Supplementary materials for:

Assessing the potential of genetic resource introduction into elite germplasm: a collaborative multiparental population for Flint maize

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File S1. Donor line selections

Genetic material

Each partner provided the parents of an elite hybrid. For each elite hybrid, the flint parent was considered as the recipient line (noted A) and the dent panel as the tester line (noted B). We pre-selected 74 candidate donor lines (noted D) from a collection of 1191 lines representative of flint diversity (Gouesnard et al. 2017). Constraint at this step were to avoid strong similarity with key founders of the Flint group (i.e. F2, F7, Ep1, D105) and to belong to the same precocity group as the elite recipient lines (B-C1 maturity groups according to French nomenclature). These lines consisted of (i) flint lines from the INRA genetic resources collection, managed by the station of Saint Martin de Hinx, (ii) DH-SSD lines derived from flint landraces in the ProMaïs DIVZEA project, (ii)i SSD lines derived from flint landraces evaluated as drought tolerant in the RESGEN European program and (iv) flint lines from the panel assembled for the CornFed project and evaluated for forage(Rincent et al. 2012).

Molecular markers

The hybrid parents and the candidate donor lines were genotyped using the Maize Illumina Infinium 50k array (Ganal et al. 2011). In the following, we only considered the 32 788 Panzea SNP markers that have been shown to prevent ascertainment bias. We obtained a set of 26 657 SNP markers after removing the monomorphic markers and filtering those with a call rate inferior to 0.9.

Phenotypic data

Each partner, except partner 7 (INRA), produced and evaluated the hybrids between the candidate donor lines and its tester (D x B) as well as between its recipient and tester (A x B). Hybrids from one partner were evaluated in its European field network for grain moisture (H2O, %) and grain yield (GY, qt/ha) in the summer of 2016. In total across partners, 26 locations were involved. In addition to GY and H2O, plant stalk lodging was recorded by 5 partners in a total of 12 locations. This phenotyping strategy was chosen to facilitate the trial implementation by the different private partners in their standard conditions, although it induces confusion between the tester effect and other partner effects (e.g. seed quality and harvest strategy). Note that the D x B hybrids were not repeated in a given location (except for partner 2) and the number of actually evaluated D x B hybrids was variable according to partners and locations (from 28 to 68). In absence of randomized check lines, no spatial heterogeneity correction was performed. Across locations, 43 outlier plots were identified and removed for GY and H2O.

Flint line value estimations and yield index computation

For a given partner, the H2O flint line LS-means were computed using the following model:

$$Y_{il} = \mu + \alpha_i + L_l + E_{il} \quad (1)$$

$$\mathrm{L} \sim N\left(0, I\sigma^2_{\mathrm{L}}\right), \mathrm{E} \sim N\left(0, I\sigma^2_{\mathrm{E}}\right)$$

$$\mathrm{L} \perp \mathrm{E}$$

where,Y_{il} is the phenotypic value of the hybrid between the tester of the partner and the flint parent i evaluated in location l. μ is the intercept term, α_i is the fixed effect of the flint parent (recipient line or candidate donor lines). L_l is the random effect of location. E_{il} is the error term.

For each partner k, the Yield Index (YI) was computed for D x B hybrids in each location l using the H20 elite flint line LS-means from (1) :

$$YI_{(D_j*B_k)_l} = GY_{(D_j*B_k)_l} - 2.5 * \left(H2O_{(D_j*B_k)_l} - H2O_{A_k*B_k}\right) \ (2)$$

where D_j is the j^{th}candidate donor line, A_k and B_k are the recipient and tester lines of the partner k.

Decomposition of hybrid values and donor value estimations

The YI DxB hybrid values were decomposed as follows:

$$Y_{jkl} = \mu + \beta_j + \gamma_k + L_{kl} + E_{jkl} \ (3)$$

$$L_k \sim N\left(0, I\sigma^2_{\mathrm{L_k}}\right), \mathrm{E} \sim N\left(0, I\sigma^2_{\mathrm{E}}\right)$$

$$\mathrm{L_k} \perp \mathrm{E}$$

where Y_{jkl} is the phenotype of the hybrid between the donor j and the tester k evaluated of the location l. μ is the intercept term. β_j is the fixed effect of the donor, γ_k is the fixed effect of the tester (confounded with a meta-environment effect). L_{kl} is the random effect of the location nested in the tester effect. E_{jkl} is the error term.

The donor effect LS-means were used to estimate the General Combining Abilities (GCA) of candidate donor lines. LS-means allowed to consider differences in the phenotyping effort made by partners: more weight was given to partners with more locations.

Plant lodging evaluation

Stalk lodging has been observed during the trials in some locations mostly in the west of France. To avoid selection pressure due to stalk lodging sensitivity during the next steps of the project, we decided to eliminate candidate lines that had high lodging levels. Since all testers were assumed to bring a roughly similar level of tolerance for plant lodging, we decided to realize a meta-analysis of all recorded scores independently of the tester. Lodging scores from 1 (high sensitivity) to 9 (low sensitivity) were transformed into proportions of lodged plants.

The candidate donor lines LS-means were computed using the following model:

$$Y_{jkl} = \mu + \beta_j + L_{kl} + E_{jkl} \ (4)$$

$$L_k \sim N\left(0, I\sigma^2_{\mathrm{L_k}}\right), \mathrm{E} \sim N\left(0, I\sigma^2_{\mathrm{E}}\right)$$

$$\mathrm{L_k} \perp \mathrm{E}$$

where Y_{jkl} is the phenotype of the hybrid between the donor j and the tester k evaluated of the location l. μ is the intercept term. β_j is the fixed effect of the donor. L_{kl} is the random effect of the location nested in the tester effect. E_{jkl} is the error term.

Parameter estimations of all models were estimated thanks to the ASREML software (Butler et al. 2017)

Selection of candidate donors

18 candidate lines, issued from five selfing generations, were discarded because of their high residual heterozygote rate (> 10%).

From the remaining candidates, those presenting more than 8% of lodged plants were eliminated. This threshold was determined using the mean lodging value of the elite A x B hybrids and the global distribution (**Fig. 1**). The candidates with higher YI GCAs were considered to be donors. Additionally, the availability in nursery of candidate D x R BC1 crosses and partners' wishes were also taken into account. Partners' wishes were considered as expert information based on the knowledge of their material (ear insertion height, sensibility to disease …) and their observations of the D x B hybrids (discriminant lodging score in their trials …). The selection procedure led to a set of 7 donor lines with diverse origins which presented an average gap performance of -19.8 qt/ha with the elite hybrids (**Table 1**).

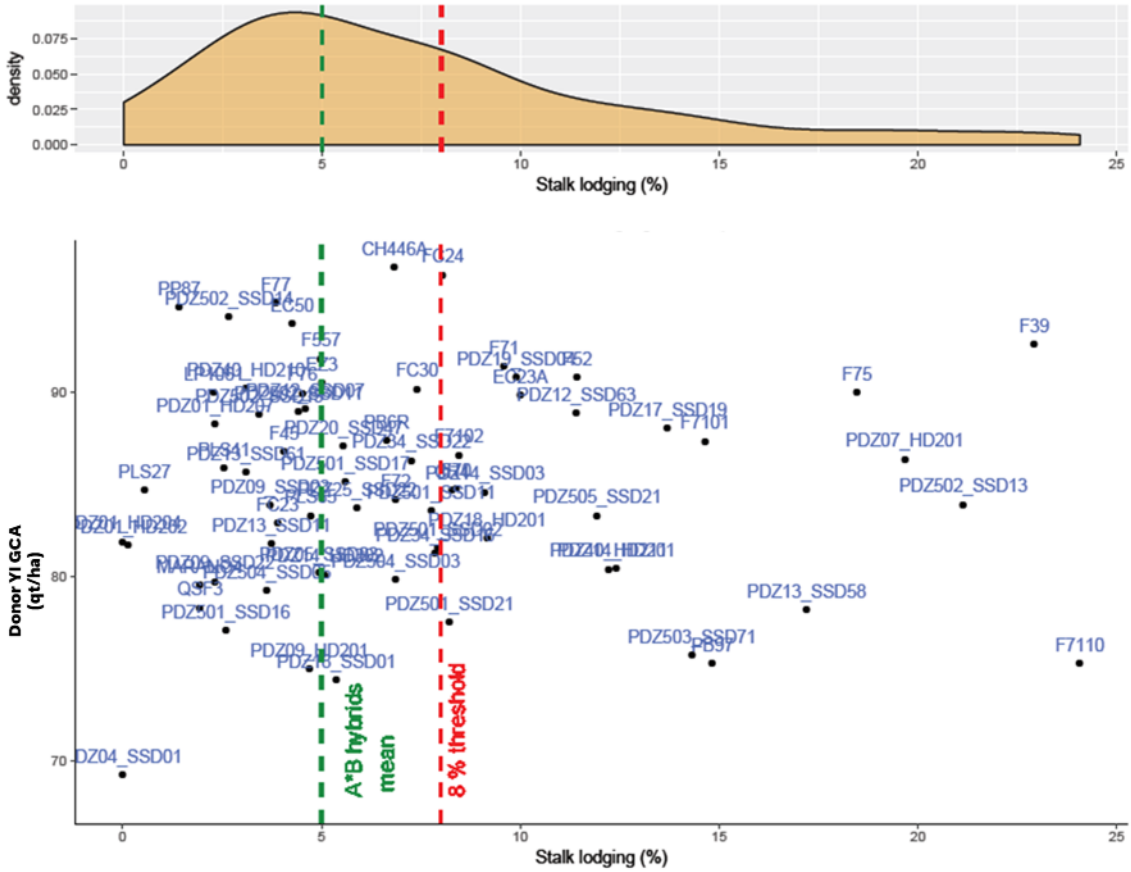

Figure 1 Density plot of stalk lodging LS-means (on top) and scatter plot between YI GCA and stalk lodging LS-means of candidate lines (on bottom)

Table 1 Set of selected donor lines

Name	Pedigree	YI GCA (qt/ha)	Stalk lodging (%)
FV77	Pop. Liesse-3.1.2 (PPS 19)	94.8 (-17.2)	4
PP87	Pop. Isola Basso	94.6 (-17.4)	1
PDZ502_SSD14	Aranga 1_14-01m-4m-1m-m	94.1 (-17.9)	3
EC50	Composite Aranga x EC18	93.7 (-18.3)	4
LP1061	Compuesto Colorado Precoz	89.9 (-22.1)	2
PDZ12_SSD07	VA5 Nostrano dell Isola_07-01m-5m-1m-1	89.1 (-22.9)	5
PDZ502_SSD11	Aranga 1_11-01m-2m-1m-m	88.9 (-23.1)	4

For YI GCA, the average performance gap between the donor line and the elite recipient lines is indicated in parenthesis.

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File S2. Spatial correction of raw phenotypic data

Modelling of spatial heterogeneity

In each trial, different models were fitted account for spatial heterogeneity in raw phenotypic data. A general model can be described as:

$$Y^R_{ircbjkhm} = \mu + \eta_i + \rho_j + \theta_k + G_h + S_{rcb} + E_{ircbjkhm}$$

where $Y^R_{ircpjkhm}$ is the raw phenotype value of the repetition m of the hybrid h derived from the recipient line j belonging to the family k located in the row r and the column c in the trial and belonging to the bloc b in the sub-trial i. η_i is the fixed effect of the sub-trial i, ρ_j is the fixed effect of the recipient line (a factor with 8 levels: one level for each recipient line and an additional level for ADEVEY) and θ_k is the fixed effect of the family (a factor with 21 levels: one level for each hybrid family and an additional level for ADEVEY and the referent hybrids). $G \sim N(0, I\sigma^2_G)\ iid$ is a random genotypic effect and $E \sim N(0, I\sigma^2_E)\ iid$ is an error term. The independence is assumed between random terms. S is a random spatial effect, which differs between spatial models, as described in the table 1 below.

The random spatial effect was decomposed into row and column ($R_r + C_c$) effects or a bloc effect (B_b). These effects are considered over the whole trial or per sub-trial. If they were declared per sub-trial, the associated variances were defined specific to each sub-trial or common between sub-trials. An AR1xAR1 model considering the rows and the columns was also fitted. (**Table 1**)

Table 1. Description of random spatial terms for the different spatial correction models

Spatial Correction Type	Approach	Spatial Effect Definition
Row x Colum	Whole trial	$\boldsymbol{R_r + C_c}$ $R \sim N(0, I\sigma^2_R),\ C \sim N(0, I\sigma^2_C)$
	Per sub-trial with common variances	$\boldsymbol{R_{ri} + C_{ci}}$ $R_i \sim N(0, I\sigma^2_R),\ C_i \sim N(0, I\sigma^2_C)$
	Per sub-trial with specific variances	$R_{ri} + C_{ci}$ $R_i \sim N(0, I\sigma^2_{R_i}),\ C_i \sim N(0, I\sigma^2_{C_i})$
Bloc	Whole trial	$\boldsymbol{B_b}$ $B \sim N(0, I\sigma^2_B)$
	Per sub-trial with common variances	$\boldsymbol{B_{bi}}$ $B_i \sim N(0, I\sigma^2_B)$
	Per sub-trial with specific variances	$\boldsymbol{B_{bi}}$ $B_i \sim N(0, I\sigma^2_{Bi})$
AR1 x AR1	Whole trial	$\boldsymbol{S_{hijkm}}$ $S \sim N(0, \Sigma_c(\omega_c) \otimes \Sigma_r(\omega_r)\sigma^2_S)\ ind$

R is a row effect, C is a column effect and B is a bloc effect. σ^2_R is the variance associated to the rows, σ^2_C is the variance associated to the columns, σ^2_B is the variance associated to the blocs. $\sigma^2_{R_i}$and $\sigma^2_{C_i}$ are specific

to the sub-trial i. Used indices have the same meaning than in the general model. Σ_c and Σ_r are the AR1 covariance matrices associated to rows and columns, respectively, with ω_c and $\omega_r$their associated auto-correlation parameters (Gilmour et al 1997; Cullis et al 1998). $\otimes$ refers to Kronecker product.

For all traits, AIC had the lowest values with the AR1xAR1 model. This spatial correction type was retained.

Modelling of genotypic effects and computation of corrected data

To improve the estimation precision of spatial effects, genotypic information was included in the data correction model by the use of a kinship matrix K computing following the recommendation given by (Vitezica et al. 2017). To this end, the following model was fitted:

$$Y^R_{ijkhm} = \mu + \eta_i + \rho_j + \theta_k + A_h + G_h + S_{hijkm} + E_{ijkhm}$$

$$A \sim N(0, K_{tot}\sigma^2_A), G \sim N(0, I\sigma^2_G)\ iid, S \sim N(0, \Sigma_c(\omega_c) \otimes \Sigma_r(\omega_r)\sigma^2_S), E \sim N(0, I\sigma^2_E)\ iid$$

$$A \perp G \perp S \perp E$$

where Y^R_{ijkhm} is the raw performance of the repetition m of the hybrid h derived from the recipient line j belonging to the family k located in the sub-trial i. The fixed terms are the same than the terms of the general model. A_h is a random additive genetic effect, G_h is a random permanent genetic effect, S_{hijkm} is a random spatial field effect and E_{hijkm} is the error.

