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Research Article

Elucidating the genetic potential of hybrids derived from elite maize (*Zea mays* L.) inbreds for economic traits under North-Western Himalayan condition

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Abstract

This study was conducted to evaluate the combining ability of newly acquired maize inbred lines over the environments. Twenty-eight crosses developed by crossing eight elite inbreds in a half-diallel mating design were evaluated during *khari*, 2019 for 12 agro-morphological traits in RBD with two replications at two different environments reflecting diverse agro-climatic and ecological conditions of North-Western Himalayas (SAREC, Kangra and HAREC, Bajaura). Analysis of variance showed that there was sufficient amount of genetic variability in the material studied. In accordance to Bartlett's test, error variance was homogeneous only for six traits. Estimates of σ^2 SCA were higher as compared to σ^2 GCA both within and across environments for all the traits, except days to 75 per cent brown husk at Kangra, representing prevalence of non-additive gene action for these traits. The inbred line B73 at Bajaura, and LM14 at Kangra were found to be good general combiner for most traits. The inbreds with good GCA can be used as potential parents for the development of high yielding single cross maize hybrids. The hybrid combinations namely, B73 \times BAJIM1811 and BAJIM1522 \times BAJIM1811 were identified as potentially superior ones at Kangra and Bajaura environments. The identified promising hybrids need further assessment for their superiority in performance across the locations and over years.

Keywords: General combining ability, specific combining ability, gene action and maize.

INTRODUCTION

Maize (*Zea mays* L.), originated from Central America, is the world's leading crop widely cultivated as a cereal grain. It is a member of *Poaceae* family, *Maydeae* tribe and one of the oldest cultivated crops. Choosing the right parent/inbred is a prerequisite for hybrid development in corn. Combining ability analysis is of particular importance in cross pollinated plants such as maize as it helps to identify potential parents that can be used to produce hybrids/synthetics. The nature and magnitude of gene action is an important factor in developing an effective breeding programme that can be interpreted through combining ability analysis. Due to genotype \times environment interactions, the information obtained under

one environment and/or with one set of genetic material might not be applicable to another because the estimates derived from one environment may be biased and would not present a true picture of genetic nature and the breeding value of population. Since, the quantitative traits are influenced by the environment, a study among different environments is likely to yield genotype \times environment interactions to accurately assess genetic variation. Assessment of genotype \times environment interaction is also critical to determine an ideal breeding strategy for releasing genotypes with stability to target environments. In any hybridization programme, identifying the best combination parental genotypes is the most critical

challenge for a plant breeder. Combining ability analysis is an important tool to identify superior parents and best specific hybrid combinations for yield and related traits. In North- Western Himalayas regions, performance of maize hybrids and varieties vary location wise and need to develop the stable and high yield hybrids and varieties, which can be obtained by assessing the genetic potential of inbred lines. The present study was carried out keeping in view the above-mentioned reasons.

MATERIALS AND METHODS

The experimental material consisted hybrids generated by crossing eight inbreds viz., P₁ (B73), P₂ (BAJIM1522), P₃ (BAJIM2010), P₄ (BAJIM1811), P₅ (LM16), P₆ (LM14), P₇ (40318) and P₈ (CML141). The inbreds were crossed during *kharif*, 2019 in a 8 × 8 diallel mating system without reciprocals. The crosses along with parents were evaluated in a Randomized Complete Block Design (RBD) with two replications in a plot size of 3.0 × 1.2m (3.6 m²) with a spacing of 60 × 20 cm, along with four checks (Palam Sankar Makka-2, Vivek Hybrid-45, Bio-9544 and DKC 7074) during *kharif*, 2020. The experiment was conducted at two environments (SAREC, Kangra and HAREC, Bajaura) representing diverse agro-climatic

and ecological conditions. SAREC, Kangra (E₁) is situated at 32°09'N latitude and 76°22'E longitude at 700 m above mean sea level. HAREC, Bajaura (E₂) is located at 32°20'N latitude and 77°E longitude and 1090 m above mean sea level. Observations were recorded on 12 agromorphological traits and combining ability analysis was performed for individual and pooled over environment to evaluate the general and specific combining ability effects. The data obtained from F₁ population and parents was evaluated for combining ability using Griffing's (1956) experimental method II, model I as it was most appropriate for the material under study. Combining ability analysis for pooled environments was carried out by procedure as per suggested by Singh (1973) using WINDOSTAT software version 9.2.

