Centre for Bioinformatics and Biometrics

Technical Report Series

Radiata Pine Breeding Company
Breeding Value MET analyses: 2018

*** Shareholders Report ***

DRAFT

Beverley Gogel, Brian Cullis, Alison Smith and Chris Lisle

National Institute for Applied Statistics and Research, Australia
School of Mathematics and Applied Statistics
University of Wollongong

May 1, 2019

Disclaimer

At the request of RPBC, the GF Plus conversions described in this report have been provided, together with the estimated breeding values, for ortets that have appeared as parents in progeny trials. However, the University of Wollongong notes that there is currently no valid statistical framework to establish that the conversion of estimated breeding values to GF Plus ratings provides a reliable indicator of genetic performance. As such, University of Wollongong does not recommend reliance on the GF plus ratings described in this report for any purpose, including the selection of germplasm for purchase.

DRAFT

Contents

DRAFT

List of Tables

List of Figures

DRAFT

1 Introduction

Breeding value analyses including data collected in 2018 (BV2018) have been undertaken by University of Wollongong (UoW) for Radiata Pine Breeding Company Limited (RPBC). Six key breeding traits have been analysed. They include: growth and form (G&F) traits *stem diameter measured at breast height* (`dbh`), *branching* (`br`) and *stem straightness* (`str`), wood quality (WQ) traits *wood density* (`dens`) and *wood stiffness* (`pme`) and *Dothistroma resistance* (`dothi`). The BV2018 MET analyses have been conducted as in previous years using the methods outlined in Cullis et al. (2014) and overall breeding values have been calculated using the methods of Smith and Cullis (2018).

2 Data summary

A summary of the MET datasets is presented in Table 1, including the total number of trials included in the MET dataset for each trait and the number of trials with phenotypic data measurements recorded in 2018. Additional information on the latter is presented in Table 2 which includes the trial planting date, region, location and design type, and the trial type. Trials marked with an asterisk (∗) indicate trials with existing data measurements, that is, phenotypic trait data recorded prior to 2018.

DRAFT

Table 1: Summary of trials included in the MET dataset for each trait including the type of trait, trait name, total number of trials included in the dataset and the number of trials with new data in 2018

Trait type	Trait name	Number of trials	Number of trials with new data in 2018
G&F	`dbh`	106	10
	`br`	106	10
	`str`	106	10
WQ	`dens`	47	5
	`pme`	47	5
Disease	`dothi`	25	3

Table 2: List of trials with new trait data in 2018

	Trial	Plant date	Region	Location	Design	Trial Type	`dbh`	`str6`	`br6`	`dens`	`tof`	`dothi`
	BC36_3	2008	Nelson	Golden Downs	Iblk	Main Population	✓	✓	✓			
	BC38_3	2008	Bathurst	Sunny Corner	Iblk	Progeny	✓	✓	✓	✓	✓	
	BC40_3	2009	Bay of Plenty	Kaingaroa	Iblk	Main Population	✓	✓	✓	✓	✓	
	BC40_4	2009	Nelson	Cut Hill	Iblk	Main Population	✓	✓	✓			
	BC42_1	2011	Tasmania	Springfield	Iblk	Prod'n Population	✓	✓	✓			
	BC46_1	2011	Tasmania	Beulah	Iblk	Main Population	✓	✓	✓			
	BC46_2	2011	Tasmania	Stoodley	Iblk	Main Population	✓	✓	✓			
	BC46_3	2011	Tasmania	Payanna	Iblk	Main Population	✓	✓	✓			
	BC37_1	2008	Gisborne	Makomako	Iblk	Main Population	✓	✓	✓	✓	✓	
	BC37_2	2008	Gisborne	Matahiia	Iblk	Main Population	✓	✓	✓	✓	✓	
∗	BC34_4	2007			Iblk	Main Population				✓	✓	
∗	BC55_2	2014			UOW	Cloned Elite						✓
	BC54_1	2014			UOW	Dothistroma Res						✓
	BC59_1	2015			UOW	Cloned Elite						✓

