

## E-SUPPLEMENTS

### Supplementary Appendix 1: Expected metafounder self-relationship with uniformly distributed base generation allele frequencies

The self-relationship of a metafounder can be computed as (Christensen, 2012; Garcia-Baccino et al., 2017):  $\gamma = 8\sigma_p^2$  where  $\sigma_p^2$  is the variance of the allele frequencies ( $p$ ) in the base population. We can write the expectation of this variance as:

$$E(\sigma_p^2) = E(p - \bar{p})^2 = \int_0^1 (p - \bar{p})^2 \varphi(p) dp$$

If the allele frequencies in the base follow a standard uniform distribution, i.e.  $U(0,1)$ , the probability density function is equal to  $\varphi(p) = \frac{1}{1-0} = 1$ . Thus, in this case:

$$E(\sigma_p^2) = \int_0^1 (p - \bar{p})^2 dp$$

Considering that  $\bar{p} = \frac{1}{2}$ , the primitive of  $(p - \bar{p})^2$  is  $F\left(\left(p - \frac{1}{2}\right)^2\right) = F\left(p^2 - p + \frac{1}{4}\right) = \frac{1}{3}p^3 - \frac{1}{2}p^2 + \frac{1}{4}p$ , so

$$E(\sigma_p^2) = \int_0^1 (p - \bar{p})^2 dp = F(1) - F(0) = \frac{1}{12}$$

Thus, if the allele frequencies in the base are uniformly distributed, the expectation of the self-relationship of a metafounder is:  $E(\gamma) = 8E(\sigma_p^2) = \frac{2}{3}$ . The above can also be derived using a Beta(1,1) distribution, noting that this is equivalent to a  $U(0,1)$  distribution.

If the distribution of the allele frequencies in the base is U-shaped, there is an increased frequency of alleles with low minor allele frequency, such that  $E(\sigma_p^2) > \frac{1}{12}$ , and  $E(\gamma) > \frac{2}{3}$ . If the distribution of the allele frequencies in the base is concave, there is a decreased frequency of alleles with low minor allele frequency, such that  $E(\sigma_p^2) < \frac{1}{12}$ , and  $E(\gamma) < \frac{2}{3}$ .

**Supplementary Table 1.** Standard errors for the estimated variance components for the related scenario for three different models: PBLUP, ssGBLUP and ssGBLUP using metafounders. Residual and genetic variances estimates are presented for purebred traits 1, 2, and 3 and crossbred traits 23 and 1(23).

Model	Trait	Residual	Genetic variances and correlations <sup>1</sup>				
			1	2	3	23	1(23)
PBLUP	1	0.034	0.035	0.130	0.103	0.093	0.079
	2	0.023	0.130	0.040	0.088	0.058	0.067
	3	0.040	0.103	0.088	0.055	0.037	0.085
	23	0.056	0.093	0.058	0.037	0.062	0.023
	1(23)	0.043	0.079	0.067	0.085	0.023	0.060
ssGBLUP	1	0.032	0.033	0.084	0.108	0.081	0.062
	2	0.022	0.084	0.040	0.068	0.059	0.053
	3	0.042	0.108	0.068	0.061	0.044	0.101
	23	0.053	0.081	0.059	0.044	0.059	0.030
	1(23)	0.037	0.062	0.053	0.101	0.030	0.060
ssGBLUP-MF	1	0.029	0.031	0.054	0.101	0.064	0.102
	2	0.022	0.054	0.038	0.078	0.056	0.054
	3	0.042	0.101	0.078	0.053	0.049	0.101
	23	0.050	0.064	0.056	0.049	0.055	0.025
	1(23)	0.043	0.102	0.054	0.101	0.025	0.054

<sup>1</sup>Standard errors for the genetic variances are on the diagonal; standard errors for the genetic correlations are on the off-diagonal.

**Supplementary Table 2.** Standard errors for the estimated variance components for the unrelated scenario for three different models: PBLUP, ssGBLUP and ssGBLUP using metafounders. Residual and genetic variances estimates are presented for purebred traits 1, 2, and 3 and crossbred traits 23 and 1(23).

Model	Trait	Residual	Genetic variances and correlations <sup>1</sup>				
			1	2	3	23	1(23)
PBLUP	1	0.039	0.055	0.080	0.108	0.084	0.083
	2	0.026	0.080	0.037	0.101	0.046	0.061
	3	0.039	0.108	0.101	0.040	0.057	0.072
	23	0.038	0.084	0.046	0.057	0.064	0.050
	1(23)	0.097	0.083	0.061	0.072	0.050	0.068
ssGBLUP	1	0.041	0.064	0.078	0.101	0.068	0.075
	2	0.025	0.078	0.041	0.103	0.052	0.073
	3	0.044	0.101	0.103	0.048	0.047	0.067
	23	0.030	0.068	0.052	0.047	0.074	0.046
	1(23)	0.090	0.075	0.073	0.067	0.046	0.057
ssGBLUP-MF	1	0.031	0.045	0.054	0.101	0.064	0.102
	2	0.023	0.054	0.035	0.078	0.056	0.054
	3	0.046	0.101	0.078	0.045	0.049	0.101
	23	0.024	0.064	0.056	0.049	0.056	0.025
	1(23)	0.077	0.102	0.054	0.101	0.025	0.036

<sup>1</sup>Standard errors for the genetic variances are on the diagonal; standard errors for the genetic correlations are on the off-diagonal.

