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Research Article

Combining ability of quality protein maize (*Zea mays* L.) inbred lines for agronomic, yield and quality traits in temperate hilly regions of Kashmir, India

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Abstract

The combining ability provides insightful information about the genetic mechanisms that govern the inheritance of traits and enables the identification of potential inbred lines ; and promising hybrid combinations for crop improvement. However, most studies on quality protein maize (QPM) have focused on nutritional aspects, and very few are focused on their combining ability. In addition, studies on the adaptation, hybrid performance and stability of QPM in temperate areas remain scarce.Therefore, the present study sought to examine the combining ability of eight QPM inbred lines (QPM13, QPM14, QPM20, QPM21, QPM49, QPM50, VQL1, and VQL17). These 8 lines were subjected to half-diallel mating. Consequently, 28 crosses obtained were further evaluated in the temperate region of Kashmir against one check and parents in the RCBD, with three replications in a single row.The results revealed significant variances for general combining ability (GCA) and specific combining ability (SCA) for most of the recorded agronomic, yield, and quality traits. The crosses QPM49 × VQL1, QPM 13 × QPM14, QPM21 × VQL17, QPM13 × QPM50 and QPM50 × VQL17 were found to perform best in terms of earliness in tasselling (-1.842), silking (-1.204), days to mature (-2.654), highest yield (12.875 g)and protein content (1.113%), respectively. These promising crosses can be viable material sources for future QPM variety development programs in temperate regions.

Keywords: Combining ability, Genral combining ability (GCA), Hybrids, Maize, Specific combining ability (SCA), Zea mays

INTRODUCTION

Maize (*Zea mays* L.) is one of the world's most important cereal crop species and is used in human diets and livestock as well as a source of edible oils and biofuels (Shah *et al*., 2016; Yu *et al*., 2020). Due to its versatility, maize is grown worldwide under tropical, subtropical and temperate agroclimatic conditions (Matin *et al*., 2016). It is the primary staple food in many parts of the world (Shah *et al*., 2016). Thus, maize plays diverse and dynamic roles in global agri-food systems and food/ nutritional security (Grote *et al*., 2021; Poole *et al*., 2021).

Therefore, further enhancing the nutrient content of maize, which is one of the most consumed staple foods (FAOSTAT, 2021), by approximately 900 million people worldwide could be one of the most practical and sustainable approaches for addressing the global malnutrition problem (Kumar *et al*., 2019). Maize contains various other crucial phytochemicals and macronutrients required for human diets and nutrition (Shah *et al*., 2016). For the development of superior maize types, understanding the genetic mechanisms conditioning the inheritance of various traits is imperative in breeding (Amegbor *et al*., 2023).

To develop superior maize plants, it is imperative to understand how inbred lines or parents combine during crossing (de Abreu *et al*., 2019). Any genetic material's performance depends on its potential per se performance and the combining ability of the lines in crosses (Vacaro *et al*., 2002; Wegary *et al*., 2013). The combining ability of lines thus generates useful information on the genetic mechanisms governing how quantitative traits are inherited (Amegbor *et al*., 2023). This approach enables the identification of the best-inbred lines and promising hybrid combinations for the production of maize hybrids (Griffing, 1956; Wolde *et al.,* 2017) for yield, agronomic (Zhang *et al*., 2017), and quality traits (Rocha *et al*., 2019). Additionally, heterosis for superior performance is controlled primarily by specific combining abilities; therefore, lines should be selected based on their combining ability with testers (Amegbor *et al*., 2023).

Notably, several studies have been conducted on QPM for yield and nutritional traits; however, paramount information on the combining ability of QPM for their combining ability remains scarce (Amegbor *et al*., 2023). Several studies on the combining ability of QPM under different environmental conditions have reported that QPM generally has a lower grain yield (Sarika *et al*., 2018). Hence, growing research interest is in improving grain yield and nutritional quality rather than focusing only on quality traits (Li and Vasal, 2016). Moreover, the rich genetic diversity of tropical maize germplasm provides ample potential for the genetic improvement of maize, and additional studies are needed to use between ecotype hybrids. Large-scale analysis of combining ability using diverse germplasm resources can significantly improve our understanding of hybrid performance and contribute to increasing genetic gains in maize hybrid breeding (Yu *et al*., 2020). Literatures on adaptation (Worral *et al*., 2015; Kostadinovic *et al*., 2016) and QPM hybrid performance and stability in temperate areas remain scarce (Ignjatovic-Micic *et al*., 2013; 2020).