This model was called *AR1xAR1_A_G*. It was compared to two sub-models: *AR1xAR1_A* (the permanent genetic effect was removed) and *AR1xAR1_G* (the genotypic information was not used to model the genetic effect). For each trial, the best linear unbiased predictors (BLUPs) of the genetic effects were calculated. These BLUPs were added to the estimated mean family performance to obtain genetic values of the individuals. These genetic values were correlated to the average raw values in other trials. These correlations were used as a precision indicator to select the most pertinent correction model for each trial (**Table 2**). The corrected field plot values were obtained by subtracting spatial BLUPs of the selected model from the raw values.

Table 2. Correlation between genetic values and raw phenotypic values between trials

Trait	Model	Blo19		Vil19		Smh19	
		Vil19	Smh19	Blo19	Smh19	Blo19	Vil19
FLOM	AR1xAR1_G	**0.597**	**0.643**	0.670	0.574	0.591	0.551
	AR1xAR1_A	0.597	0.642	**0.656**	**0.593**	**0.600**	**0.558**
	AR1xAR1_A_G	0.567	0.616	0.656	0.593	0.537	0.493
FLOF	AR1xAR1_G	**0.651**	**0.682**	**0.621**	**0.734**	0.611	0.697
	AR1xAR1_A	0.639	0.676	0.617	0.737	**0.609**	**0.707**
	AR1xAR1_A_G	0.619	0.653	0.600	0.725	0.575	0.663
ASI	AR1xAR1_G	0.555	0.546	0.554	0.554	0.561	0.556
	AR1xAR1_A	**0.561**	**0.547**	**0.559**	**0.561**	**0.570**	**0.570**
	AR1xAR1_A_G	0.542	0.539	0.555	0.557	0.558	0.550
PH	AR1xAR1_G	-	0.611	-	-	0.455	-
	AR1xAR1_A	-	**0.615**	-	-	**0.479**	-
	AR1xAR1_A_G	-	0.600	-	-	0.440	-
GY	AR1xAR1_G	**0.500**	**0.336**	0.400	0.303	0.282	0.377
	AR1xAR1_A	0.478	0.321	**0.402**	**0.308**	**0.285**	**0.389**
	AR1xAR1_A_G	0.487	0.312	0.392	0.301	0.277	0.389
H2O	AR1xAR1_G	0.573	0.368	0.439	0.365	0.488	0.558
	AR1xAR1_A	**0.599**	**0.413**	**0.436**	**0.371**	**0.510**	**0.577**
	AR1xAR1_A_G	0.597	0.401	0.415	0.361	0.485	0.565

For each model (AR1xAR1_G, AR1xAR1_A and AR1xAR1_A_G), the estimated genetic values in a trial (first row) was correlated with the raw phenotypic data in other trials (second raw). Bold values indicate which model was selected for each trial-trait pair.

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File S3 Definition of contrasts to perform pairwise comparisons between recipient or donor lines according to the genetic or additive variances in progeny

We named $\hat{\theta}$ the vector containing the estimations of the within family genetic variances given by the model M_FG$_S$. We considered two recipient lines (i and j). We named n_i (resp. n_j) the number of families derived from the recipient line i (resp. j). We defined the contrast $C\hat{\theta}$ where C is a vector containing the following coefficients:

$$\begin{cases} \frac{1}{n_i} \; for \; variance \; parameters \; associated \; to \; families \; derived \; from \; i \\ -\frac{1}{n_j} \; for \; variance \; parameters \; associated \; to \; families \; derived \; from \; j \\ 0 \; for \; other \; families \end{cases}$$

The nullity of this contrast was tested thanks to a Wald test to study the influence of the recipient line on family genetic variance. A similar approach was conducted to test the influence of the donor line used.

File S4. Comparison of the expected gain after selection for F1, BC1 and BC2 cross types

In the following document, we consider a cross between a donor line (D) and a recipient line (R) evaluated for an additive quantitative trait. We detail the expression of the expected gain after selection, considering R performance as a reference, for different populations derived from the cross. This gain can be express as:

$$Gain_p = UC_p - \mu_R \ (1)$$

where μ_R is the performance of the recipient line and UC_p is the usefulness criterion of the population p. For a given population p, the UC is computed using its mean performance (μ_p) and its genetic standard deviation (σ_{G_p}):

$$UC_p = \mu_p + ih\sigma_{G_p} \ (2)$$

where i is the selection intensity, h is the selection accuracy. For sake of simplicity, we consider that $h = 1$. The UC values will be calculated with $i = 2.07$ (selection rate of 5%).

(1) can be also be written as:

$$Gain_p = Gap_p + i\sigma_{G_p} \ (3)$$

where $Gap_p = \mu_p - \mu_R$

In a first part, we will explicit the expression of μ_p and σ_{G_p} for F1, BC1 or BC2 populations derived from the same DxR cross. In a second part, we will determine which population structure leads to maximize the UC for a range of parental performance gaps and genetic variances.

1. Expression of mean performance and genetic variance

1.1. Mean performance

We consider a population of individuals derived from a DxR cross. We note μ_D and μ_R the respective performance of the donor and recipient line. We consider that the mean performance of a population derived from this cross will be only influenced by the mean proportions of donor and recipient genomes in the individuals of this population. These proportions differ according to the cross type:

$$\mu_{F1} = \frac{\mu_D + \mu_R}{2}, \qquad \mu_{BC1} = \frac{1}{4}\mu_D + \frac{3}{4}\mu_R \ \ and \ \ \mu_{BC2} = \frac{1}{8}\mu_D + \frac{7}{8}\mu_R \ \ (4)$$

where μ_X is the expected mean performance value in the X population and in the populations derived from it ($X \in \{F1, BC1, BC2\}$).

The performance gaps between the different populations and the recipient line can be expressed as:

$$Gap_{F1} = \mu_{F1} - \mu_R = \frac{Gap_D}{2}, \qquad Gap_{BC1} = \mu_{BC1} - \mu_R = \frac{Gap_D}{4}$$

$$and\ \ Gap_{BC2} = \mu_{BC2} - \mu_R = \frac{Gap_D}{8} \quad (5)$$

where $Gap_D = \mu_D - \mu_R$

1.2. Genetic variance

1.2.1. Expression of the genetic variance for an additive trait with QTLs in linkage equilibrium

We consider a purely additive trait determined by Q biallelic QTLs. For each QTL, D and R lines are homozygous for a different allele. We note x_{iq} the number of R alleles carried by the individual i at the QTL ($x_{iq} \in \{0; 1; 2\}$). We define β_q the allelic substitution effect for the QTL q. $\sum_{q=1}^{Q} x_{iq}\beta_q$ is the genetic value of the individual i

Assuming that the QTLs are in linkage equilibrium,

we have:

$$\sigma_G^2 = var\left(\sum_{q=1}^{Q} x_{iq}\beta_q\right) = \sum_{q=1}^{Q} var(x_{iq}\beta_q) = \sum_{q=1}^{Q} var(x_{iq})\,\beta_q^2 \quad (6)$$

For a given QTL q:

$$var(x_{iq}) = f(DD)_q * \left(0 - x_{.q}\right)^2 + f(DR)_q * \left(1 - x_{.q}\right)^2 + f(RR)_q * \left(2 - x_{.q}\right)^2 \quad (7)$$

where $f(DD)$, $f(DR)$ and $f(RR)$ are the genotypic frequency at the QTL in the population q and $x_{.q}$ the mean value of allelic doses ($x_{.q} = f(DR)_q + 2 * f(RR)_q$).

1.2.2. Application to DH populations

We note DH_X a population of DH lines derived from a cross type $X\ with\ X \in \{F1, BC1, BC2\}$.

Table 1 Genotypic variances for different population structures

Population	$f(DD)$	$f(DR)$	$f(RR)$
F1	0	1	0
DH_{F1}	$\frac{1}{2}$	0	$\frac{1}{2}$
BC1	0	$\frac{1}{2}$	$\frac{1}{2}$
DH_{BC1}	$\frac{1}{4}$	0	$\frac{3}{4}$
BC2	0	$\frac{1}{4}$	$\frac{3}{4}$
DH_{BC2}	$\frac{1}{8}$	0	$\frac{7}{8}$

At a given QTL, the genotypic frequencies differ according to the population structure (**Table 1**). Using these frequencies and (2), we can give an expression of the value of σ_G^2 for the different DH populations:

$$\sigma^2_{G_{DH_{F1}}} = \sum_{q=1}^{Q} \beta_q^2 , \sigma^2_{G_{DH_{BC1}}} = \frac{3}{4}\sum_{q=1}^{Q} \beta_q^2 \ and \ \sigma^2_{G_{DH_{BC2}}} = \frac{7}{16}\sum_{q=1}^{Q} \beta_q^2 \ (8)$$

1.2.3. Application to SSD populations

We note XSn a population of lines derived from a cross type X with n generations of selfing. We will consider only the expression of the genotypic frequencies for populations derived from $BC1$ which corresponds to the populations evaluated in our paper.

In the $BC1$, at a given QTL, we have $f(DR) = \frac{1}{2} \ and \ f(RR) = \frac{1}{2}$. The genotypic frequencies after n selfing generations in progeny derived from the BC1 individuals carrying DR genotype are:

$$f(RD) = \frac{1}{2^n} \ and \ f(RR) = f(DD) = \frac{1}{4}\left(1 + \frac{1}{2} + \frac{1}{4} + \cdots + \frac{1}{2^{n-1}}\right) = \frac{1}{4}\left(\frac{\frac{1^n}{2} - 1}{\frac{1}{2} - 1}\right) = \frac{1}{2} - \frac{1}{2}^{n+1}$$

For those derived from the BC1 individuals carrying RR genotype, we have $f(RR) = 1$.

Thus, we can give the expression of the genotypic frequency in a population derive from a BC1 cross after n selfing generations:

$$f(DD) = \frac{1}{2} * \left(\frac{1}{2} - \frac{1}{2}^{n+1}\right) = \frac{1}{4} - \frac{1}{2}^{n+2} , f(DR) = \frac{1}{2} * \left(\frac{1}{2}^{n}\right) = \frac{1}{2}^{n+1}$$

$$and \ f(RR) = \frac{1}{2} + \frac{1}{2} * \left(\frac{1}{2} - \frac{1}{2}^{n+1}\right) = \frac{3}{4} - \frac{1}{2}^{n+2}$$

In this case,

$$var(x_{iq}) = \left(\frac{1}{4} - \frac{1}{2}^{n+2}\right) * \left(0 - \frac{3}{2}\right)^2 + \frac{1}{2}^{n+1} * \left(1 - \frac{3}{2}\right)^2 + \left(\frac{3}{4} - \frac{1}{2}^{n+2}\right) * \left(2 - \frac{3}{2}\right)^2 = \frac{3}{4} - \left(\frac{1}{2}\right)^{n+1}$$

and

$$\sigma^2_{G_{BC1Sn}} = \left(\frac{3}{4} - \left(\frac{1}{2}\right)^{n+1}\right)\sum_{q=1}^{Q} \beta_q^2$$

For $n = 2$, we get $\sigma^2_{G_{BC1S2}} = \frac{5}{8}\sum_{q=1}^{Q} \beta_q^2 \ (9)$.

2. Optimal cross type to maximize the UC

We wanted to determine which cross type maximizes the performance gain for virtual DxR crosses. Each DxR cross is defined thanks to two parameters: the performance gap between the donor and recipient lines (Gap_D) and the genetic variance in a DH population derived from a F1 cross ($\sigma^2_{G\,DH_{F1}}$).

In our study, we evaluated the mean performances (μ_{BC1}) and the genetic variances ($\sigma^2_{G\,DH_{F1}}$) of 20 BC1S2 families. We also obtained the performance of their recipient lines (μ_R). We used these values to determine realistic ranges of both parameters.

We had access to Gap_D as following:

$$Gap_D = 4 * Gap_{BC1} = 4 * (\mu_{BC1} - \mu_R) \quad (10)$$

We also computed the expected genetic variances in DH populations derived from F1 using those estimated in BC1S2 populations, (8) and (9):

$$\sigma^2_{G\,DH_{F1}} = \frac{8}{5}\,\sigma^2_{G\,BC1S2} \quad (11)$$

We applied (8) and (9) to each cross to obtain the values given in **Table 2**.

Table 2 Mean performances (μ_{BC1}) and genetic variances ($\sigma^2_{G\,DH_{F1}}$) of the 20 evaluated BC1S2 families and corresponding computed values of performance gaps between the donor and recipient lines (Gap_D) and the genetic variance in a DH population derived from F1 ($\sigma^2_{G\,DH_{F1}}$).

Family	Gap_{BC1}	$\sigma^2_{G\,BC1S2}$	Gap_D	$\sigma^2_{G\,DH_{F1}}$
A1D8	-11.79	32.17	-23.58	51.48
A1D5	-2.95	1.13	-5.90	1.81
A1D9	-3.36	12.89	-6.72	20.62
A2D2	-2.24	15.36	-4.48	24.57
A2D4	2.10	12.45	4.20	19.91
A3D1	-8.13	8.25	-16.26	13.20
A3D4	-7.18	9.31	-14.37	14.90
A3D6	-8.28	13.76	-16.56	22.01
A4D3	-3.86	0.00	-7.73	0.00
A4D4	-5.36	0.68	-10.71	1.09
A4D6	-2.69	0.10	-5.39	0.15
A5D1	-5.28	14.41	-10.57	23.06
A5D2	-6.46	0.01	-12.92	0.02
A5D7	-3.35	16.25	-6.71	25.99
A6D3	-10.21	2.62	-20.41	4.19
A6D5	-3.74	7.87	-7.48	12.59
A6D7	-9.31	12.01	-18.63	19.21
A7D3	-2.72	0.00	-5.43	0.01
A7D5	-5.03	7.91	-10.06	12.65
A7D6	-6.88	0.00	-13.76	0.00

We defined the following range for both parameters:

$$Gap_D \in [-30,10], \sigma^2_{G_{DH_{F1}}} \in [0,60]$$

We considered a step of 0.05 for both parameters. For each parameter pair, we computed the gains obtained for DH populations derived from F1, BC1 or BC2 crosses using (5) and (8). The cross type which maximized it was considered as optimal.

