Centre for Bioinformatics and Biometrics

Technical Report Series

Radiata Pine Breeding Company

Breeding Value MET analyses: 2018

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1 Introduction

Breeding value analyses including data collected in 2018 (BV2018) have been undertaken by University of Wollongong (UoW) for Radiata Pine Breeding Company Ltd. (RPBC). This report documents the BV2018 multi-environment trial (MET) analyses of growth and form (G&F) traits *stem diameter measured at breast height* (`dbh`), *branching* (`br`) and *stem straightness* (`str`), and wood quality (WQ) traits *wood density* (`dens`) and *wood stiffness* (`pme`). The aim was to produce predicted breeding values (additive genetic effects) of parental trees with GFPlus conversion. The MET analyses have been conducted as in previous years using the methodology outlined in Cullis et al. (2014) and include a more recent measure of the overall performance of individuals (Smith and Cullis; 2018).

The disease trait *Dothistroma septosporum* (`dothi`) is a complex longitudinal trait that is analysed using alternative (though related) statistical methods and has being reported on separately.

2 Phenotypic data

2.1 G&F and WQ traits

Trials with data to be included in BV2018 for G&F and WQ included 101 trials with existing data for some or all traits (as included in the BV2017 MET data set) and 11 trials with new WQ and/or G&F data. Table 1 is a list of the trials with new data and includes details on the trial planting date, region, location, design and trial type. The 11 trials with new WQ and/or G&F have one of three trial types (Main population, Progeny, Production population) and they all have incomplete block (Iblk) designs. We note that one trial (BC34_4) has existing G&F data but new WQ data. This gives a full MET data set for G&F/WQ that includes a total of 111 trials. See Appendix A for additional information on trials included in the BV2018 MET data set.

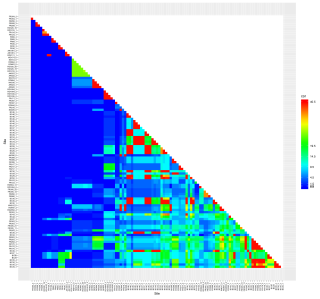
We note that the *time of flight* (tof) data for BC38_3, BC40_3, BC37_1, BC37_2 and BC34_4 has been converted to `pme` following the methodology used in previous years, see script file *pmenewfllesfix18.R*.

2.2 Dothi

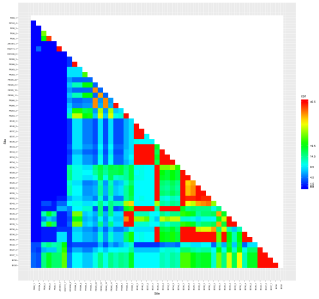
Trials with data to be included in BV2018 for `dothi` included 22 trials with existing `dothi` measurements, one trial with both an existing `dothi` measurement and a new measurement in 2018 (BC55_2) and two new trials with `dothi` measurements in 2018 (BC54_1 and BC59_1). The 3 trials with new `dothi` measurements have one of two trial types (Cloned Elite and Dothistroma Resistance) and they all have designs generated by UoW, see also Table 1 and Appendix A. The BV2018 MET analysis of `dothi` has been reported on separately.

2.3 Parental concurrence

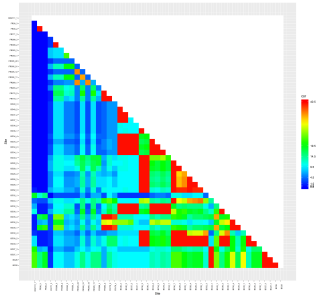
Figure 1 presents a heatmap representation of the parental connectivity between trials for (a) the three G&F traits - 111 trials, (b) `dens` - 49 trials, and (c) `pme` - 47 trials. For the three G&F traits,



(a) parental connectivity: dbh/br/str



(b) parental connectivity: dens



(c) parental connectivity: pme

Figure 1: Heatmap of the parental connectivity between trials in the BV2018 MET data set for (a) dbh/br/str, (b) dens, (c) pme

five trials had zero connectivity with all but their companion trials (comprising less than 5% of the full set of trials) and were removed from the data set for analysis of these traits (FR259_1, FR259_2, FR259_3, FR354_1 and FR354_2), see the dark blue vertical strip to the far right of Figure 1 (a). For dens, two trials had zero connectivity with more than 85% of trials and were removed from the data set for analysis of this trait (FR124_4 and FR69_1), see the dark blue vertical strip to the far right of Figure 1 (b). No trials were removed for the analysis of pme.