Therefore, considering the importance of analysing the ability of different genotypes to combine to improve the hybrid performance and genetic constitution of maize, the present study sought to examine the ability of different QPM inbred lines in the temperate hilly region of Kashmir (India).

MATERIALS AND METHODS

Study area, planting material, and field design

A total of 100 inbred lines of quality protein maize (QPM) were obtained from different locations in India, viz., CIMMYT-Hyderabad, VPKAS-Almora and Dryland Agriculture Research Station (DARS), Budgam (SKUAST-Kashmir), and their adaptability traits were evaluated at the Dryland Agriculture Research Station (DARS), Budgam (SKUAST, Kashmir), which is located at 34.084° N, 74.797° E, during the *Kharif* season of 2018-2019, with an average temperature of 24.30°C. Based on their preliminary adaptability, eight QPM inbred lines (QPM13, QPM14, QPM20, QPM21, QPM49, QPM50, VQL1, and VQL17) were selected and subsequently sent to the Winter Nursery Center, Hyderabad, South India (tropical wet region), for a half-diallel mating design during the *Rabi* season *in* 2018-19. After diallel mating, 28 crosesses were obtained; these were further evaluated in the temperate region of Kashmir against one check, the Shalimar Quality Protein Maize Hybrid-1 (Shalimar QPMH-1), and the parents. Thus, a total of 37 entries were planted in a randomized complete block design (RCBD) with three replications in a single row 4 m in length and 75 × 20 cm in spacing under rainfed conditions during *Kharif* 2020-2021 at DARS, SKUAST-Kashmir, in northern India.

DATA collection and statistical analysis

Agronomic traits

During the present investigation, data from 28 crosses of inbred QPM lines, parents and anthers were recorded for agronomic traits, viz., days to 50% tasselling (DTT), days to 50% silking (DTS), days to maturity (DTM), plant height (PH), cob height (CH), number of cobs plant^{-1} (CPP), cob length (CL), cob diameter (CD), kernel rows cob^{-1} (KRPC), number of kernels row^{-1} (KPR), 100grain weight (GW), seed yield plant^{-1} (YPP) and grain protein content (GPC).

Data analysis

The data recorded were subjected to analysis of variance (ANOVA) of the RCBD using the online statistical tool OPSTAT. F tests at 5% and 1% significance levels were calculated using different sources of variation against error variance. Diallel analysis was computed for each characteristic using Griffing formula in Windostat V9.2 (Windostat Services, Hyderabad, A.P., India). Method 2 Model 1 (fixed-effect model) of Griffing was used to determine general combining ability (GCA) and specific combining ability (SCA) effects; additive, dominance, and environmental variance; average degree of dominance; heritability (narrow sense and broad sense); and expected genetic advance. The variance in the GCA and SCA was also calculated (Singh and Chaudhary, 1985).

RESULTS AND DISCUSSION

Agronomic traits of the QPM lines

The overall ANOVA data for the agronomic traits of QPM crosses, presented in Table 1 revealed that there were significant differences among the treatments, parents, hybrids and parents vs. hybrids at either the 1 or 5% significance level, except for days to silking (DTS) and number of cobs plant^{-1} (CPP), for which no significant differences were recorded at either the 1 or 5% significance level (variable parents). Significant differences in the mean squares of agronomic traits due to parents and crosses indicate the diversity of the parental lines used for hybrid development and the different genetic backgrounds. In addition, these findings indicated substantial genetic variation in different genotypes of QPM used in the study.

Combining ability of QPM lines

Significant variations were observed in agronomic and biochemical traits for GCA at either the 1% or 5% significance level, except for cob length (CL) and number of cobs plant^{-1} (CPP). The variance attributes of GCA (σ^2s) recorded were DTT (0.243), DTS (0.157), DTM (2.103), PH (18.102), CH (28.340), CPP (0.001), CL (1.210), CD (0.070), KRPC (0.980), KPR (0.875), GW (0.278), YPP (6.920), and GPC (0.035). Similarly, a similar trend was observed for SCA, in which all the traits recorded were found to be significantly different at either the 1 or 5% significance level (Table 2). The variances attributed to SCA (σ^2s) were recorded for DTT (4.543), DTS (5.663), DTM (6.257), PH (314.160), CH (301.354), CPP (0.090), CL (18.002), CD (0.880), KRPC (2.001), KPR (24.179), GW (6.183), YPP (231.665) and GPC (0.331).