Table S1. Names and pedigrees of donor lines involved in the creation of the plant material

Donor line	Name	Pedigree	Collection	Country
D1	FV77	Pop. Liesse-3.1.2 (PPS 19)	CornFed(1)	France
D2	PP87	Pop. Isola Basso	CornFed(1)	Italy
D3	F7131 (PDZ502_SSD14)	Aranga 1_14-01m-4m-1m-m	Diversity Zea Promaïs	Spain
D4	EC50	Composite Aranga x EC18	CornFed(1)	Spain
D5	LP1061	Compuesto Colorado Precoz	INRA SMH Collection	Argentina, France, Canada, Roumania
D6	F7129 (PDZ12_SSD07)	VA5 Nostrano dell Isola_07-01m-5m-1m-1	Diversity Zea Promaïs	Italy
D7	F7130 (PDZ502_SSD11)	Aranga 1_11-01m-2m-1m-m	Diversity Zea Promaïs	Spain
D8	QSF3	Pop. Quarantin de la Sainte Famille	INRA SMH Collection	Italy
D9	Virtual line	-	-	-

D1-D7 are initial selected donor lines, D8 and D9 are putative donor lines for A1D2 and A1D7 individuals respectively identified after genotyping analysis. (1) European project « Cornfed » Rincent, Renaud, et al. "Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production." Theoretical and Applied Genetics 127.11 (2014): 2313-2331

Table S2 Adjusted means of the reference hybrids from the model M_FG

Trait	Trial	A1	A2	A3	A4	A5	A6	A7
FLOM	Blo19	90.41	91.3	91.42	91.85	90.96	91.98	91.73
	Smh19	55.13	54.84	55.73	55.18	56.51	55.99	57.54
	Vil19	92.49	93.58	92.49	94.61	94.1	94.11	93.84
	Multi	**79.34**	**79.9**	**79.88**	**80.55**	**80.52**	**80.69**	**81.04**
FLOF	Blo19	90.76	89.95	89.12	89.31	88.81	91.8	91.69
	Smh19	55.78	54.33	55.04	53.83	55.51	55.64	57.86
	Vil19	93.44	92.8	91.92	92.38	94.2	93.96	97.1
	Multi	**79.99**	**79.03**	**78.69**	**78.5**	**79.51**	**80.47**	**82.22**
ASI	Blo19	0.15	1.77	2.48	3.22	2.55	-0.08	0.41
	Smh19	-0.58	0.5	0.67	1.35	0.96	0.33	-0.25
	Vil19	-0.89	0.62	0.51	2.44	-0.18	-0.09	-3.1
	Multi	**-0.44**	**0.96**	**1.22**	**2.33**	**1.11**	**0.05**	**-0.98**
PH	Blo19	267.96	253.88	267.47	292.92	253.85	268.16	282.23
	Smh19	303.8	288.2	306.38	333.28	302.53	296.66	313.96
	Multi	**285.88**	**271.04**	**286.93**	**313.1**	**278.19**	**282.41**	**298.09**
GY	Blo19	129.83	123.13	116.47	130.04	125.78	117.04	110.85
	Smh19	117.71	115.26	128,00	123.74	129.07	125.73	113.45
	Vil19	105.58	86.99	108.77	103.97	109.33	101.47	82.76
	Multi	**117.7**	**108.46**	**117.75**	**119.25**	**121.39**	**114.75**	**102.36**
H2O	Blo19	28.49	27.02	25.52	27.43	28.12	25.8	29.35
	Smh19	24.54	21.79	22.48	25.17	23.26	23.59	22.94
	Vil19	30.3	27.54	26.64	26.07	30.33	27.06	28.32
	Multi	**27.78**	**25.45**	**24.88**	**26.22**	**27.24**	**25.49**	**26.87**
YI	Blo19	131.88	128.12	126.19	134.69	128.49	125.95	109.96
	Smh19	116.59	121.01	132.03	121.05	131.15	126.98	116.35
	Vil19	100.98	89.29	113.31	109.95	104.63	104.95	83.11
	Multi	**116.48**	**112.8**	**123.84**	**121.9**	**121.42**	**119.29**	**103.14**

Adjusted mean computed with fixed parameters of M_FG for the referent hybrid in each trial (Blo19, Smh19 and Vil19) and in multi-trial (Multi).

Table S3 Adjusted means of the hybrid families from the model M_FG

Trait	Trial	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6
FLOM	Blo19	90.65	92.78	90.09	90.49	92.51	91.56	93.15	92.15	91.58	92.45	92.33	89.46	90.88	91.11	93.1	92.21	93.41	91.35	91.38	91.46
	Smh19	55.91	57.78	55.52	55.52	55.87	56.23	57.69	56.6	55.99	57.35	56.32	55.77	57.62	57.27	57.16	56.45	57.53	56.57	56.72	56.79
	Vil19	93.54	95.13	93.29	94.15	94.93	93.96	95.67	94.06	94.48	95.07	94.69	92.81	93.83	94.77	94.84	93.99	95.16	93.6	93.83	93.45
	Multi	**80.04**	**81.9**	**79.63**	**80.05**	**81.1**	**80.58**	**82.17**	**80.94**	**80.68**	**81.62**	**81.11**	**79.34**	**80.78**	**81.05**	**81.7**	**80.88**	**82.03**	**80.51**	**80.64**	**80.56**
FLOF	Blo19	91.55	93.37	90.36	89.72	91.13	90.01	92.02	90.62	89.8	91.36	90.29	88.16	89.24	89.9	93.00	92.11	93.21	91.5	91.31	90.9
	Smh19	56.82	58.28	55.87	55.39	55.69	55.13	56.96	55.54	54.86	56.24	54.95	54.98	56.84	56.7	56.96	56.35	57.99	57.22	57.45	57.38
	Vil19	95.01	96.55	94.18	93.67	94.73	93.37	95.01	93.48	93.13	94.48	93.37	93.15	93.96	94.82	95.43	94.74	96.05	96.12	96.39	95.88
	Multi	**81.13**	**82.73**	**80.14**	**79.6**	**80.51**	**79.5**	**81.33**	**79.88**	**79.26**	**80.7**	**79.54**	**78.76**	**80.02**	**80.47**	**81.79**	**81.07**	**82.42**	**81.61**	**81.72**	**81.39**
ASI	Blo19	-0.4	-0.08	0.23	1.12	1.74	1.71	1.28	1.69	2.35	1.64	2.67	1.69	2.03	1.6	-0.1	-0.1	-0.03	0.24	0.35	0.72
	Smh19	-0.84	-0.4	-0.3	0.09	0.17	1.08	0.72	1.05	1.15	1.04	1.31	0.7	0.76	0.52	0.17	0.11	-0.51	-0.58	-0.69	-0.51
	Vil19	-1.47	-1.37	-0.82	0.3	0.04	0.59	0.62	0.56	1.58	0.79	1.52	-0.44	-0.21	-0.05	-0.8	-1.03	-1.16	-2.34	-2.33	-2.32
	Multi	**-0.9**	**-0.61**	**-0.29**	**0.5**	**0.65**	**1.12**	**0.87**	**1.1**	**1.7**	**1.16**	**1.83**	**0.65**	**0.86**	**0.69**	**-0.25**	**-0.34**	**-0.57**	**-0.89**	**-0.89**	**-0.71**
PH	Blo19	271.91	278.9	271.85	258.77	267.59	270.69	282.85	276.59	285.96	291.51	291.3	252.31	257.79	267.31	273.64	270.75	276.78	283.09	283.88	281.87
	Smh19	300.55	308.4	303.04	294.21	300.35	306.95	317.11	311.33	321.69	322.91	324.07	301.41	308.05	310.22	306.89	306.28	311.66	306.87	314.19	304.19
	Multi	**286.23**	**293.65**	**287.45**	**276.49**	**283.97**	**288.82**	**299.98**	**293.96**	**303.83**	**307.21**	**307.69**	**276.86**	**282.92**	**288.76**	**290.26**	**288.51**	**294.22**	**294.98**	**299.04**	**293.03**
GY	Blo19	118.51	127.61	123.62	115,00	126.21	113.99	117.86	116.04	124.45	125.22	127.2	125.02	125.36	127.65	110.74	116.64	114.7	105.55	104.98	101.87
	Smh19	108.2	125.46	119.63	112.72	116.28	122.67	124.54	124.25	122.21	122.77	124.24	117.01	119.8	127.67	117.84	121.75	115.9	113.11	112.77	111.4
	Vil19	92.09	99.14	98.59	90.24	93.01	99.85	101.33	97.86	97.29	96.62	98.84	104.5	100.65	103.97	89.14	94.35	92.1	82.5	79.63	77.62
	Multi	**106.27**	**117.4**	**113.94**	**105.99**	**111.83**	**112.17**	**114.58**	**112.72**	**114.65**	**114.87**	**116.76**	**115.51**	**115.27**	**119.76**	**105.91**	**110.92**	**107.57**	**100.39**	**99.13**	**96.97**
H2O	Blo19	28.78	29.97	28.84	26.98	28.28	26.67	27.68	27.01	27.44	28.25	27.7	27.65	28.06	28.7	27.36	26.25	27.51	29.06	29.4	28.9
	Smh19	24.5	25.14	24.51	21.96	22.01	22.89	22.93	23.01	23.99	24.03	24.52	23.5	23.59	24.02	23.24	23.07	23.41	23.39	23.11	23.41
	Vil19	30.4	31.47	29.54	27.18	27.58	28.14	28.92	28.54	26.43	27.66	26.74	29.88	30.52	31.13	27.55	27.03	28.11	28.82	29.79	29.11
	Multi	**27.9**	**28.86**	**27.63**	**25.37**	**25.96**	**25.9**	**26.51**	**26.18**	**25.95**	**26.64**	**26.32**	**27.01**	**27.39**	**27.95**	**26.05**	**25.45**	**26.34**	**27.09**	**27.43**	**27.14**
YI	Blo19	119.88	125.95	124.87	120.06	127.99	120.83	122.22	122.16	129.09	127.86	131.19	128.93	128.23	129.04	115.88	124.49	119.34	105.35	104,00	102.3
	Smh19	107.19	122.87	118.61	118.03	121.5	125.69	127.45	126.97	122.47	122.93	123.15	118.49	121.06	127.86	119.99	124.29	117.6	114.86	115.35	113.29
	Vil19	87.24	91.62	95.9	93.38	95.24	100.61	100.18	97.69	102.4	98.58	103.16	100.93	95.46	97.29	91.43	97.95	92.98	81.59	76.23	75.92
	Multi	**104.77**	**113.48**	**113.13**	**110.49**	**114.91**	**115.71**	**116.62**	**115.61**	**117.99**	**116.45**	**119.17**	**116.12**	**114.92**	**118.06**	**109.1**	**115.58**	**109.97**	**100.6**	**98.53**	**97.17**

Adjusted mean computed for the hybrid families in each trial (Blo19, Smh19 and Vil19) and in multi-trial (Multi). The estimations of fixed parameters of M_FG were used.

Table S4 Differences between the reference hybrid and hybrid family adjusted mean values

Trait	Trial	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6	Mean
FLOM	Blo19	0.25	2.37	-0.32	-0.81	1.21	0.14	1.73	0.74	-0.28	0.59	0.48	-1.5	-0.07	0.15	1.13	0.23	1.43	-0.38	-0.34	-0.27	0.32
	Smh19	0.78	2.65	0.39	0.68	1.03	0.5	1.96	0.87	0.81	2.17	1.14	-0.74	1.11	0.76	1.17	0.45	1.54	-0.97	-0.82	-0.76	0.74
	Vil19	1.05	2.64	0.8	0.58	1.36	1.46	3.17	1.57	-0.13	0.46	0.08	-1.29	-0.27	0.67	0.73	-0.12	1.05	-0.24	-0.01	-0.39	0.66
	Multi	**0.69**	**2.55**	**0.29**	**0.15**	**1.2**	**0.7**	**2.29**	**1.06**	**0.13**	**1.07**	**0.57**	**-1.18**	**0.26**	**0.53**	**1.01**	**0.19**	**1.34**	**-0.53**	**-0.39**	**-0.47**	**0.57**
FLOF	Blo19	0.79	2.61	-0.4	-0.23	1.17	0.88	2.9	1.5	0.5	2.06	0.98	-0.65	0.43	1.09	1.2	0.31	1.42	-0.19	-0.37	-0.78	0.76
	Smh19	1.04	2.5	0.09	1.06	1.35	0.09	1.92	0.5	1.03	2.41	1.12	-0.53	1.33	1.19	1.31	0.71	2.35	-0.64	-0.41	-0.48	0.9
	Vil19	1.58	3.12	0.75	0.87	1.93	1.45	3.09	1.57	0.75	2.1	1,00	-1.05	-0.23	0.62	1.47	0.78	2.1	-0.98	-0.71	-1.22	0.95
	Multi	**1.14**	**2.74**	**0.14**	**0.57**	**1.49**	**0.81**	**2.64**	**1.19**	**0.76**	**2.19**	**1.03**	**-0.74**	**0.51**	**0.97**	**1.33**	**0.6**	**1.95**	**-0.6**	**-0.5**	**-0.83**	**0.87**
ASI	Blo19	-0.55	-0.23	0.08	-0.64	-0.03	-0.77	-1.2	-0.79	-0.86	-1.58	-0.55	-0.86	-0.52	-0.94	-0.03	-0.02	0.05	-0.17	-0.06	0.31	-0.46
	Smh19	-0.26	0.18	0.28	-0.41	-0.33	0.41	0.06	0.38	-0.19	-0.3	-0.04	-0.26	-0.2	-0.44	-0.16	-0.22	-0.83	-0.34	-0.45	-0.27	-0.17
	Vil19	-0.58	-0.47	0.08	-0.32	-0.58	0.08	0.12	0.05	-0.86	-1.65	-0.92	-0.26	-0.03	0.13	-0.71	-0.94	-1.07	0.76	0.76	0.77	-0.28
	Multi	**-0.46**	**-0.17**	**0.15**	**-0.46**	**-0.31**	**-0.09**	**-0.34**	**-0.12**	**-0.64**	**-1.18**	**-0.5**	**-0.46**	**-0.25**	**-0.42**	**-0.3**	**-0.39**	**-0.62**	**0.08**	**0.08**	**0.27**	**-0.31**
PH	Blo19	3.94	10.93	3.89	4.89	13.71	3.21	15.38	9.11	-6.96	-1.41	-1.62	-1.54	3.94	13.46	5.48	2.59	8.62	0.86	1.65	-0.36	4.49
	Smh19	-3.25	4.59	-0.76	6.02	12.15	0.57	10.73	4.95	-11.59	-10.37	-9.21	-1.11	5.52	7.69	10.23	9.61	15,00	-7.09	0.23	-9.77	1.71
	Multi	**0.35**	**7.76**	**1.56**	**5.46**	**12.93**	**1.89**	**13.06**	**7.03**	**-9.27**	**-5.89**	**-5.41**	**-1.33**	**4.73**	**10.58**	**7.85**	**6.1**	**11.81**	**-3.12**	**0.94**	**-5.07**	**3.10**
GY	Blo19	-11.32	-2.22	-6.21	-8.13	3.08	-2.49	1.39	-0.44	-5.58	-4.82	-2.84	-0.75	-0.42	1.87	-6.3	-0.4	-2.34	-5.3	-5.87	-8.98	-3.40
	Smh19	-9.51	7.75	1.92	-2.53	1.03	-5.32	-3.46	-3.75	-1.53	-0.98	0.5	-12.06	-9.27	-1.4	-7.89	-3.97	-9.83	-0.34	-0.68	-2.05	-3.17
	Vil19	-13.48	-6.44	-6.99	3.25	6.02	-8.92	-7.43	-10.91	-6.68	-7.35	-5.13	-4.83	-8.67	-5.36	-12.33	-7.11	-9.36	-0.27	-3.13	-5.14	-6.01
	Multi	**-11.44**	**-0.3**	**-3.76**	**-2.47**	**3.38**	**-5.58**	**-3.17**	**-5.03**	**-4.6**	**-4.38**	**-2.49**	**-5.88**	**-6.12**	**-1.63**	**-8.84**	**-3.83**	**-7.18**	**-1.97**	**-3.23**	**-5.39**	**-4.20**
H2O	Blo19	0.29	1.48	0.34	-0.04	1.26	1.15	2.15	1.48	0.01	0.81	0.27	-0.47	-0.06	0.59	1.56	0.45	1.71	-0.28	0.05	-0.44	0.62
	Smh19	-0.04	0.6	-0.03	0.17	0.21	0.41	0.44	0.53	-1.18	-1.14	-0.65	0.24	0.33	0.76	-0.36	-0.52	-0.18	0.45	0.17	0.47	0.03
	Vil19	0.1	1.18	-0.75	-0.36	0.05	1.5	2.28	1.9	0.36	1.59	0.68	-0.45	0.19	0.8	0.48	-0.03	1.05	0.5	1.48	0.79	0.67
	Multi	**0.12**	**1.08**	**-0.15**	**-0.08**	**0.51**	**1.02**	**1.63**	**1.3**	**-0.27**	**0.42**	**0.1**	**-0.23**	**0.15**	**0.72**	**0.56**	**-0.03**	**0.86**	**0.22**	**0.57**	**0.27**	**0.44**
YI	Blo19	-12,00	-5.93	-7.01	-8.06	-0.13	-5.36	-3.97	-4.03	-5.6	-6.84	-3.5	0.44	-0.26	0.55	-10.07	-1.46	-6.61	-4.61	-5.96	-7.66	-4.90
	Smh19	-9.4	6.28	2.02	-2.98	0.49	-6.34	-4.58	-5.06	1.42	1.88	2.1	-12.66	-10.09	-3.29	-6.99	-2.69	-9.38	-1.49	-1,00	-3.06	-3.24
	Vil19	-13.74	-9.36	-5.08	4.09	5.95	-12.7	-13.13	-15.62	-7.55	-11.37	-6.79	-3.7	-9.18	-7.34	-13.51	-7,00	-11.96	-1.52	-6.88	-7.19	-7.68
	Multi	**-11.71**	**-3,00**	**-3.35**	**-2.32**	**2.1**	**-8.13**	**-7.22**	**-8.23**	**-3.91**	**-5.44**	**-2.73**	**-5.31**	**-6.51**	**-3.36**	**-10.19**	**-3.72**	**-9.32**	**-2.54**	**-4.61**	**-5.97**	**-5.27**

Difference between the adjusted means of the hybrid families (Table S3) and the associated referent hybrid (Table S2) in each trial (Blo19, Smh19 and Vil19) and in multi-trial (Multi).

