

Genetic analyses and association studies of yield components and kernel sugar concentration in sweet corn

Ashish Khanduri¹, B. M. Prasanna*², Firoz Hossain and P. C. Lakhera¹

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110012

¹HNB, Garhwal Vishwavidyalaya, Srinagar, Uttarakhand

²Global Maize Program, CIMMYT, Nairobi, Kenya

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Abstract

A set of sweet corn genotypes generated using line × tester (7 × 3) mating design, were evaluated at two locations (Hyderabad and Delhi) for estimating combining ability and heterosis of the genotypes and degree of association of sugar concentration with yield and its component traits. Genetic analyses revealed the importance of both additive and non-additive gene action for kernel sugar concentration, yield and its component traits, with relative predominance of dominance variance over additive variance. Significant effect of the environment on kernel sugar concentration and almost all the yield related traits indicated prominent role of environment in determining the extent of expression of these traits. L6 (RIL62) was identified as the best general combiner at both the locations for sugar concentration as well as yield traits. Some promising sweet corn genotypes, namely L6 (RIL62), L3 (DMR-2320) and L7 (RIL91) at Hyderabad and L4 (DMR-2322), L5 (RIL10), L6 (RIL62) and L7 (RIL91) were found to be promising general combiners for kernel sugar concentration at Delhi station only. Among the testers, T3 (Madhuri) was observed to be the best genotype for kernel sugar concentration and other agronomic traits. L6 × T3 (RIL62 × Madhuri) among the crosses was observed to be the best specific combiner for sweet corn trait at both the locations followed by L7 × T3 (RIL91 × Madhuri) and L5 × T2 (RIL10 × Winorange). Analysis of heterosis for sugar concentration over the popular sweet corn composites (Priya, WinOrange and Madhuri) identified L6 × T3 (RIL62 × Madhuri) as the best cross combination with a heterosis value of 48.47%, 38.82% and 24.83% at Hyderabad and 74.30%, 60.94% and 114.15% at Delhi over Priya, WinOrange and Madhuri, respectively. The analysis also showed that kernel sugar concentration was not significantly correlated with any of the grain yield and its component traits, suggesting the scope of genetic improvement of kernel sugar concentration independent of grain yield.

Key words: Sweet corn, sugar concentration, combining ability, heterosis

Introduction

Among the various types of specialty corn, sweet corn has become popular, both as a fresh and processed vegetable in several countries worldwide including India. Nearly all commercial sweet corn genotypes contain one or more recessive alleles (e.g. *su1*, *sh2*, *se1*) that alter carbohydrate content of the endosperm with higher degree of sweetness. Among the two popular theories regarding the origin of sweet corn, first theory proposes that modern sweet corn is descendent from maize landraces 'Dulce' and 'Chullpi', while the second suggests that North American sweet corn is the recent origin resulting from a mutation to *su1* in the field corn [1].

Sweet corn quality is determined mainly by the amount of sugar and starch in the endosperm. Starch synthesis mutants may be divided into two classes based on their effects on endosperm composition [2]. The Class I mutants – such as *shrunken2* (*sh2*) accumulate sugars at the expense of starch and greatly decrease total carbohydrates at the mature seed stages. Due to elevated sugar levels, varieties of these genotypes are often called 'super sweet' or 'extra sweet corn'. Among the class II mutants, *amylose extender1* (*ae1*) and *sugary1* (*su1*) alter the types and amounts of polysaccharides produced and lead to slightly less starch accumulation in the mature kernel with smaller increase in total sugar concentration at 21 days. Besides high concentration of kernel sugar among the 'super sweet', it has the added advantage of slower rate of depletion of kernel sugar after harvest as compared to *su1* type, thus enjoys the benefit of extended shelf life. Although major genes, such as *su1*, *sh2*, have major

*Corresponding author's e-mail: b.m.prasanna@cgiar.org

effects on carbohydrate composition in the endosperm, minor genes in the genetic back ground also affects carbohydrate composition.