We note that the removal of trials in BV2018 is completely consistent with those removed in BV2017.

2.4 Final phenotypic data sets

The final MET data sets for the three G&F traits comprised 106 trials, see Table 4 for summary information. We note that for br, trials have been scored using either a nine point scoring system, or more recently, a six point scoring system. Likewise for str. For both br and str, the scores have been combined to form a single trait for analysis. The final MET data set for dens included the subset of 47 trials having density data but excluding FR124_4 and FR69_1, and the final MET data set for pme included the subset of 47 trials having pme data.

Table 1: 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 Pedigree information

Pedigree information for the G&F and WQ traits is summarised in Table 2. For each trait, the `prune()` function available through the pedicure package in R (R Development Core Team; 2013) was used to prune the pedigree to remove non-informative individuals. The pruned pedigree was then further reduced to just the parents/grandparents/founders (they will be referred to collectively as the *parents*) using `prune.par()`. For example, the total number of data records in the `dbh` MET data set was 377524 corresponding to 363022 trees. Pedigree information was available on a total of 365970 trees comprising the 363022 progeny grown in the trials and 2948 parents (no parental trees were grown in any trial) and the final pedigree file included pedigree information on the 2948 parental lines only. A linear mixed model analysis including pedigree information requires the inverse of the additive relationship matrix. This was generated using the `ainv()` function in `pedicure` which has been built using the methodology of Meuwissen and Luo (1992).

Table 2: Summary of pedigree information for the G&F and WQ traits in BV2018

	dbh	br	str	dens	pme
total trials	106	106	106	47	47
total data records	377524	377045	375598	82631	81784
available pedigree information	365970	365491	364044	73649	73142
number of trees grown in trials	363022	362543	361096	72427	71958
number of parents	2948	2948	2948	1222	1184

4 Statistical methods

MET analyses of the G&F and WQ traits have been conducted as in previous years using factor analytic (FA) models and an approximate reduced animal model (ARA) as outlined in Cullis et al. (2014). The FA model fits a general covariance structure for the additive genotype by experiment (synonymous with trial) effects, that is, heterogeneity of additive genetic variance across experiments and heterogeneity of additive genetic covariance between pairs of experiments. The ARA has been used to ease the computational burden in analysing the RPBC MET data sets (which are large, see Table 2) using FA models that include pedigree information.

4.1 Baseline linear mixed model

All analyses were conducted using the ASReml-R software (Butler et al.; 2018) within R (R Development Core Team; 2013). The baseline linear mixed model for each trait included a fixed main effect for each trial, random model terms to reflect the plot structure of each trial and a set of independent errors for each trial. A random replicate term was fitted for all trials. The remaining plot structure terms for each trial can be determined from the Mtree, `Setgrp` and `Iblk` columns of Table 4 in which

- a 2 in the Mtree column indicates the trial has a multi-tree design and a `Trueplot` term was fitted for this trial ...
- a 2 in the Setgrp column indicates the trial has a setgroup design and a `Replicate:Setgroup` term

was fitted for this trial ...

- a 2 in the Iblk column indicates the trial has an incomplete block design and `Replicate:Iblk` term was fitted for this trial ...

We allowed the variances of the random model terms to differ between trials. In terms of the genetic effects, we commenced with a diagonal model for the additive genetic effects and in all analyses we fitted a set of residual genotype by trial effects for clonal entries in the clonal trials. There were 9 clonal trials among the full set of 106 trials for G&F/WQ. They comprise the set of 9 trials in Table 4 with a 2 in the Clonal column.