Table S5 Percentages of individuals in each family with higher multi-trial adjusted means than their reference hybrid

Trait	A1			A2		A3			A4			A5			A6			A7		
	A1D8	**A1D5**	**A1D9**	**A2D2**	**A2D4**	**A3D1**	**A3D4**	**A3D6**	**A4D3**	**A4D4**	**A4D6**	**A5D1**	**A5D2**	**A5D7**	**A6D3**	**A6D5**	**A6D7**	**A7D3**	**A7D5**	**A7D6**
ASI	30%	30%	56%	14%	26%	42%	32%	41%	23%	7%	25%	11%	31%	11%	29%	17%	9%	58%	50%	58%
FLOF	77%	98%	58%	76%	89%	78%	100%	79%	63%	90%	72%	27%	71%	77%	93%	71%	98%	34%	50%	33%
FLOM	75%	100%	61%	56%	93%	73%	100%	83%	47%	88%	73%	20%	63%	71%	86%	55%	95%	37%	47%	33%
PH	52%	82%	59%	75%	91%	63%	96%	79%	21%	30%	33%	49%	63%	86%	77%	77%	91%	39%	54%	31%
GY	10%	47%	24%	34%	72%	15%	39%	16%	19%	13%	33%	18%	12%	41%	4%	18%	9%	37%	32%	27%
H2O	60%	87%	44%	46%	61%	90%	100%	95%	44%	58%	53%	30%	62%	73%	68%	47%	86%	71%	79%	45%
YI	10%	25%	27%	39%	63%	8%	25%	9%	28%	13%	27%	20%	8%	29%	5%	29%	0%	26%	29%	30%

Adjusted mean of individuals were computed using model M_FG with genotypic effect declared as fixed.

Table S6 Decomposition variance with the model M_FG$_S$ (within-family genetic variances)

Trait	AIC	BIC	Variance Type	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6	Error
FLOM	4877	5145	σ^2_G	**1.16** (0.25)	**1.27** (0.27)	**1.80** (0.37)	**0.54** (0.15)	**0.46** (0.14)	**0.49** (0.12)	**0.64** (0.17)	**0.95** (0.24)	**0.51** (0.17)	**0.41** (0.13)	**0.42** (0.12)	**1.35** (0.27)	**1.08** (0.27)	**1.77** (0.38)	**0.53** (0.14)	**0.31** (0.10)	**0.39** (0.11)	**1.50** (0.43)	**2.11** (0.61)	**1.12** (0.38)	-
			$\sigma^2_{GEBlo19}$	**0** (-)	**0** (-)	**0.36** (0.21)	**0.90** (0.31)	**0.59** (0.26)	**0.47** (0.22)	**0.60** (0.27)	**0.64** (0.29)	**0** (-)	**0.11** (0.16)	**0** (-)	**0.27** (0.19)	**0.20** (0.21)	**0** (-)	**0.36** (0.21)	**0.83** (0.27)	**0.56** (0.24)	**0.95** (0.42)	**0.30** (0.32)	**0** (-)	**0.57** (0.04)
			$\sigma^2_{GESmh19}$	**0.17** (0.13)	**0.37** (0.16)	**0** (-)	**0.16** (0.13)	**0.23** (0.14)	**0** (-)	**0.30** (0.16)	**0.31** (0.19)	**0.87** (0.29)	**0.86** (0.24)	**0.99** (0.26)	**0.02** (0.12)	**0.43** (0.20)	**0.41** (0.19)	**0.13** (0.12)	**0.12** (0.11)	**0.08** (0.11)	**0.91** (0.36)	**0.97** (0.45)	**0.49** (0.30)	**0.26** (0.02)
			$\sigma^2_{GEVil19}$	**0** (-)	**0** (-)	**0** (-)	**0.35** (0.24)	**0** (-)	**0.58** (0.27)	**0.11** (0.21)	**0.52** (0.29)	**0** (-)	**0** (-)	**0** (-)	**0.62** (0.28)	**0.29** (0.26)	**0.30** (0.25)	**0** (-)	**0.27** (0.21)	**0** (-)	**0.30** (0.31)	**0** (-)	**0.51** (0.35)	**0.75** (0.04)
FLOF	5562	5829	σ^2_G	**1.62** (0.36)	**1.58** (0.36)	**2.00** (0.41)	**0.52** (0.15)	**0.67** (0.18)	**0.57** (0.15)	**0.67** (0.19)	**1.19** (0.28)	**2.31** (0.55)	**1.51** (0.33)	**1.94** (0.40)	**1.17** (0.25)	**1.18** (0.30)	**1.64** (0.36)	**0.71** (0.19)	**0.56** (0.14)	**0.43** (0.14)	**1.69** (0.52)	**2.86** (0.79)	**1.47** (0.5)	-
			$\sigma^2_{GEBlo19}$	**0.29** (0.25)	**0.59** (0.28)	**0.46** (0.24)	**0.18** (0.17)	**1.19** (0.37)	**0.71** (0.26)	**0.66** (0.29)	**0.61** (0.28)	**0.28** (0.23)	**1.13** (0.36)	**0.13** (0.17)	**0** (-)	**0.09** (0.21)	**0.14** (0.20)	**0.28** (0.21)	**0.68** (0.25)	**0.48** (0.23)	**1.29** (0.53)	**0** (-)	**0** (-)	**0.55** (0.04)
			$\sigma^2_{GESmh19}$	**0.32** (0.22)	**0.62** (0.27)	**0** (-)	**0.28** (0.16)	**0.10** (0.15)	**0** (-)	**0.63** (0.25)	**0.26** (0.19)	**0** (-)	**0.04** (0.16)	**0.04** (0.14)	**0.20** (0.15)	**0.82** (0.3)	**0.42** (0.21)	**0.32** (0.18)	**0** (-)	**0.78** (0.26)	**1.12** (0.47)	**0.95** (0.44)	**0.52** (0.34)	**0.38** (0.03)
			$\sigma^2_{GEVil19}$	**1.14** (0.42)	**0.22** (0.27)	**0.24** (0.24)	**0.20** (0.22)	**0** (-)	**0.16** (0.21)	**0** (-)	**0.02** (0.21)	**0.09** (0.24)	**0.02** (0.21)	**0.46** (0.26)	**0.20** (0.21)	**0.41** (0.31)	**0.01** (-)	**0.06** (0.21)	**0.15** (0.2)	**0** (-)	**0.99** (0.51)	**0** (-)	**1.32** (0.59)	**0.82** (0.05)
ASI	576	844	σ^2_G	**0.08** (0.03)	**0** (-)	**0.06** (0.01)	**0.03** (0.02)	**0.05** (0.01)	**0.03** (0.02)	**0.07** (0.03)	**0.04** (0.04)	**0.03** (0.04)	**0.10** (0.04)	**0.07** (0.01)	**0.04** (0.02)	**0** (-)	**0.02** (0.02)	**0.03** (0.02)	**0.01** (0.02)	**0** (-)	**0** (-)	**0.13** (0.04)	**0.07** (0.05)	-
			$\sigma^2_{GEBlo19}$	**0.15** (0.15)	**0.10** (0.13)	**0.16** (0.14)	**0.19** (0.14)	**0.44** (0.19)	**0.54** (0.21)	**0.54** (0.22)	**1.01** (0.31)	**0.78** (0.3)	**0.85** (0.27)	**0.88** (0.27)	**0.05** (0.11)	**0.06** (0.13)	**0.22** (0.16)	**0** (-)	**0** (-)	**0** (-)	**0.42** (0.20)	**0.23** (0.20)	**0** (-)	**0.59** (0.04)
			$\sigma^2_{GESmh19}$	**0.01** (0.03)	**0.07** (0.02)	**0** (-)	**0** (-)	**0** (-)	**0.01** (0.02)	**0.01** (0.03)	**0.05** (0.04)	**0.04** (0.04)	**0.02** (0.04)	**0** (-)	**0.02** (0.02)	**0.06** (0.03)	**0.01** (0.02)	**0.02** (0.02)	**0.03** (0.02)	**0.05** (0.01)	**0.04** (0.01)	**0** (-)	**0.03** (0.05)	**0.01** (0)
			$\sigma^2_{GEVil19}$	**0.84** (0.34)	**0.32** (0.24)	**0.17** (0.21)	**0.35** (0.25)	**0** (-)	**0.58** (0.28)	**0.10** (0.2)	**0.32** (0.25)	**1.47** (0.54)	**0.44** (0.24)	**0.78** (0.31)	**0** (-)	**0.26** (0.25)	**0** (-)	**0** (-)	**0.35** (0.24)	**0.01** (-)	**0.47** (0.27)	**1.08** (0.46)	**1.25** (0.51)	**1.00** (0.06)
PH	15463	15630	σ^2_G	**57.94** (21.54)	**34.42** (18.84)	**69.35** (17.51)	**27.15** (13.76)	**1.37** (24.28)	**4.85** (11.21)	**15.59** (12.33)	**20.52** (14.97)	**25.00** (32.71)	**78.43** (24.38)	**56.58** (17.51)	**62.49** (17.92)	**60.64** (16.4)	**68.75** (21.82)	**45.67** (18.29)	**42.43** (15.2)	**40.39** (18.04)	**57.40** (27.5)	**50.22** (30.97)	**160.99** (69.34)	-
			$\sigma^2_{GEBlo19}$	**16.50** (31.21)	**50.34** (35.32)	**81.50** (42.06)	**31.31** (28.92)	**240.37** (72.64)	**0** (-)	**0.85** (25.22)	**9.58** (26.71)	**296.60** (96.17)	**0** (-)	**0** (-)	**0** (-))	**27.85** (32.32)	**0** (-)	**29.64** (31.68)	**23.90** (28.03)	**0.39** (26.03)	**49.99** (40.11)	**1.79** (36.78)	**102.11** (78.35)	**115.27** (7.43)
			$\sigma^2_{GESmh19}$	**30.58** (21.56)	**36.24** (21.16)	**0** (-)	**10.27** (14.59)	**59.34** (29.57)	**39.18** (17.28)	**20.40** (15.07)	**35.37** (18.57)	**49.19** (36.35)	**34.83** (21.96)	**6.59** (14.83)	**4.69** (14.86)	**0** (-)	**15.18** (18.75)	**15.70** (18.24)	**5.49** (14.57)	**44.17** (21.18)	**55.49** (29.93)	**63.49** (37.28)	**26.12** (54.86)	**27.76** (2.23)
GY	21435	21702	σ^2_G	**43.26** (11.66)	**5.74** (4.97)	**22.54** (7.35)	**26.96** (11.01)	**15.01** (7.84)	**7.88** (4.15)	**27.24** (8.63)	**13.98** (5.75)	**9.34** (5.52)	**3.91** (3.83)	**5.19** (3.99)	**24.85** (7.5)	**16.81** (7.67)	**19.74** (7.36)	**4.02** (4.31)	**2.66** (4.66)	**10.60** (6.12)	**36.58** (15.42)	**20.33** (14.33)	**86.67** (32.28)	-
			$\sigma^2_{GEBlo19}$	**18.96** (15.02)	**28.95** (14.9)	**0** (-)	**64.59** (23.61)	**3.85** (11.34)	**0.10** (-)	**0** (-))	**0** (-)	**5.30** (12.78)	**0** (-)	**2.49** (8.9)	**2.86** (10.92)	**4.74** (12.3)	**0** (-)	**30.63** (15.85)	**11.71** (11.1)	**27.39** (15.43)	**30.39** (20.01)	**33.13** (24.61)	**58.22** (37.92)	**45.84** (2.86)
			$\sigma^2_{GESmh19}$	**16.98** (15.99)	**0** (-)	**13.29** (14.7)	**30.15** (18.24)	**46.01** (21.33)	**0** (-)	**42.75** (20.51)	**0** (-)	**0** (-))	**0** (-))	**15.14** (12.33)	**8.98** (13.35)	**22.74** (17.56)	**4.32** (13.46)	**0.02** (-)	**29.03** (15.77)	**57.31** (22.38)	**80.50** (32.84)	**7.40** (17.9)	**6.25** (24.88)	**54.23** (3.28)
			$\sigma^2_{GEVil19}$	**0** (-))	**4.67** (10.03)	**0** (-))	**35.38** (17.55)	**34.04** (16.66)	**0.01** (-)	**0** (-)	**6.13** (10.48)	**0** (-)	**11.83** (9.79)	**0** (-)	**0.01** (-)	**9.52** (12.23)	**13.95** (12.66)	**0** (-)	**10.66** (9.84)	**0** (-)	**34.67** (20.5)	**60.77** (27.56)	**55.31** (30.61)	**41.91** (2.34)
H2O	4160	4427	σ^2_G	**0.68** (0.16)	**0.77** (0.18)	**0.45** (0.13)	**0.48** (0.14)	**0.49** (0.15)	**0.20** (0.07)	**0.35** (0.11)	**0.38** (0.11)	**0.09** (0.09)	**0.50** (0.14)	**0.40** (0.13)	**0.22** (0.08)	**0.79** (0.19)	**0.37** (0.11)	**0.67** (0.17)	**0.38** (0.10)	**0.35** (0.10)	**0.20** (0.15)	**0.43** (0.17)	**0.72** (0.25)	-
			$\sigma^2_{GEBlo19}$	**0.82** (0.30)	**0.28** (0.19)	**0.49** (0.25)	**0.72** (0.27)	**1.41** (0.41)	**0.27** (0.18)	**0.28** (0.20)	**0.13** (0.17)	**0.39** (0.24)	**0** (-))	**0.16** (0.17)	**0.05** (0.14)	**0.15** (0.19)	**0.46** (0.23)	**1.34** (0.40)	**0.48** (0.21)	**0.26** (0.18)	**1.60** (0.52)	**0.78** (0.40)	**1.03** (0.53)	**0.57** (0.05)
			$\sigma^2_{GESmh19}$	**0** (-)	**0** (-)	**0.04** (0.12)	**0.11** (0.13)	**0.07** (0.13)	**0** (-)	**0** (-)	**0** (-)	**0.28** (0.15)	**0.82** (0.25)	**0.50** (0.18)	**0.06** (0.09)	**0.04** (0.13)	**0** (-))	**0** (-)	**0** (-)	**0** (-)	**0.39** (0.19)	**0** (-)	**0** (-)	**0.33** (0.02)
			$\sigma^2_{GEVil19}$	**0.30** (0.16)	**0.83** (0.25)	**0.83** (0.26)	**0.65** (0.22)	**0.49** (0.21)	**0.26** (0.14)	**0.60** (0.21)	**0.40** (0.17)	**1.10** (0.34)	**0.31** (0.16)	**0.44** (0.18)	**0.83** (0.23)	**0.50** (0.21)	**0.82** (0.25)	**0.41** (0.18)	**0.51** (0.18)	**0.38** (0.17)	**1.28** (0.41)	**0.54** (0.25)	**1.17** (0.43)	**0.36** (0.03)
YI	21713	21980	σ^2_G	**37.45** (10.74)	**1.40** (4.73)	**14.83** (6.43)	**18.33** (9.27)	**13.94** (7.43)	**6.83** (4.84)	**30.48** (9.41)	**18.15** (6.88)	**8.13** (5.98)	**7.25** (4.7)	**0.33** (3.41)	**18.34** (6.46)	**8.93** (6.16)	**20.03** (7.86)	**5.82** (5.02)	**10.95** (6.47)	**13.73** (6.96)	**45.97** (18.55)	**36.95** (19.02)	**106.61** (35.53)	-
			$\sigma^2_{GEBlo19}$	**14.98** (15.05)	**34.20** (16.25)	**0** (-)	**38.30** (18.79)	**0** (-)	**10.04** (11.89)	**0** (-)	**0** (-)	**6.84** (14.21)	**0** (-))	**5.67** (9.63)	**0** (-)	**0** (-)	**0** (-)	**57.60** (22.25)	**27.91** (15.35)	**31.12** (17.25)	**19.98** (19.69)	**39.26** (28.97)	**70.55** (42.44)	**49.71** (2.95)
			$\sigma^2_{GESmh19}$	**20.95** (17.61)	**0** (-)	**18.53** (16.26)	**33.50** (19.1)	**47.19** (22.62)	**0** (-)	**34.51** (20.15)	**0** (-)	**0** (-)	**0** (-)	**20.65** (13.85)	**10.33** (14.37)	**31.98** (20.01)	**4.61** (14.72)	**0** (-))	**19.52** (15.91)	**51.04** (22.6)	**77.63** (33.61)	**5.67** (19.79)	**0** (-)	**60.17** (3.59)
			$\sigma^2_{GEVil19}$	**0** (-)	**10.81** (11.19)	**1.58** (10.49)	**32.96** (16.63)	**32.54** (16.79)	**3.97** (10.01)	**0** (-)	**7.95** (11.47)	**2.41** (10.83)	**18.38** (11.69)	**0** (-)	**0.03** (-)	**14.36** (12.95)	**23.36** (15.02)	**0** (-)	**11.19** (11.23)	**0** (-)	**60.78** (27.62)	**43.26** (25.95)	**37.08** (25.58)	**44.09** (2.77)