In India, a few sweet corn composites (like 'Madhuri', 'Priya' and 'WinOrange') have been developed by the public sector maize breeding programmes. However, no sweet corn hybrid with high yield potential has been released so far in India. Although the composites are popular among the farming community, yet they have the inherent problem of having low yielding potential as compared to hybrids. Therefore, it is important to develop sweet corn hybrids with high yielding potential and kernel sugar concentration. In view of the above, the present study was carried out with an aim identify to genotypes with higher *per se* productivity, combining ability and nutritional quality.

Materials and methods

The basic genetic material for this experiment consisted of seven inbred lines having *su1* and/or *sh2* alleles. Four of the seven inbred lines were developed by DMR, New Delhi, while three inbred lines are from Maize Genetics Unit, IARI, New Delhi. Three popular sweet corn composites (Madhuri, Priya and WinOrange) released in India were used as broad-based testers and Golden Sweet Corn, a commercial sweet corn cultivar was used as a check in the study. Experimental crosses were generated in a Line \times Tester mating design [3] using DMR2317, DMR2318, DMR2320, DMR2322, RIL10, RIL62 and RIL91 as 'lines' and Priya, WinOrange and Madhuri as 'testers'. Crosses were generated during *Kharif* 2007 at IARI Experimental Farm, New Delhi.

The Line \times Tester set, along with the check (Golden sweet Corn), was evaluated at two locations (i) Maize Winter Nursery, Hyderabad, and (ii) IARI Experimental Farm, New Delhi, during *Rabi* 2007-08 (winter season) and *Kharif* 2008 (monsoon season), respectively. The entries were planted in a randomized complete block design (RCBD) with two replications per entry (one row per replication) with a plant-to-plant spacing of 20 cm and row-to-row spacing of 75 cm. Standard agronomical practices were followed for raising and maintenance of plants.

In each plot a uniform plant stand of 20 plants were maintained and observations were recorded for plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernels per ear row, number of kernel rows and 100 kernel weight (g) on five randomly selected open pollinated plants/ears from a plot. For measuring grain yield per plot (in kg), days to 50% male

and female flowering, data per plot was considered. In each of the plot, five randomly selected plants were controlled pollinated for the estimation of kernel sugar concentration (%) on 20th day after pollination. 'Brix' value estimated using the pocket Refractometer (ATAGO, Japan) was used for the estimation of kernel sugar concentration. Heterosis of the experimental hybrids and correlation coefficients were calculated using standard procedure. The statistical analyses of combining ability, heterosis and correlation coefficients were calculated using Windostat 8.0.

Results and discussion

ANOVA for combining ability revealed that the line, tester and line \times tester variances were significant for kernel sugar concentration and most of the yield contributing traits analyzed at both Hyderabad and Delhi (data not shown). This indicated that the 7 sweet corn inbred lines, three testers (sweet corn composites) and 21 experimental hybrids combinations used in the present study were significantly different from each other in terms of sugar concentration and all other relevant yield components. The analysis also indicated the predominance of line \times tester variance to the overall variance of the hybrids over lines and tester variances. The predominant contribution by the line \times tester variance is also in congruence with the results of other studies [4].

Genetic analyses revealed that both additive and non-additive gene actions were important, however, when proportion of dominance variance and additive variances were compared, the dominance variance were found to be relatively higher for most of the characters (data not shown), signifying the utility of heterosis breeding in sweet corn genotypes. Predominance of non-additive gene action with respect to total sugar, reducing sugar, non-reducing sugar, grain yield per plant and other agronomic traits was also reported by previous studies [4, 5]. In contrast, highly additive type of gene action for carbohydrate fractions in the US sweet corn genotypes have been reported [6]. Similarly, importance of both additive and non-additive gene action in a set of hybrids of high sugar corn has been reported [7].

