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Relationship among combining ability, heterosis and genetic distance in maize (*Zea maize* L.) inbred lines under water-deficit conditions using line × tester and molecular analysis

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ABSTRACT

This study was conducted to investigate the relationships of combining ability, hybrid performance and genetic distance using Sequence Related Amplified Polymorphism (SRAP) data and other data sets obtained from analysis of agronomic performance of the CIMMYT maize inbred lines. For this purpose, 13 lines and four testers were crossed through controlled pollination in a line × tester design scheme to develop 52 hybrids. These hybrids were evaluated together with two standard checks (KSC704 and KSC705) for grain yield under two soil moisture environments for two years (2014-2015). Pair-wise genetic distance (GD) was estimated based on Jaccard (J) and simple matching (SM) coefficients. The variance components of specific combining ability (SCA) were higher than general combining ability (GCA), hence non-additive gene effects contributed to hybrid performance. There was no coincidence between the SRAP data and morphological assessments in this study. Significant and positive association of general combining ability with mid parent heterosis (MPH) under drought stress conditions is an indicator that GCA can be useful to predict MPH during selections under water stress conditions. However, correlations of genetic distances with heterosis under both conditions were too low to be predictive of hybrid vigor.

KEY WORDS: WATER STRESS, GENETIC DISTANCE, HYBRID PERFORMANCE, LINE × TESTER, SEQUENCE RELATED AMPLIFIED POLYMORPHISM

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INTRODUCTION

Maize is one of the most important crops worldwide, which serves as food, animal feed and raw materials of bioenergy. It is stated that, maize is queen of cereal crops due to high yielding potential and genetic diversity. The global production of this crop has increased during last years. However, its yield is reduced due to water deficit, which is one of the most important environmental factors affecting agricultural productivity worldwide, (Prasanna, 2012, Aminu et al., 2014 Li et al., 2017).

Heterosis, a powerful phenomenon in the evolution of plants, has been used extensively in crop production. However, identification and selection of appropriate parental combinations which produce superior F1 hybrids, is one of the most important stages in heterosis utilization (Mohammed et al., 2014). Hybrid breeders have always been concerned to the selection of appropriate parental lines without making all of the possible crossing among the available lines. Selection of parents with various genetic backgrounds is hardly substantial in the development of hybrids having optimal expression of heterosis (Hallauer et al., 2010 Pheirim et al., 2017).

During the past decades, several procedures have been utilized for prediction of heterosis, including performance of parental lines, combining ability, genetic diversity which determined using multivariate analysis of morphological and agronomic traits and molecular markers (Mohammadi et al., 2008). Selection based on phenotypic traits is extremely influenced by environmental factors, and the presence of genotype × environment interactions can hide the actual genetic value. Moreover, because of strong dominance effects of genes controlling maize yield, hybrid performance may not be predicted from the performance of parental lines, reliably. Furthermore, in breeding programs with a large numbers of inbred lines, making and evaluation of all of the possible crosses is not only expensive and boring, but also practically difficult and time consuming (Mohammadi et al., 2008).

In maize, several methods have been expanded for the prediction of hybrid performance by means of genetic markers (Frisch et al., 2010; Maenhout et al., 2010). Considering the cost and time which is required for field evaluation of hybrids, the utilization of genetic markers for identification of best heterotic combination of parental lines can be a suitable alternative (Mohammed et al., 2014). Molecular markers have been widely utilized in breeding programs, as a tool for the selection of the best parental lines of crosses; and as potential tools for the prediction of the heterosis from a certain cross.

Parental genetic distance has been considered as a feasible indicator for hybrid performance (Melchinger, 1999). Breeders are strongly interested to the prediction of hybrid performance from parental genetic distance. Because the preferable crosses could be identified by means of genetic distance before field evaluation of all hybrid combinations. This can increase the efficiency of hybrid breeding programs, (Mohammed et al., 2014). Estimated genetic distances can be related with hybrid performance from field experiments, and the extension of molecular marker systems such as sequence related amplified polymorphisms (SRAP) have considerably amended the power of the genetic distance estimation between genotypes.