4.2 Checking for outliers

A diagonal model for the additive genetic effects is equivalent to modelling each site separately. We used the `aom=T` option for the diagonal model to check for erroneous data observations. Four data observations for `dens` had an absolute standardised conditional residual (`sres`) exceeding 9 and were removed for analysis. They are as follows:

number	Expt	Tid	dens	sres	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

All data was retained for all remaining traits.

4.3 FA analysis

For each trait, the non-genetic variance parameter estimates from the diagonal model were used as starting values for the non-genetic variance parameters in the initial FA model, which was chosen to be of the same order as the final FA model in BV2017. For the genetic variance parameters we used a *rolling MET* approach in which the FA variance parameter estimates from the final model in BV2017 were used as starting values for the FA parameters in BV2018. The final FA model for each trait, together with the mean percentage variance accounted for by each factor (%VAF) and the overall %VAF (averaged across trials) is presented in Table 3. We fitted an FA model of order 3 for the additive genetic effects for `dbh` which accounted for 79% of the total additive genetic variance. For the remaining traits we fitted an FA model of order 2, with the overall %VAF ranging from 85% to 94% for these models.

5 Results

The aim of the analysis of each trait was to obtain predicted breeding values (additive genetic effects) for the set of parents (called backward selections) to enable selection of individuals for use as parents. These have been formed for the final model for each trait, together with a measure of the overall

Table 3: Variance models for the additive genetic effects for each trait, percentage variance accounted for (%VAF) by each factor and the total percentage variance accounted for

	additive genetic	%VAF			
trait	variance model	factor 1	factor 2	factor 3	total
dbh	FA3	50.78	13.90	14.30	79.0
br	FA2	71.85	15.39		87.2
str	FA2	69.77	15.38		85.2
dens	FA2	85.62	8.35		94.0
pme	FA2	79.54	8.57		88.1

performance (OP) of each parent and associated accuracy (OPacc). OP is based on the methods of Smith and Cullis (2018) and is defined to be the set of predicted additive genetic effects constructed at the average of the loadings for the first factor. For all but `pme` for which there is a small negative first factor loading for one trial (FR260_1), the first factor loadings are all positive and are therefore considered to represent non-crossover additive genotype by experiment interaction (AE). Furthermore, the first factor accounts for between 50.8% and 85.6% of the variation in the AE effects across the five analyses (see Table 3) so that OP is considered to provide a meaningful and informative selection tool for RPBC.

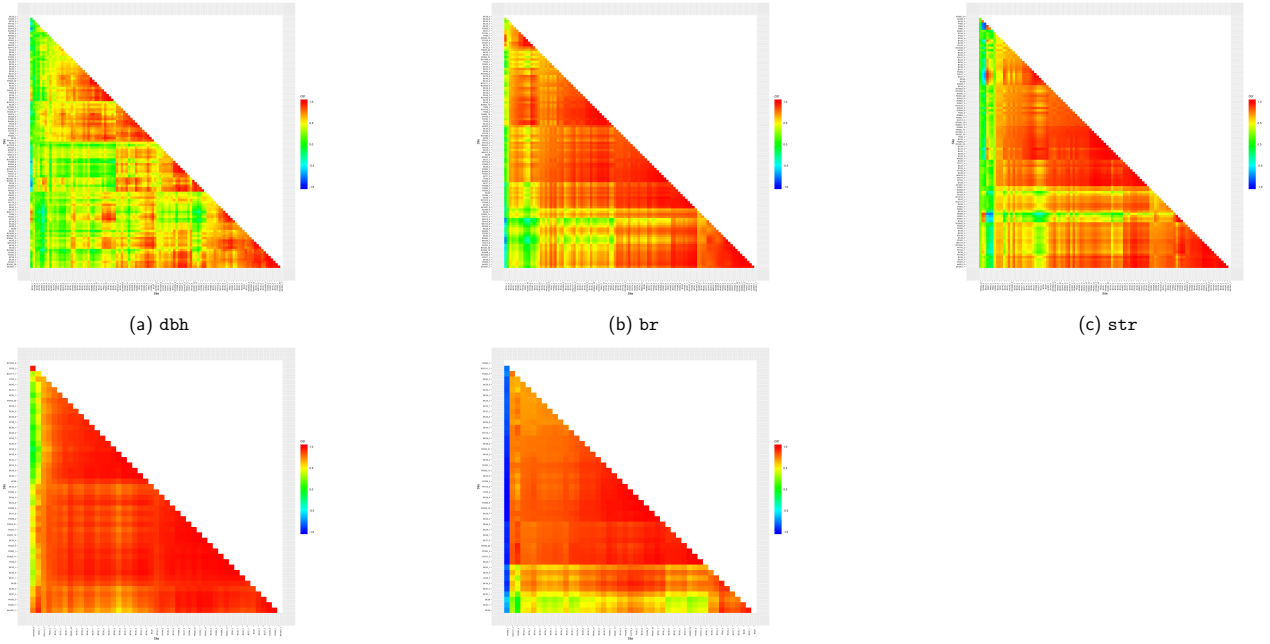
The full set of OP and OPacc for each parent and trait (see Table 2 for the number of parents for each trait) together with GFPlus conversion is presented in the results file *gfplusBV2018.csv* which has been forwarded to RPBC. Other analysis outputs include a heatmap of the estimated between trial additive genetic correlation matrix for each trait. These are presented for the five traits in Figure 2 and show substantial AE for `dbh`, with less AE for `br` and `str` and very little AE for `dens`. There is likewise little AE among a majority of trials for `pme` although one trial (FR260_1) appears to be completely uncorrelated with most other trials, see plot (e). This is not surprising given FR260_1 is the above mentioned trial with a small negative first factor loading. These results are consistent with those obtained for BV2017.

