

# 1 SUPPLEMENTARY MATERIAL

## 1.1 POPULATION MEAN

**Supplementary Table 1** Estimated yield (t.ha<sup>-1</sup>) at cycles 10, 100 and 200 of selection across-family (AF), within pre-selected families (WPSF) or within-family (WF).

Model	Strategy	10 cycles				100 cycles				200 cycles			
		Selection intensity				Selection intensity				Selection intensity			
		2.5%	5.0%	7.5%	10.0%	2.5%	5.0%	7.5%	10.0%	2.5%	5.0%	7.5%	10.0%
BayesA	AF	9.5 eA*	8.9 eB	8.5 dC	8.2 eD	25.0 kD	28.1 gC	29.2 eB	29.8 cA	25.0 mD	28.5 oC	30.5 kB	32.1 gA
	WPSF	9.0 fA	8.6 gB	8.2 eC	7.9 gD	28.9 dB	29.5 dA	29.6 dA	29.4 dA	29.5 hD	30.9 kC	31.6 iB	32.1 gA
	WF	7.8 jA	7.3 kB	6.9 jC	6.8 kD	28.9 dA	27.8 hB	26.3 jC	25.7 jD	34.1 eB	34.3 fA	33.9 eC	33.5 eD
BayesB	AF	9.4 eA	8.7 fB	8.4 dC	8.1 fD	23.1 mD	26.1 kC	27.6 iB	28.5 fA	23.1 pD	26.2 qC	28.1 oB	29.9 kA
	WPSF	8.9 fA	8.4 hB	8.1 fC	7.8 hD	27.7 gC	28.4 fB	28.7 gA	28.3 gB	28.0 kD	29.3 nC	30.2 lB	30.5 jA
	WF	7.5 kA	7.1 lB	6.8 kC	6.6 lD	27.2 hA	26.2 kB	24.8 lC	24.2 lD	32.2 gB	32.6 jA	32.0 hC	31.6 hD
FLM	AF	9.6 dA	8.8 eB	8.5 dC	8.2 dD	24.5 lD	27.5 iC	28.8 gB	29.6 dA	24.5 nD	27.8 pC	29.7 mB	31.5 hA
	WPSF	9.0 fA	8.6 gB	8.1 fC	7.8 hD	28.6 eC	29.4 dA	29.4 dA	29.1 eB	29.1 iD	30.5 lC	31.2 jB	31.7 hA
	WF	7.8 jA	7.4 kB	7.0 jC	6.8 kD	28.9 dA	27.8 hB	26.4 jC	25.7 jD	33.7 fB	34.1 gA	33.7 fB	33.4 fC
GBLUP	AF	9.6 dA	9.0 dB	8.5 dC	8.3 dD	22.1 nD	24.8 mC	26.5 jB	27.7 iA	22.1 qD	24.8 rC	26.6 pB	28.3 mA
	WPSF	9.0 fA	8.6 gB	8.2 eC	7.9 gD	27.0 hC	28.0 gB	28.2 hA	28.0 hB	27.1 lD	28.5 oC	29.1 nB	29.4 lA
	WF	7.8 jA	7.4 kB	7.0 jC	6.9 kD	27.9 fA	27.2 jB	25.7 kC	25.2 kD	32.1 gC	32.8 iA	32.5 gB	32.2 gC
Pheno	AF	8.2 gA	7.7 jB	7.4 iC	7.1 jD	28.0 fC	29.0 eA	29.0 fA	28.7 fB	32.0 gD	35.0 eC	36.3 dB	36.7 dA
	WPSF	8.1 hA	7.8 jB	7.5 hC	7.2 jD	28.8 dB	29.1 eA	28.8 gB	28.3 gC	32.0 gC	33.3 hB	33.6 fA	33.6 eA
	WF	6.3 mA	6.1 mB	5.8 lC	5.7 mC	25.5 iA	24.5 nB	22.9 mC	22.2 mD	35.3 dA	35.2 dA	33.9 eB	33.2 fC
Random	AF	3.6 oA	3.6 oA	3.6 nA	3.6 oA	3.6 qA	3.6 qA	3.6 pA	3.6 pA	3.6 sA	3.6 uA	3.6 sA	3.6 pA
	WPSF	3.6 oA	3.6 oA	3.6 nA	3.6 oA	3.5 qA	3.6 qA	3.7 pA	3.5 pA	3.5 sA	3.5 uA	3.7 sA	3.5 pA
	WF	3.6 oA	3.6 oA	3.6 nA	3.6 oA	3.6 qA	3.6 qA	3.6 pA	3.6 pA	3.6 sA	3.6 uA	3.5 sA	3.6 pA
RF	AF	8.0 iA	7.9 iA	7.7 gB	7.4 iC	12.8 pD	16.6 oC	19.4 nB	21.6 nA	12.8 rD	16.9 tC	20.0 rB	22.6 nA
	WPSF	7.2 lA	7.1 lB	6.9 jC	6.8 kD	25.2 jB	25.8 lA	25.8 kA	25.8 jA	28.2 jD	30.0 mC	30.5 kB	31.0 iA
	WF	5.1 nA	5.0 nB	4.8 mC	4.8 nC	16.0 oA	14.8 pB	13.4 oC	12.9 oD	23.5 oA	22.2 sB	20.3 qC	19.7 oD
TBV	AF	11.2 aA	10.4 aB	9.9 aC	9.5 aD	37.0 bC	39.4 bB	40.0 bA	39.9 aA	37.2 bD	40.7 bC	42.5 bB	43.8 bA
	WPSF	10.7 bA	10.0 bB	9.5 bC	8.9 bD	35.7 cC	36.3 cA	36.0 cB	35.4 bD	35.8 cC	37.1 cB	37.6 cA	37.7 cA
	WF	9.8 cA	9.3 cB	8.6 cC	8.4 cD	43.1 aA	42.7 aB	40.8 aC	39.9 aD	47.9 aC	50.2 aB	51.3 aA	51.4 aA