The above results revealed that the variance in SCA (σ^2s) was greater than those in GCA (σ^2g) for all the traits recorded, except DTM, which was greater (earlier) for GCA, implying that nonadditive gene action had greater contribution in traits.In addition, the estimates of additive (σ^2A) and nonadditive (σ^2D) genetic variances reflected that nonadditive variances had a greater magnitude of dominance than additive variances for the traits studied. This finding indicates the preponderance of nonadditive gene action, elucidating the greater effect of nonadditive gene action.

Worku *et al*. (2008) also reported the importance of both GCA and SCA effects in Maize for controlling most of the traits, although a higher proportion of sum of squares were observed for GCA than that of SCA in days to anthesis, ear height and plant height. Gelana (2000) also reported a similar result: a high GCA to SCA ratio implies greater contribution of additive gene action than nonadditive gene action in Ethiopian and CIMMYT's maize germplasm. When additive gene effects are dominant any recurrent selection method can be employed to improve the traits under study. The importance of both GCA and SCA effects observed in the current study for most traits are in line with the findings of, Nigussie and Zelleke (2001), Wegary (2002) and Tadessa (2009), who also reported the importance of both additive and nonadditive type of gene actions for the same traits. The significant GCA and SCA variances estimates suggested the importance of both additive and nonadditive gene actions for the expression of all the characters except ear diameter.

The ratio of additive to nonadditive constituents (σ^2A/σ^2D) provides insight into the underlying mechanism of action of the gene. Across all the traits, the ratio of additive genetic variance to dominance variance (σ^2A/σ^2D) was less than 1.00 (Table 2), which again elucidated the greater role of nonadditive gene action in trait inheritance (Amanah and Hadi, 2021).Additionally, the ratio $2\sigma^{\wedge2}g/2\sigma^{\wedge2}g+\sigma^{\wedge2}s$ aids in predicting the hybrid performance of a character based on a GCA less than unity for all traits (Table 2), implying that the success of a cross cannot be determined from the GCA effects of the parents alone (Yerva *et al*., 2016). The present results also indicated that genetic effects were predominantly nonadditive, which resulted in significant heterosis in maize for all the traits recorded. This finding coincides with the findings of Patel and Katherine (2016), who reported that heterosis in maize is the outcome of nonadditive effects.

General combining ability (GCA) effects

Combining ability effects: The knowledge of combining ability assists in selecting suitable parental lines. Among the various biometrical techniques available, the breeders extensively used combining ability analysis, as proposed by Griffing (1956). It provides information on the performance of genotypes in hybrid combination and also the nature of gene action involved in the control of metric traits. The parents are adjudged as best combiners based on GCA effects (Yerva *et al*.,

Table 1. Analysis of variance (ANOVA) for morphological, maturity, yield, and quality characteristics of maize (*Zea mays* L.) in hilly temperate region of Kashmir

Sr. No.	Source of Variation	d.f.	DTT	DTS	DTM	PH (cm)	CH (cm)	CPP	CL (cm)	CD (cm)	KRPC	KPR	GW (g)	YPP (g)	GPC (%)
1	Replications	2	0.026	6.419	19.541	373.665	286.331	0.900	101.450	0.061	6.470	11.210	4.825	67.005	0.085
2.	Treatments	35	14.330**	16.855**	25.110**	1212.820**	880.232**	0.150**	385.310**	2.480**	8.730**	71.130**	19.430**	602.105**	1.166**
3.	Parents	7	6.211**	4.531	48.837**	561.446**	282.314**	0.020	336.420**	0.210**	7.490**	18.840**	12.551**	112.113**	1.583**
4.	Hybrids	27	7.392**	8.313**	22.279**	628.118**	485.946**	0.160**	316.420*	0.470**	6.110*	312.200**	6.237**	102.226**	1.854**
5.	Parents vs Hybrids	1	456.600**	608.072**	108.711**	42185.171**	25413.331**	0.140**	3706.900**	157.690**	225.640**	2251.450**	842.620**	3023.380**	4.422**
6.	Error	70	1.501	1.343	3.338	106.650	105.650	0.047	109.214	0.062	2.753	1.037	2.092	16.217	0.021
Total	107	7.857	8.532	11.640	650.556	336.522	0.032	0.967	142.041	1.101	4.504	38.275	9.203	237.759	0.443