Several researchers have used genetic distance to predict hybrid performance (Dhliwayo et al., 2009; Devi and Singh, 2011; George et al., 2011); however, their results were inconsistent with each other. Some researchers reported a positive correlation between marker based genetic distance and hybrid performance (Amorim et al., 2006; Srdic et al., 2007; George et al., 2011), while other researchers have reported no correlation between these two phenomenon (Balestre et al., 2008; Dhliwayo et al., 2009; Devi and Singh, 2011). Hence, the potential utilization of molecular markers in predicting the amount of hybrid performance in maize needs more research. Though significant associations were found between hybrid performance and genetic diversity in several investigations, the level of association varied widely from one study to another. Moreover, the reliability of molecular markers in estimating genetic distance depends on several factors such as the number of markers, their mode of inheritance and uniform distribution across the genome (Hahn et al., 1995; Mohammadi et al., 2008).

To the best of our knowledge, there is a little information about the association of genetic divergence and hybrid performance in CIMMYT maize inbred lines, which asks for studies to determine genetic distance as suitable predictor of hybrid performance in this germplasm. It is also needed to examine combining ability of parents as predictor of heterosis and F1 performance comparing with genetic distance measured by molecular markers. Therefore, this study was conducted to 1) investigate the possibility of predicting the hybrid performance using SRAP data and other data sets acquired from analysis of agronomic performance of the CIMMYT maize inbred lines; 2) determine associations among genetic distance of molecular markers in parents, heterosis, F1 performance, general combining ability (GCA) and specific combining ability (SCA) effects of parents and crosses, and compare the strategies to determine hybrid performance based on parental genetic distance (GD), GCA and SCA for heterosis; and 3) evaluation of coincidence between the SRAP data and morphological data.

MATERIALS AND METHODS

PLANT MATERIALS AND EXPERIMENTAL SITE

The experiment was conducted during two years (2014-2015) at the Research Farm of Agriculture and Natural Resources Research Center, Kermanshah, Iran (longitude of 47° 26' E, latitude of 34° 8' N and altitude of 1346 m) on a silty clay loam soil. The mean annual precipitation and temperature are 538 mm and 12.2 °C for the region, respectively. In this study, a set of 13 inbred lines were selected and crossed through controlled pollination with four temperate maize testers using a line × tester matting design to produce 52 hybrid combinations. The origin and pedigree of the lines and testers are given in Table 1.

FIELD EXPERIMENT

In this experiment, 52 hybrids derived from line × tester matting scheme along with two standard checks were planted in the field according to a randomized complete block design (RCBD) with three replications, at two moisture environments (normal and water stress). Each plot was included 2 rows of 4 m long with an inter-row spacing of 0.75 m and in-row plant spacing of 18 cm. Under the normal and stress moisture environments, plants were irrigated when 50% and 65% of the total available soil water was depleted from the root zone, respectively. Soil moisture was measured based on standard gravimetric methods (Clarke Topp et al., 2008). The irrigation was applied by using a basin irrigation system. The amount of water for each irrigation treatment was measured using a volumetric counter. Grain yield per plot was recorded on five randomly selected plants per replication.

SRAP ANALYSIS OF INBRED LINES

Genetic characterization of all of the inbred lines and testers was done using a set of 30 SRAP primer pairs. Genomic DNA was extracted from fresh leaves of each line or tester according to the method of Murray and Thompson (1980). PCR reactions were performed in a 10µl reaction mix and amplified products were resolved by using 6% polyacrylamide gel followed by silver staining.

