

# GENERAL AND SPECIFIC COMBINING ABILITY IN EARLY MATURING HIGH YIELDING QUALITY PROTEIN MAIZE HYBRIDS

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## ABSTRACT

Fourteen quality protein maize (QPM) hybrids were generated by crossing seven QPM lines with two testers to estimate combining ability effects for yield and yield attributing traits. The analysis of variance revealed significant differences among the parents and  $F_1$  hybrids for all the characters except anthesis silking interval and number of cobs per plant. Combining ability analysis revealed the importance of non-additive gene action in the inheritance of majority of the characters in maize. Thus these crosses can be used directly or exploited for future hybrid breeding programmes to achieve quantum jump in maize improvement. The GCA estimates identified parental lines VIVEK-33  $VF_2$  and NBPGR 32809 as best combiner for grain yield while YHP-Panth and VIVEK-33 $VF_2$  were best combiner for earliness. Hence, these parents may be used in hybridization programmes as donors of the superior traits indicated. The best experimental hybrid, on the basis of per se performance and SCA effect for grain yield per plant and its component were observed in VIVEK-33  $VF_2$  × NBPGR 32809, followed by VIVEK-33  $VF_2$  × NBPGR 31899 and YHP Panth × NBPGR 32809.

## INTRODUCTION

Maize (*Zea mays* L.) is an important cereal crop grown widely throughout the world and is the primary staple food in many developing countries. Its uses are many, primarily for food, feed and as industrial raw materials. However, its protein quality is deficient in amino acids mainly lysine and tryptophan. Quality protein Maize (QPM) is a genotype with Opaque 2 gene along with associated modifiers. QPM contains twice the amount of lysine and tryptophan than normal maize. Higher protein content is a desirable character of the Quality Protein Maize. QPM donor with higher lysine and tryptophan content were discovered at CIMMYT, Mexico (Vasal, 1999).

The concept of general combining ability (GCA) and specific combining ability (SCA) was introduced by Sprague and Tatum (1942). In biometrical genetics two types of combining abilities are considered i.e., general combining ability (GCA) and specific combining ability (SCA). General combining ability is the average performance of a strain in series of cross combinations estimated from the performance of  $F_1$ 's from the crosses, whereas specific combining ability is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of lines involved. Studies of combining ability analysis provide useful information for selection of parents to include in a hybridization programme by defining the parents of gene action in expression of quantitative traits. This information is also useful to breeder for selection of diverse parents and hybrid combinations. Line × tester mating developed by Kempthorne (1957), provides valuable information on general and specific combining ability effects

of parents and their hybrid combination.

Development of commercial maize hybrid usually requires a good knowledge of combining ability of the breeding materials to be used. The success in commercial production of hybrid maize depends up on the availability of productive diverse quality protein maize inbred lines and clear knowledge of gene action for specific traits. Therefore, the present investigation was undertaken to study the combining ability for grain yield and yield contributing traits.

## MATERIALS AND METHODS

The genetic materials used were made up of seven inbred lines viz., NBPGR 32809 ( $T_1$ ), NBPGR 31899 ( $T_2$ ), POP 31 Q-18211 ( $L_2$ ), JP25- W95 ( $L_2$ ), CML-41 ( $L_3$ ), YHP-Panth ( $L_4$ ), CML 358 ( $L_5$ ), CML-470 B × 15 ( $L_6$ ) and VIVEK-33 $VF_2$  ( $L_7$ ). These lines were crossed in line × tester mating design (Kempthorne, 1957) during Rabi- 2016 to form 14  $F_1$  hybrids.  $F_1$  single crosses were made by hand pollination using bulk pollen from each line. The harvested ear were dried and shelled manually and in the major season Kharif-2017 field evaluation of 14  $F_1$  single crosses and their parents along with one check Shaktiman QPM-5 was conducted at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad (U.P).

The entries were arranged in Randomized Block Design with three replications. Each genotype was planted in three rows of 5 meters length with row-to-row and plant-to-plant spacing of 60 cm and 20 cm respectively. Cultural practices such as fertilization, weeding, pest and diseases control were

accompanied using normal field management practices for raising a good crop. The data were recorded from five randomly selected plants on eleven morphological traits.

The following traits were evaluated from five randomly selected plants from each replication days to 50% tasseling, days to 50% silking, anthesis-silking interval, plant height (cm), cob height (cm), cob length (cm), cob girth (cm), number of grains per row (cm), number of grains row, test weight (100 seed weight) and grain yield per plant (g).

## RESULTS AND DISCUSSION

The analysis of variance showed that mean squares due to crosses were highly significant for all the traits except for anthesis-silking interval and cob width. This indicates that the crosses were sufficiently different from each other for these traits and hence, selection is possible to identify the most desirable crosses.

The ratio of Var GCA/ Var SCA was lesser than one for all the traits except Anthesis –silking interval, cob length and grain yield which indicated that non-additive component played greater role in the inheritance of most of the traits studied. Therefore, both additive and non-additive gene actions are important in determining for the exploitation breeding behaviour of the genetic potential of the inbred lines in variety development program. Our findings are in agreement with those of Ofari *et al.* (2015), Ram *et al.* (2015) and Patel and Kathiria (2016).