\* Lower case letters indicate difference in means across selection methods and breeding strategies (vertical comparison); Capital letters indicate difference in means across selection intensity within a same generation (horizontal comparison). Statistical test of multiple comparison based on Scott-Knott clustering at 5% of error probability.

## 1.2 REGRESSION ANALYSIS BASED ON NON-LINEAR MODEL

We used non-linear regression, with model:

$$y = \theta_a(1 - e^{(-\theta_v x_1)}) + \theta_d x_2 + \varepsilon,$$

Where:  $y$ : is random variable analyzed in this case, population mean,  $\theta_a$ : is parameter of maximum value,  $\theta_v$ : is increase parameter,  $\theta_d$ : is linear parameter of intensity increase,  $x_1$ : is breeding cycle,  $x_2$ : is independent variable of selection intensity (SI),  $\varepsilon$ : is random error. This models is reparametrized (Zeviani et al., 2012), and with parameter  $\theta_v$ , is possible created  $\theta_v^*$  with relation:

$$\theta_v^* = -\frac{\log(1 - q)}{\theta_v},$$

where  $q(0 < q < 1)$  represents proportion of maximum value,  $\theta_v^*$ : represents breeding cycles that is equal  $q$  define in this case in 0.8, this model is fitted in R software, using function nls.

**Supplementary Table 2** Non-linear Regression parameters, for genetic gain select across-family (AF), within pre-selected families (WPSF) or within-family (WF).