6 Script files

For the G&F and WQ traits, each MET analysis has involved a series of six script files:

- *trait_metfix2018.R*: read in the current phenotypic and pedigree data base and undertake fixes in preparation for the MET analysis ...
- *trait_metdo2018.R*: run the models ...
- *trait_metsum2018.R*: run a summary function and produce heatmap graphics ...
- *trait_opplots2018.R*: extract the scores and loadings for the final fitted model and construct OP ...
- *trait_overall2018.R*: produce the final sets of estimated breeding values ...
- *trait_check2018.R*: series of checks that the sets of results for BV2018 align with those of BV2017 ..

In the above *trait* is generic for `dbh`, `br`, `str`, `dens` and `pme`



(a) dbh (b) br (c) str

(d) pme (e) pme

Figure 2: Heatmap of the estimated between trial additive genetic correlation matrix for (a) `dbh`, (b) `br`, (c) `str`, (d) `dens` and (e) `pme`

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A Additional information on the BV2018 MET data set

A.1 Trials with new data

The following is dot point summary of the trials included in BV2018:

- a total of 101 trials were included in the analysis of G&F (`dbh`, `br`, `str`) and WQ (`dens`, `pme`) in BV2017 ...
- a total of 11 trials were scored for G&F/WQ and 3 for `dothi` in 2018, refer to *trialsumm2018BGnew.xlsx* for a full summary ...
  - of the set of 11 trials for G&F/WQ, 1 had existing `dbh` data (BC34_4) and 10 were new trials to the analysis ...
  - of the set of 3 trials for `dothi`, 1 had existing `dothi` data (BC55_2) and 2 were assessed for `dothi` for the first time in 2018 ...
- a total of 124 trials had data for one or more traits at the time of BV2018. They comprised:
  - the 101 trials with G&F/WQ data in BV2017 ...
    - one of these had new WQ data in 2018 but existing `dbh` data and was therefore included in BV2017 ...
    - some of these had existing `dothi` measurements and were therefore also included in the BV2017

`dothi` analysis ...

- 10 new trials with G&F/WQ data ...
- 11 trials with existing `dothi` measurements but no existing G&F/WQ measurements and therefore not included in the set of 101 ...
- 2 new trials with `dothi` measurements ...

