Tables & Figures

Table 1. Morphological and agronomic traits, their genotypic (σ_g^2) and genotype x environment interaction (σ_{ge}^2) variances and heritabilities (h^2) observed for 58 flint and dent maize lines in four or six environments in South Germany.

Trait	code	UPOV code	Test sites	σ_g^2	σ_{ge}^2	$h^{2\dagger}$
Ear						
diameter (mm)	EDI	27	6	9.28**	0.47**	96.2
number of kernels	NKE	-/-	6	3108**	558**	88.6
type of grain (1-9 scale)	TGR	30	4	2.04**	0.09**	97.4
anthocyanin coloration (col.) of glumes of cob	AGC	34	4	4.48**	0.05*	98.4
anthocyanin col. of silks (1-9 scale)	ACS	17	4	1.27**	0.22**	87.7
color of dorsal side of grain (1-9 scale)	CDG	32	4	0.37**	0.02	86.6
color of tip of grain (1-9 scale)	CTG	31	4	1.13**	0.03**	96.5
length (mm)	ELG	26	6	188.9**	39.9**	92.6
number of rows of grain	NGR	29	6	1.19**	0.14**	92.8
days to silk emergence	TSE	15	4	33.1**	3.45**	96.4
Kernels						
thousand kernel weight (g)	TKW	-/-	6	1059**	168**	95.4
grain yield ($Mg*ha^{-1}$)	GYD	-/-	6	107.9**	39.2**	79.4
grain yield of 4 hand harvested ears (g)	GYE	-/-	6	3.72**	0.47**	90.4
Leaf						
angle between blade and stem (1-9 scale)	LAN	4	4	1.04**	0.21**	88.4
attitude of blade (1-9 scale)	LAT	3	4	0.72**	0.02	90.1
width of blade (mm)	WBL	24	4	0.44**	0.11**	81.3
Plant						
ear height (cm)	EHT	-/-	4	164.8**	29.0**	95.4
length (cm)	PLG	22	6	484.0**	51.3**	94.7
Tassel						
anthocyanin col. of base of glume (1-9)	ABG	8	4	2.90**	0.15**	94.7
anthocyanin col. of glume excluding base (1-9)	AEB	9	4	1.41**	0.19**	88.9
length of side branches (br.)(cm)	LSB	21	4	3.90**	1.19**	86.6
angle between main axis and lateral br. (1-9)	TAN	12	4	1.67**	0.25**	88.7
anthocyanin col. of anthers (1-9)	AAH	10	4	1.18**	0.35**	85.0
attitude of lateral branches (1-9)	ALB	13	4	1.59**	0.59**	80.6
length of main axis above lowest side br. (cm)	TLL	19	4	8.16**	2.73**	84.7
length of main axis above upper side br. (cm)	TLU	20	4	12.5**	0.44**	83.2
number of primary lateral branches	NLB	14	4	1.23**	0.18**	91.2
days to anthesis	TAH	7	4	21.7**	1.42**	96.7

$^{\dagger}h^2$ = heritability on an entry-mean basis for line *per se* performance pooled across flint and dent lines

Table 2. Estimates of mean, range, genotypic (σ_g^2) and genotype x environment interaction (σ_{ge}^2) variances, heritability (h^2_{MPH}) of mid-parent heterosis (MPH) observed for different morphological and agronomic traits of 114 flint and dent hybrids and their parental lines tested in four or six environments in South Germany as well as correlations (*r*) of MPH with coancestry (1-*f*), genetic distance based on 100 SSRs (GD_{SSR}) or 20 AFLP primer combinations (GD_{AFLP}), Euclidean (MD_{EUC}) or Mahalanobis (MD_{MAH}) morphological distances.