STATISTICAL ANALYSES

Analysis of variance (ANOVA) for each moisture environment was conducted using the PROC GLM of SAS (SAS Institute 2008). Genotypes were considered as fixed effects while years, moisture environments and replications were considered as random. The SAS program was used for the line × tester analysis to compute the SCA effects (Singh and Chaudhary, 1977). The GCA effects of lines and testers, the SCA effect of crosses, and their interactions with the year were estimated based on the factorial mating design as follows:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_k + ge_{ik} + ge_{jk} + se_{ijk}$$

Table 1. Information on maize lines and testers used in the study

Parents	Name of lines and testers/pedigree	Origin
Line 1	4-CHTSEY,2002/1389/9=1390/13=1391/10	CIMMYT germplasm
Line 2	4-CHTSEY,2002/1389/19=1390/21=1991/70	CIMMYT germplasm
Line 3	7-CHTSEY,2002/1389/33=1390/33=1391/61	CIMMYT germplasm
Line 4	7-CHTSEY,2002/1389/35=1390/37=1391/64	CIMMYT germplasm
Line 5	K18 × 2-CHTHIY, 2002/1389/59=1390/73=1391/43	derived from cross k18 × CIMMYT originated line
Line 6	K18 × 2-CHTHIY, 2002/1389/61=1390/77=1391/46	derived from k18 × CIMMYT originated line
Line 7	XT03	Derived from unknown China -source
Line 8	4-CHTSEY, 2002/1390/5=1391/6	CIMMYT germplasm
Line 9	4-CHTSEY, 2002/1390/9=1391/8	CIMMYT germplasm
Line 10	7-CHTSEY, 2002/1390/41=1391/22	CIMMYT germplasm
Line 11	20-CHTSEY,2002/1390/45=1391/25	CIMMYT germplasm
Line 12	20-CHTSEY,2002/1390/53=1391/31	derived from CIMMYT germplasm
Line 13	MO17 × 6-CHTHEY, 2002/1390/69=1391/40	derived from cross MO17 × CIMMYT originated line
Tester 1	MO17	CL. 187-2 × C103
Tester 2	0K18	derived from MO17 changes
Tester 3	A679	A B73 back-cross derived line [(A662 × B73)(3)]
Tester 4	K166B	derived from CIMMYT germplasm

Where Y_{ijk}; is performance of the hybrid when ith line is crossed to jth tester, in the kth year, μ is the overall mean, g_i is the effect of the ith line, g_j is the effect of the jth tester, s_{ij} is the interaction of the ith line with the jth tester, e_k is the effect of the kth year, $(ge)_{ik}$ is the interaction of the g_i and e_k, $(ge)_{jk}$ is the interaction of the g_j and e_k, $(se)_{ijk}$ is the interaction of s_{ij} and e_k.

For each cross combination (P1 × P2) mid parent heterosis (MPH) was calculated according to Falconer and Mackay (1996) as follows:

Mid parent heterosis (MPH) = [(F1- MP) / MP] × 100

where F1 is the mean of the F1 hybrid performance and MP is mean performance of two parental inbred lines.

Better parent heterosis (BPH) was calculated as:

BPH = [(F1- BP) / BP] × 100

where BP = mean of the better parent.

Genetic distance (GD) between each pair of parents was estimated from the binary matrix, using Jaccard and simple matching coefficients through the NTSYSpc version 2.0. Cluster analysis was done based on the UPGMA method. For evaluation of the correlation between two similarity matrices (molecular and phenotypic data), Mantel test in NTSYS software was applied. Mean of the trait in each moisture environment was used to calculate correlation coefficients between genetic distance, grain yield, MPH, BPH, GCA and SCA.

RESULTS AND DISCUSSION

Presence of an appropriate value of heterosis for grain yield and predicting hybrid performance is important in hybrid breeding programs. The degree of heterosis may influence by genetic diversity of the germplasm being used. The magnitude of heterosis which was observed in this study indicates that there is an opportunity to use this germplasm for extending hybrid varieties appropriate for stress and non-stress conditions.

Analysis of variance of grain yield for each of the two moisture environments showed significant genotype effects, indicating the existence of genetic variation among the genotypes. However genotype × year interaction was non-significant in both moisture environments, indicating that the genotypes were consistent over the years (Table 2). Nevertheless, significant differences ($p < 0.01$) among parents and F1 hybrids in both moisture environments were found and indicated that the data was suitable for genetic analysis of line × tester design. The mean squares for lines and testers which determine the GCA effects were also significant and showed the predominance of additive gene action in controlling grain yield. However, the mean squares of testers were higher than that of the lines in normal conditions and it was vice versa for water stress conditions.

