**Manuscript G3-2021-402668: Supplementary Materials**

**Methods**

**SM.M1 – Single site analyses**

The races listed in Table S1.C were included as fixed genetic group effects within the pedigree (Westell et al. 1988). Fixed effects were included for the overall mean, replicates, and checklots. Random effects were additive and family-specific genetic effects of full-sib families, incomplete blocks, and row-plots. The dispersion matrices contained elements **A**$\hat{σ}\_{a}^{2}$, **I**$\hat{σ}\_{f}^{2}$, **I**$\hat{σ}\_{b}^{2}$**¸** **I**$\hat{σ}\_{p}^{2}$*,*and **I**$\hat{σ}\_{e}^{2}$*,* where $\hat{σ}\_{a}^{2}$is the estimated additive genetic variance fitted to full-sib families, $\hat{σ}\_{f}^{2}$is the estimated non-additive full-sib family-specific variance, $\hat{σ}\_{b}^{2}$is the estimated incomplete block variance, $\hat{σ}\_{p}^{2} $is the plot variance, $\hat{σ}\_{e}^{2} $is the residual variance, **A** was previously defined, and **I** is the identity matrix. OP families were not included in relationship matrices and were represented with separate random effects to avoid bias in estimates of $\hat{σ}\_{a}^{2}$. Additional within-plot error was fitted for checklots. A two-dimensional autoregressive structure fitted to ordered row and column effects in VOL was used to model the spatial trend in each trial: $\hat{σ}\_{ξ}^{2}\left[AR1\left(ρ\_{col}\right)⊗AR1(ρ\_{row})\right]$, where $\hat{σ}\_{ξ}^{2}$ is the estimated spatial variance, and AR1(ρ) represents a first-order autoregressive correlation matrix (Dutkowski et al. 2002). Spatial effects on VOL were retained for all but one site after significance testing by two-tailed likelihood ratio tests (LRT; Gilmour et al. 2015), fitting additional random row or column effects where necessary, and visual inspection of two-dimensional smoothness. The effect of multi-stemmed form on VOL was determined to be significant by one-tailed LRT at seven sites.

VOL data from each of the EG2 trials were then analysed on a single-site basis using both **A** without groups and **H** (single-site HBLUP) as the numerator relationship matrix (NRM). Goodness of fit was compared amongst single-site EG2 models using the Akaike Information Criterion (AIC; Akaike 1974), for which lower values indicate better fit. Single-site coefficient of additive variation ($\hat{CV}\_{a}$), narrow-sense heritability ($\hat{h}^{2}$) and dominance proportion ($\hat{d}^{2}$) were calculated using **A**, with and without genetic groups, and **H** as the NRM:

$$\begin{array}{c}\hat{CV}\_{a}=\frac{100 \sqrt{\hat{σ}\_{a}^{2}}}{\overbar{X}}\#\end{array}$$

$$\begin{array}{c}\hat{h}^{2}=\frac{\hat{σ}\_{a}^{2}}{\overbar{\hat{σ}\_{a}^{2}+\hat{σ}\_{f}^{2}+\hat{σ}\_{b}^{2}+\hat{σ}\_{p}^{2}+\hat{σ}\_{e}^{2}}}\#\end{array}$$

$$\begin{array}{c}\hat{d}^{2}=\frac{4\hat{σ}\_{f}^{2}}{\overbar{\hat{σ}\_{a}^{2}+\hat{σ}\_{f}^{2}+\hat{σ}\_{b}^{2}+\hat{σ}\_{p}^{2}+\hat{σ}\_{e}^{2}}}\#\end{array}$$

where $\overbar{X}$ is the trait mean. Parameter estimates did not vary substantially from expectation and all trials were retained for across site analyses.

**SM.M2** **– Preliminary cross site analyses**

Two preliminary cross-site analyses for VOLadj were then conducted for each program and each used **A** with genetic groups as the NRM. In the first, $\hat{σ}\_{a}^{2}$ and $\hat{σ}\_{f}^{2}$ were heterogenous and the ratio $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ was determined for each site. Non-additive genetic effects differed considerably among trials and the preliminary across model accommodated this heterogeneity by sub-setting trials to provide $\hat{σ}\_{f}^{2}$ estimates for four sets of trials where dominance to additive variance estimates near zero, low, moderate and high. Trials were classed into four groups with similar non-additive to additive variance ratios: Group 1 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ less than 0.04 (mean 0.02; seven sites), Group 2 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$between 0.06 and 0.30 (mean 0.15; 34 sites representing all regions), Group 3 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ between 0.30 and 0.38 (mean 0.33; four sites), and Group 4 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ between 0.58 and 0.85 (mean 0.73; three sites).