Trait†	MPH			σ_g^2	σ_{ge}^2	h^2_{MPH}‡	*r*				
	Mean	Min.	Max.				1-*f*	GD_{SSR}	GD_{AFLP}	MD_{EUC}	MD_{MAH}
EDI	0.09	0.01	0.18	< 0.001	< 0.001	91.3	0.68**	0.78**	0.76**	0.65**	0.55**
NKE	0.59	0.03	1.34	0.070**	0.012**	96.3	0.76**	0.86**	0.87**	0.69**	0.60**
ELG	0.25	0.02	0.53	0.010**	< 0.001	96.9	0.78**	0.85**	0.89**	0.68**	0.63**
NGR	0.06	-0.02	0.16	0.010**	0.001**	73.2	0.38**	0.56**	0.50**	0.43**	0.39**
TSE	-0.06	-0.17	0.03	0.001**	0.001**	65.9	-0.70**	-0.66**	-0.70**	-0.58**	-0.51**
TKW	0.10	-0.04	0.42	0.004**	0.002**	90.1	0.66**	0.71**	0.76**	0.55**	0.53**
GYD	0.79	0.14	2.14	0.150**	0.054**	92.1	0.73**	0.84**	0.86**	0.72**	0.61**
GYE	0.75	0.06	1.84	0.130**	0.021**	96.9	0.80**	0.90**	0.92**	0.66**	0.63**
EHT	0.27	0.01	0.63	0.010**	0.005**	83.8	0.75**	0.78**	0.80**	0.58**	0.57**
PLG	0.17	0.01	0.36	0.010**	0.001**	95.2	0.75**	0.85**	0.87**	0.63**	0.55**
TAH	-0.05	-0.17	0.04	< 0.001	< 0.001	72.1	-0.59**	-0.76**	-0.74**	-0.49**	-0.42**

*,** Significant at the 0.05 or 0.01 probability level, respectively
† For abbreviations, see Table 1.
‡ h^2_{MPH} = heritability on a triplet-mean basis for mid-parent heterosis pooled across flint and dent lines.

Table 3. Simple correlations between coancestry coefficient (1-*f*), genetic distances based on 100 SSRs (GD_{SSR}) and 20 AFLP primer combinations (GD_{AFLP}) as well as Euclidean (MD_{EUC}) and Mahalanobis (MD_{MAH}) morphological distances based on 25 traits (see Table 1) for 24 flint (below diagonal) and 34 dent inbreds (above diagonal).

	1-*f*	**GD_{SSR}**	**GD_{AFLP}**	**MD_{EUC}**	**MD_{MAH}**
1-*f*		0.75**	0.85**	0.58**	0.31**
GD_{SSR}	0.88**		0.92**	0.57**	0.40**
GD_{AFLP}	0.88**	0.97**		0.68**	0.40**
MD_{EUC}	0.55**	0.65**	0.65**		0.62**
MD_{MAH}	0.44**	0.49**	0.59**	0.76**	