A.2 Phenotypic and pedigree data bases and associated data objects

The following is a record of the data objects created in the R environment (R Development Core Team; 2013) in the process of updating the phenotypic and pedigree data bases used in BV2017 in preparation for BV2018. The base directory in which this work was undertaken is *U:/bgogel/UoW/RPBC/analyses2019/*. The phenotypic data used by Brian Cullis (BC) for G&F/WQ in BV2017 was cross-matched to the data base compiled by Chris Lisle (CL) and Jesse Rand (JR) in *.../dbhcheck*. The phenotypic data for BV2017 was updated and cross-checked (mostly) in *.../dbhcheck/newdata*. The pedigree data base was checked in *.../dbhcheck/Brian* with subsequent updates to the phenotypic data base also undertaken in this workspace.

The final phenotypic and pedigree data bases for BV2018 were produced as follows:

- *RPBCdatacheck.R* was used to cross match the data used by BC for G&F/WQ in BV2017 (101 trials) with the matching trials extracted from the data base compiled by CL and JR including all traits (`dbh`, `br`, `str`, `dens`, `pme`, `dothi`) ...
- `kdat` (from BC) and `gfdat` (from CL/JR) are data frames for the set of 101 trials precluding and including `NA dbh` data, respectively ...
  - the `NA`s in `gfdat` corresponded to trees for which there was `dothi` data but no `dbh` data ...
  - this can happen if the tree dies after the `dothi` measurements are taken but before the tree is the right age to have `dbh` scored...
- `pheno.df` was created in *bgset1BG.R* and is a data frame containing the full set of 181 trials, but with G&F/WQ/`dothi` data for trials included in BV2017 only. `pheno.df` has been updated with new data measured in 2018 for inclusion in BV2018 ...
- `kpednew` was created in *allfixBG.R* and is the pruned pedigree data frame matching `gfdat` (for the 101 trials used in the G&F/WQ analyses in BV2017 expanded to include trees with `dothi` but no `dbh` measurement) ...
  - `kpednew` was used as the base pedigree data frame in the analysis of all traits ...
- `pheno.df050319` was `pheno.df` updated by Alison Smith (AS) with new `dothi` data measured in 2018 ...
- `pheno18.df` was an extract of `pheno.df` for the 11 trials with new G&F/WQ data in 2018 (10 new trials plus BC34_4), updated with the new data ...

A Additional information on the BV2018 MET data set

- `pheno.df070319` was a merge by Bev Gogel (BG) of the new G&F/WQ data in `pheno18.df` into `pheno.df050319`, see *alldatacheckASphenodf.R* ...
- `pheno070319.drone` is a summary of `pheno.df070319` generated by running `droneBGall()` over `pheno.df070319`: these summaries were generated along the way and have been cross-checked throughout ...
- `pheno.df190319` was `pheno.df070319` updated by BG based on pedigree checks, see *fix180319.R* ...
- `pheno.df010419` was the final phenotypic data base updated by BG to remove all (known) outstanding issues, see *fixBV2018final.R* ...
  - `pheno.df010419` saved to `finalfilesBV2018/pheno010419.RData` ...
- `data123` is a subset of `pheno.df010419` corresponding to 123 trials being the 124 trials with data for BV2018 with one trial (BC51_2) removed, as directed by RPBC ...
  - `data123` saved to `finalfilesBV2018/data123_010419.RData` ...
- `kped123` is `kpednew` updated to include
  - new trees from the 22 (= 123 - 101) new trials to be included in BV2018
  - NSW pedigree information (for 25 5 digit Fcln codes) ...
- `ped123` is the pruned pedigree for data123 using `kped123` ...
  - `ped123` saved to `finalfilesBV2018/ped123_010419.RData` ...