In the second preliminary cross-site model for VOLadj also allowed heterogeneous $\hat{σ}\_{a}^{2}$, however $\hat{σ}\_{f}^{2}$ at each site was constrained to a common $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ ratio within groups 2 to 4 and $\hat{σ}\_{f}^{2}$ was not fitted to Group 1 trials that had near zero family variance. Family effects were fit at the region level with inter-region correlation and across sites included for Group 2 trials while separate family effects were fit for Group 3 and 4. The $\hat{σ}\_{a}^{2}$ estimates for each site provided by this preliminary cross-site model were used to standardize data from each site. VOLadj data were standardised by site to have a zero mean and an additive standard deviation of one.

 A similar procedure was used for modelling DENS and CELL across sites. Three site groups were formed for DENS on the basis of $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ ratio: Group 1 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ of zero (seven sites), Group 2 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$between 0.04 and 0.31 (mean 0.15; 12 sites), and Group 3 contained a single site with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ of 1.12. Two site Groups were formed for CELL on the basis of $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ ratio: Group 1 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$ of zero (six sites) and Group 2 with $\hat{σ}\_{f}^{2}:\hat{σ}\_{a}^{2}$between 0.05 and 0.38 (mean 0.18; 18 sites). Additive and non-additive genetic effects were fitted across sites to DENS and CELL regardless of region.

**Supplementary Materials tables S1.A to S1D** provide summaries of the *E. globulus* breeding populations, the structure of the treatments evaluating in the trials, the composition of the native range provenances and external populations and phenotypic data collected for different strata in each breeding population.