AIC and BIC criterion are indicated for each model. The estimations of variance components are indicated in bold and their standard errors are given in parenthesis. (The standard error is not computed if the estimated variance value is close to 0)

Table S7 Likelihood ratio test to test the within-family variances homogeneity

Model 1	Model 2	Trait	Likelihood-ratio	DF	P-value
M_FG	M_FG_S	FLOM	238.15	76	5.83E-28
		FLOF	229.89	76	1.52E-26
		ASI	215.99	76	3.43E-24
		PH	132,83	57	3,53E-24
		GY	215,91	76	7,12E-14
		H2O	192.51	76	2.66E-20
		YI	203.64	76	3.94E-22
M_FA	M_FA_S	FLOM	200.82	76	1.15E-21
		FLOF	242.63	76	9.87E-29
		ASI	182.98	76	9.28E-19
		PH	122.97	57	2.60E-12
		GY	186.29	76	2.72E-19
		H2O	164.39	76	8.11E-16
		YI	184.24	76	5.82E-19
M_FAP	$M\_FA_SP_S$	FLOM	313.30	152	3.52E-27
		FLOF	321.92	152	1.72E-28
		ASI	223.99	152	1.62E-14
		PH	180.08	114	5.55E-13
		GY	253.51	152	1.72E-18
		H2O	236.89	152	3.19E-16
		YI	249.99	152	5.28E-18

The likelihood ratio test were performed with the function pchisqmix of the R package TcGSA which used a chi-squared mixtures distribution. P-value<0.01 were considered as significant.

Table S8 Variance decomposition with the model M_FA$_s$ (within-family additive variances)

Trait	AIC	BIC	Variance Type	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6	Error
FLOM	4673	4941	σ^2_A	**1.57** (0.37)	**1.14** (0.29)	**1.37** (0.32)	**0.64** (0.21)	**0.57** (0.19)	**0.68** (0.19)	**0.72** (0.23)	**1.03** (0.29)	**0.66** (0.26)	**1.14** (0.37)	**0.39** (0.14)	**1.37** (0.31)	**1.33** (0.35)	**2.29** (0.54)	**0.55** (0.16)	**0.34** (0.13)	**0.39** (0.13)	**2.21** (0.63)	**2.05** (0.62)	**1.66** (0.56)	-
	$\sigma^2_{AEBlo19}$	**0.03** (0.13)	**0** (-)	**0.21** (0.20)	**0.71** (0.37)	**0.43** (0.25)	**0.08** (0.16)	**0.51** (0.31)	**0.49** (0.34)	**0** (-)	**0** (-)	**0** (-)	**0.17** (0.16)	**0.05** (0.18)	**0** (-)	**0.02** (0.14)	**0.91** (0.42)	**0.43** (0.27)	**0.61** (0.40)	**0.09** (0.29)	**0** (-)	**0.71** (0.04)
	$\sigma^2_{AESmh19}$	**0.03** (0.11)	**0.25** (0.18)	**0** (-)	**0.09** (0.14)	**0.19** (0.15)	**0** (-)	**0.26** (0.18)	**0.24** (0.20)	**1.17** (0.45)	**1.94** (0.65)	**1.15** (0.37)	**0** (-)	**0.51** (0.25)	**0.28** (0.20)	**0.08** (0.10)	**0.13** (0.13)	**0.03** (0.09)	**1.45** (0.55)	**1.24** (0.61)	**0.40** (0.30)	**0.29** (0.02)
	$\sigma^2_{AEVil19}$	**0.08** (0.15)	**0** (0.11)	**0** (-)	**0.27** (0.26)	**0** (-)	**0.61** (0.30)	**0.20** (0.23)	**0.51** (0.32)	**0** (-)	**0** (-)	**0** (-)	**0.80** (0.36)	**0.26** (0.25)	**0.27** (0.28)	**0** (-)	**0.24** (0.20)	**0** (-)	**0.10** (0.33)	**0** (-)	**0.47** (0.36)	**0.77** (0.04)
FLOF	5386	5654	σ^2_A	**2.12** (0.51)	**1.53** (0.40)	**1.65** (0.39)	**0.60** (0.19)	**0.64** (0.21)	**0.70** (0.20)	**0.89** (0.28)	**1.34** (0.35)	**4.85** (1.21)	**4.79** (1.06)	**2.65** (0.60)	**1.24** (0.30)	**1.45** (0.40)	**1.81** (0.45)	**0.75** (0.21)	**0.68** (0.20)	**0.37** (0.15)	**2.52** (0.77)	**2.78** (0.82)	**1.62** (0.57)	-
	$\sigma^2_{AEBlo19}$	**0** (-)	**0.46** (0.32)	**0.04** (0.16)	**0** (-)	**0.94** (0.40)	**0.40** (0.28)	**0.34** (0.32)	**0.36** (0.29)	**0.13** (0.20)	**1.21** (0.54)	**0.05** (0.15)	**0** (-)	**0** (-)	**0** (-)	**0.05** (0.17)	**0.37** (0.26)	**0.33** (0.26)	**0.87** (0.58)	**0** (-)	**0** (-)	**0.74** (0.04)
	$\sigma^2_{AESmh19}$	**0.43** (0.27)	**0.56** (0.31)	**0.01** (0.09)	**0.26** (0.15)	**0.09** (0.13)	**0** (-)	**0.50** (0.25)	**0.22** (0.21)	**0** (-)	**0** (-)	**0.06** (0.14)	**0.17** (0.13)	**1.01** (0.40)	**0.31** (0.20)	**0.14** (0.15)	**0.07** (0.12)	**0.57** (0.25)	**2.11** (0.80)	**1.14** (0.60)	**0.41** (0.32)	**0.40** (0.03)
	$\sigma^2_{AEVil19}$	**1.03** (0.52)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0.02** (-)	**0** (-)	**0.05** (0.20)	**0** (-)	**0.01** (-)	**0.33** (0.26)	**0** (-)	**0.43** (0.34)	**0** (-)	**0** (-)	**0.04** (0.16)	**0** (-)	**0.85** (0.60)	**0** (-)	**1.03** (0.56)	**0.91** (0.04)
ASI	-355	-87	σ^2_A	**0.04** (0.02)	**0** (-)	**0.04** (0.01)	**0.02** (0.01)	**0.03** (0.02)	**0.03** (0.02)	**0.05** (0.02)	**0.03** (0.02)	**0.03** (0.04)	**0.05** (0.03)	**0.05** (0.01)	**0.02** (0.01)	**0** (0.02)	**0.01** (0.01)	**0.02** (0.02)	**0.01** (0.01)	**0** (-)	**0** (-)	**0.10** (0.03)	**0.04** (0.04)	-
	$\sigma^2_{AEBlo19}$	**0.07** (0.12)	**0** (-)	**0.08** (0.11)	**0.13** (0.13)	**0.33** (0.19)	**0.01** (-)	**0.39** (0.23)	**0.98** (0.37)	**0.78** (0.38)	**0.95** (0.39)	**0.94** (0.37)	**0.04** (0.08)	**0.10** (0.12)	**0.19** (0.14)	**0** (-)	**0** (-)	**0** (-)	**0.38** (0.21)	**0.14** (0.19)	**0** (-)	**0.68** (0.03)
	$\sigma^2_{AESmh19}$	**0.02** (0.02)	**0.04** (0.01)	**0** (-)	**0** (0.01)	**0** (0.02)	**0** (0.02)	**0** (0.02)	**0.02** (0.02)	**0.02** (0.04)	**0.01** (0.03)	**0** (-)	**0.01** (0.01)	**0.05** (0.02)	**0** (0.01)	**0.01** (0.02)	**0.02** (0.01)	**0.03** (0.01)	**0.04** (0.01)	**0** (-)	**0.03** (0.04)	**0** (0)
	$\sigma^2_{AEVil19}$	**0.61** (0.37)	**0** (-)	**0.07** (0.16)	**0.03** (0.14)	**0** (-)	**0.33** (0.25)	**0.10** (0.18)	**0.01** (-)	**1.47** (0.68)	**0.07** (0.16)	**0.64** (0.37)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0.12** (0.17)	**0** (-)	**0.39** (0.28)	**1.02** (0.54)	**1.06** (0.51)	**1.15** (0.05)
PH	15384	15552	σ^2_A	**58.94** (22.09)	**45.27** (26.3)	**49.97** (16.65)	**37.05** (16.75)	**0** (-)	**9.68** (9.67)	**18.93** (13.02)	**26.45** (17.55)	**78.03** (54.53)	**183.65** (53.8)	**93.83** (28.94)	**51.16** (17.75)	**53.77** (18.55)	**64.72** (20.01)	**51.74** (18.04)	**50.85** (17.37)	**45.17** (20.62)	**86.52** (34.84)	**55.40** (33.83)	**112.90** (71.21)	-
	$\sigma^2_{AEBlo19}$	**5.55** (26.26)	**28.76** (35.22)	**76.32** (41.62)	**0** (-)	**353.34** (117.43)	**0** (-)	**0** (-)	**0.55** (22.06)	**420.34** (156.52)	**0** (-)	**0** (-)	**0.49** (19.09)	**26.71** (28.82)	**0** (-)	**19.01** (27.02)	**5.22** (20.75)	**0** (-)	**0** (-)	**0** (-)	**76.46** (76.74)	**122.76** (6.26)
	$\sigma^2_{AESmh19}$	**10.48** (19.01)	**48.14** (30.06)	**0** (-)	**0.02** (-)	**65.74** (23.79)	**21.22** (14.4)	**11.57** (15.04)	**26.11** (20.74)	**8.79** (53.06)	**16.16** (22.11)	**0** (-)	**4.58** (13.5)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**26.74** (20.19)	**59.55** (34.88)	**64.27** (45.84)	**88.80** (71.77)	**35.47** (2.32)
GY	21341	21608	σ^2_A	**37.04** (12.18)	**5.60** (5.31)	**17.61** (7.11)	**21.48** (12.09)	**18.08** (9.8)	**8.59** (4.46)	**35.31** (12.27)	**13.06** (6.63)	**3.27** (4.84)	**2.88** (3.02)	**6.41** (4.05)	**25.81** (9.5)	**14.05** (8.14)	**21.22** (8.94)	**4.74** (4.35)	**1.43** (4.53)	**12.82** (8.3)	**49.18** (19.74)	**24.14** (17.52)	**139.14** (49.66)	-
	$\sigma^2_{AEBlo19}$	**15.98** (13.76)	**16.25** (14.28)	**0** (-)	**63.88** (27.01)	**2.52** (9.72)	**0** (-)	**0** (-)	**0** (-)	**14.50** (13.26)	**0** (-)	**0.31** (5.24)	**9.81** (10.52)	**7.77** (12.1)	**0.01** (-)	**21.93** (15.11)	**7.22** (8.24)	**21.91** (16.79)	**21.42** (20.98)	**30.69** (28.58)	**61.85** (45.46)	**48.18** (2.51)
	$\sigma^2_{AESmh19}$	**20.39** (14.83)	**0** (-)	**7.39** (11.1)	**32.76** (22.2)	**49.72** (26.61)	**0.39** (7.73)	**32.43** (19.7)	**5.77** (9.95)	**0** (-)	**0** (-)	**7.30** (9.76)	**12.06** (12.01)	**25.07** (18.37)	**8.64** (11.32)	**0** (-)	**34.74** (18.07)	**63.46** (29.1)	**96.16** (42.21)	**4.19** (19.63)	**10.08** (28.05)	**55.36** (2.91)
	$\sigma^2_{AEVil19}$	**0** (-)	**8.59** (9.16)	**0** (-)	**31.07** (20.33)	**28.61** (18.31)	**0.81** (6.93)	**0** (-)	**10.27** (10.63)	**3.09** (7.68)	**7.77** (8.71)	**0** (-)	**3.57** (8.58)	**11.14** (12.03)	**9.21** (11.07)	**0.57** (6.24)	**16.88** (10.53)	**0.58** (9.45)	**30.71** (22.77)	**78.71** (37.48)	**50.97** (35.18)	**43.28** (2.25)
H2O	3753	4021	σ^2_A	**0.56** (0.16)	**0.72** (0.20)	**0.43** (0.15)	**0.42** (0.15)	**0.37** (0.14)	**0.19** (0.08)	**0.41** (0.14)	**0.33** (0.11)	**0.10** (0.11)	**0.95** (0.26)	**0.47** (0.17)	**0.25** (0.10)	**0.71** (0.20)	**0.36** (0.12)	**0.50** (0.15)	**0.46** (0.14)	**0.23** (0.09)	**0.51** (0.26)	**0.59** (0.24)	**0.65** (0.25)	-
	$\sigma^2_{AEBlo19}$	**0.83** (0.38)	**0.35** (0.22)	**0.33** (0.23)	**0.70** (0.31)	**1.15** (0.40)	**0.19** (0.15)	**0.30** (0.21)	**0.15** (0.14)	**0.32** (0.25)	**0** (-)	**0.14** (0.18)	**0.14** (0.14)	**0.23** (0.19)	**0.34** (0.23)	**1.43** (0.49)	**0.48** (0.24)	**0.21** (0.16)	**1.51** (0.58)	**0.75** (0.44)	**0.92** (0.50)	**0.60** (0.04)
	$\sigma^2_{AESmh19}$	**0** (-)	**0** (-)	**0.11** (0.14)	**0.06** (0.12)	**0.05** (0.13)	**0** (-)	**0** (-)	**0** (-)	**0.25** (0.16)	**1.07** (0.38)	**0.56** (0.24)	**0.03** (0.10)	**0.05** (0.13)	**0** (-)	**0.02** (0.12)	**0** (-)	**0** (-)	**0.53** (0.30)	**0** (-)	**0** (-)	**0.32** (0.02)
	$\sigma^2_{AEVil19}$	**0.25** (0.16)	**0.78** (0.30)	**0.62** (0.27)	**0.73** (0.32)	**0.64** (0.29)	**0.23** (0.14)	**0.65** (0.27)	**0.36** (0.18)	**1.22** (0.46)	**0.02** (0.10)	**0.34** (0.20)	**0.97** (0.32)	**0.49** (0.24)	**0.74** (0.28)	**0.33** (0.19)	**0.43** (0.20)	**0.33** (0.18)	**1.67** (0.63)	**0.62** (0.34)	**1.55** (0.59)	**0.43** (0.03)
YI	21648	21915	σ^2_A	**31.14** (11.04)	**2.38** (4.42)	**12.28** (5.86)	**16.40** (10.57)	**16.48** (9.07)	**8.68** (4.71)	**38.80** (13.43)	**16.67** (7.85)	**2.88** (5.39)	**5.68** (4.55)	**0.24** (2.94)	**16.55** (7.75)	**4.90** (5.59)	**21.51** (9.63)	**5.20** (4.93)	**10.23** (7.19)	**18.20** (9.13)	**75.14** (26.96)	**48.18** (24.48)	**183.18** (59.63)	-
	$\sigma^2_{AEBlo19}$	**12.45** (13.1)	**13.18** (12.91)	**0** (-)	**36.84** (21.11)	**0** (-)	**0** (-)	**0** (-)	**0.01** (-)	**12.15** (13.67)	**0.03** (-)	**1.65** (6.12)	**6.30** (9.79)	**0** (-)	**0.01** (-)	**47.13** (24.78)	**16.08** (13.75)	**17.87** (17.05)	**0.40** (18.6)	**25.47** (29.36)	**76.52** (51.77)	**54.70** (2.75)
	$\sigma^2_{AESmh19}$	**23.49** (16.13)	**0** (-)	**17.66** (14.12)	**32.23** (22.23)	**43.04** (26.15)	**0.01** (-)	**29.65** (19.33)	**5.99** (10.59)	**3.75** (9.74)	**0** (-)	**17.48** (13.3)	**16.43** (13.52)	**39.18** (22.45)	**10.90** (12.97)	**0** (-)	**24.37** (17)	**57.55** (28.85)	**92.23** (41.21)	**0.15** (-)	**0** (-)	**60.31** (3.12)
	$\sigma^2_{AEVil19}$	**0** (-)	**11.28** (10.3)	**0** (-)	**31.09** (19.5)	**23.87** (17.09)	**3.04** (8.07)	**0** (-)	**11.54** (11.4)	**9.19** (10.83)	**15.98** (11.82)	**2.94** (5.72)	**3.68** (8.92)	**15.42** (12.09)	**22.25** (15.66)	**0** (-)	**15.84** (11.72)	**0.19** (-)	**60.61** (32.22)	**51.21** (32.21)	**28.71** (24.72)	**45.73** (2.36)