Table 4: Summary of trials included in the BV2018 G&F and WQ analyses including the mean trait value for each trial

										mean				
Expt	Pldate	TrialType	Fcln	Mcln	Mtree	Setgrp	Iblk	Clonal	Reps	`dbh`	`br`	`str`	`dens`	`pme`
AK1061_1	1987	Progeny	467	1	1	2	1	1	25	202.8	6.4	5.5	459.2	
AK1061_2	1987	Progeny	467	1	1	2	1	1	25	192.4	5.9	5.6		
AK290_0	1971	Progeny	271	1	2	2	1	1	5	220.6	7.5	7.3		
AK622_1	1975	BValues	101	1	1	2	1	1	10	193.0	5.5	5.9		
AK622_2	1975	Diallel	20	20	1	2	1	1	6	212.5	5.3	6.0		
AK623_1	1975	BValues	107	1	1	2	1	1	10	150.4	5.6	5.9		
AK623_2	1975	Diallel	21	21	1	2	1	1	6	169.2	6.0	6.4		
BC25	2003	Elite	62	55	1	2	1	1	30	201.4	3.5	5.5	321.8	5.0
BC26	2003	Elite	62	54	1	2	1	1	30	162.9	3.5	5.6	311.4	4.7
BC27_1	2003	Elite	62	55	1	2	1	1	24	192.9	4.9	6.6	334.6	6.7
BC27_3	2003	Elite	41	36	1	1	1	1	20	158.9	2.9	4.9	331.6	7.3
BC28_1	2004	Breeding	126	6	1	2	1	1	30	204.9	3.3	5.7	310.2	6.0
BC28_3	2004	Breeding	127	6	1	2	1	1	30	191.3	3.6	5.6	318.8	4.8
BC28_4	2004	Breeding	126	6	1	2	1	1	30	195.1	3.6	6.4	343.0	5.3
BC29_1	2005	Breeding	119	6	1	2	1	1	30	213.5	3.7	5.4	340.8	5.9
BC29_2	2005	Breeding	122	6	1	2	1	1	30	177.7	3.6	5.1	319.3	4.6
BC29_3	2005	Guad Hyb	50	51	1	1	1	1	30	161.3	2.9	6.2		
BC30_1	2006	Breeding	163	28	1	1	2	1	25	226.4	5.1	7.6	362.6	8.4
BC30_2	2006	Breeding	163	28	1	1	2	1	25	196.8	2.3	3.8	358.1	8.9
BC30_4	2006	Breeding	105	16	1	1	2	1	15	281.4	2.8	3.8	377.5	8.4
BC30_7	2005	Progeny	232	6	1	1	2	1	20	169.8	3.0	6.2	331.9	5.1
BC32_1	2006	Cl Elite	41	37	1	1	2	2	4	187.1	2.5	4.1	310.8	6.8
BC34_1	2007	Main Pop	141	6	1	1	2	1	25	209.0	2.2	4.1	340.2	5.7
BC34_2	2007	Main Pop	177	6	1	1	2	1	25	208.7	2.5	3.2	327.7	6.1
BC34_3	2007	Main Pop	177	5	1	1	2	1	25	163.9	2.3	4.1	317.4	5.9

A Additional information on the BV2018 MET data set

Summary of trials included in the BV2018 G&F and WQ analyses including the mean trait value for each trial