**Table S1.A** Summary of trial sites and data collected from thebreeding populations.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trial | Program | Region | Year Planted | Latitude | Longitude | CP FAMS | SizeMeas Yr | n(HT) | HT.sample | n(DBH,VOL) | n(DENS) | n(CELL) |
| 1 | EG1 | WA | 1998 | -34.874 | 117.606 | 125 | 8 | 3844 | 100% | 3844 |  |  |
| 2 | EG1 | WA | 1998 | -34.805 | 118.105 | 155 | 8 | 3320 | 100% | 3320 | 1725 | 298 |
| 3 | EG1 | WA | 1999 | -34.515 | 117.219 | 155 | 5 | 4905 | 100% | 4905 | 2097 | 909 |
| 4 | EG1 | WA | 1999 | -34.443 | 118.503 | 154 | 5 | 4091 | 100% | 4091 | 1792 |  |
| 5 | EG1 | WA | 1999 | -34.780 | 118.194 | 147 | 5 | 4050 | 100% | 4050 | 1790 |  |
| 6 | EG1 | WA | 2001 | -34.846 | 118.022 | 85 | 5 | 1510 | 100% | 1510 | 754 | 321 |
| 7 | EG1 | WA | 2001 | -33.750 | 122.017 | 85 | 5 | 1319 | 100% | 1319 | 762 | 337 |
| 8 | EG1 | WA | 2003 | -34.974 | 118.000 | 39 | 5 | 960 | 100% | 960 | 418 |  |
| 9 | EG1 | WA | 2003 | -33.834 | 122.653 | 28 | 5 | 629 | 100% | 629 |  |  |
| 10 | EG1 | WA | 2003 | -34.598 | 117.603 | 35 | 3 | 938 | 100% | 938 |  |  |
| 11 | EG1 | WA | 2004 | -33.813 | 122.374 | 61 | 5 | 1654 | 100% | 1654 | 718 |  |
| 12 | EG1 | WA | 2004 | -34.543 | 118.669 | 45 | 5 | 1244 | 100% | 1244 | 557 |  |
| 13 | EG1 | WA | 2005 | -34.721 | 118.377 | 78 | 5 | 2263 | 100% | 2263 | 1273 |  |
| 14 | EG1 | WA | 2005 | -33.812 | 120.726 | 26 | 5 | 2324 | 100% | 2324 | 1326 |  |
| 15 | EG1 | WA | 2005 | -33.816 | 122.721 | 59 | 5 | 1930 | 100% | 1930 |  |  |
| 16 | EG1 | WA | 2005 | -33.792 | 122.711 | 71 | 3 | 2377 | 100% | 2377 |  |  |
| 17 | EG1 | WA | 2007 | -34.875 | 117.876 | 306 | 5 | 7399 | 100% | 7399 | 2551 | 1023 |
| 18 | EG1 | WA | 2007 | -34.874 | 117.887 | 306 | 5 | 6214 | 100% | 6214 |  |  |
| 19 | EG1 | WA | 2007 | -33.785 | 122.199 | 306 | 5 | 5103 | 100% | 5103 |  |  |
| 20 | EG1 | WA | 2010 | -34.563 | 116.988 | 75 | 5 | 2111 | 100% | 2111 |  |  |
| 21 | EG1 | WA | 2010 | -34.893 | 117.754 | 137 | 5 | 4204 | 100% | 4204 |  |  |
| 22 | EG1 | WA | 2012 | -34.779 | 118.323 | 345 | 5 | 10189 | 100% | 10189 | 1564 | 1523 |
| 23 | EG1 | WA | 2012 | -34.854 | 117.904 | 308 | 5 | 7335 | 100% | 7335 | 991 | 988 |
| 24 | EG1 | WA | 2015 | -34.833 | 117.769 | 265 | 3 | 3111 | 100% | 3111 |  |  |
| 25 | EG1 | WA | 2015 | -34.710 | 118.022 | 262 | 3 | 3071 | 100% | 3071 |  |  |
| 26 | EG2 | WA | 2005 | -34.770 | 117.598 | 122 | 4 | 2719 | 100% | 2712 |  |  |
| 27 | EG2 | WA | 2006 | -34.893 | 117.924 | 107 | 4 | 2298 | 100% | 2259 |  |  |
| 28 | EG2 | WA | 2006 | -34.769 | 117.857 | 114 | 4 | 1939 | 100% | 1934 |  |  |
| 29 | EG1 | GT | 1999 | -37.909 | 141.729 | 134 | 5 | 4059 | 100% | 4059 | 1735 |  |
| 30 | EG1 | GT | 2001 | -37.821 | 140.862 | 59 | 3 | 2726 | 100% | 2726 |  |  |
| 31 | EG1 | GT | 2011 | -37.960 | 141.071 | 36 | 5 | 3636 | 100% | 3636 |  |  |
| 32 | EG1 | GT | 2012 | -37.714 | 140.999 | 210 | 5 | 3994 | 100% | 3994 |  |  |
| 33 | EG1 | GT | 2015 | -37.925 | 141.028 | 265 | 3 | 2670 | 100% | 2670 |  |  |
| 34 | EG2 | GT | 2003 | -38.182 | 142.089 | 93 | 5 | 2162 | 100% | 2154 | 330 | 330 |
| 35 | EG2 | GT | 2004 | -38.055 | 142.678 | 177 | 4 | 375 | 10% | 3584 |  |  |
| 36 | EG2 | GT | 2004 | -38.055 | 142.678 | 171 | 4 | 301 | 9% | 3470 | 566 | 566 |
| 37 | EG2 | GT | 2005 | -37.677 | 142.068 | 114 | 4 | 298 | 12% | 2428 |  |  |
| 38 | EG2 | GT | 2009 | -37.917 | 141.040 | 141 | 4 | 2639 | 100% | 2623 |  |  |
| 39 | EG2 | GT | 2009 | -37.782 | 141.127 | 109 | 4 | 2280 | 100% | 2242 |  |  |
| 40 | EG2 | GT | 2011 | -37.840 | 141.746 | 248 | 5 | 630 | 12% | 5462 | 261 | 261 |
| 41 | EG2 | GT | 2011 | -38.171 | 141.815 | 207 | 5 | 537 | 11% | 4775 |  |  |
| 42 | EG2 | GT | 2011 | -37.307 | 141.478 | 139 | 5 | 472 | 10% | 4580 |  |  |
| 43 | EG2 | GIPPS | 2003 | -38.298 | 146.256 | 84 | 3 | 305 | 17% | 1807 | 196 | 196 |
| 44 | EG2 | GIPPS | 2004 | -38.264 | 146.259 | 158 | 8 | 251 | 8% | 3128 |  |  |
| 45 | EG2 | GIPPS | 2004 | -37.406 | 149.018 | 119 | 5 | 77 | 3% | 2322 |  |  |
| 46 | EG2 | GIPPS | 2005 | -38.316 | 145.978 | 101 | 5 | 80 | 4% | 2154 |  |  |
| 47 | EG2 | GIPPS | 2009 | -38.253 | 146.085 | 161 | 4 | 3225 | 100% | 3168 | 290 | 290 |
| 48 | EG2 | GIPPS | 2011 | -38.328 | 146.269 | 228 | 5 | 600 | 15% | 4070 |  |  |

***Table* S1.B*.*** *Summary of breeding programs providing number of trials, number of full-sib (control pollinated (CP)) families, and number of CP progeny by breeding program and planting region.*

|  |  |  |
| --- | --- | --- |
|  | **EG1** | **EG2** |
| *Western Australia* |  |  |
| Trials | 25 | 3 |
| CP Families | 1256 | 222 |
| CP Progeny | 68,816 | 5924 |
| *Green Triangle* |  |  |
| Trials | 5 | 9 |
| CP Families | 655 | 592 |
| CP Progeny | 12,263 | 23,065 |
| *Gippsland* |  |  |
| Trials | 0 | 6 |
| CP Families | 0 | 632 |
| CP Progeny | 0 | 16,399 |