3 Data exclusions

A detailed account of the BV2018 MET analyses is presented in the final report *RPBCbv2018final.pdf*, which includes information on data exclusions. In summary:

- the five trials FR259_1, FR259_2, FR259_3, FR354_1 and FR354_2 had zero parental connectivity with all but their companion trials (comprising less than 5% of the full set of trials) for `dbh`, `br` and `str` and were removed from the MET data set for analysis (this is consistent with BV2017) ...
- the two trials FR124_4 and FR69_1 had zero parental connectivity with more than 85% of trials for `dens` and were removed from the MET data set for analysis (this is consistent with BV2017) ...
- four data observations for `dens` had large absolute standardised conditional residuals (`scres`) and were removed for analysis ...

number	Expt	Tid	`dens`	`scres`	comment
1	BC30_2	56006210	570.00	9.01	removed in BV2017
2	FR399_2	50005257	536.30	9.40	not removed in BV2017
3	BC37_2	58021436	629.91	10.16	new in BV2018
4	BC30_4	56015503	891.00	17.09	removed in BV2017

- with the exception of the seven trials listed above, all data was retained for `dbh`, `br`, `str` and `pme`.

DRAFT

4 GF Plus conversions

For a given trait, the GF Plus conversion is computed by regressing the current year breeding values (for BV2018 here, constructed following Smith and Cullis (2018)) onto the previous year GF Plus ratings. The resulting regression equation is then used for the conversion. Table 3 gives the BV2018 GF Plus regression equations for each trait, where BV denotes the BV2017 GF Plus ratings. The predicted breeding values together with their accuracies and corresponding GF Plus conversion are presented for the full set of parents and all six traits in the results file *gfplusBV20128.csv*, which has been forwarded to RPBC.

Table 3: GF Plus regression for each trait

Trait type	Trait name	Regression equation	R^2
G&F	`dbh`	$15.677 + 0.544\mathtt{BV}$	0.981
	`br`	$19.208 + 3.603\mathtt{BV}$	0.959
	`str`	$16.026 + 4.859\mathtt{BV}$	0.990
WQ	`dens`	$18.900 + 0.515\mathtt{BV}$	0.974
	`pme`	$14.648 + 3.031\mathtt{BV}$	0.975
Disease	`dothi`	$17.920 + 0.903\mathtt{BV}$	0.912

Figures 1 to 6 are for `dbh`, `br`, `str`, `dens`, `pme` and `dothi`, respectively. Plot **A** is a plot of the estimated breeding values for BV2018 against the BV2017 GF Plus conversion, with estimated regression equation.