RESULTS AND DISCUSSION

Analysis of variance: Significant differences among parents and their crosses indicated inherent genetic differences among genotypes for traits studied. Analysis of variance showed significant differences indicating genetic variations among genotypes for all the traits except shelling (%) in E₁ (Table 1). Similar results were also reported by Kumar *et al.* (2017) for grain yield, 1000 grain

Table 1. Analysis of variance for different traits across the environments

| Traits | d.f. | Env. | Rep | Gen | Parents | Crosses | P vs C | Error | Bartlett |
|-------------------------------|------|----------------|--------|----------|----------|----------|-----------|-------|----------|
| | | | 1 | 35 | 7 | 27 | 1 | 35 | 1 |
| Days to 50% pollen shedding | | E ₁ | 10.12 | 15.61* | 5.96* | 7.33* | 306.68* | 1.27 | 0.01 |
| | | E ₂ | 1.68 | 35.86* | 2.29 | 21.31* | 663.81* | 1.22 | |
| Days to 50% silking | | E ₁ | 6.12 | 21.27* | 6.28* | 8.90* | 460.08* | 1.52 | 0.005 |
| | | E ₂ | 2.00 | 39.61* | 1.92 | 21.94* | 780.52* | 1.49 | |
| Days to 75% brown husk | | E ₁ | 0.12 | 3.75* | 5.63* | 3.35* | 1.36 | 0.84 | 0.13 |
| | | E ₂ | 6.72 | 4.37* | 4.29* | 2.51* | 55.25* | 0.95 | |
| Plant height | | E ₁ | 34.72 | 695.48* | 529.06* | 77.09* | 18557.17* | 6.60 | 15.76* |
| | | E ₂ | 17.01 | 879.48* | 753.41* | 313.94* | 17031.51* | 26.90 | |
| Ear height | | E ₁ | 156.06 | 2607.57* | 1953.57* | 300.83* | 69467.68* | 20.63 | 14.07* |
| | | E ₂ | 85.37 | 3263.73* | 2732.29* | 1148.20* | 64103.05* | 77.30 | |
| Number of kernel rows per ear | | E ₁ | 0.93 | 11.14* | 11.21* | 1.75 | 264.14* | 1.18 | 25.07* |
| | | E ₂ | 0.28 | 4.82* | 1.03* | 4.44* | 41.53* | 0.19 | |
| Number of kernels per row | | E ₁ | 3.17 | 169.13* | 40.60* | 13.49 | 5271.31* | 7.56 | 15.40* |
| | | E ₂ | 2.88 | 74.09* | 9.98* | 46.29* | 1273.50* | 1.89 | |
| Ear length | | E ₁ | 6.08 | 25.82* | 6.24* | 2.71 | 786.70* | 2.03 | 14.22* |
| | | E ₂ | 0.48 | 10.82* | 3.35* | 7.13* | 162.88* | 0.54 | |
| Ear circumference | | E ₁ | 2.45 | 8.87* | 3.38* | 1.06* | 258.12* | 0.36 | 1.68 |
| | | E ₂ | 1.34 | 3.65* | 2.38* | 2.60* | 40.74* | 0.56 | |
| 1000-grain weight | | E ₁ | 924.50 | 3810.19* | 4573.71* | 1547.62* | 59555.06* | 73.44 | 0.30 |
| | | E ₂ | 3.12 | 3815.01* | 5038.99* | 1612.22* | 54722.55* | 61.01 | |
| Shelling | | E ₁ | 9.62 | 14.91 | 9.96 | 14.77 | 53.48* | 10.21 | 14.53* |
| | | E ₂ | 7.39 | 15.72* | 27.69* | 9.40* | 102.40* | 2.66 | |
| Grain Yield | | E ₁ | 17.78 | 1035.40* | 27.61* | 259.06* | 29051.27* | 5.72 | 0.20 |
| | | E ₂ | 0.16 | 2070.01* | 9.80 | 467.77* | 59752.00* | 6.66 | |