AIC and BIC criterion are indicated for each model. The estimations of variance components are indicated in bold and their standard errors are given in brackets. (The standard error is not computed if the estimated variance value is close to 0)

Table S9. Variance decomposition with the model M_FA$_s$P$_s$ (within-family additive and permanent effect variances)

Trait	AIC	BIC	Variance Type	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6	Error
FLOM	4681	5077	σ^2_A	**1.33** (0.59)	**1.06** (0.27)	**1.35** (0.43)	**0.55** (0.18)	**0.13** (0.15)	**0.27** (0.2)	**0.45** (0.26)	**0.50** (0.29)	**0.15** (0.23)	**0** (-)	**0.42** (0.14)	**1.34** (0.4)	**1.29** (0.35)	**1.06** (0.51)	**0.52** (0.15)	**0.31** (0.15)	**0.36** (0.17)	**0.59** (0.63)	**2.01** (0.61)	**0** (-)	**0.51** (0.02)
			σ^2_G	**0.07** (0.23)	**0** (-)	**0.01** (0.16)	**0** (-)	**0.26** (0.14)	**0.24** (0.15)	**0.13** (0.14)	**0.26** (0.18)	**0.35** (0.21)	**0.42** (0.13)	**0** (-)	**0.02** (0.13)	**0** (-)	**0.56** (0.31)	**0** (-)	**0.02** (0.07)	**0** (-)	**0.80** (0.55)	**0** (-)	**1.17** (0.37)	
			$\overline{\sigma^2_{AE}}$	**0.06** (-)	**0.01** (-)	**0.04** (-)	**0.06** (-)	**0.25** (-)	**0.23** (-)	**0.24** (0.15)	**0.28** (-)	**0.36** (-)	**0.05** (-)	**0.29** (-)	**0.32** (-)	**0.27** (0.15)	**0.07** (-)	**0.04** (-)	**0.13** (-)	**0.03** (-)	**0.31** (-)	**0** (-)	**0.28** (-)	
			$\overline{\sigma^2_{GE}}$	**0.05** (-)	**0.12** (-)	**0.09** (-)	**0.44** (-)	**0.03** (-)	**0.16** (-)	**0.16** (-)	**0.25** (-)	**0.01** (-)	**0.28** (-)	**0.06** (-)	**0.06** (-)	**0.05** (-)	**0.18** (-)	**0.14** (-)	**0.29** (-)	**0.20** (-)	**0.45** (-)	**0.42** (-)	**0** (-)	
FLOF	5389	5785	σ^2_A	**1.24** (0.58)	**1.41** (0.39)	**1.51** (0.48)	**0.39** (0.21)	**0.29** (0.2)	**0.53** (0.24)	**0.24** (0.22)	**0.91** (0.41)	**0.62** (0.72)	**0.08** (0.26)	**1.66** (0.67)	**1.21** (0.29)	**1.04** (0.57)	**1.20** (0.52)	**0.73** (0.21)	**0.66** (0.19)	**0.27** (0.18)	**0.50** (0.71)	**2.81** (0.81)	**1.03** (0.76)	**0.56** (0.02)
			σ^2_G	**0.39** (0.29)	**0** (-)	**0.02** (0.17)	**0.11** (0.12)	**0.24** (0.15)	**0.05** (0.13)	**0.32** (0.18)	**0.15** (0.23)	**1.68** (0.68)	**1.43** (0.39)	**0.40** (0.27)	**0.01** (-)	**0.22** (0.3)	**0.31** (0.27)	**0** (-)	**0** (-)	**0.01** (0.1)	**1.10** (0.67)	**0** (-)	**0.45** (0.55)	
			$\overline{\sigma^2_{AE}}$	**0.18** (-)	**0.04** (-)	**0** (-)	**0.09** (-)	**0.40** (-)	**0** (-)	**0.20** (-)	**0.05** (-)	**0.11** (-)	**0** (-)	**0.11** (0.11)	**0.06** (-)	**0.39** (0.21)	**0.09** (-)	**0** (-)	**0.04** (-)	**0.26** (-)	**0.47** (-)	**0** (-)	**0.50** (-)	
			$\overline{\sigma^2_{GE}}$	**0.43** (-)	**0.44** (0.16)	**0.25** (-)	**0.14** (-)	**0.03** (-)	**0.35** (-)	**0.27** (-)	**0.31** (-)	**0.04** (-)	**0.41** (0.16)	**0.13** (-)	**0.11** (-)	**0.11** (-)	**0.11** (0.12)	**0.22** (0.11)	**0.25** (-)	**0.20** (-)	**0.67** (0.33)	**0.34** (-)	**0** (-)	
ASI	-247	149	σ^2_A	**0.05** (0.03)	**0** (-)	**0.04** (0.01)	**0.01** (0.01)	**0.03** (0.02)	**0.03** (0.02)	**0.05** (0.02)	**0.03** (0.02)	**0.02** (0.04)	**0.06** (0.03)	**0.05** (0.01)	**0.02** (0.01)	**0** (-)	**0.01** (0.01)	**0.02** (0.01)	**0.01** (0.01)	**0** (-)	**0** (-)	**0.09** (0.03)	**0.04** (0.04)	**0.52** (0.02)
			σ^2_G	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	
			$\overline{\sigma^2_{AE}}$	**0.05** (0.11)	**0.01** (-)	**0.07** (-)	**0.05** (-)	**0.09** (-)	**0.04** (-)	**0.09** (0.1)	**0.25** (-)	**0.53** (0.31)	**0.01** (-)	**0.21** (-)	**0.03** (-)	**0.06** (-)	**0.08** (-)	**0** (-)	**0.04** (0.07)	**0.01** (-)	**0.24** (0.17)	**0** (-)	**0.39** (-)	
			$\overline{\sigma^2_{GE}}$	**0.29** (-)	**0.15** (-)	**0.06** (-)	**0.15** (-)	**0.06** (-)	**0.35** (-)	**0.16** (-)	**0.22** (-)	**0.30** (-)	**0.46** (-)	**0.38** (-)	**0** (-)	**0.09** (-)	**0** (-)	**0** (-)	**0.10** (-)	**0** (-)	**0.10** (-)	**0.46** (-)	**0.01** (-)	
PH	15408	15661	σ^2_A	**58.28** (22.41)	**9.48** (23.28)	**52.29** (20.18)	**28.35** (22.77)	**15.51** (13.5)	**10.42** (9.52)	**19.08** (12.85)	**8.08** (12.92)	**0** (-)	**0.05** (-)	**5.45** (15.21)	**53.58** (18.2)	**55.11** (28.13)	**63.75** (21.69)	**35.63** (21.86)	**31.27** (19.09)	**31.77** (22.27)	**0** (-)	**52.24** (30.09)	**95.86** (79.96)	**69.44** (3.54)
			σ^2_G	**0** (-)	**24.20** (22.71)	**1.17** (10.47)	**6.02** (11.89)	**0** (-)	**0** (-)	**0** (-)	**12.44** (17.62)	**31.65** (32.58)	**78.29** (24.23)	**51.23** (21.34)	**0** (-)	**2.39** (19.35)	**0** (-)	**1.88** (17.99)	**12.98** (16.19)	**7.28** (17.21)	**57.60** (27.6)	**0** (-)	**5.75** (67.6)	
			$\overline{\sigma^2_{AE}}$	**12.35** (22.7)	**20.24** (24.73)	**41.40** (-)	**3.88** (-)	**0.02** (-)	**12.86** (-)	**5.63** (-)	**3.69** (-)	**10.86** (42.29)	**4.35** (11.88)	**0** (-)	**6.65** (12.34)	**16.64** (-)	**0** (-)	**14.81** (-)	**0** (-)	**10.01** (14.26)	**0** (-)	**0** (-)	**38.94** (-)	
			$\overline{\sigma^2_{GE}}$	**5.11** (20.7)	**27.47** (25.87)	**0** (-)	**21.07** (-)	**136.63** (35.02)	**0** (-)	**4.62** (13.92)	**20.04** (21.01)	**157.52** (65.05)	**13.66** (-)	**3.40** (-)	**0** (-)	**0.68** (-)	**4.58** (-)	**13.22** (-)	**17.48** (15.38)	**11.77** (-)	**54.54** (25.11)	**32.16** (-)	**44.50** (56.17)	
GY	21426	21821	σ^2_A	**37.79** (12.14)	**0** (-)	**17.08** (8.44)	**20.76** (10.96)	**10.69** (9.7)	**9.25** (4.56)	**19.00** (15.23)	**12.11** (9.14)	**0** (-)	**0.67** (3.23)	**6.50** (3.95)	**27.18** (9.66)	**11.15** (10)	**16.54** (11.05)	**4.10** (5.39)	**0.96** (4.53)	**10.29** (6.62)	**30.39** (30.73)	**5.52** (17.43)	**0** (-)	**44.77** (1.52)
			σ^2_G	**0** (-)	**4.13** (4.49)	**1.76** (5.96)	**0** (-)	**2.54** (8.47)	**0** (-)	**11.73** (11.59)	**1.95** (6.64)	**8.85** (5.31)	**3.23** (4.72)	**0** (-)	**0** (-)	**3.42** (7)	**2.66** (7.74)	**0.25** (5.94)	**0** (-)	**0** (-)	**10.60** (22.99)	**14.12** (21.47)	**89.49** (34.07)	
			$\overline{\sigma^2_{AE}}$	**13.78** (-)	**4.29** (-)	**2.30** (-)	**28.36** (13.31)	**3.00** (-)	**1.45** (-)	**5.22** (-)	**6.57** (-)	**5.30** (-)	**0.43** (-)	**0.91** (-)	**9.80** (6.12)	**17.48** (8.52)	**5.08** (6.22)	**2.10** (-)	**21.27** (7.79)	**1.20** (-)	**21.56** (20.74)	**0** (-)	**7.99** (21.62)	
			$\overline{\sigma^2_{GE}}$	**0** (-)	**10.73** (-)	**1.99** (-)	**18.04** (-)	**29.64** (-)	**0** (-)	**9.61** (-)	**0** (-)	**0** (-)	**4.75** (-)	**4.37** (-)	**0** (-)	**0** (-)	**5.70** (-)	**10.07** (-)	**3.08** (-)	**30.84** (-)	**29.21** (19.36)	**35.84** (13.68)	**32.06** (-)	
H2O	3825	4220	σ^2_A	**0.56** (0.15)	**0.61** (0.25)	**0.44** (0.15)	**0.37** (0.14)	**0.32** (0.13)	**0.19** (0.08)	**0.07** (0.11)	**0.24** (0.13)	**0.09** (0.1)	**0.32** (0.22)	**0.47** (0.17)	**0.09** (0.1)	**0.67** (0.28)	**0.32** (0.11)	**0.50** (0.15)	**0.45** (0.14)	**0.23** (0.11)	**0** (-)	**0.39** (0.35)	**0.55** (0.36)	**0.40** (0.02)
			σ^2_G	**0** (-)	**0.06** (0.11)	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0.25** (0.12)	**0.08** (0.09)	**0** (-)	**0.23** (0.16)	**0** (-)	**0.10** (0.08)	**0.03** (0.13)	**0** (-)	**0** (-)	**0** (-)	**0** (0.06)	**0.21** (0.14)	**0.06** (0.25)	**0.08** (0.25)	
			$\overline{\sigma^2_{AE}}$	**0.11** (-)	**0.35** (-)	**0.31** (0.15)	**0.33** (0.16)	**0.46** (0.17)	**0.13** (-)	**0.39** (-)	**0.19** (-)	**0.47** (0.22)	**0.11** (-)	**0.36** (0.13)	**0.42** (-)	**0.29** (0.11)	**0.30** (-)	**0.45** (0.22)	**0.29** (-)	**0.19** (-)	**0.58** (0.35)	**0.01** (-)	**0.32** (-)	
			$\overline{\sigma^2_{GE}}$	**0.27** (-)	**0.06** (-)	**0.09** (-)	**0.19** (-)	**0.17** (-)	**0.07** (-)	**0** (-)	**0.01** (-)	**0.17** (-)	**0.27** (-)	**0.03** (-)	**0.03** (-)	**0** (-)	**0.18** (-)	**0.15** (-)	**0.07** (-)	**0.04** (-)	**0.54** (0.28)	**0.44** (-)	**0.43** (-)	
YI	21728	22123	σ^2_A	**32.17** (11.28)	**1.13** (3.71)	**12.89** (5.99)	**15.36** (9.15)	**12.45** (8.98)	**8.25** (4.9)	**9.31** (14.63)	**13.76** (10.45)	**0** (-)	**0.68** (4.23)	**0.10** (2.8)	**14.41** (9.87)	**0.01** (-)	**16.25** (11.66)	**2.62** (6.08)	**7.87** (6.69)	**12.01** (7.84)	**0** (-)	**7.91** (22.18)	**0** (-)	**48.31** (1.64)
			σ^2_G	**0** (-)	**0** (-)	**0** (-)	**0** (-)	**0.32** (8.03)	**0** (-)	**22.52** (14.11)	**4.07** (7.62)	**6.25** (5.41)	**6.18** (5.91)	**0.08** (-)	**3.13** (6.42)	**8.32** (5.83)	**3.27** (8.32)	**3.96** (7.2)	**0** (-)	**0.02** (-)	**48.42** (18.8)	**27.77** (27.26)	**109.24** (35.87)	
			$\overline{\sigma^2_{AE}}$	**13.94** (-)	**5.02** (-)	**6.37** (-)	**18.62** (11.56)	**0** (-)	**1.36** (-)	**7.38** (-)	**7.45** (6.02)	**9.70** (6.3)	**1.06** (-)	**3.72** (5.41)	**10.55** (6.35)	**19.71** (8.69)	**8.39** (7.71)	**2.64** (-)	**18.76** (8.53)	**2.25** (-)	**26.45** (22.04)	**0** (-)	**3.33** (-)	
			$\overline{\sigma^2_{GE}}$	**0.16** (-)	**12.42** (-)	**1.50** (-)	**18.87** (-)	**30.51** (-)	**4.84** (-)	**5.18** (-)	**0** (-)	**0** (-)	**7.06** (-)	**8.22** (-)	**0** (-)	**0** (-)	**7.21** (-)	**16.63** (-)	**8.93** (-)	**31.95** (-)	**27.84** (21.03)	**31.74** (14.51)	**33.54** (-)	