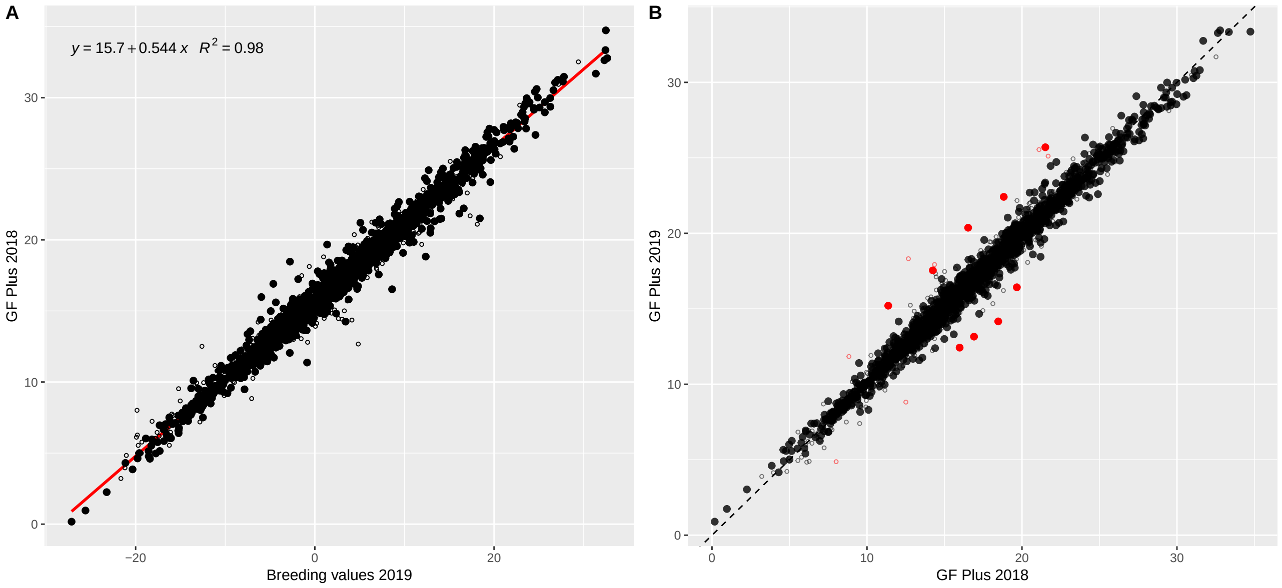

Figure 1: `dbh` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `dbh` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Points coloured in red represent a change in three GF Plus points between years. Open circles correspond to breeding values with accuracy less than 0.8.

Plot **B** is a plot of the BV2018 GF Plus conversion against the BV2017 GF Plus conversion. Where present (for all but `str`), points coloured in red indicate a change in three GF Plus points between years. Points represented by an open circle correspond to those ortets with for which the accuracy of their breeding value is less than 0.8.

DRAFT

5 Recommendation

Our recommendation from BV2017 remains unchanged (see Shareholder report for MET analyses including phenotypic data recorded in 2017), that is, that the GF Plus ratings be replaced by their estimated breeding values (with accuracies) constructed following the methods of Smith and Cullis (2018).

5 Recommendation

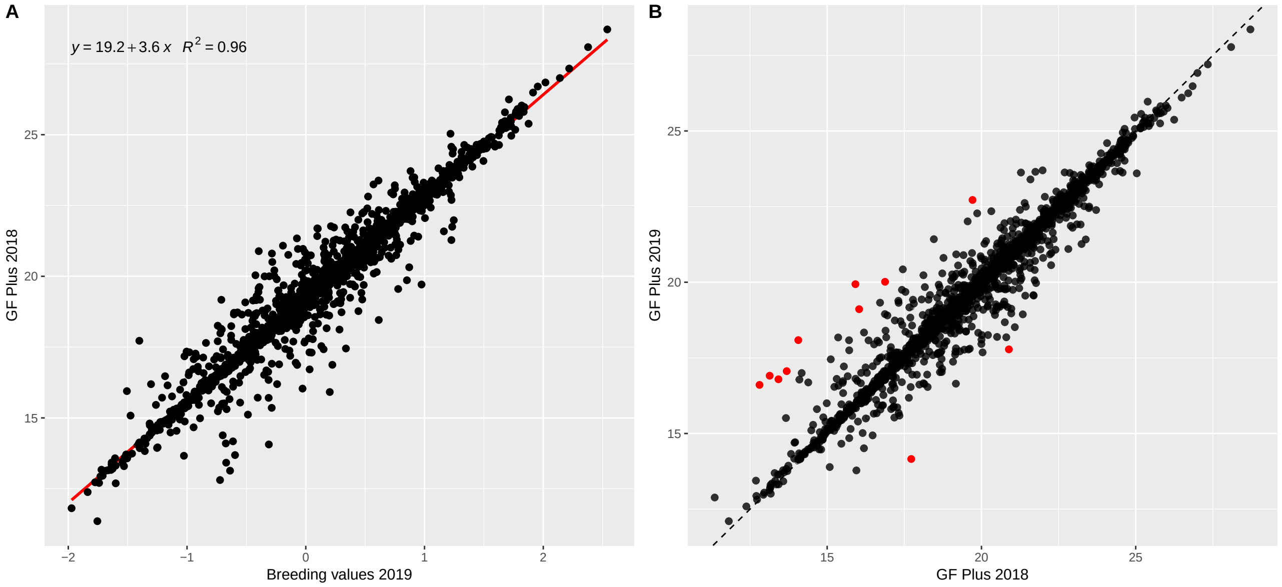

Figure 2: `br` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `br` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Points coloured red represent a change in three GF Plus points between years.