Pooled analysis revealed significant effects of the environment on kernel sugar concentration and yield related traits suggesting the prominent role of environment in determining the extent of expression of these traits (Table not shown). Besides significant effects of environment \times lines variance and environment \times tester variances; variances for environment \times crosses

were significant, suggesting the presence of genotypes \times environment interactions. Significant influence of planting and harvesting dates on sweet corn traits, establishing strong $G \times E$ effects was also reported in various studies [8, 9].

Among the lines, L6 (3.43), L3 (0.59) and L7 (0.51) at Hyderabad, and L6 (5.06), L7 (1.64), L4 (1.05) and L5 (0.68) at Delhi showed significant positive GCA effects, and were found to be good general combiner for kernel sugar concentration (Table 1). Importantly, L6 showed the highest and significant GCA value at both the locations. Pooled analysis also revealed L6 and L7 as promising general combiners for kernel sugar concentration. Also, L4 (0.28) and L1 (0.09) were found to be best general combiner for grain yield at Hyderabad, while at Delhi, L6 (0.41) was identified as the best general combiner followed by L4 (0.12) (value not presented in the Table). Analysis of pooled data set also revealed the L4 (0.20) and L6 (0.18) as the promising general combiners for grain yield. In case of testers, T2 (0.09) at Hyderabad and T1 (0.11) at Delhi were noted to be best general combiners for grain yield per plot.

Considering all the traits, L6 (RIL62) among all the lines was found to be the best general combiner at Delhi for total sugar concentration, besides having significant positive GCA effects for grain yield, ear diameter and 100-kernel weight. At Hyderabad, the same line showed 35.50% sugar concentration and was also identified as the best general combiner for sugar concentration and 100-kernel weight. Pooled analysis also identified L6 (RIL62) as the best general combiner for kernel sugar concentration, grain yield and related traits, such as 100-kernel weight and ear diameter (Table 1). Among the testers, T3 (Madhuri) was found to be the best general combiner for kernel sugar concentration at both Hyderabad (0.29) and Delhi (1.96) and was identified as the best genotype. The choice of three composite varieties as testers in the present study is primarily due to more efficient evaluation of GCA by broad based testers as compared to narrow based testers such as inbred lines [10, 11].

Among the crosses at Hyderabad, L3 \times T1 (3.95) was found to be best specific combiner for kernel sugar concentration, followed by L6 \times T3 (3.94) (Table 1). At Delhi location, L6 \times T3 (7.47) was identified as the best cross combination for kernel sugar concentration. Other promising cross combinations at Delhi included L3 \times T2 (3.87), L5 \times T1 (3.48), L7 \times T3 (3.09), L5 \times T2 (1.62) and L2 \times T1 (1.14). The present study thus led to the

identification of L6 \times T3 (RIL62 \times Madhuri) as the best specific combiner with kernel sugar concentration of 27.88% and 34.65% at Hyderabad and Delhi, respectively. Taken into consideration of grain yield, L7 \times T2 had the highest SCA effects (0.39) for grain yield at Hyderabad, followed by L6 \times T2 (0.22), L5 \times T3 (0.22), L3 \times T1 (0.21), L4 \times T2 (0.18), L2 \times T1 (0.16) and L5 \times T1 (0.12) (value not presented in the table). Among the crosses at Delhi, L3 \times T2 (0.34) was the promising specific combiner for grain yield.

Considering the mean performance and combining ability for sugar concentration, grain yield and its component traits, L6 \times T3 (RIL62 \times Madhuri) was identified as the best genotype at both the locations. The analysis of SCA effect revealed that in most of the cases the parents involved in experimental crosses having higher SCA possess higher GCA effect as was also reported earlier [12]. In the present study, both L6 and T3 were found to be the best general combiner for kernel sugar concentration and L6 \times T3 also showed high SCA effects, suggesting that having one or both parents with high GCA effects would lead to desirable SCA effects in the cross combination.

Several studies analyzed the combining ability of sweet corn \times sweet corn or field corn \times sweet corn crosses for diverse traits such as sugar concentration, grain yield and its components, prolificacy, seed processing potential and resistance to biotic and abiotic stresses [4, 5, 13]. Estimation of gene action using combining ability analysis have led to the identification of promising sweet corn inbred lines and cross combinations for various target traits.