Table 2. Analysis of variance (ANOVA) for combining ability of total grain yield based on line × tester matting design under normal and drought stress conditions.

Source of variation	df	Mean squares (MS)	
		NS	S
Year (Y)	1	18.11	17.41
Block (R)	4	37.18**	1.20
Genotype (G)	53	14.99**	19.33**
F1 vs. Check	1	2.65	39.26
Check	1	35.02**	6.02*
F1	51	14.84*	19.20**
Lines (L)	12	21.31**	36.36**
Testers (T)	3	46.94**	35.45**
L×T	36	10.00**	11.89**
G×Y	53	2.56	0.85
(F1 vs. Check) × Y	1	0.65	5.38
Check × Y	1	1.84	0.04
F1 × Y	51	2.61	0.77
L × Y	12	2.85	0.38
T × Y	3	0.71	0.86
L × T × Y	36	2.69	0.95
Error	212	2.32	1.12
σ^2A	-	1.96	1.91
σ^2D	-	4.88	7.29

*,**Significant at 0.05 and 0.01 probability levels, respectively. NS: Non-stress, S: Stress

The significance of line × tester interaction revealed that SCA was also important in the control of grain yield and indicated that non-additive gene effects also play an important role in the controlling of this trait (Table 2).

Average grain yield for parents (Table 3) and hybrid combinations (Table 4) showed a remarkable reduction under water stress and it ranged from 8.68 ton/ha for L8 × T1 to 15.16 ton/ha for L9 × T4 under normal conditions. However, under water stress conditions, this ranged from 4.95 ton/ha for L10 × T1 to 11.99 ton/ha for L5 × T3. The GCA effect was positive and significant for two parents of T3 and T4 under both normal and water stress conditions (Table 3). However, under normal conditions four parents and under water stress conditions five parents showed significant and positive values of GCA for grain yield (Table 3). Under normal conditions five hybrids and under water stress conditions seven hybrids expressed significant and positive values of SCA for grain yield (Table 4). Moreover, under normal conditions five hybrids and under water stress conditions eight hybrids showed significant and negative SCA for this trait.

Table 3. Grain yield (GY) means and general combining ability (GCA) values for parental lines used in this study under normal (NS) and water stress (S) conditions.

Parents	Grain yield (GY) (Ton/ha)		General combining ability (GCA) (Ton/ha)
	NS	S	NS
L1	5.85	2.77	-1.12
L2	4.14	3.07	0.41
L3	5.49	2.40	0.57
L4	6.39	3.85	0.98**
L5	5.30	2.72	0.37
L6	6.33	3.22	0.54
L7	3.77	2.73	0.07
L8	4.91	2.82	-1.90**
L9	4.17	2.62	0.65
L10	7.15	3.05	-0.83*
L11	6.18	3.21	-0.98**
L12	5.74	2.57	1.33**
L13	5.70	2.88	-0.09
T1	4.56	2.34	-0.71**
T2	4.80	2.71	-0.63**
T3	5.27	3.06	0.75**
T4	5.53	3.04	0.59**

*, ** Significant at 0.05 and 0.01 probability levels, respectively.
NS: Non-stress, S: Stress

Mid parent heterosis (MPH) and better parent heterosis (BPH) values were significant and positive for all hybrids under both normal and water stress conditions. MPH ranged from 70% for L10 × T1 to 230% for L7 × T3 under normal conditions and from 0.63% for L10 × T3 to 3.15% for L5 × T3 under water stress conditions. The range of BPH was from 39% for L10 × T1 to 183% for L7 × T3 under normal conditions, and from 0.62% for L10 × T3 to 2.92% for L5 × T3 under water stress conditions (Table 4).