*, ** Significant at 5 and 1 percent level, respectively; DTT = days to 50% tasselling, DTS = days to 50% silking, DTM = days to maturity, PH = plant height, CH = cob height, CPP = number of cobs plant^{-1}, CL = cob length, CD = cob diameter, KRPC = kernel rows cob^{-1}, KPR = number of kernels row^{-1}, GW = 100 grain weight, YPP = grain yield plant^{-1} and GPC = grain protein content

Table 2. ANOVA for combining ability and estimation of components of genetic variation for morphological, yield and quality characters of maize (*Zea mays* L.) in the hilly temperate region of Kashmir

S.No.	Source of variation	d.f	DTT	DTS	DTM	PH (cm)	CH (cm)	CPP	CL (cm)	CD cm)	KRPC	KPR	GW (g)	YPP (g)	GPC (%)
1.	GCA	7	4.180 **	3.210 **	24.681**	221.640**	402.756**	0.023	38.287	0.142**	1.246*	14.256**	4.611**	98.144**	0.489**
2.	SCA	35	5.854 **	7.401 **	20.434**	485.372**	356.165**	0.048*	74.089**	0.818**	2.116**	29.186**	7.212**	201.313**	0.711**
3.	Error $\hat{\sigma}^2 g$	70	1.105	1.316	1.348	85.721	38.701	0.019	48.511	0.018	0.978	0.887	0.802	8.811	0.014
4.			0.243	0.157	2.103	18.102	28.340	0.001	1.210	0.070	0.980	0.875	0.278	6.920	0.035
5.	$\hat{\sigma}^2 s$		4.543	5.663	6.257	314.160	301.354	0.090	18.002	0.880	2.001	24.179	6.183	231.665	0.311
6.	$\hat{\sigma}^2 A$		0.486	0.314	4.116	36.204	56.680	0.002	2.420	0.140	1.960	1.750	0.556	13.840	0.070
7.	$\hat{\sigma}^2 D$		4.543	5.663	6.257	314.160	301.354	0.09	18.002	0.880	2.001	24.179	6.183	231.665	0.311
8.	$\sigma^{\wedge 2}A/\sigma^{\wedge 2}D$		0.106	0.055	0.657	0.115	0.188	0.022	0.134	0.159	0.970	0.070	0.089	0.059	0.225
9.	$2\sigma^{\wedge 2}g/2\sigma^{\wedge 2}g+\sigma^{\wedge 2}s$		0.097	0.059	0.387	0.075	0.157	0.118	0.070	0.017	0.082	0.069	0.078	0.046	0.160

*, ** Significant at 5 and 1 percent level;DTT = days to 50% tasselling, DTS = days to 50% silking, DTM = days to maturity, PH = plant height, CH = cob height, CPP = number of cobs plant^{-1}, CL = cob length, CD = cob diameter, KRPC = kernel rows cob^{-1}, KPR = number of kernels row^{-1}, GW = 100 grain weight, YPP = grain yield plant^{-1} and GPC = grain protein content (%)

2016). The high positive value of GCA effect of these parents indicates that their contribution in transferring those traits to their hybrids is high. This is in accordance with the findings of Huang *et al.* (2015), who found that parents with higher GCA in inbred lines of rice can produce hybrids with higher yield, which indicates that combining ability can be used to predict heterosis in yield traits further, and can be combined with other parameters to select excellent parents in a hybrid breeding system.

The GCA effects of parental lines found for different traits are presented in Table 3. A significant GCA effect in the negative but desired direction for DTT was shown by parents' QPM13 (-0.712), QPM14 (-0.419) and QPM50 (-0.340). Only one parent, QPM13, exhibited a significantly negative but desirable GCA effect for all three maturity traits, indicating its early maturity. Therefore, these lines are expected to contribute to developing early-maturing/short-duration hybrids adaptable to targeted temperate hill ecologies.

