

Genomic prediction of hybrid performance: comparison of the efficiency of factorial and tester designs used as training sets in a multiparental connected reciprocal design for maize silage.

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Supplementary materials

File S1 Spatial corrections

The BLUPs of spatial effects were estimated on raw performance using model (S.1) on the factorial designs and model (S.2) on the tester designs.

The model implemented on the factorial designs (F-1H and F-4H) was:

$$Y_{hkk'lxyz} = \mu + \lambda_l + \tau_h \times t_h + H_{h(kk')} \times (1 - t_h) + (R_{x(l)} + C_{y(l)}) \times (1 - d_l) + B_{z(l)} \times d_l + E_{hkk'lxyz}, \quad (\text{S.1})$$

where $Y_{hkk'lxyz}$ is the phenotypic value of hybrid h produced by crossing the parental lines k and k' , evaluated in environment, l located at row x , column y and in block z . μ is the intercept, λ_l is the fixed effect of environment l , t_h distinguishes the type of hybrid, it is set to 0 for the experimental hybrids and set to 1 for the controls, τ is the vector of fixed effect of the control with 18 levels (two for the commercial hybrids and 16 for the founder controls). With $H_{h(kk')}$ the random genetic effect of hybrid h produced by crossing the dent line k' and the flint line k . The genetic value of the hybrid $H_{h(km)}$, is defined as follows: $H_{h(kk')} = U_k + U'_{k'} + S_{kk'}$, where U_k (respectively $U'_{k'}$) is the random GCA effect of the flint line k (respectively dent line k'), we assume that U_k ($U'_{k'}$) are independent and identically distributed (iid) and follow a normal distribution: $U_k \sim \mathcal{N}(0, \sigma_{GCA_f}^2)$ (and $U'_{k'} \sim \mathcal{N}(0, \sigma_{GCA_d}^2)$). $S_{kk'}$ is the random SCA effect of the interaction between the parental lines k and k' , with $S_{kk'} \sim \mathcal{N}(0, \sigma_{SCA}^2)$ iid. $R_{x(l)}$ is the random effect of row x in environment l , $C_{y(l)}$ is the random effect of column y in environment l and $B_{z(l)}$ is the random effect of block z in environment l , with $R_{x(l)} \sim \mathcal{N}(0, \sigma_{R_l}^2)$, $C_{y(l)} \sim \mathcal{N}(0, \sigma_{C_l}^2)$ and $B_{z(l)} \sim \mathcal{N}(0, \sigma_{B_l}^2)$ which are assumed to be independent and identically distributed (iid). d_l indicates the spatial

effect to consider in environment l , it is set to 1 if the spatial effect is modeled by a block effect and by 0 if modeled by row and column effects. To construct the vector d , for each trait and each trial, two types of spatial effects were tested the line and column effects or the block effect. The best spatial effect was chosen based on the AIC criterion. $E_{hkk'lxyz}$ is the error term of the model, with $E_{hkk'lxyz} \sim \mathcal{N}(0, \sigma_{E_l}^2)$ iid within trial and independent between trials. The different random effects of the model are assumed to be independent.

The model implemented on the T-F was:

$$Y_{hkmlxyz} = \mu + \lambda_l + \tau_h \times t_h + \gamma_m + H_{h(km)} \times (1 - d_l) + (R_{x(l)} + C_{y(l)}) \times (1 - d_l) + B_{z(l)} \times d_l + E_{hkmlxyz}, \quad (\text{S.2})$$

where λ_l , t_h , τ_h , ρ_{lh} , $R_{x(l)}$, $C_{y(l)}$, $B_{z(l)}$ and d_l are defined as in model (S.1). $Y_{hkmlxyz}$ is the phenotypic value of hybrid h produced by crossing the dent parental line m used as tester and the flint parental line k , evaluated in environment l located at row x , column y and in block z . γ_m is the fixed effect of line m used as tester. $H_{h(km)}$ is the random genetic effect of hybrid h produced by crossing the dent parental line m used as tester and the flint parental line k evaluated for its GCA. The genetic value of the hybrid $H_{h(km)}$, is defined as follows:

$$H_{h(km)} = U_k + S_{km},$$

where U_k is the random GCA effect of the flint line k , with $U_k \sim \mathcal{N}(0, \sigma_{GCA_f}^2)$ iid and S_{km} is the random effect of the interaction between the flint line k and the dent line m used as tester, with $S_{km} \sim \mathcal{N}(0, \sigma_S^2)$ iid. $E_{hkmlxyz}$ is the error term of the model, we assume that it follows: $E_{hkk'lxyz} \sim \mathcal{N}(0, \sigma_{E_l}^2)$ iid. The same model was adapted and implemented on T-D. The different random effects of the model are assumed to be independent.

51 **Table S1** Broad-sense heritability (H^2),percentage of genetic variance assigned to SCA variance (%SCA) and variance components estimated on phenotypic data corrected for
52 the spatial effects for all the designs (F-1H, F-4H, T-D and T-F) without using marker information.

Trait	Design	$\sigma_{GCA_d}^2$	$\sigma_{GCA_f}^2$	σ_{SCA}^2	$\sigma_{GCA_d \times E}^2$	$\sigma_{GCA_f \times E}^2$	$\sigma_{SCA \times E}^2$	%SCA ^a	σ_E^2 min-max ^b	H^2 ^c
DMY	F-1H	0.72(0.10)	0.25(0.10)	0.25(0.11)	0.03(0.06)	0.19(0.06)	0.12(0.09) ns	20	0.70(0.06)-3.09(0.17)	0.84
	F-4H	0.74(0.14)	0.54(0.11)	0.13(0.03)	0.18(0.03)	0.17(0.03)	0.11(0.05)	9	0.44(0.06)-3.15(0.26)	0.89
	T-D	0.70(0.13)	-	0.17(0.04)	0.03(0.04) ns	-	0.21(0.06)	20	0.26(0.06)-2.22(0.27)	0.88
	T-F	-	0.52(0.10)	0.14(0.03)	-	0.09(0.03)	0.09(0.05)	21	0.34(0.07)-1.42(0.18)	0.87
DMC	F-1H	0.84(0.27)	2.25(0.26)	0.55(0.27)	0.33(0.10)	0.30(0.10)	0.20(0.15) ns	15	0.71(0.07)-4.96(0.28)	0.91
	F-4H	1.32(0.24)	2.78(0.46)	0.28(0.05)	0.40(0.06)	0.45(0.06)	0.25(0.09)	6	0.68(0.10)-4.15(0.37)	0.93
	T-D	1.89(0.34)	-	0.32(0.08)	0.56(0.10)	-	0.35(0.12)	14	0.59(0.13)-2.63(0.37)	0.89