DRAFT

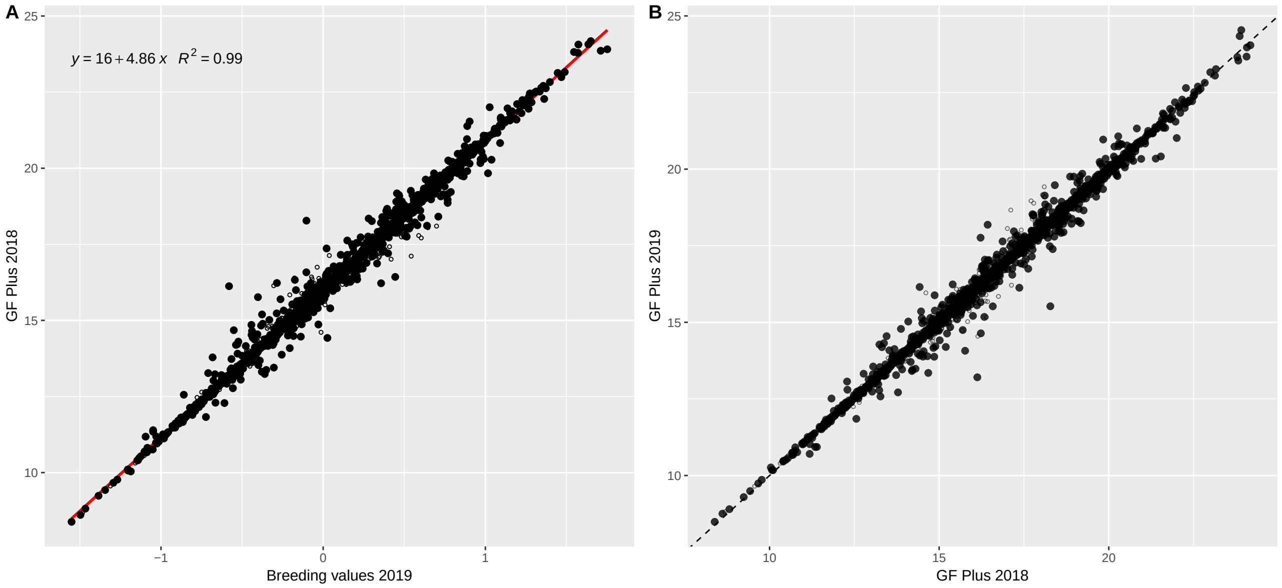

Figure 3: `str` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `str` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Open circles correspond to breeding values with accuracy less than 0.8.