***Table* S1.C*.*** *Number of families within E. globulus races represented in the pedigree of EG1 and EG2 full-sib families.*

|  |  |  |
| --- | --- | --- |
| Race | EG1 | EG2 |
| W Otways | 8 | 12 |
| E Otways | 3 | 5 |
| Strzelecki Ranges | 7 | 30 |
| Furneaux | 25 | 8 |
| NE Tasmania | 17 | 3 |
| SE Tasmania | 7 | 8 |
| S Tasmania | 1 | 3 |
| W Tasmania | 7 | 0 |
| King Is. | 13 | 6 |
| Portugal | 18 | 8 |
| California | 6 | 0 |
| TOTAL | 112 | 83 |

***Table* S1.D*.*** *Summary of phenotypic data describing the number of trials, number of control pollinated families, number of control pollinated progeny and total number of trees in each breeding program.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Program | Stem Volume | Basic Density | Cellulose Content |
| Trials | EG1 | 30 | 15 | 15 |
|  | EG2 | 18 | 5 | 5 |
|  | Total | 48 | 20 | 20 |
| CP Families | EG1 | 1282 | 744 | 564 |
|  | EG2 | 691 | 308 | 308 |
|  | Total | 1973 | 1052 | 872 |
| CP Progeny1 | EG1 | 80,905 (100%) | 14,847 (18%) | 4612 (6%) |
|  | EG2 | 45,384 (100%) | 1491 (3%) | 1489 (3%) |
|  | Total | 126,289 (100%) | 16,338 (13%) | 6101 (5%) |
| All Trial Trees | EG1 | 103,180 | 19,755 | 5384 |
|  | EG2 | 54,872 | 1643 | 1640 |
|  | Total | 158,052 | 21,398 | 7024 |

1Percentages in brackets represent proportion of trees present that were phenotyped

**Table S2.A.**Mean and standard error of prediction error variance and prediction accuracy for cohorts of parents, genotyped individuals, and progeny in the EG1 program