The phenomenon of heterosis has been exploited extensively in maize breeding starting with the single-cross, double-cross, three-way cross, and coming back to the single-cross hybrid development [14]. The study on the extent of heterosis among the sweet corn hybrid combinations would not only help in understanding the extent of complementation of alleles coming from the diverse parents but would also having potential of release of some of the promising top cross hybrid combinations directly as variety.

The best parent heterosis for kernel sugar concentration in the present study ranged from -45.70 to 28.78% at Hyderabad and from -27.04 to 54.00% at Delhi. L3 \times T1 was found to be the best combination with 28.78% best parent heterosis at Hyderabad, while at Delhi, L6 \times T3 performed best with 54.00% best parent heterosis, followed by L7 \times T3 (25.00%) and L5 \times T1

Table 1. Mean performance and GCA/SCA effects of kernel sugar concentration and yield contributing traits

Genotypes	Hyderabad			Delhi			Pooled		
	GCA/SCA effect of sugar conc.	Mean of sugar conc.	Yield and yield component with significant value	GCA/SCA effect of sugar conc.	Mean of sugar conc.	Yield and yield component with significant value	GCA/SCA effect of sugar conc.	Mean of sugar conc.	Yield and yield component with significant value
Parents (line and tester)									
L ₁	-0.86**	22.73	YLD,NKR,KPR,PH	-3.33**	20.25	KPR	-2.10**	21.49	NKR,KPR
L ₂	-2.85**	20.48	KPR,PH,EH	-4.02**	22.05	-	-3.44**	21.27	KPR,PH, EH,MF
L ₃	0.59**	19.20	EL,KPR,PH,MF	-1.07**	19.58	EL,PH	-0.24	19.39	EL,PH,FF
L ₄	-0.67**	19.48	YLD,EL,KPR, 100KW,PH,EH	1.05**	22.18	YLD,100KW	0.19	20.83	YLD,ED, 100KW,PH
L ₅	-0.14	21.48	PH, EH	0.68*	17.20	MF,FF	0.27	19.34	-
L ₆	3.43**	35.50	100 KW	5.06**	22.50	YLD,ED, 100KW	4.24**	29.00	YLD,ED, 100KW,
L ₇	0.51**	19.80	EH	1.64**	21.48	-	1.08**	20.64	EH
T ₁	-0.03	18.80	-	-1.16**	19.88	YLD,EL	-0.60**	19.34	-
T ₂	-0.26*	20.08	YLD,EL,ED, NKR,KPR,FF	-0.80**	21.53	-	-0.53**	20.81	EL,NKR, 100KW,PH,FF
T ₃	0.29**	22.33	PH,EH	1.96**	16.18	EH	1.13**	19.26	PH,EH
Cross combinations (line x tester)									
L ₁ x T ₁	1.16**	20.48	EL,KPR	-0.87	14.78	-	0.14	17.63	EL
L ₂ x T ₁	0.54	17.88	YLD,EL,ED, KPR,100KW	1.14*	16.10	-	0.84**	16.99	ED,100KW
L ₃ x T ₁	3.95**	24.73	YLD,PH,EH	-0.36	17.55	-	1.79**	21.14	PH
L ₄ x T ₁	1.18**	20.63	EL	0.76	20.80	KPR	0.94**	20.72	-
L ₅ x T ₁	-1.72**	18.33	YLD,100KW	3.48**	23.15	100 KW	0.88*	20.74	100KW
L ₆ x T ₁	-4.33**	19.28	EH	-2.77**	21.28	NKR	-3.55**	20.28	EH
L ₇ x T ₁	-0.72*	19.98	NKR	-1.37*	19.25	-	-1.05**	19.62	NKR
L ₁ x T ₂	-0.57*	18.53	-	0.76	16.78	NKR,100KW	0.10	17.66	NKR
L ₂ x T ₂	1.02**	18.13	100KW,PH	0.77	16.10	MF,FF	0.90**	17.12	-
L ₃ x T ₂	-2.92**	17.63	-	3.87**	22.15	YLD,ED	0.47	19.89	-
L ₄ x T ₂	1.89**	21.18	YLD,KPR,100KW	-0.60	19.80	-	0.65*	20.49	100KW
L ₅ x T ₂	1.56**	21.38	EL,PH,EH	1.62**	21.65	EL,KPR	1.59**	21.52	EL,NKR, PH,EH
L ₆ x T ₂	0.39	23.78	YLD,EL,NKR, 100KW,PH,EH	-4.71**	19.70	ED,100KW	-2.16**	21.74	ED,NKR, 100KW
L ₇ x T ₂	-1.37**	19.10	YLD,EL,KPR,EH	-1.71**	19.28	-	-1.54**	19.19	-
L ₁ x T ₃	-0.59*	19.05	100KW,PH,EH	0.12	18.90	EL,KPR	-0.24	18.98	KPR
L ₂ x T ₃	-1.56**	16.10	EL,EH	-1.91**	16.18	-	-1.74**	16.14	-
L ₃ x T ₃	-1.03**	20.08	EL,100KW	-3.51**	17.53	100KW	-2.27**	18.81	100KW
L ₄ x T ₃	-3.01**	16.83	PH	-0.16	23.00	MF	-1.59**	19.92	-
L ₅ x T ₃	0.16	20.53	YLD	-5.10**	17.70	-	-2.47**	19.12	-
L ₆ x T ₃	3.94**	27.88	EL,KPR	7.47**	34.65	-	5.71**	31.27	EL,KPR
L ₇ x T ₃	2.08**	23.10	100KW,PH,EH	3.09**	26.85	100KW	2.59**	24.98	100KW,PH,EH