** Significant at the 0.01 probability level.

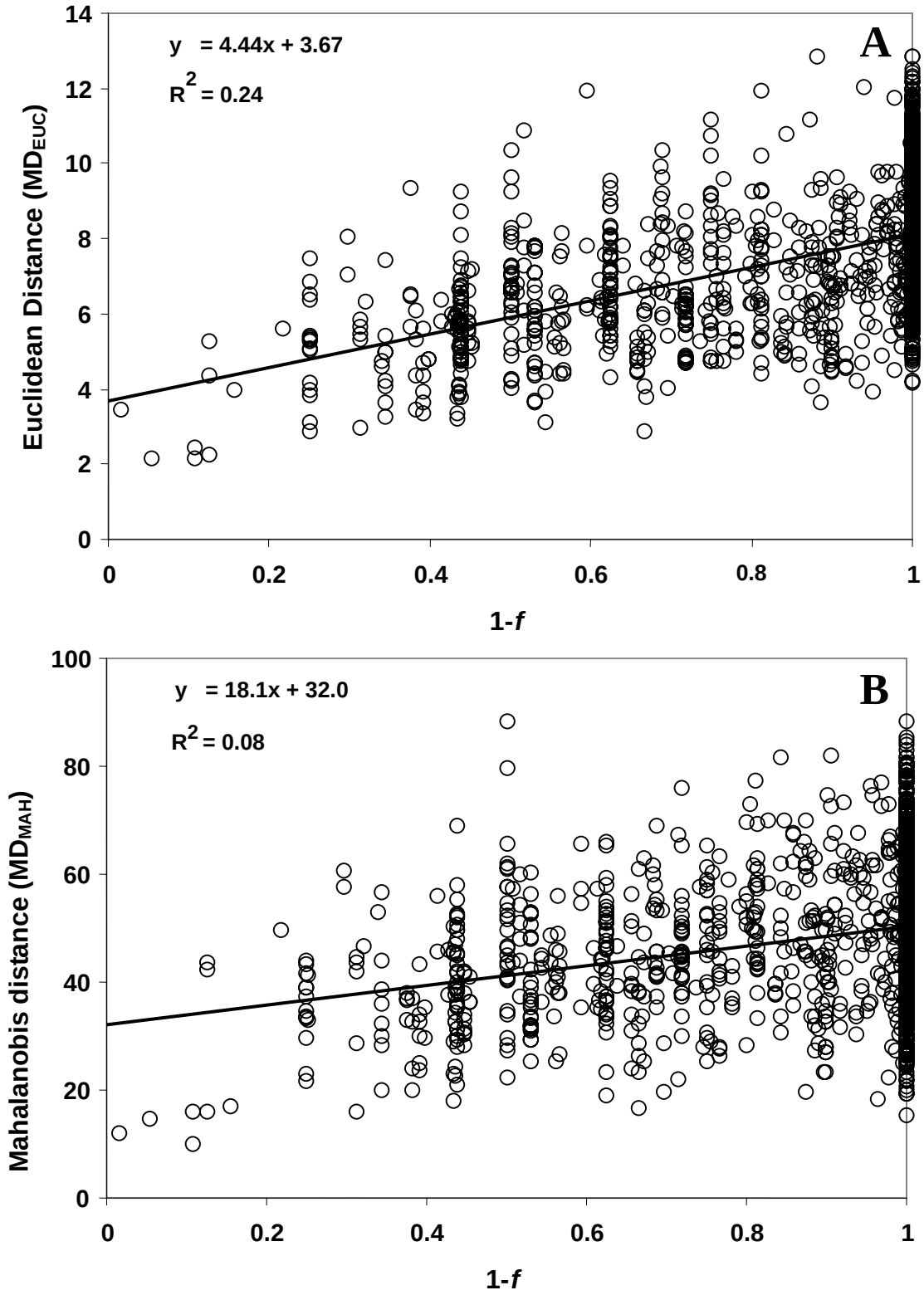

Figure 1. Relationship of the coancestry coefficient (*f*) with (A) Euclidean (MD_{EUC}) and (B) Mahalanobis (MD_{MAH}) distances based on 25 morphological traits observed for 1767 pairwise comparisons of maize inbred lines.