SRAP data showed low genetic distances among parental lines. Distances ranged from 0.181 for L12 × T4 to 0.423 for L11 × T2 based on Jaccard coefficient, and from 0.142 for L12 × T4 to 0.358 for L9 × T1 based on simple matching coefficient (Table 4). The average genetic distance among inbred lines of this study based on Jaccard and simple matching coefficients were 0.33 and 0.25, respectively; indicating low levels of polymorphism among them. Ndhlela et al. (2015) stated that low genetic distances can be attributed to the mixing of germplasm by CIMMYT for population improvement at the expense of hybrid breeding.

In field experiments, the most expensive and time consuming step of hybrid breeding programs is the identification of inbred lines expressing higher heterosis (Mohammadi et al., 2008). Plant breeders often have used SCA of hybrids in identifying better parental lines for extension of hybrid combinations. However, when a large numbers of inbred lines are available in a breeding program, more useful tools are needed. In maize, genetic distance determined by molecular markers is the main strategy which has been followed for determination of hybrid performance and its potential for this purpose has been evaluated in several researches. In these researches, the extent of correlation differed greatly from one trait to another and also varied extensively with the germplasm used in different studies.

The correlation coefficients of GD calculated based on Jaccard and simple matching coefficients were negligible and non-significantly different from zero for each of TGY, MPH and BPH (Table 5). Therefore, prediction of hybrid performance for grain yield based on genetic distance estimated by SRAP markers cannot be a practical approach and this was in agreement with the results of Dhliwayo et al. (2009), Devi and Singh (2011) and Ndhlela et al. (2015). However, some studies have reported powerful correlation between hybrid performance and parental genetic distance (Melchinger, 1999; Singh and Singh, 2004).

Mohammadi et al. (2008) suggested that insufficient genome coverage, sample size of the parental lines and progenies and different levels of dominance effects on traits are some important reasons for the low correlation between genetic distance and hybrid performance. Other possible reason for this issue is utilization of unlinked markers to the trait in estimation of genetic distance. For solving this problem, Bernardo (1992) suggested identifying of specific marker loci with close linkage to chromosomal segments controlling target traits. Although genetic distance was not a reliable predictor of hybrid performance, some promising approaches such as BLUP (Best Linear Unbiased Prediction) along with molecular marker data have been extended for predicting hybrid performance using genetic distances. However, in this study significant and positive associations were observed between TGY, BPH and MPH with SCA effects of crosses. Moreover, a significant and positive correlation was found between GCA and MPH under water stress conditions (Table 5). This correlation is an indicator that GCA can be useful to predict MPH during selections under water stress conditions.

In this study, correlations based on genetic distance estimates using simple matching coefficient were relatively higher than correlations based on GD estimated using Jaccard coefficient. This shows that the extent of correlation coefficient was not only impressed by the germplasm under study, but also by the genetic distance measures.

Cluster analysis grouped the 17 lines and testers into three major groups (Fig. 1). However, the cluster analy-

Table 4. Grain yield (GY) means, specific combining ability (SCA), mid parent heterosis (MPH) and better parent heterosis (BPH) estimates for 52 F_1 hybrids of line × tester under normal (NS) and water stress (S) conditions, and genetic distance (GD) between respective parental lines using simple matching (SM) and Jaccard's (J) coefficients based on SRAP markers.