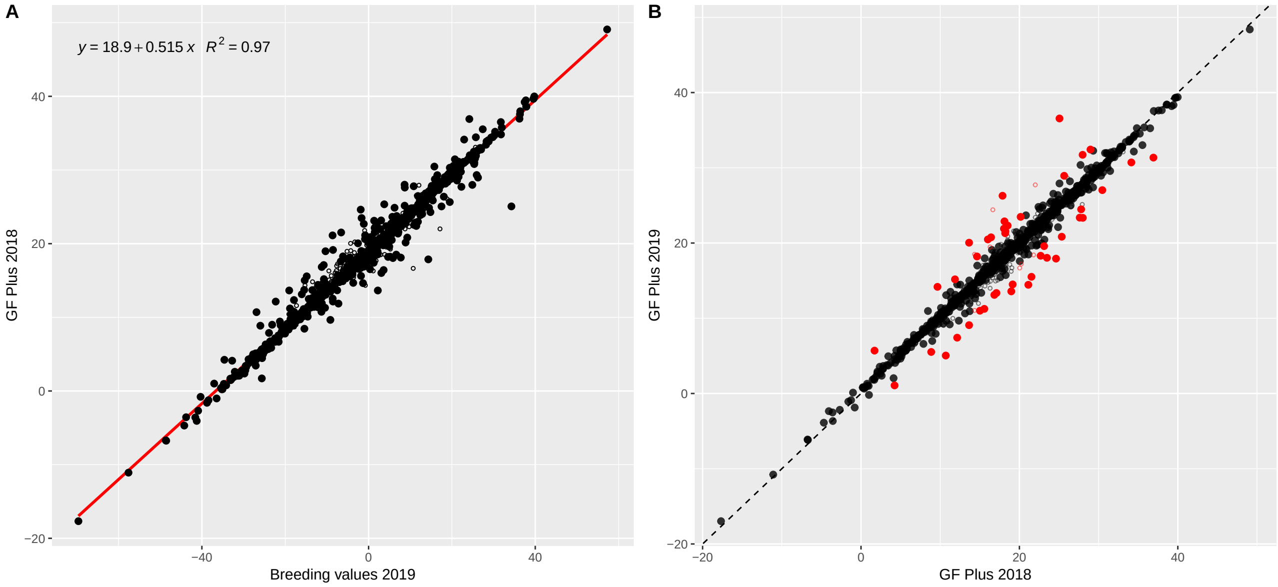

Figure 4: `dens` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `dens` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Points coloured red represent a change in three GF Plus points between years. Open circles correspond to breeding values with accuracy less than 0.8.

DRAFT

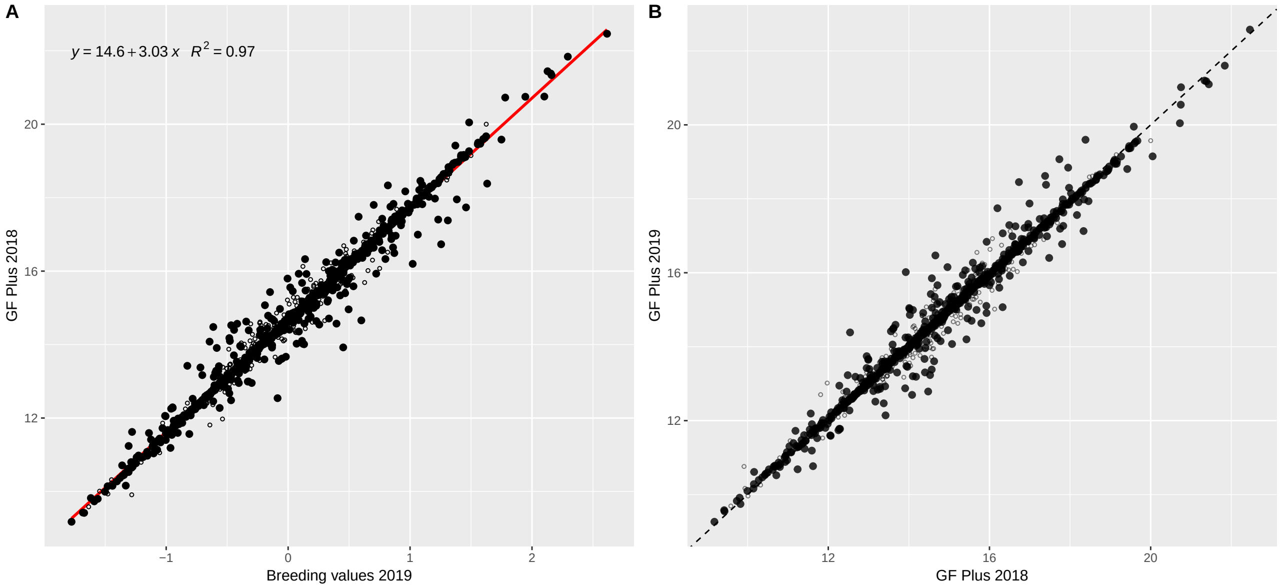

Figure 5: `pme` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `pme` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Points coloured red represent a change in three GF Plus points between years. Open circles correspond to breeding values with accuracy less than 0.8.