* Significant at 5% probability level, E₁ = Kangra, E₂ = Bajaura

weight, number of kernels per row, ear circumference, days to 50% anthesis, days to 50% silking, ear height, ear length and plant height. El-Hosary *et al.* (2018) reported insignificant differences for shelling (%). By further partitioning of genotypic variance, significant mean square due to parents were observed for all traits except shelling (%) in E_1 ; days to 50 per cent pollen shedding, days to 50 per cent silking and grain yield in E_2 . Mean squares due to crosses showed significance for most traits except number of kernel rows per ear, number of kernels per row, ear length and shelling (%) in E_1 , whereas, parents vs. crosses were significant for all traits, except days to 75 per cent brown husk in E_1 . These results were in agreement with the reports of Lal and Kumar (2012) for days to 50% pollen shedding, days to 50% silking, days to 75% brown husk, ear height, plant height and grain yield/plant. The Bartlett's test revealed that error variance was homogeneous for days to 50 per cent pollen shedding, days to 50 per cent silking, days to 75 per cent brown husk, ear circumference, 1000-grain weight and grain yield and hence pooled analysis was performed for these traits only. The pooled analysis elucidated significant differences between the environments for all traits, except days to 50 per cent silking. Significant mean squares due to genotypes, parents, crosses, parents vs crosses and genotype \times environment interaction were observed for all the pooled traits, representing environmental influence on the expression of these traits (Table 2). Similar results were reported by Chandel *et al.* (2014) and Kumar *et al.* (2017) for genotypes and GEI for grain yield and 1000-grain weight.

Combining ability ANOVA and estimates of genetic components: ANOVA for combining ability unveiled significant mean sum of squares due to GCA and SCA for all traits, except mean sum of squares due to GCA for ear length and SCA for shelling (%) in E_1 (Table 3).

This revealed the presence of additive as well as non-additive gene action for different traits. Significant GCA and SCA mean square were previously observed for days to 50% pollen shedding, days to 50% silking, plant height, ear height, ear length, number of kernels per row and grain yield by Rajesh *et al.* (2018) and Kumar *et al.* (2019). In pooled analysis, significant mean squares due to environment, GCA, SCA, GCA \times environment and SCA \times environment were observed for all traits, except for days to 50 per cent silking in environment and GCA \times environment for days to 75 per cent brown husk (Table 4). This revealed that expression of the traits is strongly influenced by environmental effect and its interaction with combining ability effects. Non-significant GCA \times environment interaction for days to 75 per cent brown husk revealed that the trends in variation of GCA effects were similar across the environments for this trait (Bello and Olaoye, 2009). Mean sum of squares for both GCA \times environment and SCA \times environment were significant for days to 50 per cent pollen shedding, days to 50 per cent silking, ear circumference, 1000-grain weight and grain yield suggesting that both additive and non-additive genetic components were equally influenced by environments. The magnitude of interaction observed in case of GCA was higher than that of SCA for days to 50 per cent pollen shedding, days to 50 per cent silking, days to 75 per cent brown husk and 1000-grain weight suggesting that additive component was less stable over environments than dominance components. However, the magnitudes of GCA \times environment mean squares were invariably lesser than GCA mean squares for most of the traits except grain yield suggesting that the interaction effects may be of minor relevance in comparison to main effects. Present findings suggested that environment must be taken into consideration while evaluating genotypes for different traits particularly grain yield. Significant differences among environment,