L₁ = DMR-2317sh₂/sh₂, L₂ = DMR-2318sh₂/sh₂, L₃ = DMR-2320sh₂/sh₂, L₄ = DMR-2322sh₂/sh₂, L₅ = RIL10sh₂/sh₂, L₆ = RIL62su/su, L₇ = RIL62su/su, T₁ = Priya, T₂ = Winorange, T₃ = Madhuri; *Significant at P = 0.05; **Significant at P = 0.01; YLD: Yield per plot; EL: Ear length; ED: Ear diameter; NKR: No. of kernel rows per ear; KPR: No. of kernels per row; 100KW: 100-kernel weight; PH: Plant height; EH: Ear height; MF: Days to 50% anthesis; FF: Days to 50% silking.

(16.45%) (Table 2). Standard parent heterosis over 'Golden Sweet Corn' was found to vary from -9.80 and 56.16% at Hyderabad and from 0.99 to 136.80% at Delhi. L6 × T3 was identified as the best cross combination over standard check.

Analysis of heterosis for kernel sugar concentration over the popular sweet corn composites revealed L6 × T3 (RIL62 × Madhuri) as the best cross combination among all the experimental hybrids with a heterosis value of 48.47%, 38.82% and 24.83% over Priya, WinOrange and Madhuri, respectively, at Hyderabad (Table 2). At Delhi also, the same cross combination (RIL62 × Madhuri) recorded the highest heterosis of 74.30%, 60.94% and 114.15% over the three testers Priya, WinOrange and Madhuri, respectively. The present study thus, suggests the utility of RIL62 × Madhuri across the environments. In case of heterosis over Priya, L3 × T1 (31.52%) and L6 × T2 (26.46%) were found to be the best cross combinations at Hyderabad, whereas at Delhi, L7 × T3 (35.06%) was found to be the promising combination. The results of heterosis over Winorange showed that L3 × T1 (23.13%), L6 × T2 (18.40%) and L7 × T3 (15.04%) at Hyderabad, and L2 × T3 (24.87%) and L7 × T3 (24.71%) at Delhi were the best cross combinations. In case of heterosis over Madhuri, L7 × T3 (65.95%), L5 × T1 (43.08%), L4 × T3 (42.15%) and L3 × T2 (36.90%) were identified as the most promising combinations at Delhi (Table 2).