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **N** | ABLUP+race1 | (se) | ABLUP-race 2 | (se) | EG1-HBLUP3 | (se) | JOINT-HBLUP4 | (se) | Drace5 | (se)6 | Drace+markers7 | (se)6 | Drace+markers +joint8 | (se)6 |
| ***Program EG1 IN WA*** |  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| PEV.geno.parent.represented9 | **162** | 0.127 | (0.006) | 0.132 | (0.007) | 0.120 | (0.006) | 0.123 | (0.006) | 0.005 | (0.002)\*\* | -0.007 | (0.002)\*\*\* | -0.004 | (0.002)\* |
| PEV.geno.parent.correlated10 | **2** | 0.294 | (0.018) | 0.333 | (0.018) | 0.297 | (0.010) | 0.305 | (0.016) | 0.039 | (0.001)\* | 0.003 | (0.008) | 0.011 | (0.002) |
| PEV.geno.related11 | **32** | 0.295 | (0.003) | 0.339 | (0.003) | 0.296 | (0.011) | 0.299 | (0.011) | 0.044 | (<0.001)\*\*\* | 0.001 | (0.010) | 0.005 | (0.010) |
| PEV.geno.unrelated12 | **52** | NA23 | - | NA23 | - | 0.887 | (0.014) | 0.459 | (0.011) | NA | - | NA | - | NA | - |
| PEV.ungeno.parent.represented13 | **182** | 0.187 | (0.009) | 0.185 | (0.008) | 0.182 | (0.008) | 0.179 | (0.008) | -0.002 | (0.003) | -0.004 | (0.003) | -0.008 | (0.004) |
| PEV.ungeno.parent.correlated14 | **1** | NA24 | - | NA | - | NA | - | NA | NA | NA | - | NA | - | NA | - |
| PEV.progeny15 | **63521** | 0.273 | (<0.001) | 0.308 | (<0.001) | 0.302 | (<0.001) | 0.322 | (<0.001) | 0.035 | (<0.001)\*\*\* | 0.030 | (<0.001)\*\*\* | 0.05 | (<0.001)\*\*\* |
| rgg.geno.parent.represented16 | **162** | 0.864 | (0.008) | 0.882 | (0.006) | 0.892 | (0.006) | 0.898 | (0.005) | 0.018 | (0.003)\*\*\* | 0.027 | (0.004)\*\*\* | 0.034 | (0.004)\*\*\* |
| rgg.geno.parent.correlated17 | **2** | 0.661 | (0.027) | 0.674 | (0.021) | 0.709 | (0.012) | 0.729 | (0.017) | 0.013 | (0.005) | 0.048 | (0.014) | 0.068 | (0.010) |
| rgg.geno.related18 | **32** | 0.660 | (0.004) | 0.667 | (0.003) | 0.707 | (0.014) | 0.732 | (0.012) | 0.008 | (0.001)\*\*\* | 0.047 | (0.012)\*\*\* | 0.072 | (0.011)\*\*\* |
| rgg.geno.unrelated19 | **52** | NA | - | NA | - | 0.401 | (0.016) | 0.531 | (0.016) | NA | - | NA | - | NA | - |
| rgg.ungeno.parent.represented20 | **182** | 0.788 | (0.012) | 0.827 | (0.009) | 0.825 | (0.009) | 0.845 | (0.008) | 0.039 | (0.005)\*\*\* | 0.038 | (0.005)\*\*\* | 0.057 | (0.006)\*\*\* |
| rgg.ungeno.parent.correlated21 | **1** | NA | - | NA | - | NA | - | NA | NA | NA | - | NA | - | NA | - |
| rgg.progeny22 | **63521** | 0.691 | (0.000) | 0.704 | (0.000) | 0.702 | (0.000) | 0.71 | (<0.001) | 0.013 | (<0.001)\*\*\* | 0.012 | (<0.001)\*\*\* | 0.019 | (<0.001)\*\*\* |
| ***Program EG1 IN GT*** |  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| PEV.geno.parent.represented | **152** | 0.380 | (0.227) | 0.363 | (0.100) | 0.348 | (0.096) | 0.268 | (0.008) | -0.018 | (0.021) | -0.033 | (0.021) | -0.112 | (0.022)\*\*\* |
| PEV.geno.parent.correlated | **12** | 0.402 | (0.022) | 0.442 | (0.027) | 0.436 | (0.042) | 0.313 | (0.033) | 0.040 | (0.005)\*\*\* | 0.034 | (0.034) | -0.089 | (0.027)\*\* |
| PEV.geno.related | **32** | 0.463 | (0.010) | 0.536 | (0.003) | 0.549 | (0.018) | 0.438 | (0.014) | 0.073 | (0.007)\*\*\* | 0.086 | (0.019)\*\*\* | -0.025 | (0.016) |
| PEV.geno.unrelated | **52** | NA | - | NA | - | 0.887 | (0.014) | 0.631 | (0.016) | NA | - | NA | - | NA | - |
| PEV.ungeno.parent.represented | **110** | 0.365 | (0.018) | 0.374 | (0.019) | 0.376 | (0.019) | 0.32 | (0.015) | 0.009 | (0.003)\*\* | 0.010 | (0.003)\*\*\* | -0.046 | (0.004)\*\*\* |
| PEV.ungeno.parent.correlated | **73** | 0.774 | (0.070) | 0.562 | (0.020) | 0.576 | (0.021) | 0.423 | (0.015) | -0.213 | (0.055)\*\*\* | -0.198 | (0.055)\*\*\* | -0.351 | (0.061)\*\*\* |
| PEV.progeny | **9055** | 0.437 | (0.001) | 0.497 | (0.001) | 0.497 | (0.001) | 0.445 | (<0.001) | 0.060 | (<0.001)\*\*\* | 0.060 | (<0.001)\*\*\* | 0.008 | (<0.001)\*\*\* |
| rgg.geno.parent.represented | **152** | 0.729 | (0.015) | 0.795 | (0.007) | 0.805 | (0.007) | 0.832 | (0.006) | 0.066 | (0.010)\*\*\* | 0.076 | (0.010)\*\*\* | 0.102 | (0.011)\*\*\* |
| rgg.geno.parent.correlated | **12** | 0.713 | (0.020) | 0.748 | (0.018) | 0.746 | (0.032) | 0.799 | (0.026) | 0.035 | (0.001)\*\*\* | 0.033 | (0.028) | 0.086 | (0.023)\*\* |
| rgg.geno.related | **32** | 0.659 | (0.012) | 0.685 | (0.002) | 0.67 | (0.014) | 0.707 | (0.012) | 0.026 | (0.010)\* | 0.011 | (0.018) | 0.048 | (0.017)\*\* |
| rgg.geno.unrelated | **52** | NA | - | NA | - | 0.331 | (0.018) | 0.52 | (0.017) | NA | - | NA | - | NA | - |
| rgg.ungeno.parent.represented | **110** | 0.727 | (0.016) | 0.783 | (0.012) | 0.782 | (0.012) | 0.79 | (0.011) | 0.057 | (0.005)\*\*\* | 0.055 | (0.005)\*\*\* | 0.064 | (0.006)\*\*\* |
| rgg.ungeno.parent.correlated | **73** | 0.495 | (0.038) | 0.651 | (0.017) | 0.638 | (0.017) | 0.713 | (0.013) | 0.156 | (0.024)\*\*\* | 0.143 | (0.024)\*\*\* | 0.218 | (0.029)\*\*\* |
| rgg.progeny | **9055** | 0.681 | (0.001) | 0.709 | (0.001) | 0.709 | (0.001) | 0.701 | (<0.001) | 0.028 | (<0.001)\*\*\* | 0.027 | (<0.001)\*\*\* | 0.02 | (<0.001)\*\*\* |