Table 2. Pooled analysis of variance for heterogeneous traits over the environments

| Traits | d.f. | Days to 50% pollen shedding | Days to 50% silking | Days to 75% brown husk | Ear circumference | 1000-grain weight | Grain yield |
|-------------------------------|------|-----------------------------|---------------------|------------------------|-------------------|-------------------|-------------|
| Env | 1 | 23.36* | 3.67 | 458.67* | 422.30* | 1870.56* | 22825.17* |
| Rep | 2 | 5.90* | 4.06 | 3.42* | 189.44* | 463.81* | 8.97 |
| Genotype | 35 | 47.10* | 55.51* | 6.25* | 1029.08* | 6611.16* | 2884.86* |
| Parents | 7 | 6.91* | 5.20* | 7.50* | 331.94* | 9131.74* | 27.31* |
| Crosses | 27 | 24.58* | 25.44* | 4.79* | 314.72* | 1971.92* | 544.94* |
| P vs C | 1 | 936.45* | 1219.56* | 36.97* | 25196.91* | 114226.50* | 86065.43* |
| G \times E | 35 | 4.37* | 5.37* | 1.87* | 223.13* | 1014.05* | 220.56* |
| Parent \times E | 7 | 1.34 | 3.00 | 2.42* | 244.54* | 480.10* | 10.09 |
| Crosses \times E | 27 | 4.06* | 5.41* | 1.07 | 52.20 | 1187.92* | 181.89* |
| Parents vs Crosses \times E | 1 | 34.05* | 21.05* | 19.643* | 4688.46* | 51.11 | 2737.84* |
| Pooled Error | 70 | 1.25 | 1.50 | 0.89 | 45.78 | 67.23 | 6.19 |

* Significant at 5% probability level

Table 3. Analysis of variance for combining ability across the environments

| Traits | d.f. | Env. | Source | | |
|-------------------------------|------|----------------|----------|----------|-------|
| | | | GCA | SCA | ERROR |
| | | | 7 | 28 | 35 |
| Days to 50% pollen shedding | | E ₁ | 13.28* | 6.44* | 0.63 |
| | | E ₂ | 22.01* | 16.91* | 0.61 |
| Days to 50% silking | | E ₁ | 14.74* | 9.61* | 0.76 |
| | | E ₂ | 19.24* | 19.95* | 0.74 |
| Days to 75% brown husk | | E ₁ | 5.63* | 0.94* | 0.42 |
| | | E ₂ | 3.34* | 1.90* | 0.48 |
| Plant height | | E ₁ | 1011.69* | 1376.81* | 10.32 |
| | | E ₂ | 2649.08* | 1377.57* | 38.64 |
| Ear height | | E ₁ | 263.58* | 368.78* | 3.3 |
| | | E ₂ | 727.96* | 367.69* | 13.45 |
| Number of kernel rows per ear | | E ₁ | 3.30* | 6.14* | 0.59 |
| | | E ₂ | 4.30* | 1.93* | 0.1 |
| Number of kernels per row | | E ₁ | 14.47* | 102.09* | 3.78 |
| | | E ₂ | 42.26* | 35.74* | 0.95 |
| Ear length | | E ₁ | 1.39 | 15.79* | 1.02 |
| | | E ₂ | 3.65* | 5.85* | 0.27 |
| Ear circumference | | E ₁ | 0.74* | 5.36* | 0.18 |
| | | E ₂ | 2.84* | 1.57* | 0.28 |
| 1000-grain weight | | E ₁ | 3310.54* | 1553.74* | 36.72 |
| | | E ₂ | 2421.27* | 1779.07* | 30.5 |
| Shelling | | E ₁ | 13.36* | 5.98 | 5.11 |
| | | E ₂ | 10.62* | 7.17* | 1.33 |
| Grain Yield | | E ₁ | 54.67* | 633.46* | 2.86 |
| | | E ₂ | 244.80* | 1232.56* | 3.33 |