Hybrids	GY (Ton/ha)		SCA (Ton/ha)		MPH (%)		BPH (%)		GD J	GD SM
	NS	S	NS	S	NS	S	NS	S		
L1×T1	10.55	7.35	-0.01	-0.43	103**	188**	80**	166**	0.327	0.245
L1×T2	10.73	7.56	0.08	1.04*	101**	176**	83**	173**	0.359	0.250
L1×T3	12.59	8.24	0.56	-0.81	126**	183**	115**	170**	0.308	0.221
L1×T4	11.23	9.00	-0.63	0.20	97**	210**	92**	196**	0.350	0.275
L2×T1	12.32	6.87	0.23	-0.34	183**	154**	170**	124**	0.353	0.270
L2×T2	12.57	7.79	0.38	0.45	181**	170**	162**	154**	0.292	0.196
L2×T3	11.62	6.79	-1.94**	-1.17*	147**	122**	121**	121**	0.290	0.206
L2×T4	14.72	10.92	1.32	1.06*	204**	257**	166**	255**	0.312	0.240
L3×T1	14.21	7.28	1.96**	-0.28	183**	207**	159**	203**	0.276	0.211
L3×T2	12.21	7.63	-0.13	0.37	137**	199**	122**	182**	0.349	0.255
L3×T3	11.61	7.71	-2.11**	-0.80	116**	183**	112**	152**	0.301	0.225
L3×T4	13.84	7.75	0.28	0.71	151**	185**	150**	155**	0.280	0.221
L4×T1	12.20	6.66	-0.46	-0.26	123**	115**	91**	73**	0.395	0.324
L4×T2	11.42	8.41	-1.33	-0.75	104**	157**	79**	119**	0.388	0.289
L4×T3	14.73	8.93	0.60	-0.39	153**	159**	130**	132**	0.350	0.270
L4×T4	15.15	10.00	1.19	1.40**	154**	191**	137**	160**	0.376	0.314
L5×T1	14.59	6.76	2.54**	-0.11	196**	167**	175**	148**	0.388	0.324
L5×T2	10.82	8.36	-1.33	-1.56**	114**	208**	104**	207**	0.370	0.279
L5×T3	14.51	11.99	0.98	0.80	175**	315**	174**	292**	0.333	0.260
L5×T4	11.16	9.57	-2.20**	0.87	106**	232**	102**	215**	0.398	0.343
L6×T1	11.97	7.22	-0.26	-0.48	120**	160**	89**	124**	0.291	0.216
L6×T2	12.21	6.77	-0.10	-0.87	119**	129**	93**	111**	0.297	0.201
L6×T3	12.79	10.58	-0.90	-0.24	121**	237**	102**	229**	0.283	0.201
L6×T4	14.79	10.86	1.26	1.59**	149**	247**	134**	238**	0.306	0.235
L7×T1	11.78	6.47	0.03	0.92*	183**	155**	158**	137**	0.240	0.181
L7×T2	11.70	9.90	-0.14	-0.35	173**	264**	144**	262**	0.347	0.255
L7×T3	14.92	9.98	1.70*	0.40	230**	245**	183**	227**	0.331	0.255
L7×T4	11.46	10.74	-1.59*	-0.96*	146**	272**	107**	254**	0.256	0.201
L8×T1	8.68	7.62	-1.10	0.43	83**	195**	77**	170**	0.232	0.176
L8×T2	10.11	5.09	0.24	-0.20	108**	84**	106**	80**	0.327	0.240
L8×T3	11.21	5.21	-0.04	0.91*	120**	77**	113**	71**	0.290	0.221
L8×T4	11.98	5.71	0.90	-1.14*	129**	95**	117**	88**	0.259	0.206
L9×T1	12.38	8.84	0.05	0.71	184**	256**	172**	237**	0.422	0.358
L9×T2	11.61	5.79	-0.81	-1.07*	159**	117**	142**	114**	0.408	0.314
L9×T3	13.02	7.16	-0.78	0.32	176**	152**	147**	134**	0.390	0.314
L9×T4	15.16	8.76	1.53*	0.04	212**	210**	174**	188**	0.412	0.358
L10×T1	9.92	4.95	-0.93	0.00	70**	84**	39**	62**	0.342	0.265
L10×T2	11.92	6.79	0.98	0.02	100**	136**	67**	123**	0.340	0.240
L10×T3	12.75	4.96	0.43	0.89	105**	63**	78**	62**	0.336	0.250
L10×T4	11.67	6.23	-0.48	-0.90*	84**	105**	63**	105**	0.354	0.284
L11×T1	11.07	5.42	0.38	-1.18**	106**	95**	79**	69**	0.373	0.324
L11×T2	11.59	10.48	0.80	1.82**	111**	254**	87**	227**	0.423	0.348
L11×T3	11.60	6.67	-0.56	0.81	103**	113**	88**	108**	0.368	0.309
L11×T4	11.39	5.82	-0.61	-1.45**	94**	86**	84**	81**	0.356	0.314