	T-F	-	3.00(0.51)	0.44(0.09)	-	0.30(0.07)	0.12(0.10)	13	0.50(0.10)-2.26(0.31)	0.94
DtSilk	F-1H	1.26(0.18)	0.73(0.19)	0.41(0.18)	0.12(0.05)	0.16(0.06)	0.00(0.08) ns	17	0.66(0.06)-5.57(0.28)	0.91
	F-4H	0.76(0.14)	1.55(0.26)	0.14(0.03)	0.15(0.03)	0.20(0.03)	0.09(0.06) ns	6	9.69(0.08)-2.34(0.22)	0.93
	T-D	0.63(0.11)	-	0.08(0.03)	0.06(0.03)	-	0.09(0.06)	11	0.37(0.07)-2.06(0.25)	0.86
	T-F	-	1.07(0.19)	0.22(0.05)	-	0.14(0.04)	0.01(0.08)	17	0.51(0.09)-3.34(0.39)	0.90
PH	F-1H	89.26(10.94)	41.69(11.68)	23.40(11.90)	8.36(3.50)	1.95(3.76)	3.03(5.78) ns	15	33.87(3.39)-215.58(11.31)	0.90
	F-4H	120.75(20.40)	57.37(10.36)	5.40(1.96)	11.68(2.38)	6.99(2.16)	0.00 ns	3	55.38(6.60)-169.29(14.29)	0.92
	T-D	115.58(18.90)	-	5.80(2.49)	10.66(3.68)	-	0.00	5	46.16(7.77)-128.96(16.56)	0.92
	T-F	-	56.86(11.64)	24.98(5.22)	-	10.12(3.28) ns	0.00	31	38.26(7.06)-91.75(12.70)	0.89
DINAG	F-1H	1.55(0.18)	0.90(0.18)	0.00 ns	0.09(0.11)	0.11(0.12)	0.23(0.18) ns	0	1.45(0.13)-6.47(0.34)	0.85
	F-4H	2.11(0.36)	1.17(0.21)	0.08(0.05)	0.36(0.07)	0.23(0.06)	0.00 ns	2	1.12(0.11)-5.36(0.43)	0.87
	T-D	2.68(0.45)	-	0.15(0.08) ns	0.38(0.12)	-	0.24(0.20)	5	1.28(0.24)-3.27(0.46)	0.88
	T-F	-	1.25(0.23)	0.21(0.08)	-	0.18(0.10) ns	0.04(0.17)	14	0.99(0.21)-3.60(0.44)	0.81
DINAGZ	F-1H	1.47(0.17)	0.86(0.15)	0.00 ns	0.21(0.12)	0.25(0.13)	0.00 ns	0	2.10(0.16)-5.88(0.33)	0.79
	F-4H	1.88(0.34)	0.97(0.20)	0.11(0.08) ns	0.43(0.10)	0.28(0.09)	0.00 ns	4	2.13(0.25)-8.84(0.71)	0.78
	T-D	2.53(0.44)	-	0.08(0.10) ns	0.21(0.14)	-	0.36(0.25)	3	1.16(0.24)-5.67(0.71)	0.82
	T-F	-	1.10(0.23)	0.25(0.12)	-	0.10(0.14) ns	0.00 ns	19	1.39(0.25)-5.78(0.68)	0.71