### General combining ability effects

The GCA effects of nine inbred lines (7 lines  $\times$  2 testers) were estimated for determining their genetic worth for production of superior lines. Selection of parents with good general combining ability is a prime requisite for any successful breeding programme especially for heterosis breeding. The estimates of gca effects revealed that for flowering traits, CML-41, YHP- Panth and VIVEK-33 VF<sub>2</sub> were having highly significant negative GCA effects. Martin *et al.* (2016) also reported the importance of negative general combining ability estimates for days to 50 per cent tasseling and days to 50 per cent silking for characterising the parents as good combiners. For days to 50% tasseling and days to 50% silking, negative estimates are considered desirable as those were observed to be associated with earliness. For anthesis - silking interval CML470BX15 showed the best combiner. These inbred lines

possessed favourable genetic architecture for imparting earliness to their progenies.

For plant height, POP 31Q-18311 was found to be best general combiners followed by JP25 W95. This indicates that these two lines had the tendency to reduce plant height in the hybrid progenies. In maize, shorter plant height is desirable for lodging resistance. For cob height, two inbred lines showed negative and significant GCA effects which indicated that POP 31Q-18311 and CML-41 were good general combiners and has the tendency to decrease the cob height.

For grain yield VIVEK-33 VF<sub>2</sub> was identified as best combiner followed by NBPGR 32809. These can be used directly as parents for developing high yielding single cross hybrids. VIVEK-33VF<sub>2</sub> was also accompanied with significant GCA in desired direction for 100 grain weight, number of grains per row, cob length, number of cobs per plant, cob width and flowering traits *viz.*, days to 50% tasseling and days to 50% silking. With respect to cob width, cob length, number of grains per row and test weight, L<sub>7</sub> (VIVEK-33 VF<sub>2</sub>) showed positive and significant GCA effects. The positive GCA effect is desired for these characters as it is the most important yield component that directly contributes to increased grain yield. Hence, inbred lines with high GCA effects for these traits can be suitable parents for hybrid formation as well as for inclusion in future breeding programs. The similar trends for combining ability in maize were also reported by Rajitha *et al.* (2014), Patel *et al.* (2016) and Varalakshmi and Wali (2017).

### Estimation of specific combining ability

The SCA effect is an important criterion to determine the potential and effectiveness of hybrids. For grain yield, both negative and positive and significant estimates of SCA effects were observed among the crosses. Cross L<sub>1</sub>  $\times$  T<sub>2</sub> was good specific combiners. Highly significant SCA effects of the crosses indicate that significant deviation from what would have been predicted based on their parental performances. These crosses with highly positive and significant estimates of SCA effect could be selected for their specific combining ability to use in maize improvement program. The results of the current study are in agreement with the findings of Shams *et al.* (2010) and Abrha *et al.* (2013) who reported significant to highly significant level of SCA effects in most of the crosses they studied for grain yield in maize. With respect to number of days to anthesis, crosses L<sub>1</sub>  $\times$  T<sub>2</sub> and L<sub>4</sub>  $\times$  T<sub>1</sub> showed the best SCA effects indicating earliness of the hybrids. For plant height and cob

**Table 1: General combining ability effects of parents for different quantitative parameters in quality protein maize**

Genotypes	Days to 50 % tasseling	Days to 50% silking	Anthesis silking interval	Cob height	Plant height	Cob width	Cob length	Number of grains per row	Number of grain row	Test weight	Grain yield
POP 31Q-18211	3.02**	3.60**	0.57**	-11.24**	-24.55**	0.03	-0.82*	-4.35**	-0.22	-0.88*	-5.88**
JP25 W95	-0.48	-0.40	0.07	0.56	-12.11**	0.07	0.57	3.99**	-0.29	1.11**	1.36
CML-41	-0.98*	-1.07*	-0.10	-3.69**	15.89**	0.64**	-1.48**	-0.82	0.31	0.22	-1.74
YHP- Panth	-1.48**	-1.24**	0.24	-0.84*	11.22**	-0.62**	0.81*	-0.31	0.88**	-2.20**	-8.85**
CML-358	0.86*	0.60	-0.26	2.28**	-1.35	-0.26	-2.41**	-3.24**	-0.75**	-0.29	0.21
CML-470 BX15	0.69	0.26	-0.43**	7.66**	8.15**	-0.54**	-0.55	-1.57*	-0.44	0.38	-0.21
VIVEK-33 VF <sub>2</sub>	-1.64**	-1.74**	-0.10	5.25**	2.75	0.67**	3.89**	6.29**	0.51	1.66**	15.10**
NBPGR 32809	0.02	0.02	0.00	-0.53*	-0.34	0.11	0.27	0.35	0.01	0.36	5.16**
NBPGR 31899	-0.02	-0.02	0.00	0.53*	0.34	-0.11	-0.27	-0.35	-0.01	-0.36	-5.16**