Interestingly, most of the cross combinations exhibited negative, better-parent heterosis for kernel sugar concentration indicating that although non-additive gene action is playing an important role (as evident from the proportion of additive and dominance variance), there is a need to accumulate favorable alleles in the inbred lines so that the heterosis for kernel sugar concentration can be achieved in the positive direction. For examples, L3 × T1, L4 × T1 and L4 × T2 at Hyderabad and L6 × T3, L7 × T3 and L5 × T1 at Delhi exhibited positive better parent heterosis indicating the positive complementation of alleles responsible for sweet corn trait. Data on standard heterosis (over Golden Sweet Corn) revealed the worth of L6 × T3, L7 × T3, L6 × T2, L5 × T2 and L4 × T2 cross combinations for kernel sugar concentrations at both the locations. However the potential of these promising cross combinations needs to be further validated by evaluating them at multiple locations/seasons. Although, the cross combinations refers to the top cross hybrids (since the female parent being a inbred line and male parent being

a composite), the promising combinations can be considered for release as they are better than the existing composites (Priya, WinOrange and Madhuri) in terms of both kernel sugar concentration trait as well as for yield performance. Kumari et al. [4] identified heterotic combination for field emergence, kernel quality traits and yield among crosses made between field corn and sweet corn genotypes.

In many genotypes such as L1, L2 and T2 were observed to be the excellent performer for yield and its contributing traits, but simultaneously they were identified as the poor combiners for kernel sugar concentration. On the other hand genotypes, such as L7 and T3 were promising combiner for kernel sugar concentration but were the poor performer in terms of yield and its contributing traits. Similar trend was also observed in many of the cross combinations. This trend necessitated to study the degree and direction of associations among kernel sugar concentration, yield and its component traits. Phenotypic and genotypic correlation analyses revealed that kernel sugar concentration was not correlated with any of the grain yield and its component traits (Table 3). This suggests that improvement of kernel sugar concentration in sweet corn genotypes can be undertaken independently of that of grain yield and its component traits. Saleh et al. [15] also reported non-association between ear yield and brix value while experimenting with nine advanced sweet corn population at the University Putra Malaysia during 2000 and 2001. This suggests that there is a need for further breeding efforts in combining the sweet corn trait with the yield component traits in otherwise agronomically superior genetic backgrounds. Several studies have analyzed field corn × sweet corn cross combination and identified best field corn donors for favorable alleles for grain yield and yield contributing traits for introgression into sweet corn genotypes [4, 13, 16]. However, in case of phenotypic correlations, grain yield was found to be positively correlated with number of kernel rows per ear (0.35), number of kernels per ear row (0.47) and 100-kernel weight (0.40) at Hyderabad and with ear length (0.68), ear diameter (0.63), number of kernel rows per ear (0.40), number of kernels per ear row (0.43), 100-kernel weight (0.49) and plant height (0.50) at Delhi (Table 3). Similar trend in case of genotypic correlations were observed in the present study. Positive association between grain yield and yield component traits has also been reported [15, 17], indicating that selection for yield component traits could help in improving grain yield in the sweet corn genotypes as well.