* Significant at 5% probability level, E₁ = Kangra, E₂ = Bajaura

Table 4. Pooled analysis of variance for combining ability for different traits over the environments

| Traits | d.f. | Source of variation | | | | | Pooled error |
|-----------------------------|------|---------------------|----------|-----------|-----------|-----------|--------------|
| | | GCA | SCA | ENV | GCA × ENV | SCA × ENV | |
| | | 7 | 28 | 1 | 7 | 28 | |
| Days to 50% pollen shedding | | 31.94* | 21.45* | 11.67* | 3.35* | 1.90* | 0.62 |
| Days to 50% silking | | 30.41* | 27.08* | 1.83 | 3.58* | 2.46* | 0.75 |
| Days to 75% brown husk | | 8.26* | 1.84* | 229.33* | 0.7 | 0.99* | 0.45 |
| Ear circumference | | 2.70* | 5.76* | 2.11* | 0.89* | 1.17* | 0.23 |
| 1000-grain weight | | 5157.06* | 2842.72* | 935.22* | 574.72* | 490.09* | 33.61 |
| Grain Yield | | 134.17* | 1769.49* | 11412.56* | 165.29* | 96.53* | 3.10 |

* Significant at 5% probability level

GCA × environment and SCA × environment among most of the traits were observed earlier by Chandel and Mankotia (2014) and Kumar *et al.* (2017) for days to 50 per cent silking, ear girth and grain yield.

Estimates of genetic components viz., σ^2 GCA, σ^2 SCA

and σ^2 GCA/ σ^2 SCA for different traits across E₁, E₂ as well as for pooled over environment have been presented in **Table 5**. σ^2 SCA were higher in comparison to σ^2 GCA in both the environments and in pooled environment except for days to 75 per cent brown husk in E₁. This represented higher influence of non-additive genetic effects than

Table 5. Estimates of genetic components for different traits in maize across the environments and pooled over environment

| Trait | Env | Genetic Components | | |
|-----------------------------|----------------|--------------------|------------------|---------------------------------|
| | | σ^2_{gca} | σ^2_{sca} | $\sigma^2_{gca}/\sigma^2_{sca}$ |
| Days to 50% pollen shedding | E ₁ | 1.26 | 5.81 | 0.22 |
| | E ₂ | 2.14 | 16.30 | 0.13 |
| | P | 1.54 | 10.15 | 0.15 |
| Days to 50% silking | E ₁ | 1.40 | 8.85 | 0.16 |
| | E ₂ | 1.85 | 19.20 | 0.10 |
| | P | 1.45 | 12.85 | 0.11 |
| Days to 75% brown husk | E ₁ | 0.52 | 0.52 | 1.01 |
| | E ₂ | 0.29 | 1.42 | 0.20 |
| | P | 0.38 | 0.62 | 0.62 |
| Ear circumference | E ₁ | 0.06 | 5.18 | 0.01 |
| | E ₂ | 0.26 | 1.29 | 0.20 |
| | P | 0.11 | 2.62 | 0.04 |
| 1000-grain weight | E ₁ | 327.38 | 1517.02 | 0.22 |
| | E ₂ | 239.08 | 1748.56 | 0.14 |
| | P | 248.28 | 1325.60 | 0.19 |
| Grain Yield | E ₁ | 5.18 | 630.60 | 0.01 |
| | E ₂ | 24.15 | 1229.22 | 0.02 |
| | P | 4.77 | 865.33 | 0.01 |

E₁ = Kangra, E₂ = Bajaura, P = Pooled

additive genetic effects in the expression of various traits in hybrids. The ratio of variance of GCA to SCA was less than unity hence non-additive gene action played key role in the inheritance of these traits. GCA/SCA ratio was equal to unity for days to 75 per cent brown husk at E₁ revealing the significance of additive as well as non-additive gene actions. Prevalence of non-additive gene action was previously reported for days to 50% pollen shedding, days to 50% silking, days to 75% maturity, ear circumference, 1000 grain weight and grain yield by Chandel and Mankotia (2014); Darshan and Marker (2019) and Sharma *et al.* (2019).