Models	Strategy	R <sup>2</sup>	$\theta_a$ (Max Gain)	$\theta_d$ (baseline SI)	$\theta_v$ (Gain/cycle)	$\theta_v^*$ (cycle to 80% total)
BayesA	AF	0.949	26.732(±0.017)*	0.439(±0.002)	0.027(±0.001)	58.964(±0.112)
	WPSF	0.984	30.894(±0.011)	0.094(±0.001)	0.026(±0.001)	62.506(±0.064)
	WF	0.978	35.290(±0.018)	-0.137(±0.002)	0.017(±0.001)	96.612(±0.137)
BayesB	AF	0.945	24.368(±0.016)	0.460(±0.002)	0.030(±0.001)	53.391(±0.104)
	WPSF	0.981	29.341(±0.011)	0.100(±0.001)	0.027(±0.001)	59.552(±0.064)
	WF	0.976	33.192(±0.017)	-0.113(±0.002)	0.017(±0.001)	96.558(±0.143)
FLM	AF	0.949	26.021(±0.017)	0.449(±0.002)	0.028(±0.001)	56.634(±0.107)
	WPSF	0.983	30.502(±0.011)	0.091(±0.001)	0.026(±0.001)	61.184(±0.064)
	WF	0.979	34.977(±0.017)	-0.126(±0.002)	0.017(±0.001)	94.994(±0.132)
GBLUP	AF	0.939	22.910(±0.015)	0.462(±0.002)	0.034(±0.001)	47.585(±0.095)
	WPSF	0.978	28.315(±0.011)	0.096(±0.001)	0.030(±0.001)	54.383(±0.062)
	WF	0.978	33.299(±0.016)	-0.096(±0.002)	0.018(±0.001)	90.843(±0.124)
Pheno	AF	0.982	34.686(±0.017)	0.201(±0.002)	0.016(±0.001)	100.310(±0.138)
	WPSF	0.988	33.448(±0.011)	0.050(±0.001)	0.019(±0.001)	83.798(±0.083)
	WF	0.977	39.328(±0.036)	-0.126(±0.002)	0.010(±0.001)	156.934(±0.331)
RF	AF	0.870	12.678(±0.018)	0.881(±0.002)	0.030(±0.001)	53.520(±0.225)
	WPSF	0.987	29.809(±0.011)	0.168(±0.001)	0.017(±0.001)	92.010(±0.101)
	WF	0.914	23.356(±0.034)	-0.116(±0.002)	0.011(±0.001)	142.523(±0.513)
TBV	AF	0.973	40.415(±0.019)	0.284(±0.002)	0.024(±0.001)	68.179(±0.097)
	WPSF	0.983	37.896(±0.013)	-0.021(±0.002)	0.027(±0.001)	59.384(±0.061)
	WF	0.990	54.048(±0.021)	-0.106(±0.002)	0.015(±0.001)	105.945(±0.115)

\*Estimated parameter followed by standard error

### 1.3 GENETIC VARIANCE

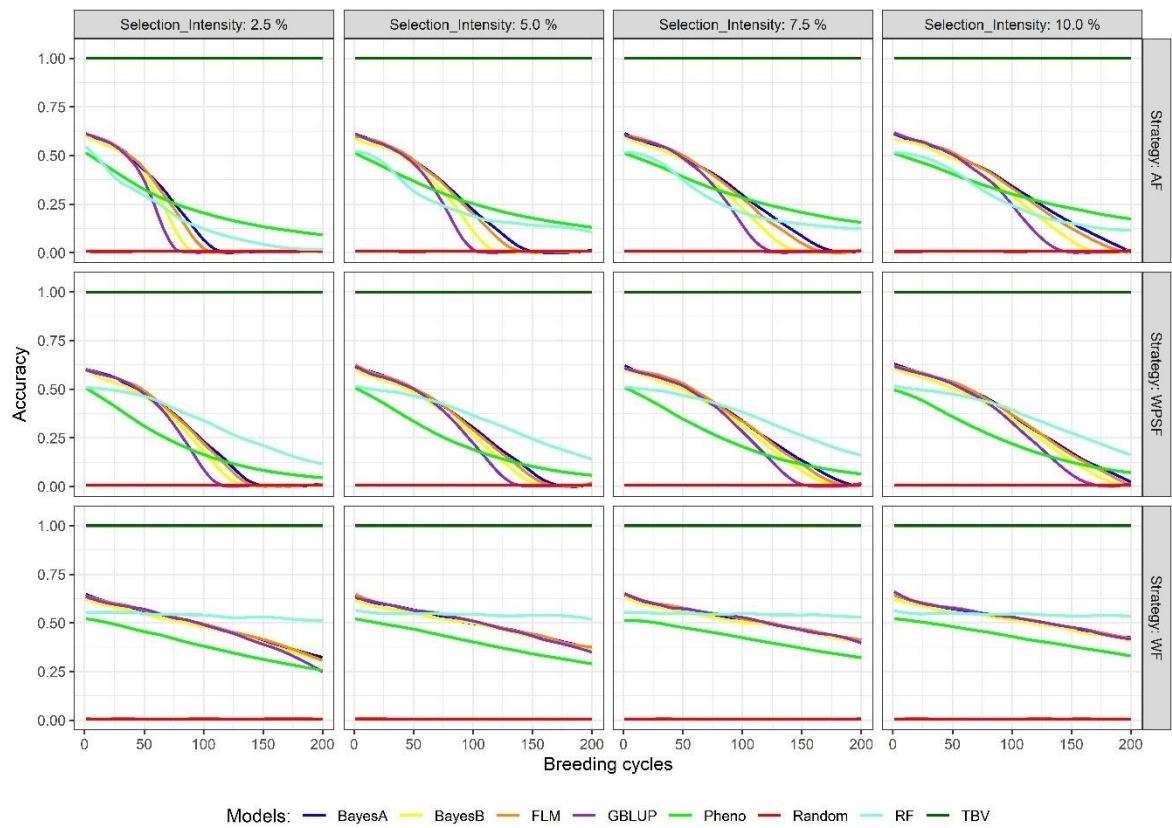
**Supplementary Table 3** Number of breeding cycles necessary to exhaust 80% of genetic variance (E80GV); Estimated final population performance (Max) and the number of cycles to reach 80% of total genetic gains (NC80GG) considering prediction methods, selection intensity and the breeding strategy across-family (AF), within pre-selected families (WPSF) or within-family (WF)