Similarly, negative and desirable results for DTS were observed for QPM13 (-0.416), QPM21 (-0.442) and QPM50 (-0.510), and for DTM, QPM13 (-1.500), QPM14 (-1.879) and QPM49 (-0.413) were observed. It was observed from the GCA effects that none of the parents individually showed good general combiner for all the characters. Various studies have reported positive and negative GCA effects in maize (Fan *et al*., 2008; Mutimaamda *et al.,* 2020; Matongera *et al*., 2023). The high GCA effect in the negative direction indicates that they were good general combiners for earliness.

Crosses that showed longer days to anthesis and silking could be considered late maturing types. Conversely, crosses with shorter days to flowering could be regarded as early maturing types. Crosses exhibiting early anthesis and silking are desirable, especially in moisture-stress environments, since early-type crosses can escape terminal moisture stresses during the growth stages (Bänziger *et al*., 2006).

In general, crosses that exhibited short anthesis-silking intervals indicate that the cross had short gaps between anthesis and silking days and it is a desired character for good seed setting since these crosses may show anthesis-silking intervals within an acceptable range. If the gap between days of anthesis and silking is large, the viability of pollen would be minimized and abnormal fertilization might occur, or fertilization may not happen. In general, shorter ASI improves pollen-silk synchronization, a major trait that is affected under moisture-stress areas. The need for a shorter ASI to achieve high grain yield has been observed by Anderson *et al*. (2004), where the potential number of florets that could become grains was limited by the receptivity of the silks. In this regard, ASI has been widely used in the indirect selection of higher grain yield under drought conditions (Bänziger *et al*., 2006). Days to anthesis and anthesis-silking interval follow the same trends as days to silking, in which parents with GCA positive and significant GCA effects are considered poor general combiners while those with negative and significant GCA effects are considered good general combiners in breeding for the early type of variety for the short rainy season.

Additionally, three inbred lines, viz., QPM13 (-6.121), QPM14 (-3.100) and QPM49 (-3.192) for PH and QPM13 (-7.342), QPM14 (-4.506) and QPM49 (-2.310) for CH, concerning GCA effects were recorded, which reflects moderate to high GCA effects in the negative direction for PH and CH (Table 3). A negative GCA for both of these traits is desirable, as such parental lines with negative and significant GCA effects could contribute alleles for short-stature plant types and thus impart lodging resistance, which is a favorable trait, especially in hill ecologies where the wind speed is always high. According to Matin *et al*. (2016) earliness is generally associated with days to silk and the shorter plants with low ear height are associated with resistance to lodging.

However, for individual yield-attributing traits, QPM13 (4.571), QPM14 (2.329) and QPM50 (3.143) had significant GCA effects on CL; QPM14 (0.480) and VQL50 (0.351) had significant effects on KRPC; QPM13 (1.589) and QPM49 (0.938) had the greatest effect on KPR; QPM13 (0.750) and QPM49 (0.430) had the greatest effect on GW; and QPM13 (4.118), QPM49 (2.159) and QPM50 (1.454) had the greatest effect on YPP. These lines could be used in the development of high-yielding hybrids. Additionally, QPM13 (0.117), QPM14 (0.134) and QPM21 (0.96) had significant GCA effects on GPC. Our findings were in line with the results of Srivastava and Singh (2003), Badu *et al*. (2016), and Ünay *et al*. (2016), who also reported that maize inbred lines with high positive GCA values for yield-attributing traits could result in greater yields of hybrids. Nevertheless, good performance of the parental line per se is not an authentication factor for producing better hybrids via hybridization (Chigeza *et al*., 2014).

Specific combining ability (SCA) effects

SCA effects were found for the tested traits during the present study, as presented in Table 4. Most of the crosses depicted varied but had significant SCA effects for most traits. However, no cross-combination demonstrated a significant SCA effect for any of the traits in a favorable direction. Most crosses showed a significant SCA effect for different maturity traits in the desired negative direction. Among these, three cross combinations, viz., QPM21 × VQL1 (-1.95), QPM 14 × VQL 1 (-1.968), and QPM21 × QPM 50 (-2.125), had the highest SCA effect in the desired direction. However, QPM 49 × QPM 50 (-2.770) had the most significant SCA effect in the desirable negative direction for days to maturity.