Combining ability effects: Estimates of all parental GCA effects and significant SCA effects for hybrids are represented in graphical form in **Fig. 1 and 2**. In case of days to 50 per cent pollen shedding, GCA effects ranged from -1.59 (P₆) to 2.01 (P₈) in E₁; -2.11 (P₁) to 2.69 (P₈) in E₂ and -1.67 (P₁) to 2.35 (P₈) in pooled environment. From the results, it was observed that parent P₆, P₁ in E₁; P₁, P₅, P₆ in E₂ and P₁, P₆, P₅ in pooled environment, exhibited significant negative values for GCA effects. Negative GCA effects were observed for the above trait by Chandel *et al.* (2019) who suggested that these parents can be good sources of genes for earliness. Estimates of SCA effects elucidated that out of the 28 crosses, 9 crosses in E₁; 16 crosses in E₂ and 15 crosses in pooled environment showed significant negative SCA effects. Cross P₁ × P₃ followed by P₁ × P₅ and P₂ × P₄ had highest significant negative values in pooled over environment.

Parents P₆, P₁, P₅ in E₁; P₁, P₅, P₆ in E₂ and P₁, P₆, P₅ in pooled environment, showed significant negative GCA values for days to 50 per cent silking. Significant negative SCA effects for 13 crosses in E₁ and 18 crosses in E₂ were observed. In pooled over environment, P₁ × P₅ followed by P₁ × P₃ and P₄ × P₆ had highest significant SCA values in negative direction. Kumar *et al.* (2022) also reported significant negative SCA effects for days to 50 per cent silking.

Analysis of days to 75 per cent brown husk for GCA effects ranged from -1.26 (P₁) to 1.14 (P₄) in E₁; -0.90 (P₁) to 1.00 (P₄) in E₂ and -1.08 (P₁) to 1.07 (P₄) in pooled environment. Significant negative values for GCA effects were observed for parent P₁ (-1.26), P₂ (-0.61) in E₁, P₁ (-0.90), P₅ (-0.55) in E₂ and P₁ (-1.08), P₅ (-0.41) in pooled environment, which is desirable as it represents earliness. The crosses P₃ × P₈, P₅ × P₆, P₁ × P₈ and P₄ × P₇ in E₁; P₆ × P₇, P₂ × P₃, P₁ × P₃, P₅ × P₆ in E₂ and P₂ × P₃, P₅ × P₆, P₃ × P₈ and P₁ × P₃ in pooled over environment showed significant negative SCA effects.

For ear circumference parent P₂ in E₁ and P₂, P₁ in E₂ as well as pooled over environment, had significant positive values for GCA effects. The crosses P₂ × P₄ (1.63) followed by P₁ × P₄ (1.58) and P₄ × P₆ (1.55) exhibited highest significant positive SCA effects in pooled over environment. For 1000-grain weight, parent P₇, P₈, P₄ in E₁; P₇, P₈, P₄, P₂, P₅ in E₂ and P₇, P₈, P₄ in pooled over environment, showed significant positive values for GCA