										mean				
Expt	Pldate	TrialType	Fcln	Mcln	Mtree	Setgrp	Iblk	Clonal	Reps	dbh	br	str	dens	pme
BC34_4	2007	Main Pop	172	6	1	1	2	1	25	232.4	2.9	3.7	357.9	9.3
BC35_1	2007	BValues	95	6	1	1	2	1	25	191.8	3.7	4.3	317.2	5.5
BC35_2	2007	BValues	69	5	1	1	2	1	25	175.2	3.3	4.1	320.7	6.8
BC35_3	2007	BValues	93	6	1	1	2	1	25	205.4	2.7	2.8		
BC35_4	2007	BValues	93	6	1	1	2	1	25	205.4	2.5	3.1	332.4	6.9
BC36_1	2008	Main Pop	177	6	1	1	2	1	25	181.8	3.1	5.4		6.1
BC36_2	2008	Main Pop	165	6	1	1	2	1	25	152.9	2.5	4.4	320.7	6.2
BC36_3	2008	Main Pop	177	6	1	1	2	1	9	236.4	4.1			
BC37_1	2008	Main Pop	69	6	1	1	2	1	25	275.3	3.3	3.5	355.3	8.7
BC37_2	2008	Main Pop	107	6	1	1	2	1	25	246.0	3.1	3.6	373.8	9.3
BC38_1	2008	Progeny	272	30	1	1	2	1	15	185.2	3.7	7.4		7.8
BC38_3	2008	Progeny	206	28	1	1	2	1	20	169.5	3.2	4.2	409.1	7.7
BC40_2	2009	Main Pop	158	6	1	1	2	1	25	122.3	2.3	4.3	312.5	4.3
BC40_3	2009	Main Pop	158	6	1	1	2	1	25	215.3	2.7	3.0	342.0	6.5
BC40_4	2009	Main Pop	142	6	1	1	2	1	25	191.7	3.8	4.0		
BC42_1	2010	Prod Pop	37	23	1	1	1	1	26	208.4	3.5	4.2		
BC43_1	2011	Comp Wood	79	27	1	1	2	1	30	167.1	3.0	3.9	310.8	3.9
BC46_1	2011	Main Pop	104	4	1	1	2	1	25	163.4	3.0	3.8		
BC46_2	2011	Main Pop	139	6	1	1	2	1	25	167.4	2.9	4.1		
BC46_3	2011	Main Pop	143	6	1	1	2	1	20	183.1	3.1	4.1		
BC52_3	2013	Cl Elite	56	51	1	1	2	2	5	131.6	3.1	4.5	347.3	5.6
FR123_1	1990	Guad Hyb	19	1	1	1	1	1	35	204.3	6.4	6.3		
FR123_4	1990	Guad Hyb	19	1	1	1	1	1	30	247.7	5.3	5.4		
FR124_1	1990	Breeding	63	80	1	2	1	1	32	208.8	2.7	5.5		
FR124_4	1990	Breeding	52	67	1	2	1	1	31	220.1	2.4	5.2		
FR170_1	1992	Fem Tester	125	6	1	2	1	1	30	197.2	6.6	7.2		9.9
FR170_2	1992	Fem Tester	152	6	1	2	1	1	30	201.4	6.1	6.4		9.6
FR170_3	1992	Fem Tester	152	6	1	2	1	1	30	173.9	5.8	6.1		
FR171_3	1992	Farm Fld	128	1	1	2	1	1	32	221.1	6.0	5.3		12.7
FR202_3	1993	Adv Gen	46	67	1	2	1	1	25	204.8	6.2	6.3		
FR203_1	1993	Fem Tester	189	5	1	2	1	1	30	248.5	6.3	5.9	343.0	
FR203_2	1993	Fem Tester	165	5	1	2	1	1	30	187.4	6.1	6.1	352.8	7.1
FR203_3	1993	Fem Tester	98	5	1	2	1	1	30	214.2	6.0	6.4		
FR216_1	1994	Fem Tester	17	18	1	2	1	1	32	159.3	5.9	6.3		
FR217_1	1994	Elite	29	24	1	2	1	1	30	233.4	6.0	6.1		
FR217_2	1994	Elite	29	24	1	2	1	1	30	223.5	6.0	6.2		
FR217_3	1994	Elite	27	22	1	2	1	1	30	243.0	6.1	6.0		
FR260_1	1995	Elite	26	21	1	2	1	1	30	200.8	5.6	5.7	345.4	3.7
FR260_3	1995	Elite	24	19	1	2	1	1	30	168.8	6.0	6.0	351.7	
FR305_11	1997	Cl Elite	25	18	1	2	1	2	6	232.6	6.3	6.5	328.0	6.8
FR305_12	1997	Cl Elite	19	16	1	2	1	2	6	210.4	6.0	6.2	352.4	7.5
FR305_21	1997	Cl Elite	25	18	1	2	1	2	6	198.4	6.7	7.0	348.2	9.0
FR305_22	1997	Cl Elite	19	16	1	2	1	2	6	201.9	6.9	6.8	363.9	8.4
FR307_2	1997	Fem Tester	52	6	1	2	1	1	30	219.9	5.4	6.1		
FR307_3	1997	Fem Tester	52	6	1	2	1	1	30	200.1	4.6	6.7		
FR353_1	1999	Clonal	18	15	1	1	2	2	5	213.3	4.4	6.2	358.9	12.5
FR353_2	1999	Clonal	18	15	1	1	2	2	5	180.5	3.8	6.2		
FR353_3	1999	Clonal	17	14	1	1	2	2	5	175.2	5.6	7.1	384.9	13.4
FR38_1	1988	Progeny	224	1	1	2	1	1	33	161.5	6.2	5.6	448.6	
FR38_2	1988	Progeny	224	1	1	2	1	1	32	211.9	4.4	5.0	329.7	5.2
FR38_3	1988	Progeny	224	1	1	2	1	1	29	219.0	6.0	5.2	344.1	6.8
FR399_1	2000	Guad Hyb	56	60	1	2	1	1	26	172.9	3.0	6.3		
FR399_2	2000	Guad Hyb	54	58	1	2	1	1	30	152.1	2.9	6.4	353.5	6.6
FR399_3	2000	Guad Hyb	56	61	1	2	1	1	30	159.0	3.5	6.8	358.4	4.6
FR69_1	1989	Progeny	329	1	1	2	1	1	32	190.5	6.3	6.4		
FR69_2	1989	Progeny	329	1	1	2	1	1	32	206.7	4.6	5.0		
FR69_3	1989	Progeny	329	1	1	2	1	1	32	171.7	3.9	4.8		
NN330_1	1975	BValues	105	1	1	2	1	1	10	144.9	5.1	6.1		
RO1015_1	1972	Breeding	104	1	2	2	1	1	10	233.5	4.2	5.4		
RO1015_2	1972	Breeding	23	4	1	1	1	1	15	251.7	5.9	4.5		
RO1804_0	1980	Diallel	86	96	1	2	1	1	46	234.5	5.8	5.9		
RO1836_0	1981	Progeny	171	1	1	2	1	1	45	206.0	5.9	5.4	383.5	