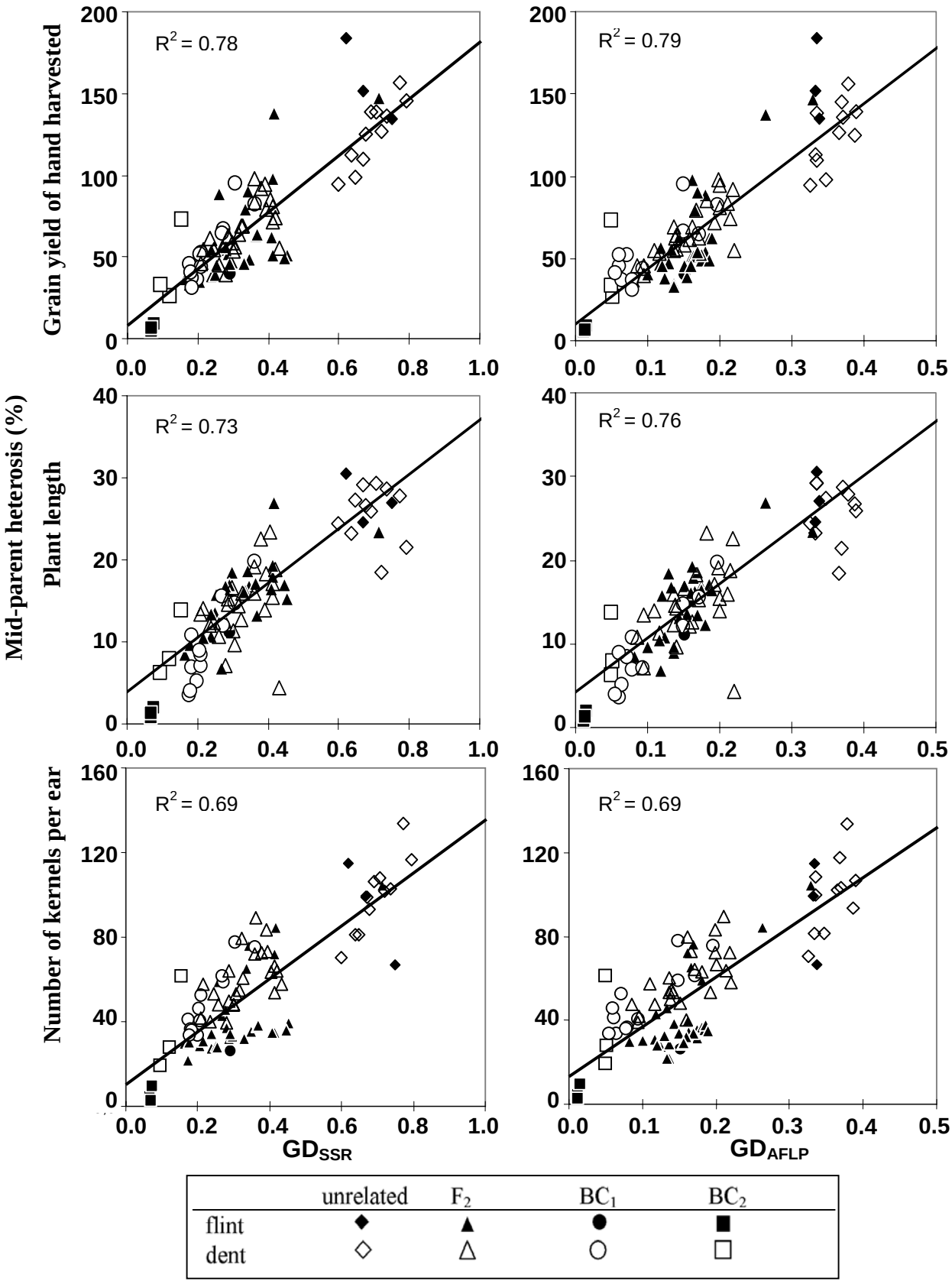

Figure 2. Relationship of genetic distances based on 100 SSRs (GD_{SSR}) or 20 AFLP primer combinations (GD_{AFLP}) with mid-parent heterosis (in %) of 84 intra-pool hybrids with given pedigree relationships of their parental maize lines.