**Supplementary Table 3.** Unscaled genetic variances estimated with ssGBLUP using metafounders for purebred traits 1, 2, and 3 and crossbred traits 23 and 1(23), for the related and unrelated scenario.

Trait	Related	Unrelated
1	1.214	1.722
2	1.171	1.630
3	1.308	1.750
23	1.267	1.313
1(23)	1.268	1.329

**Supplementary Table 4.** Accuracies (averages across 10 replicates; SE within brackets) for purebred performance in lines 1, 2 and 3 (PB1, PB2, PB3) and crossbred performance in lines 1, 2 and 3 (CB1, CB2, CB3), for the related and unrelated scenarios.

Trait	Related			Unrelated		
	PBLUP	ssGBLUP	ssGBLUP_MF	PBLUP	ssGBLUP	ssGBLUP_MF
PB1	0.415 (0.018)	0.514 (0.013)	0.510 (0.013)	0.433 (0.017)	0.575 (0.015)	0.575 (0.014)
PB2	0.467 (0.022)	0.586 (0.016)	0.585 (0.016)	0.452 (0.021)	0.588 (0.019)	0.587 (0.018)
PB3	0.371 (0.025)	0.471 (0.015)	0.471 (0.015)	0.398 (0.022)	0.542 (0.015)	0.540 (0.014)
CB1	0.265 (0.033)	0.364 (0.027)	0.338 (0.037)	0.264 (0.046)	0.395 (0.026)	0.398 (0.022)
CB2	0.139 (0.030)	0.290 (0.026)	0.295 (0.026)	0.134 (0.025)	0.277 (0.021)	0.267 (0.026)
CB3	0.224 (0.019)	0.339 (0.022)	0.336 (0.024)	0.193 (0.037)	0.310 (0.034)	0.297 (0.037)

**Supplementary Table 5.** Bias of the level of the (G)EBV (average for the 10 replicates; SE within brackets), measured as the intercept of the regression of TBV on (G)EBV, for purebred performance in lines 1, 2 and 3 (PB1, PB2, PB3) and crossbred performance in lines 1, 2 and 3 (CB1, CB2, CB3) for the related and unrelated scenarios.

Trait	Related			Unrelated		
	PBLUP	ssGBLUP	ssGBLUP_MF	PBLUP	ssGBLUP	ssGBLUP_MF
PB1	0.106 (0.116)	0.124 (0.127)	0.115 (0.120)	-0.591 (0.473)	-0.723 (0.464)	-0.433 (0.466)
PB2	-0.045 (0.108)	-0.004 (0.123)	0.016 (0.124)	-0.134 (0.385)	-0.083 (0.366)	-0.133 (0.383)
PB3	0.164 (0.112)	0.112 (0.120)	0.137 (0.107)	-0.286 (0.269)	-0.290 (0.289)	-0.166 (0.249)
CB1	0.096 (0.188)	0.138 (0.184)	0.124 (0.179)	0.019 (0.329)	-0.061 (0.339)	0.138 (0.335)
CB2	-0.098 (0.187)	-0.076 (0.174)	-0.089 (0.185)	-0.011 (0.250)	0.087 (0.232)	0.098 (0.238)
CB3	0.158 (0.150)	0.160 (0.154)	0.176 (0.148)	-0.006 (0.483)	0.021 (0.418)	0.120 (0.408)

**Supplementary Table 6.** Bias of the scale of the (G)EBV (average for the 10 replicates; SE within brackets), measured as the slope of the regression of TBV on (G)EBV, for purebred performance in lines 1, 2 and 3 (PB1, PB2, PB3) and crossbred performance in lines 1, 2 and 3 (CB1, CB2, CB3) for the related and unrelated scenarios.

Trait	Related			Unrelated		
	PBLUP	ssGBLUP	ssGBLUP_MF	PBLUP	ssGBLUP	ssGBLUP_MF
PB1	0.961 (0.042)	0.959 (0.030)	0.944 (0.029)	1.050 (0.051)	1.087 (0.044)	0.998 (0.033)
PB2	1.054 (0.058)	1.050 (0.041)	1.023 (0.038)	1.022 (0.042)	1.078 (0.024)	0.988 (0.024)
PB3	0.924 (0.050)	0.942 (0.036)	0.915 (0.034)	0.960 (0.057)	1.052 (0.048)	0.954 (0.041)
CB1	0.859 (0.091)	0.883 (0.042)	0.797 (0.073)	1.097 (0.229)	1.048 (0.078)	1.019 (0.086)
CB2	0.679 (0.137)	0.934 (0.094)	0.885 (0.099)	0.689 (0.149)	0.895 (0.095)	0.705 (0.081)
CB3	0.845 (0.088)	0.886 (0.075)	0.864 (0.062)	0.865 (0.162)	0.954 (0.085)	0.819 (0.096)