5	91.6	46.3	21.2	4.3
FS	IE836	5	84.3	62.2	22.6	4.0
FS	LE834	5	69.0	69.0	18.8	3.7
FS	SE833	5	95.2	19.9	17.0	3.2
FS	WE837	5	89.6	59.3	21.3	4.3

SINGLE-SITE ANALYSIS

- Comparison of sites within and among experiment designs, trials series, and trait expression levels.
- Narrow-sense heritability h^2 estimated for all sites (both FS and HS heritability), and dominance d^2 estimated for sites with FS entries.
- This analysis was used to eliminate *noisy* sites, detect outliers, etc.

SINGLE-SITE ANALYSIS

$$y = \mu + rep + rep{:}row + rep{:}col + indiv + e \qquad \text{PMX1}$$

$$y = \mu + rep + rep{:}iblock + indiv + at(CP){:}family + e \qquad \text{PMX2}$$

$$y = \mu + rep + rep{:}iblock + indiv + family + e \qquad \text{FS}$$

rep	fixed effect of replicate
rep:row	random effect of row within replicate
rep:col	random effect of row within replicate
rep:iblock	random effects of incomplete block within replicate
indiv	random effect of genotype within a test, $indiv \sim MVN(\mathbf{0}, \mathbf{A})$
at(CP):family	random effect of family (where it corresponds)
e	random residual term, with $e \sim MVN(\mathbf{0}, \mathbf{D})$

SINGLE-SITE ANALYSIS

Summary Genetic Parameters

			vtree - CP		vtree - OP	CRust - CP		CRust - OP	Selected	Selected
Project	Test	age	h^2	d^2	h^2	h^2	d^2	h^2	vtree	CRust
PMX1	BE766	8	*	*	0.416	*	*	0.431	Yes	Yes
PMX1	CE762	8	*	*	0.465	*	*	**0.024**	Yes	No
PMX1	EE764	5	*	*	0.318	*	*	*	Yes	No
PMX1	EE764	8	*	*	*	*	*	0.368	No	Yes
PMX1	FE765	8	*	*	0.380	*	*	**0.088**	Yes	No
PMX1	HE761	8	*	*	0.173	*	*	0.257	Yes	Yes
PMX1	IE760	8	*	*	0.309	*	*	0.354	Yes	Yes
PMX1	LE763	8	*	*	0.404	*	*	0.356	Yes	Yes
PMX1	SE767	8	*	*	0.344	*	*	0.346	Yes	Yes
PMX2	BE775	6	0.325	0.000	0.383	0.260	0.006	0.281	Yes	Yes
PMX2	EE769	6	0.488	0.052	0.237	0.246	0.000	0.180	Yes	Yes
PMX2	FE773	6	0.291	0.174	0.198	**0.000**	0.000	**0.001**	Yes	No
PMX2	HE768	6	0.171	0.000	0.135	0.148	0.000	**0.098**	Yes	No
PMX2	IE772	6	0.432	0.205	0.275	0.271	0.000	0.195	Yes	Yes
PMX2	ME774	6	0.148	0.000	0.284	**0.040**	0.000	**0.049**	Yes	No
PMX2	SE770	6	0.554	0.000	0.310	0.217	0.246	0.162	Yes	Yes
PMX2	WE771	6	0.466	0.214	0.411	0.267	0.000	0.183	Yes	Yes
FS	AE830	5	0.197	0.426	*	0.221	0.120	*	Yes	Yes
FS	BE832	5	0.219	0.259	*	0.218	0.099	*	Yes	Yes
FS	FE831	5	0.155	0.256	*	0.116	0.126	*	Yes	Yes
FS	HE835	5	0.279	0.229	*	0.294	0.199	*	Yes	Yes
FS	IE836	5	0.257	0.246	*	0.255	0.131	*	Yes	Yes
FS	LE834	5	0.166	0.161	*	0.272	0.062	*	Yes	Yes
FS	SE833	5	0.128	0.335	*	0.184	0.000	*	Yes	Yes
FS	WE837	5	0.140	0.297	*	0.318	0.097	*	Yes	Yes

MET ANALYSES

- **All data analyzed together with an animal model**
  - MET model based on complex additive variance-covariance structure between sites (corh)
  - *All* individuals in pedigree have a breeding value (BV) estimation (or predicted genetic value) at each site!
  - Overall BV is obtained by averaging BVs across 'relevant' sites.

$$\mathbf{G} = \begin{bmatrix} \sigma_1^2 & \rho\sigma_1\sigma_2 & \rho\sigma_1\sigma_3 & \rho\sigma_1\sigma_4 \\ \rho\sigma_1\sigma_2 & \sigma_2^2 & \rho\sigma_2\sigma_3 & \rho\sigma_2\sigma_4 \\ \rho\sigma_1\sigma_3 & \rho\sigma_2\sigma_3 & \sigma_3^2 & \rho\sigma_3\sigma_4 \\ \rho\sigma_1\sigma_4 & \rho\sigma_2\sigma_4 & \rho\sigma_3\sigma_4 & \sigma_4^2 \end{bmatrix}$$

MET ANALYSES

$$y = \mu + test + test{:}rep + at(test){:}rep{:}row + at(test){:}rep{:}col + at(test){:}rep{:}iblock + test{:}indiv + at(CP){:}family + at(CP){:}test{:}family + e$$

test	fixed effect of trial
test:rep	fixed effect of replicate nested within trial
at(test):rep:row	random effect of row within replicate
at(test):rep:col	random effect of row within replicate
at(test):rep:iblock	random effects of incomplete block within replicate
test:indiv	random effect of genotype within a test, $test{:}indiv \sim MVN(\mathbf{0}, \mathbf{G} \otimes \mathbf{A})$
at(CP):family	random effect of family
at(CP):test:family	random interaction of family within a trial
e	random residual term, with $e \sim MVN(\mathbf{0}, \mathbf{D})$