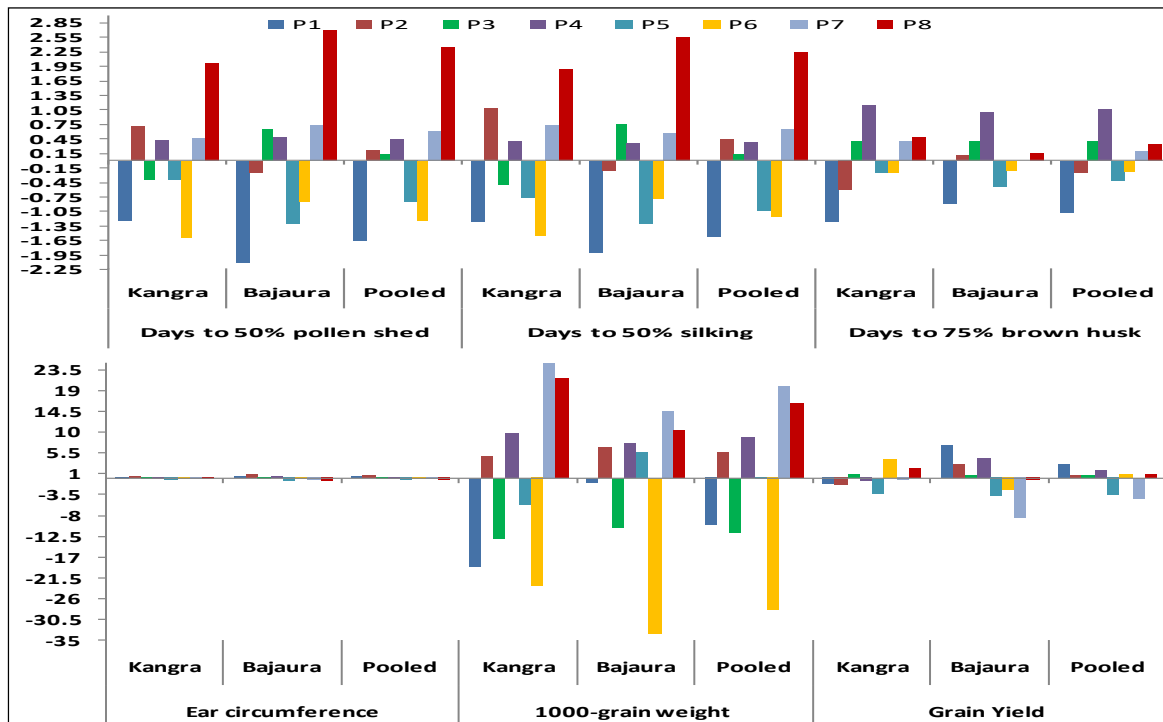


Fig. 1. GCA effects of parents

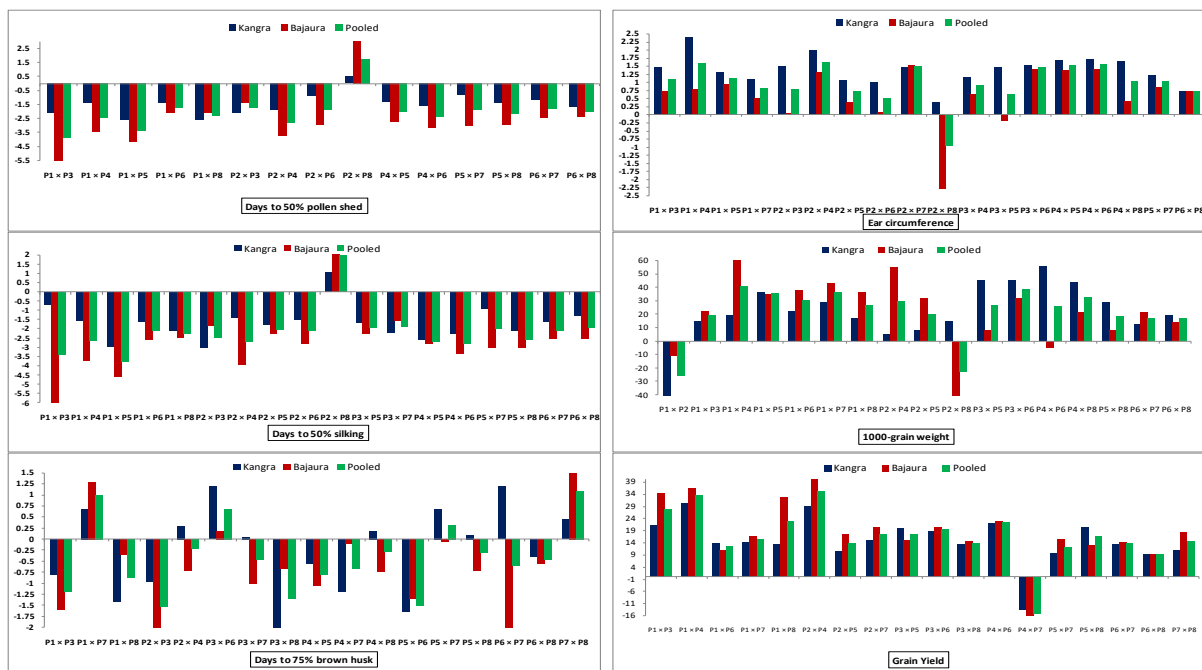


Fig. 2. SCA effects of crosses

effects. The estimates of SCA effects for 1000-grain weight ranged from -40.21 ($P_1 \times P_2$) to 55.99 ($P_4 \times P_6$) in E_1 , -59.94 ($P_2 \times P_8$) to 61.66 ($P_1 \times P_4$) in E_2 and -25.35 ($P_1 \times P_2$) to 40.7 ($P_1 \times P_4$) in pooled environment. Highest significant positive values for this trait were observed by $P_1 \times P_4$, $P_3 \times P_6$ and $P_1 \times P_7$ in pooled environment.

For grain yield, GCA effects ranged from -3.32 (P_5) to 4.03 (P_6) in E_1 ; -8.46 (P_7) to 7.23 (P_1) in E_2 and -4.42 (P_7) to 2.79 (P_1) in pooled environment. Parent P_6 , P_8 in E_1 ; P_1 , P_4 , P_2 in E_2 and P_1 in pooled environment, depicted significant positive values for GCA effects. These genotypes likely to possess favourable alleles for the trait of interest and

are predominantly additive in nature. SCA effects ranged from -13.65 ($P_4 \times P_7$) to 30.17 ($P_1 \times P_4$) in E_1 , -16.62 ($P_4 \times P_7$) to 41.28 ($P_2 \times P_4$) in E_2 and -15.14 ($P_4 \times P_7$) to 35.04 ($P_2 \times P_4$) in pooled over environment. In pooled over environment, highest significant positive values for this trait were observed by $P_2 \times P_4$ followed by $P_1 \times P_4$ and $P_1 \times P_3$ revealed that non-additive genetic effects (dominance and/or epistasis) are important for this trait and heterosis is likely to occur in these specific combinations. Similar results were observed by Katragadda *et al.* (2020).