Additionally, seven cross combinations for PH, viz., QPM 14 × QPM 21 (-7.186), QPM 14 × QPM 49 (-9.165), QPM 14 × QPM 50 (-10.932), QPM 20 × QPM 21 (-18.875), QPM 21 × VQL 1 (-10.165), QPM 21 × VQL 17 (-7.101) and QPM 50 × VQL 17 (-8.093), and seven cross combinations for CH viz., QPM 13 × VQL 17 (-11.114), QPM 14 × QPM 21(-7.150), QPM 14 × QPM 49 (-7.129), QPM 20 × VQL 1 (-7.150), QPM 21 × VQL 1 (-13.393), QPM 49 × VQL 1 (-6.821) and QPM 50 × VQL 17 (-8.214), were identified as having a negatively significant but desirable SCA effect. The results revealed that a good GCA effect generally results in a good SCA effect in crosses (Fasahat *et al*., 2016). SCA effects for plant height, which is undesirable as tallness contributes to susceptibility to lodging. As mentioned above, the present results of cross combinations for SCA showed negative and highly significant effects, indicating the better specific combining ability of these crosses for plant height, which is desirable as short-statured plants are mostly lodging tolerant.

Estimates of significant positive SCA effects for cob length, cob diameter and TSW are more frequently associated with significant estimates of SCA effect of kernel yield. Amiruzzaman *et al.* (2010) reported a positive relationship between SCA effect of kernel yield and yield contributory characters. For grain yield estimates due to SCA effect were observed in both, negative and positive directions. The higher estimates of SCA effects in the present study is deviation from the prediction based on their parental performance. The crosses with significant and positive estimates of SCA effect are very useful for QPM maize hybrid development programme. The results of the current study are in agreement with the findings of Abrha *et al*. (2013), who reported high and significant SCA effects in most of the crosses they studied for grain yield in maize. Singh *et al*. (2013) reported that cross-combining any parental lines may create hybrid vigour over the parents, which might be due to dominant, over dominant, or epistatic type of gene action. Therefore, the crosses could be selected for their specific combining ability for grain yield improvement. When high-yielding specific combinations are desired, especially in hybrid maize development, SCA effects could help select parental material for hybridization.

Furthermore, the comparative GCA:SCA data indicated that those crosses with a high SCA effect mostly had at least one parent with a good GCA effect (high × low) or, in other cases, both parents with a good GCA effect (high × high). However, there were few high SCA cross combinations where both parents reflected a nonsignificant/low GCA effect (low × low). The high SCA effect depicted by cross combinations in this study can be attributed to additive × additive gene action when both

Table 3. GCA effects for morphological, maturity, yield and quality traits found during the present study in maize (*Zea mays* L.) in hillytemperate region of Kashmir

Lines	DTT	DTS	DTM	PH (cm)	CH (cm)	CPP	CL (cm)	CD (cm)	KRPC	KPR	GW(g)	YPP (g)	GPC (%)
QPM13	-0.712**	-0.416*	-1.500**	-6.121**	-7.342**	0.013	4.571**	-0.003	0.104	1.589**	0.750**	4.118**	0.117**
QPM14	-0.419*	-0.189	-1.879**	-3.100*	-4.506*	0.043*	2.329*	-0.012	0.480**	-0.043	-0.423**	-1.782*	0.134**
QPM20	0.102	0.105	-0.520	3.108*	1.001	-0.003	-2.330*	-0.97	-0.118	-0.325*	-0.700	-1.157*	0.035
QPM21	-0.198	-0.442*	0.301	0.450	1.100	-1.006*	-0.145	-0.116	0.035	0.218	0.152	-0.782	0.96*
QPM49	-0.980	-0.003	-0.413*	-3.192*	-2.310*	0.018	-2.143*	-0.75	0.110	0.938*	0.430**	2.159**	-0.157**
QPM50	-0.340*	-0.510*	-0.250	-1.087	-1.427	1.070*	3.143**	0.67	0.351*	-0.246	-0.015	1.454*	-0.660*
VQL1	-0.030	-0.520	0.415*	3.744*	3.951*	0.050*	-1.026	0.91	0.218	-0.546**	-0.223*	-1.415*	-0.153**
VQL17	-0.227	-0.311	-0.180	-0.037	-0.187	-0.025	-1.120	0.011	-0.343*	-0.632**	-0.028	-1.782*	0.036
SE±(gi)	0.129	0.201	0.185	1.304	1.459	0.021	1.107	0.023	0.150	0.116	0.131	0.515	0.013
SE±(gi-gj)	0.224	0.243	0.371	1.981	1.345	0.032	2.657	0.033	0.223	0.218	0.196	1.106	0.035