MFU (x10²)	F-1H	2.06(0.30)	1.03(0.33)	0.33(0.34) ns	0.13(0.23)	0.01(0.24)	0.86(0.39)	10	3.39(0.28)-12.83(0.69)	0.79
	F-4H	1.74(0.31)	1.67(0.30)	0.10(0.06) ns	0.37(0.08)	0.29(0.07)	0.00 ns	3	1.29(0.12)-7.61(0.60)	0.86
	T-D	2.23(0.40)	-	0.28(0.10)	0.46(0.12)	-	0.00	11	1.04(0.16)-6.31(0.74)	0.85
	T-F	-	1.46(0.27)	0.23(0.09)	-	0.21(0.11)	0.23(0.16)	14	0.46(0.12)-6.53(0.77)	0.78
NDF	F-1H	0.80(0.21)	0.89(0.22)	0.25(0.24) ns	0.06(0.19)	0.13(0.19)	0.71(0.31)	13	2.51(0.22)-10.23(0.55)	0.72
	F-4H	0.71(0.15)	1.31(0.24)	0.12(0.07) ns	0.17(0.07)	0.23(0.08)	0.23(0.19) ns	6	2.07(0.24)-5.32(0.47)	0.80
	T-D	0.79(0.19)	-	0.27(0.11)	0.48(0.14)	-	0.00	25	1.42(0.27)-4.03(0.53)	0.71
	T-F	-	1.46(0.29)	0.31(0.12)	-	0.08(0.14) ns	0.62(0.24)	18	1.15(0.23)-4.30(0.59)	0.79
LIGN (x10²)	F-1H	0.08(0.01)	0.02(0.01)	0.00(0.01) ns	0.01(0.00)	0.00	0.01(0.01) ns	0	0.05(0.00)-1.03(0.06)	0.89
	F-4H	0.13(0.02)	0.03(0.01)	0.00 ns	0.02(0.00)	0.01(0.00)	0.01(0.01) ns	0	0.05(0.01)-0.11(0.01)	0.86
	T-D	0.12(0.02)	-	0.01(0.00) ns	0.01(0.00)	-	0.00	8	0.04(0.01)-0.09(0.01)	0.88
	T-F	-	0.05(0.01)	0.00 ns	-	0.01(0.00)	0.01(0.01)	0	0.03(0.01)-0.12(0.02)	0.70
CELL (x10²)	F-1H	0.21(0.03)	0.10(0.03)	0.01(0.03) ns	0.05(0.02)	0.03(0.02)	0.00 ns	3	0.34(0.03)-1.03(0.06)	0.78
	F-4H	0.40(0.08)	0.25(0.05)	0.02(0.02) ns	0.10(0.03)	0.07(0.03)	0.03(0.04) ns	3	0.26(0.04)-12.98(0.96)	0.57
	T-D	0.40(0.08)	-	0.07(0.03)	0.12(0.04)	-	0.00(0.06)	15	0.29(0.06)-7.65(0.83)	0.58
	T-F	-	0.20(0.05)	0.03(0.03) ns	-	0.09(0.04)	0.01(0.06)	13	0.28(0.06)-7.03(0.82)	0.39
HCELL (x10²)	F-1H	0.55(0.06)	0.21(0.06)	0.00(0.05) ns	0.08(0.03)	0.04(0.03)	0.00 ns	0	0.54(0.04)-2.01(0.11)	0.84
	F-4H	0.94(0.17)	0.36(0.08)	0.04(0.03) ns	0.20(0.04)	0.17(0.04)	0.05(0.06) ns	3	0.38(0.05)-9.81(0.76)	0.73
	T-D	0.89(0.16)	-	0.12(0.05)	0.19(0.06)	-	0.00	12	0.49(0.10)-6.22(0.70)	0.76
	T-F	-	0.32(0.07)	0.04(0.04) ns	-	0.17(0.06)	0.05(0.08)	11	0.39(0.08)-7.41(0.82)	0.48