MET ANALYSES RESULTS

ivol

$h^2 = 0.201$
$d^2 = 0.107$

$r_{Ba} = 0.729$
$r_{Bd} = 0.851$

CRust

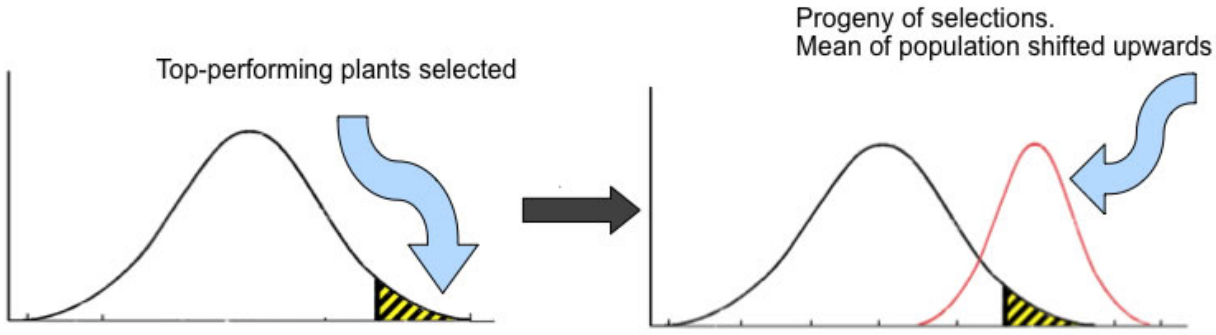
$h^2 = 0.246$
$d^2 = 0.055$

$r_{Ba} = 0.878$
$r_{Bd} = 0.600$

- Genetic parameters are within expected ranges for slash pine.
- High value of r_{Ba} for both traits (> 0.73): low levels of GxE across the evaluated environments.
- Low levels of d^2 for both traits (< 0.11); additional gain that can be achieved by selecting the best families but not much.

MET ANALYSES

- **Selection candidates were evaluated using predictions**
  - Mean values of individual predictions across sites were used for ranking.
  - These values were used to compute volume gain (GVOL) and R50.
  - Breeding values were used for the entire pedigree (grandparents, parents and offspring) for references.



SELECTION STRATEGY

- Selections within a BG with ranking for GVOL, CRust.
- Index: 50/50 for CRust (~R50) and ivol within a single breeding group.
- 40 individuals per BG (~400 total).
- No more than 2 individuals per FS family.
- No more than 4 individuals per HS family.
- Ideal case: ~10-20% backward selection.
- Rust-infected, forked, or otherwise poor form excluded.
- Favor complementary mating and increased genetic diversity.

ESTIMATING GENETIC GAIN

- **Normal approach: have a designated 'average' or 'reference'.**
  - Difficult to have if data for analyses changes.
  - Mean site is not possible as management, site quality, silviculture practices, have changed.

- **Gains were evaluated relative to an 'arbitrary' baseline.**
  - Rust: mean of data was 49.79% incidence, so we assume that this is functionally R50.
  - Stem Volume Increment:
    - 2nd generation parents were chosen as baseline of a genetic gain of ~5.75%.

SUMMARY OF SELECTIONS

- 393 individuals selected:
  34 backward and 359 forward selections.
- 294/359 forward selections were first choice.
- Average estimated genetic gains:
  - R50 25.15
  - GVOL 10.89%.
- Some individuals were found to be outliers:
  -13.8 for R50 and 37.6% for GVOL
- Note: values are relative to an arbitrary reference.
- Important differences were noted between breeding groups, but all showed interesting levels of genetic gain.

ESTIMATES OF GENETIC GAIN

Breeding Group	Population (Selection)			Selected		
	n	R50	GVOL	n	R50	GVOL
B	4,624	39.43	-0.14	35	18.27	10.86
C	3,276	50.66	-0.49	41	31.17	11.13
E	3,340	28.52	5.92	36	**10.71**	13.89
F	2,838	49.05	-6.15	42	29.14	3.51
H	2,330	49.45	-0.65	42	34.09	9.15
I	1,652	37.33	4.78	40	24.29	14.30
L	3,611	40.02	-1.14	40	19.19	9.42
M	2,141	40.91	6.64	35	25.10	**16.79**
S	3,213	46.23	-7.04	38	29.23	6.59
W	2,598	46.87	3.41	44	27.20	14.17
Elite	2,554	34.26	9.61	0	-	-
Average	32,177	41.94	0.85	393	25.15	10.89

DISCUSSION

- Forward and backward selections were satisfactory – a large amount of gain can be obtained for each breeding group.
- Statistical analyses demonstrates reasonable genetic control (heritability and dominance ratio) with acceptable levels of GxE.
- It can be expected that similar levels of genetic gain will be obtained in upcoming breeding cycles.
- The levels of genetic gain reported here for both R50 and GVOL are obtained in relation to an *arbitrary* baseline.
- The BVs of the parents, and their rankings, have changed with this analysis in relation to previous studies.

DISCUSSION

- BV estimates are available for each genotype at every site:
  - Users may extract more gain for their selections by evaluating/selecting genotypes from a subset of the trials (and BVs) tested.
  - Reasonable low levels of GxE justify averaging, across sites, BV's for parental rankings.

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SFRC