*, ** significant at 5 and 1% level; DTT = days to 50% tasselling, DTS = days to 50% silking, DTM = days to maturity, PH = plant height, CH = cob height, CPP = number of cobs plant^{-1}, CL = cob length, CD = cob diameter, KRPC = kernel rows cob^{-1}, KPR = number of kernels row^{-1}, GW = 100 grain weight, YPP = grain yield plant^{-1} and GPC = grain protein content (%)

Table 4. SCA of crosses on morphological, maturity, yield and quality characteristics found during the present study in maize (*Zea mays* L.) in temperate hilly region of Kashmir

Cross	DTT	DTS	DTM	PH (cm)	CH (cm)	CPP	CL (cm)	CD (cm)	KRPC	KPR	GW (g)	YPP (g)	GPC (%)
QPM 13 × QPM 14	-1.790*	-1.204*	-0.415	24.321**	11.364**	-0.71	1.035	0.218*	1.440**	3.504**	1.446**	3.895*	-0.201**
QPM 13 × QPM 20	-1.181*	-1.090*	-2.006*	7.478*	12.193**	-0.98	0.206	0.202**	1.075	0.02	1.001*	5.842**	0.293**
QPM 13 × QPM 21	0.035	-0.271	-1.861*	10.107**	7.129*	0.033	1.249	0.219*	-2.011**	1.117	-1.172*	0.145	-0.321**
QPM 13 × QPM 49	-1.230*	-1.13	-1.197	7.178	1.379	0.129*	2.159	0.417**	-1.014	1.447**	0.194	1.198	-0.061
QPM 13 × QPM 50	-0.88	-0.314	2.146*	9.164	4.146	0.243**	1.259	0.146*	0.319	1.361**	1.447**	12.875**	-0.475**
QPM 13 × VQL 1	-0.435	-0.313	1.218	3.162	1.407	-2.674**	1.032	0.326**	1.232*	1.961**	1.190**	5.842**	0.321**
QPM 13 × VQL 17	2.060**	1.351	1.960*	-1.016	-11.114*	-0.62	3.106*	0.85	3.146**	3.017**	1.280**	6.395**	0.331**
QPM 14 × QPM 20	-0.047	-0.25	-0.348	-1.103	1.693	0.65	0.356	1.020**	1.625*	0.34	2.271**	10.538**	1.011**
QPM 14 × QPM 21	-0.315	-0.401	-1.327*	-7.186	-7.150*	-0.022	-4.251*	0.404**	-1.002	-0.118	1.069*	3.449*	0.07
QPM 14 × QPM 49	-0.74	-0.78	1.016	-9.165**	-7.129*	-0.148	-0.69	0.317**	0.112	-3.275**	-0.634	-3.158	0.136
QPM 14 × QPM 50	-1.09	-0.215	1.332**	-10.932**	-3.627	-0.013	1.127	0.217**	0.319	3.047**	1.060*	3.445**	0.119**
QPM 14 × VQL 1	-1.904**	-2.400**	-1.968**	3.415	7.157	0.201*	-0.107	0.212	-1.44	1.182*	1.429**	3.592**	0.461*
QPM 14 × VQL 17	-0.432	-1.98	-1.682	1.004	2.293	-0.158	3.156*	-0.442**	0.175	4.175**	1.374**	8.645**	-0.254
QPM 20 × QPM 21	1.818*	2.014**	3.012**	-18.875**	-6.257	-0.102	1.556	-0.035	2.168*	2.125**	-0.209	3.515**	-0.454
QPM 20 × QPM 49	1.189	1.021	1.015	16.181**	8.750**	0.122	5.016*	-0.126	0.315	-2.160*	0.369	0.127	-0.127
QPM 20 × QPM 50	1.239	1.221	1.216	15.199**	7.271*	0.275*	-1.101	0.564**	2.118**	3.760**	1.012*	5.842**	-0.033
QPM 20 × VQL 1	1.01	1.886	1.531	-2.979	-7.150*	-0.001	2.163	-0.609**	1.932**	5.125**	0.626	3.145	-0.89
QPM 20 × VQL17	1.005	0.389	0.31	2.149	-1.443	-0.76	-0.207	-0.542**	2.120**	1.918*	1.292**	6.288**	0.216**
QPM 21 × QPM 49	-0.98	-0.157	-1.31	1.471	-5.114	-0.182*	-1.994	0.312*	-1.197*	2.961**	-0.759	-3.551*	0.209**
QPM21 × QPM 50	-2.147**	-1.979**	-2.125*	7.192	11.436**	0.041	3.135	-0.901**	-0.982	-2.896**	2.037**	10.592**	-0.196**
QPM 21 × VQL 1	-2.182**	-2.450**	-1.95	-10.165*	-13.393**	0.216*	1.85	0.7	1.105	4.125**	1.356**	3.645*	-0.025
QPM 21 × VQL 17	-1.094	-1.01	-2.654	-7.101*	1.421	0.165*	3.177	0.181**	1.996**	1.981**	1.603**	10.842**	-0.107
QPM 49 × QPM 50	-0.204	-0.326	-2.770**	-1.808	0.271	-0.79	0.373	0.107	-1.74	2.861**	0.744	6.931**	-0.327**
QPM 49 × VQL 1	-1.842*	-1.279*	-2.027**	3.178	-6.821**	-0.035	1.377	0.453**	-0.941	0.615	1.052*	3.926*	-0.401**
QPM 49 × VQL 17	-1.322	-1.079	-1.815**	8.657**	4.1	0.208*	-0.38	0.405**	0.312	-1.925*	0.965*	4.538**	1.043**
QPM 50 × VQL 1	-0.7	0.136	1.718	9.478**	6.879*	0.700	1.225	0.215**	-0.314	3.981**	0.695	3.408*	1.000**
QPM 50 × VQL 17	1.433*	1.034	2.139**	-8.093**	-8.214*	0.027	0.265	0.254**	-0.325	3.154**	-0.329	2.765*	1.113**
VQL 1 × VQL 17	-1.240*	1.183	1.51	-7.272*	0.103	0.198*	-0.373	0.021	2.718**	1.917	1.844**	9.895**	0.042
S.E± (Sij)	1.009	1.004	1.108	3.501	4.071	0.78	2.184	0.314	1.093	1.053	0.513	2.943	0.53
S.E ± (Sij-Sik)	1.234	1.35	1.035	8.896	9.904	0.131	5.186	0.135	1.598	1.237	1.013	3.016	0.98