53 ^a Percentage of SCA variance computed as $\frac{\sigma_{SCA}^2}{\sigma_{GCA_d}^2 + \sigma_{GCA_f}^2 + \sigma_{SCA}^2} \times 100$

54 ^b Minimum residual variance and maximum residual variance across all environments

55 ^c Broad-sense heritability

56 ^d Standard error in brackets

57 ^e Significance of the variance components assessed by likelihood ratio test with χ^2 mixed distributions ($\alpha=0.05$). Non-significant variance component is indicated by **ns**

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Table S2 Variance components and percentage of genetic variance assigned to SCA variance (%SCA) estimated with marker information (GBLUP model) for all the designs (F-1H, F-4H, T-D and T-F).

Trait	Design	$\sigma_{GCA_d}^2$	$\sigma_{GCA_f}^2$	σ_{SCA}^2	%SCA ^a	σ_E^2
DMY	F-1H	0.62(0.12) ^b	0.48(0.09)	0.13(0.06)	11	0.52(0.06)
	F-4H	0.68(0.15)	1.04(0.21)	0.03(0.05)	2	0.31(0.05)
	T-D	0.47(0.13)	-	0.08(0.06)	15	0.25(0.05)
	T-F	-	0.86(0.17)	0.10(0.05)	10	0.11(0.03)
DMC	F-1H	1.41(0.25)	1.79(0.28)	0.00	0	1.07(0.08)
	F-4H	2.79(0.53)	4.45(0.78)	0.01(0.08)	0	0.62(0.10)
	T-D	4.27(0.79)	-	0.19(0.12)	4	0.41(0.09)
	T-F	-	3.95(0.76)	0.28(0.18)	7	0.51(0.12)
DtSilk	F-1H	1.21(0.21)	2.03(0.29)	0.09(0.06)	3	0.73(0.08)
	F-4H	1.67(0.32)	2.65(0.46)	0.11(0.06)	2	0.24(0.05)
	T-D	0.99(0.23)	-	0.04(0.04)	4	0.21(0.05)
	T-F	-	2.29(0.42)	0.17(0.11)	7	0.24(0.06)
PH	F-1H	70.90(11.74)	68.85(11.28)	6.59(4.31)	5	33.18(4.62)
	F-4H	76.78(14.91)	103.47(18.80)	0.61(2.81)	0	20.42(3.16)
	T-D	75.91(15.80)	-	1.12(2.38)	1	16.75(3.11)
	T-F	-	100.13(21.72)	17.53(10.18)	15	20.85(5.92)
DINAG	F-1H	0.78(0.13)	0.60(0.11)	0.00	0	0.69(0.05)
	F-4H	1.03(0.22)	1.10(0.23)	0.08(0.09)	4	0.47(0.09)
	T-D	1.67(0.39)	-	0.00	0	0.63(0.09)
	T-F	-	1.13(0.28)	0.47(0.24)	29	0.32(0.11)
DINAGZ	F-1H	0.84(0.15)	0.58(0.12)	0.00	0	0.90(0.06)
	F-4H	1.11(0.26)	0.79(0.21)	0.00	0	0.92(0.09)
	T-D	1.97(0.49)	-	0.00	0	0.85(0.12)
	T-F	-	0.90(0.28)	0.24(0.22)	21	0.72(0.15)
MFU (x10²)	F-1H	1.14(0.22)	1.31(0.24)	0.00	0	1.50(0.10)
	F-4H	1.19(0.27)	2.17(0.42)	0.26(0.14)	7	0.48(0.11)
	T-D	1.38(0.38)	-	0.07(0.10)	5	0.81(0.14)
	T-F	-	2.11(0.44)	0.12(0.13)	5	0.55(0.11)
NDF	F-1H	0.77(0.16)	0.99(0.19)	0.02(0.05)	1	1.32(0.10)
	F-4H	0.88(0.23)	1.54(0.32)	0.09(0.10)	4	0.66 (0.11)
	T-D	0.62(0.23)	-	0.01(0.07)	2	0.84(0.12)
	T-F	-	1.80(0.44)	0.10(0.14)	5	0.77(0.14)
LIGN (x10²)	F-1H	0.04(0.01)	0.02(0.00)	0.00	1	0.02(0.00)
	F-4H	0.07(0.01)	0.05(0.01)	0.00	2	0.02(0.00)
	T-D	0.06(0.01)	-	0.00	0	0.03(0.00)
	T-F	-	0.06(0.01)	0.00	5	0.03(0.00)
CELL (x10²)	F-1H	0.09(0.02)	0.08(0.02)	0.00	0	0.15(0.01)
	F-4H	0.33(0.09)	0.51(0.13)	0.00	0	0.50(0.05)
	T-D	0.25(0.10)	-	0.06(0.06)	19	0.37(0.06)
	T-F	-	0.24 (0.10)	0.04(0.05)	14	0.39(0.06)
HCELL (x10²)	F-1H	0.23(0.04)	0.17(0.03)	0.00	0	0.23(0.01)
	F-4H	0.50(0.12)	0.65(0.16)	0.00	0	0.50(0.05)
	T-D	0.37(0.12)	-	0.13(0.10)	26	0.35(0.07)
	T-F	-	0.36 (0.13)	0.05(0.06)	12	0.46(0.07)

^a Percentage of SCA variance computed as $\frac{\sigma_{SCA}^2}{\sigma_{GCA_d}^2 + \sigma_{GCA_f}^2 + \sigma_{SCA}^2} \times 100$

^b Standard error in brackets

Table S3 Predictive abilities obtained for the F-4H and for each of the tester designs using the F-1H as TRS.