AIC and BIC criterion are indicated for each model. The estimations of variance components are indicated in bold and their standard errors are given in brackets. The standard error is not computed if the estimated variance value is close to 0. AxE and PxE interaction terms were averaged over environments. If the standard errors were available for each environment, the standard errors associated to the mean values were computed with the following formula: $SE_{\overline{\sigma^2}} = \sqrt{SE^2_{\sigma^2_{Blo19}} + SE^2_{\sigma^2_{Smh19}} + SE^2_{\sigma^2_{Vil19}}}$

Table S10 Additive and genetic variance ratios between M_FG$_S$. M_FA$_S$ and M_FA$_S$P$_S$

Variance ratio	Trait	A1D8	A1D5	A1D9	A2D2	A2D4	A3D1	A3D4	A3D6	A4D3	A4D4	A4D6	A5D1	A5D2	A5D7	A6D3	A6D5	A6D7	A7D3	A7D5	A7D6	Mean
$\frac{\hat{\sigma}^2{}_{A_{M\_FA_S}}}{\hat{\sigma}^2{}_{G_{M\_FG_S}}}$	**FLOM**	1.35	0.90	0.76	1.19	1.22	1.38	1.13	1.09	1.31	2.74	0.92	1.01	1.23	1.30	1.03	1.10	1.01	1.48	0.97	1.49	**1.23**
	FLOF	1.31	0.97	0.82	1.15	0.95	1.22	1.34	1.12	2.10	3.18	1.37	1.06	1.23	1.10	1.06	1.22	0.86	1.49	0.97	1.10	**1.28**
	ASI	0.54	1.43	0.70	0.55	0.54	0.91	0.65	0.80	0.97	0.53	0.64	0.43	0.61	0.65	0.73	0.56	0.21	5962	0.72	0.64	**298.75**
	PH	1.02	1.32	0.72	1.36	0.00	2.00	1.21	1.29	3.12	2.34	1.66	0.82	0.89	0.94	1.13	1.20	1.12	1.51	1.10	0.70	**1.27**
	GY	0.86	0.98	0.78	0.80	1.20	1.09	1.30	0.93	0.35	0.74	1.24	1.04	0.84	1.07	1.18	0.54	1.21	1.34	1.19	1.61	**1.01**
	H2O	0.82	0.94	0.96	0.88	0.76	0.97	1.15	0.85	1.22	1.89	1.18	1.17	0.89	0.97	0.74	1.23	0.66	2.59	1.36	0.90	**1.11**
	YI	0.83	1.69	0.83	0.89	1.18	1.27	1.27	0.92	0.35	0.78	0.72	0.90	0.55	1.07	0.89	0.93	1.33	1.63	1.30	1.72	**1.05**
$\frac{\hat{\sigma}^2{}_{A_{M\_FA_SP_S}}}{\hat{\sigma}^2{}_{G_{M\_FG_S}}}$	**FLOM**	1.14	0.84	0.75	1.02	0.29	0.54	0.71	0.53	0.31	0.00	0.98	0.99	1.19	0.60	0.97	1.01	0.93	0.39	0.95	0.00	**0.71**
	FLOF	0.76	0.89	0.75	0.76	0.43	0.93	0.36	0.77	0.27	0.05	0.86	1.03	0.88	0.73	1.02	1.18	0.64	0.29	0.98	0.70	**0.71**
	ASI	0.64	0.25	0.70	0.52	0.53	0.80	0.60	0.69	0.79	0.54	0.68	0.39	0.60	0.69	0.73	0.57	0.06	469.20	0.71	0.61	**24.02**
	PH	1.01	0.28	0.75	1.04	11.29	2.15	1.22	0.39	0.00	0.00	0.10	0.86	0.91	0.93	0.78	0.74	0.79	0.00	1.04	0.60	**1.24**
	GY	0.87	0.00	0.76	0.77	0.71	1.17	0.70	0.87	0.00	0.17	1.25	1.09	0.66	0.84	1.02	0.36	0.97	0.83	0.27	0.00	**0.67**
	H2O	0.82	0.79	0.97	0.78	0.65	0.97	0.19	0.62	1.08	0.63	1.18	0.42	0.84	0.85	0.75	1.19	0.65	0.00	0.91	0.76	**0.75**
	YI	0.86	0.81	0.87	0.84	0.89	1.21	0.31	0.76	0.00	0.09	0.29	0.79	0.00	0.81	0.45	0.72	0.87	0.00	0.21	0.00	**0.54**
$\frac{\hat{\sigma}^2{}_{A_{M\_FA_SP_S}} + \hat{\sigma}^2{}_{P_{M\_FA_SP_S}}}{\hat{\sigma}^2{}_{G_{M\_FG_S}}}$	**FLOM**	1.20	0.84	0.75	1.02	0.86	1.03	0.92	0.80	1.00	1.02	0.98	1.01	1.20	0.92	0.97	1.08	0.94	0.93	0.95	1.05	**0.97**
	FLOF	1.00	0.90	0.76	0.98	0.79	1.02	0.84	0.90	1.00	1.00	1.06	1.03	1.07	0.92	1.02	1.18	0.66	0.94	0.98	1.01	**0.95**
	ASI	0.64	0.25	0.70	0.52	0.53	0.80	0.60	0.69	0.79	0.54	0.68	0.39	0.60	0.69	0.73	0.57	0.06	479.7	0.71	0.61	**24.54**
	PH	1.01	0.98	0.77	1.27	11.29	2.15	1.22	1.00	1.27	1.00	1.00	0.86	0.95	0.93	0.82	1.04	0.97	1.00	1.04	0.63	**1.56**
	GY	0.87	0.72	0.84	0.77	0.88	1.17	1.13	1.01	0.95	1.00	1.25	1.09	0.87	0.97	1.08	0.36	0.97	1.12	0.97	1.03	**0.95**
	H2O	0.82	0.87	0.97	0.78	0.65	0.97	0.89	0.83	1.08	1.08	1.18	0.88	0.89	0.85	0.75	1.20	0.66	1.07	1.06	0.87	**0.92**
	YI	0.86	0.81	0.87	0.84	0.92	1.21	1.04	0.98	0.77	0.95	0.52	0.96	0.93	0.97	1.13	0.72	0.88	1.05	0.97	1.02	**0.92**
$\frac{\hat{\sigma}^2{}_{A_{M\_FA_SP_S}}}{\hat{\sigma}^2{}_{A_{M\_FA_SP_S}} + \hat{\sigma}^2{}_{P_{M\_FA_SP_S}}}$	**FLOM**	0.95	1.00	0.99	1.00	0.33	0.52	0.78	0.66	0.31	0.00	1.00	0.99	1.00	0.65	1.00	0.94	0.99	0.42	1.00	0.00	**0.73**
	FLOF	0.76	1.00	0.99	0.77	0.54	0.92	0.43	0.86	0.27	0.05	0.81	0.99	0.82	0.80	1.00	1.00	0.98	0.31	1.00	0.70	**0.75**
	ASI	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00	**1.00**
	PH	1.00	0.28	0.98	0.82	1.00	1.00	1.00	0.39	0.00	0.00	0.10	1.00	0.96	1.00	0.95	0.71	0.81	0.00	1.00	0.94	**0.70**
	GY	1.00	0.00	0.91	1.00	0.81	1.00	0.62	0.86	0.00	0.17	1.00	1.00	0.77	0.86	0.94	1.00	1.00	0.74	0.28	0.00	**0.70**
	H2O	1.00	0.91	1.00	1.00	1.00	1.00	0.22	0.75	1.00	0.58	1.00	0.48	0.95	1.00	1.00	1.00	0.98	0.00	0.86	0.87	**0.83**
	YI	1.00	1.00	1.00	1.00	0.98	1.00	0.29	0.77	0.00	0.10	0.56	0.82	0.00	0.83	0.40	1.00	1.00	0.00	0.22	0.00	**0.60**

$\hat{\sigma}^2{}_{G_{M\_FG_S}}$ is the within-family genetic variance estimated with M_FG_S, $\hat{\sigma}^2{}_{A_{M\_FA_S}}$ is the within-family additive variance estimated with M_FA_S, $\hat{\sigma}^2{}_{A_{M\_FA_SP_S}}$ is the within-family additive variance estimated with $M\_FA_SP_S$ and $\hat{\sigma}^2{}_{P_{M_FA_SP_S}}$is the within-family permanent effect variance estimated with $M\_FA_SP_S$

Table S11 Usefulness criterion values for the different families

		A1			A2			A3			A4			A5			A6			A7		
Trait	**UC Type**	**A1D8**	**A1D5**	**A1D9**	**A2D2**	**A2D4**	**A3D1**	**A3D4**	**A3D6**	**A4D3**	**A4D4**	**A4D6**	**A5D1**	**A5D2**	**A5D7**	**A6D3**	**A6D5**	**A6D7**	**A7D3**	**A7D5**	**A7D6**
GY	**UC1**	118.9	121.6	122.9	115.5	119.3	118.4	126.0	120.4	120.8	119.1	122.0	126.3	123.2	128.8	110.2	112.9	114.2	113.4	108.3	116.0
	UC2	118.9	117.5	122.5	115.5	118.6	118.4	123.6	119.9	114.7	116.7	122.0	126.3	122.2	128.1	110.0	112.9	114.2	111.6	104.0	96.5
YI	**UC1**	116.4	115.7	120.5	118.6	122.3	121.6	128.3	124.3	123.2	121.9	120.1	124.8	120.9	127.2	114.4	121.3	117.1	114.8	110.4	117.8
	UC2	116.4	115.7	120.5	118.6	122.2	121.6	123.0	123.2	118.1	118.2	119.8	124.0	115.2	126.4	112.4	121.3	117.1	100.6	103.9	96.3

For the family k, $UC_{1k} = \widehat{\mu_k} + ih\widehat{\sigma_{Gk}}$, $UC_{2k} = \widehat{\mu_k} + ih\widehat{\sigma_{Ak}}$ and $UC_{\text{bis}2k} = \widehat{\mu_k} + ih\widehat{\sigma_{Ak}}^{*}$. $\widehat{\mu_k}$ is the mean performance of the family, i the intensity of selection (i=2.07), h is the selection accuracy (h = 1) and $\widehat{\sigma_{Gk}} = \widehat{\sigma_{Ak}} + \widehat{\sigma_{Pk}}$ with $\widehat{\sigma_{Ak}}$ and $\widehat{\sigma_{Pk}}$ the additive and permanent effect variances of the family estimated with M_FA$_S$P$_S$.

Table S12 Theoretical and observed diversity in each family

Family	He_O	He_E	$\frac{He_O - He_E}{He_E}$ (%)
A1D8	0.156	0.154	1%
A1D5	0.153	0.161	-5%
A1D9	0.133	0.143	-7%
A2D2	0.153	0.150	2%
A2D4	0.136	0.145	-6%
A3D1	0.145	0.152	-5%
A3D4	0.148	0.154	-4%
A3D6	0.154	0.159	-3%
A4D3	0.137	0.152	-10%
A4D4	0.136	0.148	-8%
A4D6	0.139	0.149	-7%
A5D1	0.152	0.156	-3%
A5D2	0.165	0.162	2%
A5D7	0.147	0.157	-6%
A6D3	0.141	0.146	-3%
A6D5	0.156	0.158	-1%
A6D7	0.136	0.149	-9%
A7D3	0.160	0.158	1%
A7D5	0.164	0.162	1%
A7D6	0.157	0.156	1%

$\boldsymbol{He_O = \frac{1}{m}\sum_{i=1}^{m} 2p_{i_O}(1 - p_{i_O})}$ is the observed Nei index where $\boldsymbol{m}$ is the number of markers and $\boldsymbol{p_{i_O}}$ is the observed frequency of the referent allele for the marker $\boldsymbol{i}$ in a given family. $\boldsymbol{He_E = \frac{1}{m}\sum_{i=1}^{m} 2p_{i_E}(1 - p_{i_E})}$ is the expected Nei index where $\boldsymbol{p_{i_E}}$ is the expected frequency of the referent allele for the marker $\boldsymbol{i}$ in absence of selection and genetic drift. $\boldsymbol{p_{i_E}}$ was computed taking into account the parental genotypes and the cross type used to create families (BC1).