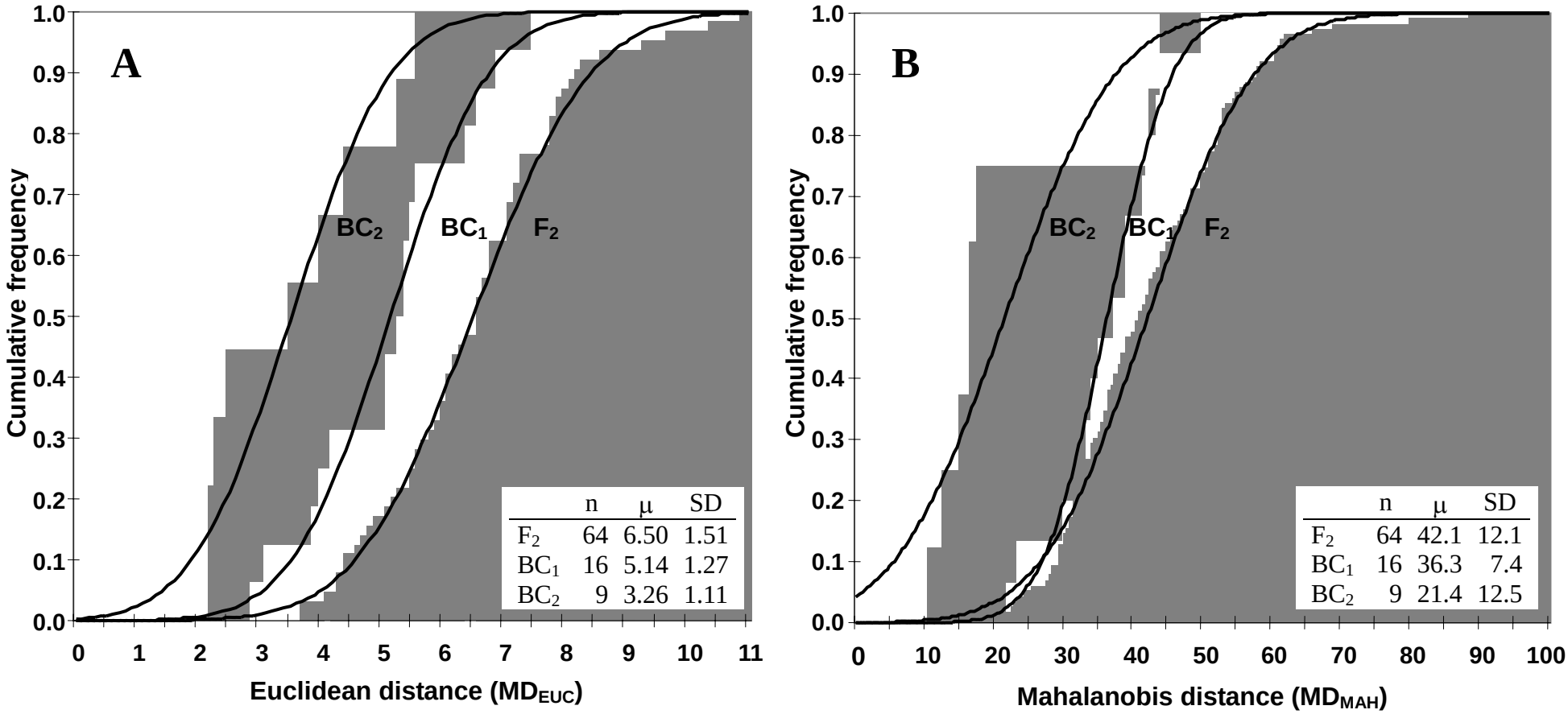

Figure 3. Cumulative histograms (columns) and approximated normal distributions (curves) for (A) Euclidean (MD_{EUC}) or (B) Mahalanobis (MD_{MAH}) morphological distances based on 25 morphological traits for F_2-, BC_1-, and BC_2-derived progeny lines. Variables n, μ, and SD refer to the number of values, the mean, and the standard deviation of MD values for the particular distribution, respectively.

Table 4. Evaluation of different scenarios for thresholds T based on morphological distances, heterosis, and genetic distances based on SSRs and AFLPs.

Parameter	F_2 *vs.* BC_1				BC_1 *vs.* BC_2			
	α=0.05		$\alpha=\beta$		α=0.05		$\alpha=\beta$	
	T	1-β	T	$\alpha = \beta$	T	1-β	T	$\alpha = \beta$
Morphological distances								
Euclidean (MD_{EUC})	4.0	0.18	5.8	0.32	3.1	0.40	4.1	0.21
Mahalanobis (MD_{MAH})	22.5	0.03	38.5	0.39	24.5	0.60	31.0	0.28
Heterosis								
Grain yield (GYE)	0.24	0.05	0.58	0.39	0.24	0.47	0.41	0.25
Plant length (PLG)	0.08	0.29	0.13	0.31	0.03	0.30	0.08	0.29
Number of kernels per ear (NKE)	0.17	0.02	0.48	0.47	0.22	0.52	0.36	0.24
Cumulative[†]	0.14	0.07	0.29	0.38	0.13	0.49	0.21	0.25
Genetic distances								
100 SSRs (GD_{SSR})	0.21	0.68	0.25	0.14	0.08	0.38	0.12	0.18
20 AFLP PCs (GD_{AFLP})	0.12	0.65	0.14	0.21	0.04	0.37	0.05	0.10

[†]Average relative heterosis of five traits (GYE, ELG, NKE, PLG, EHT) showing highest correlation with 1-*f*; for abbreviations, see Table 1.