*, ** significant at 5 and 1 percent level;DTT = days to 50% tasselling, DTS = days to 50% silking, DTM = days to maturity, PH = plant height, CH = cob height, CPP = number of cobs plant^{-1}, CL = cob length, CD = cob diameter, KRPC = kernel rows cob^{-1}, KPR = number of kernels row^{-1}, GW = 100 grain weight, YPP = grain yield plant^{-1} and GPC = grain protein content (%).

parents have good GCA effects (good GCA × good GCA). However, the high SCA affected by good × poor general combiner parents can be ascribed to the additive effect of the parent with a good GCA × epistatic effect of the poor GCA parent, thus producing the non-fixable-overdominance effect. Some cross combinations that resulted from parental lines with nonsignificant GCA effects (low × low) may be due to nonallelic (dominant × dominant) gene interactions. In general, the gca effects of the parents were reflected in the sca effects of the crosses in most of the studied traits. This is corroborated by the results of Hussain *et al.* (2003). Besides, good general combining parent do not show high sca effects in their hybrid combinations. On the contrary, Talukder *et al*. (2016) obtained high estimates of SCA from high GCA parents in their study.

Conclusion

The present investigation revealed highly significant differences among parents of Quality Protein Maize (*Zea mays* L.) and their crosses for all traits, indicating the diverse nature of the experimental materials used in the study. None of the cross combinations in the experiment exhibited significant SCA effects for any of the traits in a desirable direction. However, several cross-combinations demonstrated significant SCA effects in desirable directions for both maturity and yield traits. The earliest tasselling, silking, days to mature, highest yield and protein content were recorded best for QPM49 × VQL1, QPM 13 × QPM14, QPM21 × VQL17, QPM13 × QPM50 and QPM50 × VQL17, respectively, in terms of specific combining ability. These promising crosses can serve as viable sources of material for future breeding programs for early-maturing hybrids and high-yield and high-protein-content QPM varieties in temperate regions.

Conflict of interest

The authors declare that they have no conflict of interest.

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