The relative importance of GCA vs. SCA can inform breeding strategies and help predict genetic gain. If GCA effects are predominant, recurrent selection methods might be more effective. If SCA effects are significant, hybrid breeding programs might be more suitable. Genotypes with high GCA are valuable for developing improved inbred lines or varieties. The crosses with best specific combination for grain yield would be obtained from poor \times average, good \times good or average \times average parental combinations. High SCA effects where both parents were good general combiners could be attributed to additive \times additive gene action. The results, therefore, revealed that parents with good GCA effects did not always result in high SCA crosses which further indicated that SCA effects are attributable to dominance and epistatic interactions. High SCA effects expressed by poor \times average might be due to diverse genetic background of parental lines. The poor \times poor crosses can perform better in comparison to good \times good and good \times poor combinations because of the complimentary gene action.

In present study, adequate amount of genetic variability was observed for the experimental material that can be used for maize improvement programme. Analysis of variance depicted genetic diversity among the genotypes studied. The inbred line B73 at E_2 , pooled over environment and LM14 at E_1 were found to be good general combiner for grain yield and can be used as potential inbred parental lines for further development of high yielding single cross maize hybrids. Based on high *per se* performance, SCA effects and days to 75 per cent brown husk, the crosses B73 \times BAJIM1811 and BAJIM1522 \times BAJIM1811 identified as potential hybrids at E_1 , E_2 as well as pooled over environment may be commercially exploited after further evaluation for its performance superiority across the locations and over years.

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