Training Set	F-1H			
Validation Set	F-4H		T-D	T-F
Predicted hybrid value	GCA _f + GCA _d	GCA _f + GCA _d + SCA	GCA _d	GCA _f
DMY	0.78	0.77	0.69	0.80
DMC	0.78	0.78	0.84	0.74
DtSilk	0.79	0.79	0.84	0.76
PH	0.87	0.87	0.75	0.87
DINAG	0.86	0.86	0.82	0.85
DINAGZ	0.79	0.79	0.77	0.78
MFU	0.82	0.82	0.79	0.79
NDF	0.69	0.69	0.76	0.57
LIGN	0.87	0.87	0.78	0.91
CELL	0.72	0.72	0.58	0.73
HCELL	0.80	0.80	0.61	0.83

Table S4 Predictive ability obtained for the F-1H using the F-4H (using a model including or not the SCA effect) or the tester designs as TRS.

Training set	F-4H		Tester designs
Validation set	F-1H		
Predicted hybrid value	GCA _f + GCA _d	GCA _f + GCA _d + SCA	GCA _f + GCA _d
DMY	0.56	0.56	0.54
DMC	0.64	0.64	0.65
DtSilk	0.55	0.55	0.56
PH*	0.69	0.69	0.66
DINAG*	0.78	0.78	0.75
DINAGZ*	0.73	0.73	0.70
MFU	0.67	0.67	0.65
NDF	0.51	0.51	0.50
LIGN	0.80	0.80	0.81
CELL	0.64	0.64	0.63
HCELL	0.73	0.73	0.72

* Significant difference assessed by Williams tests between the predictive abilities obtained when calibrating on the F-4H or on the tester designs ($\alpha = 0.05$)

Table S5 Correlations between the GCA BLUPs of the F-1H predicted using the F-4H or the tester designs as TRS.

BLUPs correlated	DMY	DMC	DtSilk	PH	DINAG	DINAGZ	MFU	NDF	LIGN	CELL	HCELL
GCA _f	0.85	0.95	0.94	0.89	0.94	0.92	0.93	0.90	0.89	0.86	0.84
GCA _d	0.90	0.88	0.86	0.94	0.94	0.91	0.92	0.76	0.95	0.94	0.96