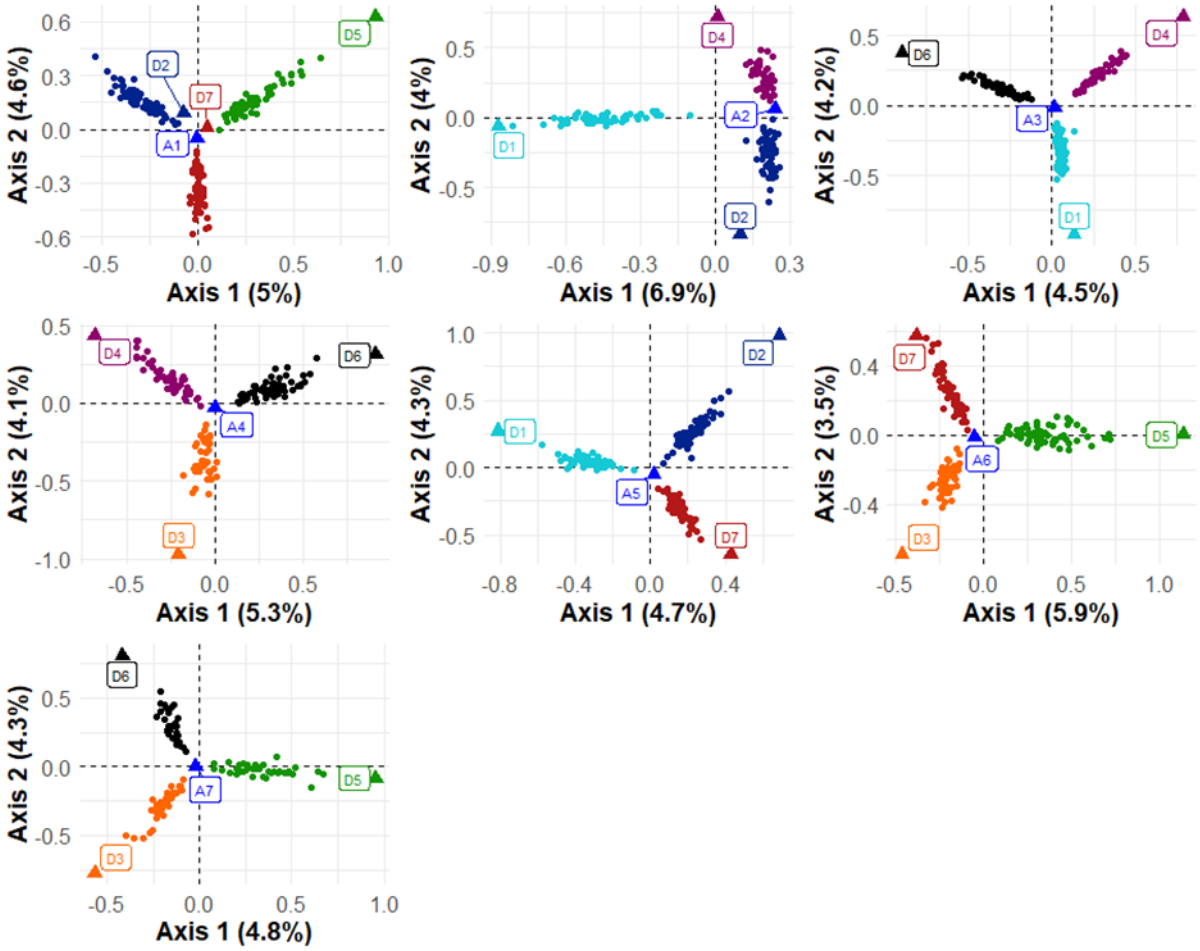

Fig S1. Multi correspondence analysis (MCA) based on BC1S2 individual genotypic information. MCA analyses were performed using a 25K genotyping matrix (coded with IUPAC standard and "failed" if the genotyping information was not available). Each MCA analysis included one of the recipient line (blue triangle) and BC1S2 individuals derived from this recipient line (dots colored by declared donor line). Declared donor lines are treated as supplemental individuals (triangles). 16 individuals were removed before analysis because of high illegitimate rates.

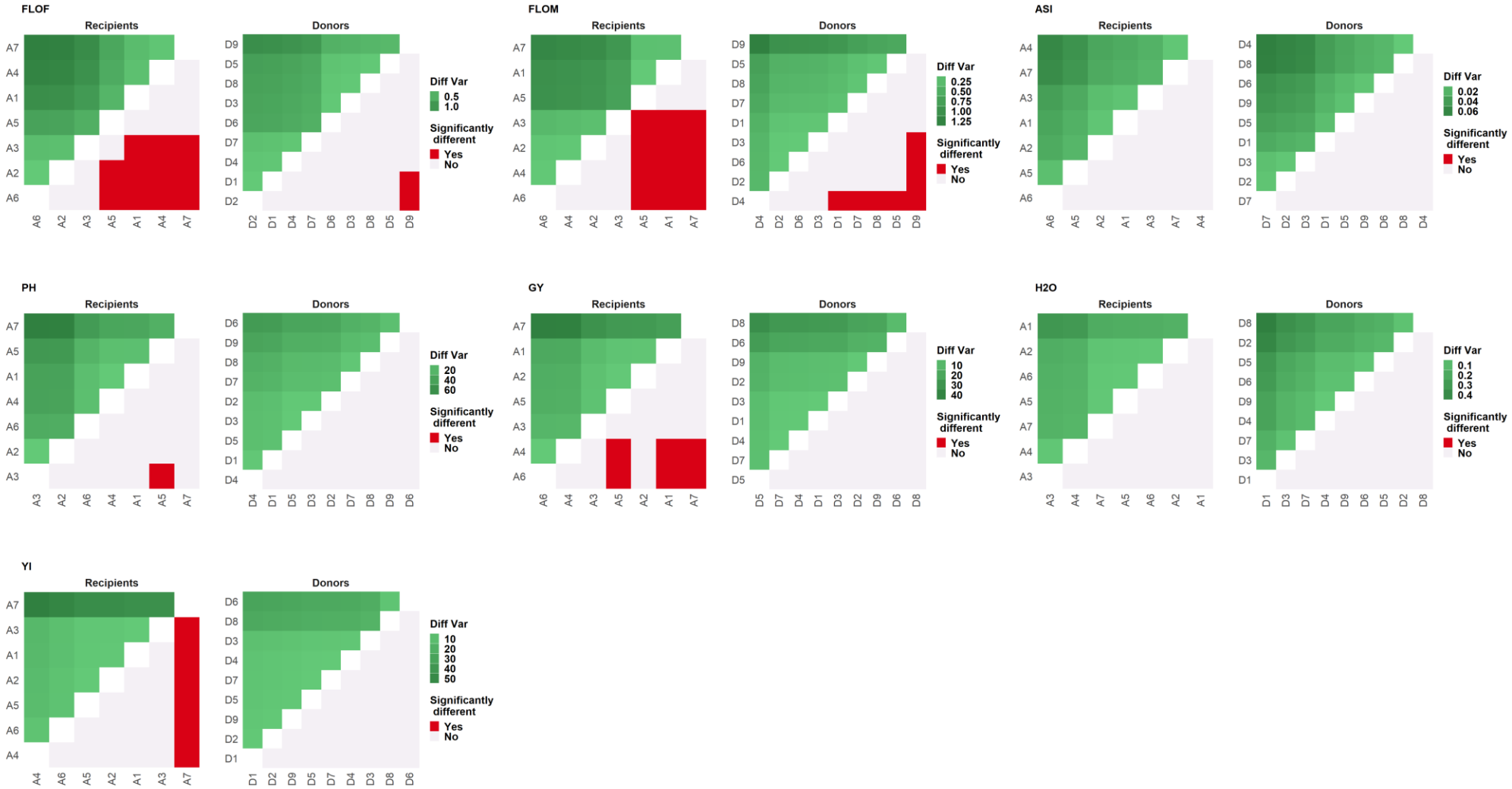

Fig S2. Recipient and donor pairwise comparisons of genetic variance values (model M_FG$_S$). For each trait, the mean genetic variance of the families derived from the same recipient or donor was computed. The recipients and the donors were ranked according to this value. **Upper triangle:** mean differences of genetic variances between two recipients or two donors (Diff Var). **Lower triangle**: Significance of the variance difference between each pair of recipients or donors. For each pair, a contrast was defined as presented in File S4 and its nullity was tested. The difference is declared significant for the pairs with an FDR adjusted p-values inferior to 0.05.

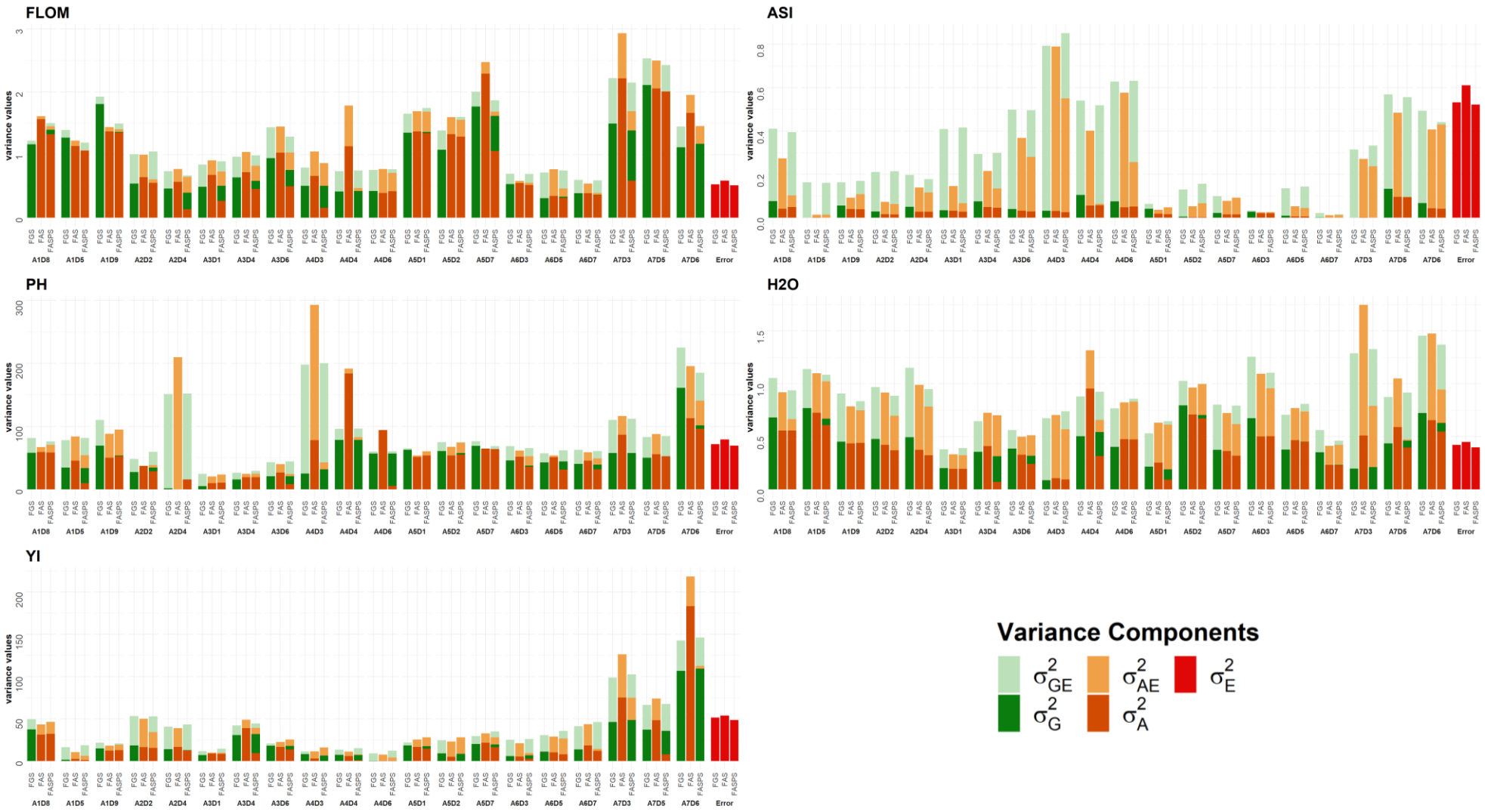

Fig S3 Within-family genetic and additive variance estimation with the models M_FG$_S$. M_FAs and M_FA$_S$P$_S$ for FLOM. ASI. PH. H2O and YI. For M_FAs and M_FA$_S$P$_S$, within-family additive variances are indicated in orange. The within-family genetic (model M_FG$_S$) and permanent effect (model M_FA$_S$P$_S$) variances are in dark green. The interaction (AxE: light orange and GxE: light green) and error (red) terms are trial specific and represented by their respective average values

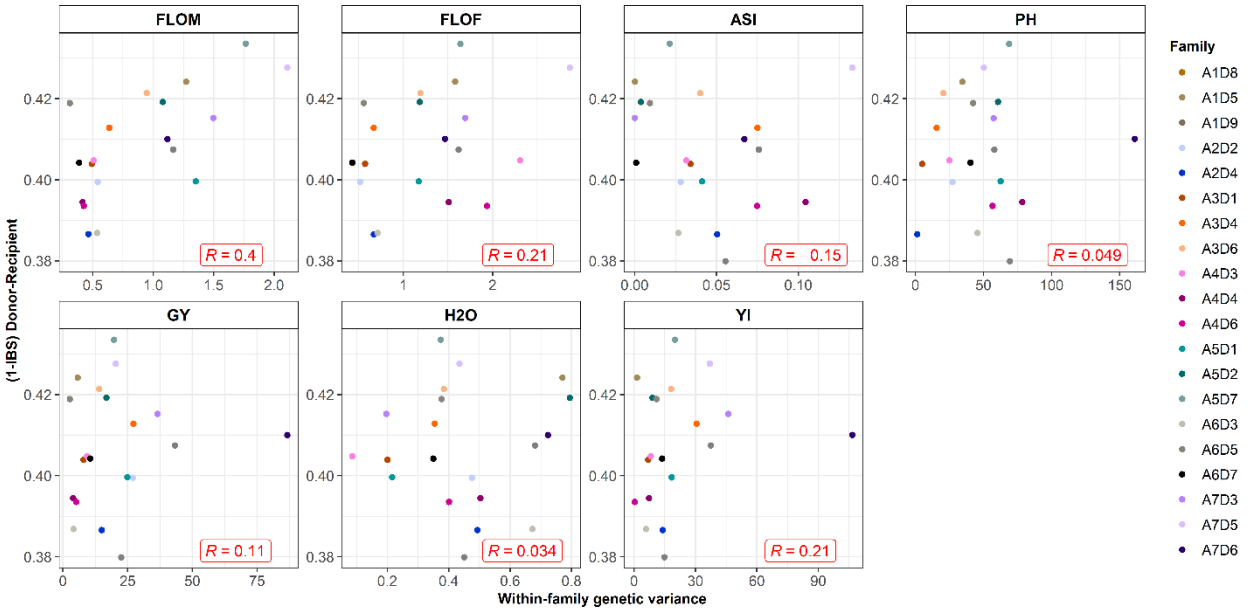

Fig S4 Correlation between the genetic distances between parents and the within-family genetic variances. For each parent pair, the genetic distance was computed as 1-IBS (Identity-By-State). For each trait, R is the Pearson correlation coefficient value between the genetic distance between the parents and the within-family genetic variance.