L12×T1	12.78	7.57	-0.24	0.34	148**	208**	123**	194**	0.220	0.172
L12×T2	13.20	7.82	0.09	0.40	150**	196**	130**	189**	0.385	0.304
L12×T3	14.88	8.88	0.39	0.06	170**	216**	159**	191**	0.298	0.235
L12×T4	14.07	8.62	-0.25	-0.80	150**	207**	145**	184**	0.181	0.142
L13×T1	9.41	5.26	-2.18**	0.69	83**	102**	65**	83**	0.329	0.240
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*, **Significant at 0.05 and 0.01 probability levels, respectively.
NS: Non-stress, S: Stress

Table 5. Correlation coefficients of grain yield (GY), Mid parent heterosis (MPH) and Better parent heterosis (BPH) with each of SRAP-based genetic distance estimates using Jaccard (GDJ) and simple matching (GDSM) coefficients, general and specific combining ability (GCA and SCA, respectively) under normal (NS)and water stress (S) conditions.

Environments	GY (Ton/ha)		MPH (%)		BPH (%)	
	NS	S	NS	S	NS	S
GDJ	-0.023	0.028	-0.028	-0.03	-0.063	-0.045
GDSM	0.027	0.062	0.006	0.012	-0.02	-0.015
GCA	0.012	-0.243	0.049	0.661**	0.202	-0.073
SCA	0.689**	0.323**	0.565**	0.318**	0.528**	0.309**

*, **Significant at 0.05 and 0.01 probability levels, respectively.
NS: Non-stress, S: Stress
GY, grain yield; MPH, Mid parent heterosis; BPH, Better parent heterosis; GDJ, Jaccard genetic distance; GDSM, Simple matching genetic distance; GCA, General combining ability; SCA, Specific combining ability.

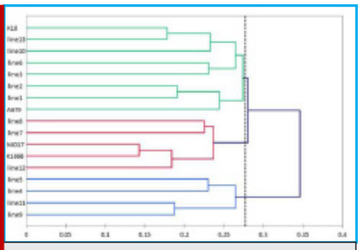

FIGURE 1. Dendrogram depicting genetic relationships among parental lines involved in line × tester analysis, based on SRAP data using UPGMA method and Jaccard's coefficient.

sis based on phenotypic traits and SRAP markers could not separate parents based on geographical or ecological data. Moreover, in this study there was no coincidence between the SRAP data and morphological estimations, which indicated poor association and agreement of molecular marker diversity with that of phenotypic one (r= 0.15 under normal and r= 0.10 under water stress conditions). Several reasons are given for the discordance between these two sets of data. Accumulation of some characteristics having adaptive value in specific habitats subjected to similar ecologic conditions (Steiner and Los Santos, 2001), differences between the evolutionary rates of phenotypic traits with adaptive value and those originating from selectively neutral DNA (Linhart and Grant, 1996), selection pressure for homogenization of different traits in parental germplasm and the different genomic regions evaluated with both markers (Amini et al., 2011), are some of these probable reasons.

In conclusion, prediction of heterosis is critical and valuable in hybrid breeding programs. In this regard, a potentially powerful approach is the application of genetic distance specified by molecular markers. In this study, associations between genetic distance estimates (GDJ and GDSM) with heterosis effects were negligible and non-significant. Thus, prediction of heterosis based on genetic distances estimated by SRAP markers cannot be a practical approach. Use of unlinked markers to the target traits, insufficient genome coverage, sample size of the parental lines and progenies and different levels of dominance effects on target traits are some of probable reasons for the low correlations between genetic distance and hybrid performance. On the other hand, identifying of specific marker loci with close linkage to chromosomal segments controlling target traits and application of statistical methods such as BLUP along with molecular marker data are some of the solutions for this problem. A significant and positive association

among GCA and MPH under drought stress conditions is an indicator that GCA can be useful to predict MPH during selections under water stress conditions.

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