Table 2. Best parent, mid-parent and standard heterosis for kernel sugar concentration among promising cross combinations

Crosses	% Best parent heterosis		% Mid-Parent heterosis		% Standard heterosis		% hetrosis over Priya		% Hetrosis over Winorange		% Hetrosis over Madhuri	
	Hyd	Del	Hyd	Del	Hyd	Del	Hyd	Del	Hyd	Del	Hyd	Del
L ₃ x T ₁	28.78**	-11.72**	30.13**	-11.05**	38.52**	19.96**	31.52**	-11.72**	23.13**	-18.49**	10.73**	8.47
L ₄ x T ₁	5.88**	-6.22	7.76**	-1.09	15.55**	42.17**	9.71**	4.63	2.71	-3.39	-7.64**	28.55**
L ₅ x T ₁	-14.69**	16.45**	-9.01**	24.87**	2.66	58.24**	-2.53	16.45**	-8.74**	7.52*	-17.94**	43.08**
L ₆ x T ₁	-45.70**	-5.44	29.01**	0.40	7.98**	45.42**	2.53	7.02	-4.01*	-1.18	-13.68**	31.49**
L ₇ x T ₁	0.88	-10.38**	3.5*	-6.91*	11.9**	31.58**	6.25**	-3.17	-0.52	-10.59**	-10.55**	18.97**
L ₃ x T ₂	-12.23**	2.88	-10.26**	7.76*	-1.26	51.4**	-6.25**	11.42**	-12.23**	2.88	-21.07**	36.90**
L ₄ x T ₂	5.45**	-10.73**	7.05**	-9.40**	18.63**	35.34**	12.63**	-0.40	5.45**	-8.04*	-5.17**	22.37**
L ₅ x T ₂	-0.49	0.56	2.86	11.80**	19.75**	47.98**	13.70**	8.90**	6.45**	0.56	-4.28*	33.81**
L ₆ x T ₂	-33.03**	-12.44**	-14.45**	-10.52**	33.19**	34.65**	26.46**	-0.91	18.40**	-8.50*	6.47**	21.76**
L ₇ x T ₂	-4.88*	-10.47**	-4.21*	-10.37**	7.00**	31.75**	1.60	-3.02	-4.88*	-10.45**	-14.46**	19.16**
L ₁ x T ₃	-16.19**	-6.67	-15.45**	3.76	6.72**	29.19**	1.33	-4.93	-5.13**	-12.22**	-14.69**	16.81**
L ₂ x T ₃	-29.17**	-26.64**	24.77**	-15.38**	-9.8**	10.56*	-14.36**	-18.64**	-19.82**	24.87**	-27.90**	-0.03
L ₄ x T ₃	-24.65**	3.70	19.50**	19.92**	-5.74**	57.21**	-10.51**	15.69**	-16.21**	6.83	-24.65**	42.15**
L ₅ x T ₃	-8.08**	2.91	-6.28**	6.05	14.99**	20.98**	9.18**	-10.97**	2.22	-17.79**	-8.08**	9.39*
L ₆ x T ₃	-21.48**	54.00**	-3.58**	79.16**	56.16**	136.8**	48.47**	74.30**	38.82**	60.94**	24.83**	114.15**
L ₇ x T ₃	3.45*	25.00**	9.69**	42.59**	29.41**	85.53**	22.87**	35.06**	15.04**	24.71**	3.45*	65.95**
SE±	0.37	0.74	0.32	0.64	0.37	0.74	0.37	0.74	0.37	0.74	0.37	0.74

L₁ = DMR-2317sh₂/sh₂, L₂ = DMR-2318sh₂/sh₂, L₃ = DMR-2320sh₂/sh₂, L₄ = DMR-2322su/su, L₅ = RIL10sh₂/sh₂, L₆ = RIL62su/su, L₇ = RIL91 sh₂/sh₂, T₁ = Priya, T₂ = Winorange; T₃ = Madhuri; *Significant at P = 0.05; **Significant at P = 0.01; Hyd: Hyderabad; Del: Delhi