\*,\*\* Significant at 5 % and 1 % level of significance respectively

**Table 2(a): Specific combining ability effects for different quantitative parameters in quality protein maize**

Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis silking interval	Cob height	Plant height	Cob width
POP 31Q-18211 × NBPGR 32809	1.64**	1.64**	0.11	-6.17**	-10.86**	-0.32
POP 31Q-18211 × NBPGR 31899	-1.64**	-1.64**	0.11	6.17**	10.86**	0.32
JP25 W95 × NBPGR 32809	-1.19*	-1.02	0.17	1.83**	-3.56	0.64*
JP25 W95 × NBPGR 31899	1.19*	1.02	-0.17	-1.83**	3.56	-0.64*
CML-41 × NBPGR 32809	-0.36	-0.36	0.00	0.08	5.70**	-0.16
CML-41 × NBPGR 31899	0.36	0.36	0.00	-0.08	-5.70**	0.16
YHP-Panth × NBPGR 32809	-1.19*	-1.19*	0.13	-3.71**	-5.30*	-0.41
YHP-Panth × NBPGR 31899	1.19*	1.19*	0.13	3.71**	5.30*	0.41
CML -358 × NBPGR 32809	0.81	0.98	0.17	7.58**	18.60**	0.43
CML- 358 × NBPGR 31899	-0.81	-0.98	-0.17	-7.58**	-18.60**	-0.43
CML-470 B X15 × NBPGR 32809	0.31	-0.02	-0.33	0.39	-5.63**	-0.15
CML-470 B X15 × NBPGR 31899	-0.31	0.02	0.33	-0.39	5.63**	0.15
VIVEK-33 VF <sub>2</sub> × NBPGR 32809	-0.02	-0.02	0.00	0.01	1.04	-0.02
VIVEK-33 VF <sub>2</sub> × NBPGR 31899	0.02	0.02	0.00	-0.01	-1.04	0.02

\*,\*\* Significant at 5 % and 1 % level of significance respectively

**Table 2(b): Specific combining ability effects for different quantitative characters in quality protein maize**

Genotypes	Cob length	Number of grains per row	Number of grain row	Test weight	Grain yield
POP 31Q-18211 × NBPGR 32809	0.63	-2.49*	-0.61	0.12	-7.07**
POP 31Q-18211 × NBPGR 31899	-0.63	2.49*	0.61	-0.12	7.07**
JP25 W95 × NBPGR 32809	-0.37	0.58	0.79*	0.84	2.59
JP25 W95 × NBPGR 31899	0.37	-0.58	-0.79*	-0.84	-2.59
CML-41 × NBPGR 32809	0.21	2.80**	-0.34	0.97	5.69*
CML-41 × NBPGR 31899	-0.21	-2.80**	0.34	-0.97	-5.69*
YHP-Panth × NBPGR 32809	-0.14	-2.32*	-0.31	-0.52	3.57
YHP-Panth × NBPGR 31899	0.14	2.32*	0.31	0.52	-3.57
CML -358 × NBPGR 32809	1.27*	2.35*	1.26**	-1.00	-2.48
CML- 358 × NBPGR 31899	-1.27*	-2.35*	-1.26**	1.00	2.48
CML-470 B X15 × NBPGR 32809	-0.75	-0.96	-0.79*	-0.72	-3.10
CML-470 B X15 × NBPGR 31899	0.75	0.96	0.79*	0.72	3.10
VIVEK-33 VF <sub>2</sub> × NBPGR 32809	-0.86	0.05	-0.01	0.31	0.80
VIVEK-33 VF <sub>2</sub> × NBPGR 31899	0.86	-0.05	0.01	-0.31	-0.80

\*,\*\* Significant at 5 % and 1 % level of significance respectively

height,  $L_5 \times T_2$  and  $L_1 \times T_1$  were found to be the best two crosses evaluated in the current study. The shortened plant is advantageous in case of lodging resistance. Crosses  $L_3 \times T_1$  and  $L_5 \times T_1$  were found to exhibit significant level of SCA effects for number of grains per row and number of rows respectively. This shows that most of the crosses evaluated in the current study did not significantly deviate from what would have been predicted based on their parental performance.

## CONCLUSION

The study identified valuable genetic materials which can be exploited for subsequent breeding activities. The GCA estimates identified parental lines VIVEK-33 VF<sub>2</sub> and NBPGR 32809 as best combiner for yield while YHP-Panth and VIVEK-33VF<sub>2</sub> were most suitable for earliness. Hence, these parents may be used in hybridization programmes as donors of the superior traits indicated. Hybrids POP 31Q-18211 × NBPGR 31899 and CML-41 × NBPGR 32809 exhibited positive significant SCA effects for grain yield per plant while POP 31Q-18211 × NBPGR 31899, JP25 W95 × NBPGR 31899 and VIVEK-33VF<sub>2</sub> × NBPGR 32809 for days to maturity indicating these crosses are good combiner for earliness. The analysis of experimental result revealed the importance of non-

additive gene action in the inheritance of majority of the characters in maize. Thus, these crosses can be used directly or exploited for future hybrid breeding programmes to achieve quantum jump in maize improvement.

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