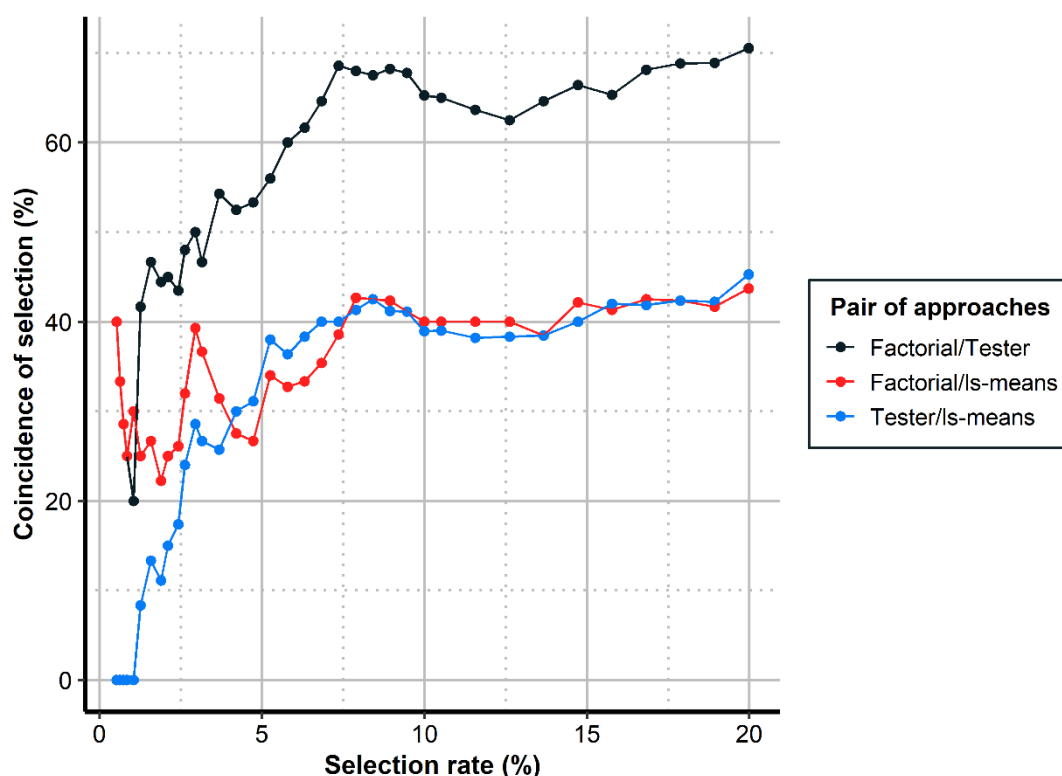


Fig.S1 Coincidence of selection of the F-1H single-cross hybrids computed for different selection rates (%). The coincidence of selection was computed in black between the factorial and the tester approaches (GBLUP), in red between the factorial approach (GBLUP) and the phenotypic values (ls-means) and in blue between the tester approach (GBLUP) and the phenotypic values (ls-means).

Table S6 Predictive abilities obtained by calibrating a GS model on the F-4H or on the tester designs to predict different hybrid types of the F-1H (VS).

Training set	F-4H ^a				Tester designs			
Hybrid type in the VS ^b	T1D	T1F	T0	All	T1D	T1F	T0	All
Number of hybrids in the VS	106	95	742	951	107	95	741	951
DMY	0.61	0.74	0.49	0.56	0.60	0.75	0.49	0.54
DMC	0.72	0.81	0.61	0.64	0.73	0.78	0.62	0.65
DtSilk	0.61	0.72	0.50	0.55	0.63	0.73	0.52	0.56
PH	0.75	0.78	0.65	0.69	0.74	0.75	0.62	0.66
DINAG	0.79	0.84	0.77	0.78	0.76	0.84	0.73	0.75
DINAGZ	0.70	0.81	0.72	0.73	0.66	0.80	0.69	0.70
MFU	0.70	0.78	0.64	0.67	0.68	0.75	0.63	0.65
NDF	0.63	0.70	0.47	0.51	0.60	0.65	0.47	0.50
LIGN	0.83	0.83	0.79	0.80	0.84	0.84	0.79	0.81
CELL	0.59	0.71	0.62	0.64	0.62	0.73	0.61	0.63
HCELL	0.71	0.77	0.72	0.73	0.73	0.78	0.71	0.72

^a TRS used to calibrate the Model (5.1) including SCA effect

^b Different hybrids types in the VS: T0 hybrids where none of the parental lines was in the TRS, T1F hybrids where only the flint line was in the TRS) and T1D where only the dent line was in the TRS.

Table S7 Predictive ability obtained (i) when calibrating on 216 hybrids of the F-1H design to predict 216 hybrids of the F-4H design and (ii) when calibrating on 216 hybrids of the F-4H design to predict the F-1H.

TRS	F-1H		F-4H	
	Mean ^a	Sd ^b	Mean	Sd
DMY	0.55	0.04	0.50	0.05
DMC	0.62	0.03	0.60	0.03
DtSilk	0.57	0.04	0.44	0.05
PH	0.71	0.03	0.62	0.04
DINAG	0.77	0.02	0.76	0.02
DINAGZ	0.71	0.03	0.70	0.03
MFU	0.71	0.03	0.65	0.03
NDF	0.55	0.04	0.46	0.05
LIGN	0.80	0.02	0.78	0.02
CELL	0.58	0.03	0.60	0.03
HCELL	0.69	0.03	0.70	0.03

^a Mean of the predictive abilities over the 100 repetitions

^b Standard deviation of the 100 repetitions