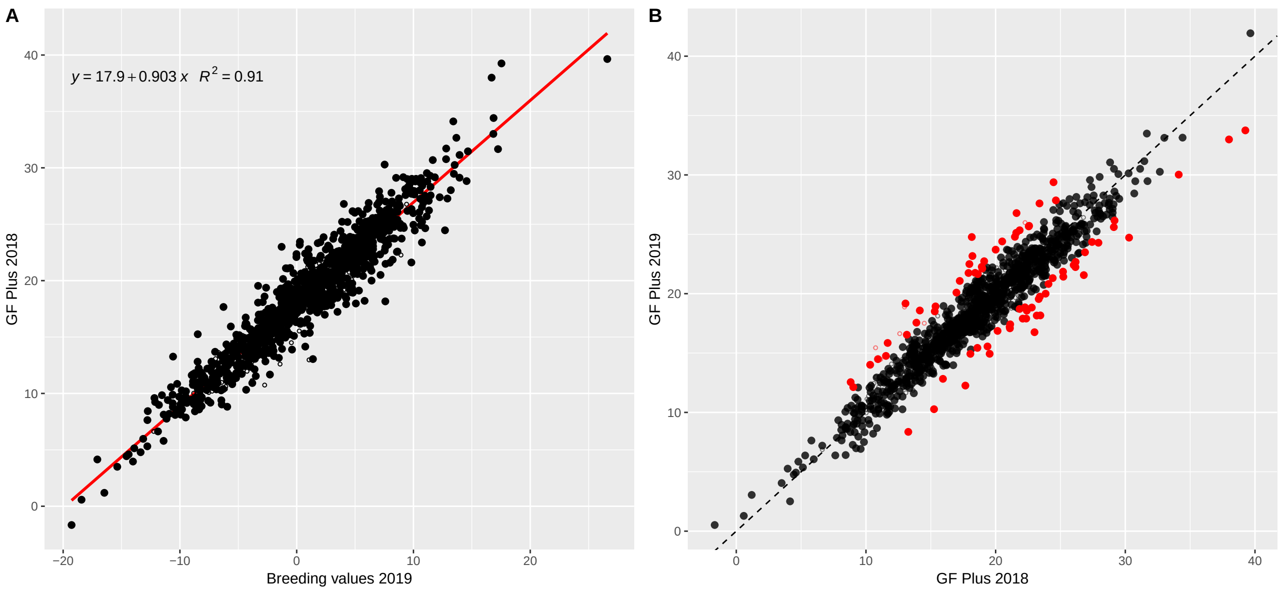

Figure 6: `dothi` Estimated regression equation and plot of the estimated breeding values for the BV2018 MET analysis of `dothi` against the BV2017 GF Plus conversion, plot **A**. Plot of the GF Plus conversion for BV2018 against BV2017, plot **B**. Points coloured red represent a change in three GF Plus points between years. Open circles correspond to breeding values with accuracy less than 0.8.

References

Cullis, B. R., Jefferson, P., Thompson, R. and Smith, A. B. (2014). Factor analytic and reduced animal models for the investigation of additive genotype-by-environment interaction in outcrossing pllant species with application to a *pinus radiata* breeding programme, *Theoretical and Applied Genetics* **114**(8): 1319–1332.
URL: *http://dx.doi.org/10.1007/s00122-007-0515-3*

Smith, A. and Cullis, B. R. (2018). Plant breeding selection tools built on factor analytic mixed models for multi-environment trial data, *Euphytica* **214**(8): 143.

DRAFT