1ABLUP+Race derived from pedigree with genetic groups, 2ABLUP derived from pedigree, 3EG1-HBLUP derived from EG1-wide analysis using pedigree and GRM, 4JOINT-HBLUP derived from joint-program analysis using pedigree and GRM, 5Drace is change in estimate from ABLUP+race when genetic groups are removed from the model, 6Result of two-way t-test result for *H1*: mean change from ABLUP+race significantly different to zero : \* p<0.05, \*\* p<0.01, \*\*\* p<0.001, 7Drace+markers is change in estimate from ABLUP+race when genetic groups are removed from the model and the H matrix is used, 8 Drace+markers+joint is change in estimate from ABLUP+race when genetic groups are removed, the H matrix is used, and the analysis is jointly across programs, 9PEV.geno.parent.represented is prediction error variance for genotyped parents with progeny represented in the region, 10PEV. geno.parent.correlated is prediction error variance for genotyped parents estimated through inter-region correlation because progeny unrepresented in the region, 11PEV.geno.related is prediction error variance for genotyped individuals that were not parents of tested progeny and were related through the pedigree, 12PEV.geno.unrelated is prediction error variance for genotyped individuals that were not parents of tested progeny and were not related through the pedigree, 13PEV.ungeno.parent.represented is prediction error variance for ungenotyped parents with progeny represented in the region, 14PEV.ungeno.parent.correlated is prediction error variance for ungenotyped parents estimated through inter-region correlation because progeny unrepresented in the region,  15PEV.progeny is prediction error variance for progeny (none genotyped) in the region, 16rgg.geno.parent.represented is prediction accuracy for genotyped parents with progeny represented in the region, 17rgg.geno.parent.correlated is prediction accuracy for genotyped parents estimated through inter-region correlation because progeny unrepresented in the region, 18rgg.geno.related is prediction accuracy for genotyped individuals that were not parents of tested progeny and were related through the pedigree, 19rgg.geno.unrelated is prediction accuracy for genotyped individuals that were not parents of tested progeny and were not related through the pedigree, 20rgg.ungeno.parent.represented is prediction accuracy for ungenotyped parents with progeny represented in the region, 21rgg.ungeno.parent.correlated is prediction accuracy for ungenotyped parents estimated through inter-region correlation because progeny unrepresented in the region,  22rgg.progeny is prediction accuracy for progeny (none genotyped) in the region, 23Unrelated individuals were not included in ABLUP+race or ABLUP models, 24Means not presented for classes with 0 or 1 individuals

**Table S2.B.** Mean and standard error of prediction error variance and prediction accuracy for cohorts of parents, genotyped individuals, and progeny in the EG2 program1