		Number of cycles to E80GV				Max t.ha <sup>-1</sup>	NC80GG
Model	Strategy	Selection Intensity					
		2.5%	5.0%	7.5%	10.0%		
BayesA	AF	29 kD	39 mC	47 kB	54 iA	26	58
	WPSF	41 iD	47 kC	52 iB	58 hA	30	62
	WF	104 dD	139 dC	172 cB	184 cA	35	96
BayesB	AF	28 kD	38 mC	45 lB	52 iA	24	53
	WPSF	41 iD	47 kC	53 iB	57 hA	29	59
	WF	115 cD	149 cC	186 bB	195 bA	33	96
FLM	AF	28 kD	38 mC	45 lB	52 iA	26	56
	WPSF	39 jD	47 kC	52 iB	57 hA	30	61
	WF	101 eD	136 eC	168 dB	179 dA	34	94
GBLUP	AF	25 lD	33 nC	40 mB	46 jA	22	47
	WPSF	37 jD	44 lC	49 jB	53 iA	28	54
	WF	100 eD	131 fC	167 dB	180 dA	33	90
Pheno	AF	62 fD	81 gC	97 eB	108 eA	34	100
	WPSF	57 gD	64 iC	68 gB	75 fA	33	83
	WF	171 bC	197 bB	200 aA	200 aA	39	156
Random	AF	200 aA	200 aA	200 aA	200 aA	-	-
	WPSF	200 aA	200 aA	200 aA	200 aA	-	-
	WF	200 aA	200 aA	200 aA	200 aA	-	-
RF	AF	11 mD	21 oC	29 oB	38 lA	12	53
	WPSF	57 gD	67 hC	72 fB	76 fA	29	92
	WF	200 aA	200 aA	200 aA	200 aA	23	142
TBV	AF	25 lD	32 nC	37 nB	42 kA	40	68
	WPSF	27 kD	33 nC	37 nB	42 kA	37	59
	WF	48 hD	55 jC	66 hB	69 gA	54	105

\* Lower case letters indicate difference in means across selection methods and breeding strategies (vertical comparison); Capital letters indicate difference in means across selection intensity (horizontal comparison). Statistical test of multiple comparison based on Scott-Knott clustering at 5% of error probability.

## 1.4 ACCURACY

The accuracy of genomic selection models is a key factor at many researches used for selection the model for used. Based on this result displayed in **Error! Reference source not found.**, we can see that the accuracy of models has interaction between breeding strategy and selection intensity, in long term. In BayesA for example, we can see in AF strategy that lowest selection intensity (2.5%), lost 80% of your variance with 87 breeding generation, and for 10% of selection intensity, this value is 154 breeding generation, it is very significative different. For this same model, BayesA, in strategy WF the results show that of end 200 breeding generation the 80% of accuracy is not loser. Similar conclusion can be extending for all Bayesian models, where for strategy WF, all never lost 80% of genetic variance, the strategy of WPSF and AF demonstrate similar behavior.



**Supplementary Figure 1.** Prediction accuracy across 200 breeding cycles. Colors correspond to different selection methods, grid columns represent selection intensity (2.5, 5, 7.5, 10%) and grid rows represent breeding strategies, where individuals are selected across-family (AF), within pre-selected families (WPSF) or within-family (WF).