Table 3. Phenotypic and genotypic correlation coefficients among various traits

Traits	SUG	YLD	EL	ED	NKR	KPR	100KW	PH	EH	MF	FF
SUG	-	0.03 (0.31)	0.23 (0.08)	0.06 (0.01)	0.06 (-0.06)	0.08 (-0.19)	0.11 (0.13)	-0.18 (0.13)	-0.25 (0.21)	-0.28 (0.07)	-0.22 (0.03)
YLD	0.02 (0.34)	-	0.45 (0.68**)	0.34 (0.63**)	0.35* (0.40*)	0.47** (0.43*)	0.40* (0.49*)	-0.03 (0.50**)	-1.18 (0.18)	-0.36* (0.29)	-0.40* (0.24)
EL	0.23 (0.07)	0.50** (0.66**)	-	0.46** (0.50**)	0.45** (0.53**)	0.70** (0.65**)	0.29 (0.19)	0.23 (0.55**)	-0.16 (0.28)	-0.56** (0.31)	-0.57** (0.30)
ED	0.05 (0.02)	0.43** (0.80**)	0.58** (0.61**)	-	0.41* (0.50**)	0.32 (0.39*)	0.29 (0.50**)	-0.00 (0.57**)	-0.14 (0.32)	-0.16 (0.34)	-0.19 (0.30)
NKR	0.05 (-0.09)	0.41* (0.45**)	0.51** (0.52**)	0.44* (0.65**)	-	0.41* (0.36*)	0.10 (0.26)	0.19 (0.50**)	-0.11 (0.36*)	-0.42* (0.11)	-0.42* (0.05)
KPR	0.09 (-0.21)	0.50** (0.38*)	0.73** (0.63**)	0.38* (0.45**)	0.45** (0.34)	-	0.22 (-0.01)	0.23 (0.46**)	-0.18 (0.24)	-0.57** (0.30)	-0.56** (0.30)
100KW	0.11 (0.14)	0.56** (0.59**)	0.30 (0.27)	0.37* (0.61**)	0.11 (0.34)	0.23 (0.03)	-	-0.04 (0.26)	-0.12 (0.09)	-0.13 (0.22)	-0.18 (0.22)
PH	-0.18 (0.14)	-0.03 (0.59**)	0.24 (0.69**)	-0.02 (0.79**)	0.21 (0.65**)	0.25 (0.54**)	-0.04 (0.29)	-	0.70** (0.79**)	-0.32 (0.33)	-0.39* (0.30)
EH	-0.25 (0.26)	-0.20 (0.37**)	-0.17 (0.55**)	-0.21 (0.44**)	-0.13 (0.61**)	-0.20 (0.45**)	-0.12 (0.06)	0.70** (0.89**)	-	0.02 (0.12)	-0.03 (0.08)
MF	-0.37 (0.11)	-0.45** (0.28)	-0.72** (0.31)	-0.32 (0.20)	-0.68** (0.07)	-0.71 (0.30)	-0.21 (0.29)	-0.43* (0.54**)	0.03 (0.32)	-	0.87** (0.77**)
FF	-0.31 (0.07)	-0.44* (0.18)	-0.80** (0.37)	-0.46** (0.37*)	-0.72** (0.14)	-0.76 (0.32)	-0.29 (0.30)	-0.57** (0.37*)	-0.06 (0.20)	1.06** (1.02**)	-

Above diagonal: Phenotypic correlation coefficients; Below diagonal: Genotypic correlation coefficients; value without parenthesis represents; Hyderabad location, value within parenthesis represents Delhi locations. *Significant at P = 0.05; **Significant at P = 0.01; SUG: % kernel sugar; YLD: Yield per plot; EL: Ear length; ED: Ear diameter; NKR: No. of kernel rows per ear; KPR: No. of Kernels per row; 100KW: 100-kernel weight; PH: Plant height; EH: Ear height; MF: Days to 50% male flowering; FF: Days to 50% female flowering.

The study thus identified L6 (RIL62) and T3 (Madhuri) as best general combiners and L6 × T3 (RIL62 × Madhuri) as the best specific combiner at both the locations. Based on heterosis for kernel sugar concentration and grain yield and its component traits, L6 × T3 (RIL62 × Madhuri) was identified as the best cross combination at both the locations. The analysis also showed that kernel sugar concentration was not correlated with any of the grain yield and its component traits suggesting the possibility to bring favourable alleles for grain yield and its components from suitable genetic background.

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