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **N** | ABLUP+race | (se) | ABLUP-race | (se) | EG2-HBLUP | (se) | JOINT-HBLUP | (se) | Drace | (se)1 | Drace+markers | (se)1 | Drace+markers +joint | (se)1 |
| ***Program EG2 IN WA*** |  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| PEV.geno.parent.represented | **61** | 0.245 | (0.017) | 0.25 | (0.019) | 0.238 | (0.017) | 0.164 | (0.009) | 0.005 | (0.003) | -0.007 | (0.003)\* | -0.081 | (0.017)\*\*\* |
| PEV.geno.parent.correlated | **32** | 0.541 | (0.023) | 0.57 | (0.028) | 0.491 | (0.023) | 0.277 | (0.011) | 0.029 | (0.013)\* | -0.049 | (0.013)\*\*\* | -0.264 | (0.016)\*\*\* |
| PEV.geno.related | **39** | 0.697 | (0.027) | 0.892 | (0.031) | 0.815 | (0.029) | 0.375 | (0.012) | 0.195 | (0.012)\*\*\* | 0.118 | (0.022)\*\*\* | -0.322 | (0.025)\*\*\* |
| PEV.geno.unrelated | **5** | NA | - | NA | - | 1.092 | (0.129) | 0.47 | (0.050) | NA | - | NA | - | NA | - |
| PEV.ungeno.parent.represented | **10** | 0.307 | (0.036) | 0.305 | (0.038) | 0.295 | (0.036) | 0.205 | (0.020) | -0.001 | (0.010) | -0.012 | (0.008) | -0.102 | (0.017)\*\*\* |
| PEV.ungeno.parent.correlated | **4** | 0.695 | (0.129) | 0.715 | (0.093) | 0.674 | (0.088) | 0.394 | (0.043) | 0.020 | (0.038) | -0.021 | (0.043) | -0.300 | (0.088)\* |
| PEV.progeny | **5924** | 0.532 | -(0.001) | 0.670 | -(0.001) | 0.644 | -(0.001) | 0.363 | (<0.001) | 0.138 | (<0.001)\*\*\* | 0.112 | (<0.001)\*\*\* | -0.169 | (<0.001)\*\*\* |
| rgg.geno.parent.represented | **61** | 0.870 | (0.010) | 0.906 | (0.008) | 0.906 | (0.007) | 0.862 | (0.008) | 0.035 | (0.002)\*\*\* | 0.036 | (0.003)\*\*\* | -0.008 | (0.011) |
| rgg.geno.parent.correlated | **32** | 0.685 | (0.017) | 0.77 | (0.014) | 0.796 | (0.011) | 0.755 | (0.012) | 0.085 | (0.007)\*\*\* | 0.111 | (0.009)\*\*\* | 0.070 | (0.011)\*\*\* |
| rgg.geno.related | **39** | 0.541 | (0.030) | 0.594 | (0.022) | 0.62 | (0.019) | 0.645 | (0.015) | 0.053 | (0.014)\*\*\* | 0.079 | (0.023)\*\* | 0.104 | (0.029)\*\*\* |
| rgg.geno.unrelated | **5** | NA | - | NA | - | 0.383 | (0.118) | 0.503 | (0.079) | NA | - | NA | - | NA | - |
| rgg.ungeno.parent.represented | **10** | 0.836 | (0.021) | 0.885 | (0.015) | 0.883 | (0.015) | 0.826 | (0.019) | 0.048 | (0.008)\*\*\* | 0.047 | (0.007)\*\*\* | -0.011 | (0.006) |
| rgg.ungeno.parent.correlated | **4** | 0.503 | (0.169) | 0.699 | (0.050) | 0.703 | (0.049) | 0.620 | (0.057) | 0.196 | (0.120) | 0.200 | (0.120) | 0.117 | (0.114) |
| rgg.progeny | **5924** | 0.696 | (<0.001) | 0.726 | (<0.001) | 0.723 | (<0.001) | 0.665 | (<0.001) | 0.030 | (<0.001)\*\*\* | 0.027 | (<0.001)\*\*\* | -0.031 | (<0.001)\*\*\* |
| ***Program EG2 IN GT*** |  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| PEV.geno.parent.represented | **91** | 0.151 | (0.023) | 0.156 | (0.024) | 0.147 | (0.021) | 0.143 | (0.010) | 0.005 | (0.001)\*\*\* | -0.004 | (0.002)\*\* | -0.009 | (0.016) |
| PEV.geno.parent.correlated | **2** | 0.670 | (0.013) | 0.739 | (0.030) | 0.680 | (0.093) | 0.524 | (0.086) | 0.069 | (0.017) | 0.009 | (0.080) | -0.146 | (0.073) |
| PEV.geno.related | **39** | 0.535 | (0.018) | 0.765 | (0.029) | 0.699 | (0.027) | 0.486 | (0.017) | 0.23 | (0.034)\*\*\* | 0.164 | (0.030)\*\*\* | -0.049 | (0.023)\* |
| PEV.geno.unrelated | **5** | NA | - | NA | - | 0.959 | (0.114) | 0.639 | (0.074) | NA | - | NA | - | NA | - |
| PEV.ungeno.parent.represented | **14** | 0.271 | (0.050) | 0.271 | (0.047) | 0.263 | (0.045) | 0.247 | (0.036) | -0.001 | (0.005) | -0.008 | (0.006) | -0.024 | (0.015) |
| PEV.ungeno.parent.correlated | **0** | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - |
| PEV.progeny | **23063** | 0.497 | (<0.001) | 0.572 | (<0.001) | 0.562 | (<0.001) | 0.446 | (<0.001) | 0.075 | (<0.001)\*\*\* | 0.065 | (<0.001)\*\*\* | -0.051 | (<0.001)\*\*\* |
| rgg.geno.parent.represented | **91** | 0.921 | (0.008) | 0.933 | (0.007) | 0.936 | (0.006) | 0.914 | (0.007) | 0.011 | (0.001)\*\*\* | 0.015 | (0.002)\*\*\* | -0.008 | (0.010) |
| rgg.geno.parent.correlated | **2** | 0.595 | (0.010) | 0.636 | (0.019) | 0.663 | (0.057) | 0.633 | (0.077) | 0.041 | (0.009) | 0.068 | (0.047) | 0.038 | (0.066) |
| rgg.geno.related | **39** | 0.689 | (0.016) | 0.603 | (0.023) | 0.643 | (0.018) | 0.664 | (0.016) | -0.086 | (0.027)\* | -0.045 | (0.022)\* | -0.025 | (0.020) |
| rgg.geno.unrelated | **5** | NA | - | NA | - | 0.399 | (0.120) | 0.497 | (0.086) | NA | - | NA | - | NA | - |
| rgg.ungeno.parent.represented | **14** | 0.851 | (0.033) | 0.88 | (0.023) | 0.882 | (0.023) | 0.843 | (0.027) | 0.029 | (0.011)\*\* | 0.030 | (0.011)\*\* | -0.008 | (0.008) |
| rgg.ungeno.parent.correlated | **0** | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| rgg.progeny | **23063** | 0.722 | (<0.001) | 0.734 | (<0.001) | 0.734 | (<0.001) | 0.703 | (<0.001) | 0.013 | (<0.001)\*\*\* | 0.012 | (<0.001)\*\*\* | -0.019 | (<0.001)\*\*\* |
| ***Program EG2 IN GIPPS*** |  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| PEV.geno.parent.represented | **90** | 0.233 | (0.016) | 0.219 | (0.015) | 0.219 | (0.015) | 0.16 | (0.008) | -0.014 | (0.002)\*\*\* | -0.014 | (0.003)\*\*\* | -0.073 | (0.017)\*\*\* |
| PEV.geno.parent.correlated | **3** | 0.608 | (0.011) | 0.601 | (0.011) | 0.662 | (0.047) | 0.334 | (0.027) | -0.007 | (0.018) | 0.054 | (0.052) | -0.274 | (0.034)\* |
| PEV.geno.related | **39** | 0.599 | (0.030) | 0.633 | (0.027) | 0.66 | (0.024) | 0.302 | (0.010) | 0.034 | (0.008)\*\*\* | 0.061 | (0.020)\*\* | -0.297 | (0.029)\*\*\* |
| PEV.geno.unrelated | **5** | NA | - | NA | - | 0.894 | (0.106) | 0.385 | (0.042) | NA | - | NA | - | NA | - |
| PEV.ungeno.parent.represented | **14** | 0.295 | (0.046) | 0.27 | (0.039) | 0.29 | (0.043) | 0.205 | (0.023) | -0.025 | (0.009)\* | -0.005 | (0.007) | -0.090 | (0.024)\*\* |
| PEV.ungeno.parent.correlated | **0** | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - |
| PEV.progeny | **16398** | 0.468 | (<0.001) | 0.505 | (<0.001) | 0.564 | (<0.001) | 0.295 | (<0.001) | 0.037 | (<0.001)\*\*\* | 0.097 | (<0.001)\*\*\* | -0.173 | (<0.001)\*\*\* |
| rgg.geno.parent.represented | **90** | 0.851 | (0.012) | 0.876 | (0.010) | 0.893 | (0.008) | 0.823 | (0.010) | 0.025 | (0.002)\*\*\* | 0.043 | (0.004)\*\*\* | -0.028 | (0.014)\* |
| rgg.geno.parent.correlated | **3** | 0.557 | (0.011) | 0.619 | (0.009) | 0.635 | (0.033) | 0.583 | (0.044) | 0.062 | (0.017) | 0.077 | (0.038) | 0.026 | (0.051) |
| rgg.geno.related | **39** | 0.529 | (0.038) | 0.56 | (0.031) | 0.627 | (0.019) | 0.629 | (0.016) | 0.03 | (0.008)\*\*\* | 0.098 | (0.026)\*\*\* | 0.100 | (0.036)\*\* |
| rgg.geno.unrelated | **5** | NA | - | NA | - | 0.385 | (0.118) | 0.455 | (0.096) | NA | - | NA | - | NA | - |
| rgg.ungeno.parent.represented | **14** | 0.804 | (0.039) | 0.846 | (0.025) | 0.856 | (0.024) | 0.765 | (0.032) | 0.042 | (0.015)\* | 0.052 | (0.016)\*\* | -0.039 | (0.013)\*\* |
| rgg.ungeno.parent.correlated | **0** | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - | NA | - |
| rgg.progeny | **16398** | 0.684 | (<0.001) | 0.694 | (<0.001) | 0.701 | (<0.001) | 0.647 | (<0.001) | 0.01 | (<0.001)\*\*\* | 0.017 | (<0.001)\*\*\* | -0.037 | (<0.001)\*\*\* |

1See Table S2.A for details of terms