A Additional information on the BV2018 MET data set

Summary of trials included in the BV2018 G&F and WQ analyses including the mean trait value for each trial

										mean			
Expt	Pldate	TrialType	Fcln	Mcln	Mtree	Setgrp	Iblk	Clonal	Reps	dbh	br	str	dens	pme
RO1838_0	1981	Progeny	170	1	1	2	1	1	35	90.8	5.2	5.1		
RO1884_2	1983	Dothi Res	169	1	1	2	1	1	33	144.0	5.6	5.1		
RO1884_3	1983	Dothi Res	169	1	1	2	1	1	33	156.8	5.4	5.9		
RO2052_4	1985	Fact Prog	75	74	1	2	1	1	15	143.9	6.0	6.9		
RO2111_1	1987	Progeny	540	1	1	2	1	1	25	189.2	3.3	5.1	357.2	12.5
RO320_15	1972	Breeding	23	4	2	1	1	1	15	244.6	5.1	6.0		
RO320_16	1972	Progeny	104	1	2	2	1	1	7	225.7	4.3	5.4		
RO320_25	1975	Diallel	20	20	1	2	1	1	6	235.7	5.4	6.1		
RO663_0	1975	Diallel	20	20	1	2	1	1	6	205.9	5.1	5.0		
RO664_1	1975	BValues	106	1	1	2	1	1	10	227.9	4.5	5.7		
RO664_13	1980	Diallel	86	96	1	2	1	1	50	180.5	5.8	6.8		
RO664_2	1975	Diallel	21	21	1	2	1	1	6	255.8	5.3	6.0		
RO944_8	1968	Progeny	372	1	2	2	1	1	5	240.1	5.7	5.7		
RO947_2	1969	Progeny	588	1	2	2	1	1	5	237.7	5.0	5.6		
SD228_0	1971	Progeny	298	1	2	2	1	1	5	248.3	5.2	5.9		
SD413_0	1975	Diallel	20	20	1	2	1	1	6	166.7	3.3	5.4		
SD415_0	1975	BValues	100	1	1	2	1	1	10	114.9	4.9	5.7		
WD174_0	1975	Diallel	20	20	1	2	1	1	6	192.7	6.0	5.5		
WN212_0	1969	Progeny	564	1	2	2	1	1	5	229.0	5.8	5.6		

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