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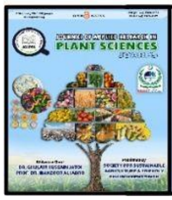

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Heterosis and Combining Ability Studies in A 5 x 5 Diallel Crosses of Maize Inbred Lines

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Abstract

The present study was conducted to evaluate the genetic architecture of five diverse maize genotypes using combining ability analyses. General combining ability (GCA) mean squares were non-significant for grain yield and its related components. Specific combining ability (SCA) mean squares were highly significant for grain yield, the number of grains per row and cob girth while non-significant for days to tasseling, days to silking, plant height, cob height and cob length. The genotypes MIL2020-51 and MIL2020-52 were good general combiners for grain yield, grains per row, cob height and plant height. These lines were the poorest general combiner for days to 50% tasseling and days to 50% silking which suggested that these genotypes had sufficient genes for inducing earliness. The crosses MIL2020-51 x MIL2020-54, MIL2020-52 x MIL2020-53, MIL2020-51 x MIL2020-55, MIL2020-53 x MIL2020-55and MIL2020-52 x MIL2020-55 were the best performing combinations for grain yield. These crosses involved good x good and good x poor general combiners. The reciprocal cross combinations MIL2020-55 x MIL2020-53, MIL2020-52 x MIL20220-51, MIL2020-54I x MIL2020-52, MIL2020-55 x MIL2020-51, MIL2020-54 x MIL2020-51and MIL2020-55 x MIL2020-54 showed large positive estimates for grain yield suggesting that cytoplasmic inheritance also had a role in the expression of grain yield. SCA variances were higher than GCA variances for grain yield, plant height, cob height, number of grains per row, cob girth and cob length which highlighted major role of non-additive genes in the inheritance of these traits. Additive gene action was found more important for number of days to 50% tasseling and number of days to 50% silking.

Keywords: *Combining ability, Diallel crosses, Gain yield, Heterosis, Maize inbred lines*

Introduction

In Pakistan Maize is widely grown as cross-pollinated cereal crop after wheat and rice. Its average area under cultivation is 1418 thousand hectares with a total production of 8940 thousand tons. Its average production is (2388 kg/acre), Pakistan economic survey (2020-21). Hybrid cultivars have played a vital role in increasing the acreage and productivity of maize (Kanagarasu *et al.*, 2010). In Pakistan, Maize hybrids have been contributing a lot in increasing productivity of maize per unit area of production, therefore high yielding maize hybrids are in dire need of time to alleviate poverty. The study revealed that every plant species have different number of paralogs representing correspondence towards the plant genomic size viz. higher genome keeps higher gene number but change in gene number resulted due to tandem gene duplication or complete genome duplication while evolutionary process ultimately resulted to special feature in any plant species even under biotic and abiotic stresses (Hussain *et al.*, 2022). To fulfill this aim, combining ability studies have prime significance in maize hybrid development program as it provides information for the selection of parents and provides information on the nature and magnitude of gene actions present in the gene pool (Zeleke, 2015). Combining ability analysis is the quickest method of understanding the genetic nature of quantitatively inherited traits; it also provides essential information about the selection of parents resulting in better segregates (Griffing, 1956a). The variance due to general combining ability (GCA) is usually considered for the additive type of gene action, whereas specific combining ability (SCA) is taken as the measure of the non-additive type of gene action in heterosis breeding. The present study was undertaken to estimate the combining ability of parents and hybrids and hence the nature and Magnitude of gene action for yield and yield components in 5 x 5 diallel analysis at Maize Breeding Sub Station, Chharrapani Murree, Pakistan.

Materials And Methods

Five maize inbred lines viz. MIL2020-51, MIL2020-52, MIL2020-53, MIL2020-54 and MIL2020-55 were crossed in all possible combinations during the spring season of 2020. Twenty crosses along with five parents were sown on 06-04-2021 in the research area of Maize Breeding Sub Station Chharrapani-Murree, Pakistan. A randomized complete block design was used with two replications. Inter row and inter-plant spacing was kept at 75cm and 25cm respectively. To get a good quality crop recommended agronomic and cultural practices were performed. Data were recorded from ten randomly selected plants from each block for grain yield and its related components. Mean values were analyzed using the procedure of Steel *et al.* (1980), Table 1. General and specific combining ability analyses were performed using Griffing's procedure Method-I, Model-II (Griffing, 1956a, 1956b).

Results and Discussion

Analysis of variance showed highly significant differences for all the traits under study (Table 1). This suggested that the parents had sufficient genetic variability for all the parameters studied. General combining ability (GCA) mean squares (Table 2) were non-significant for all the characters under study. Specific combining ability (SCA) mean squares were highly significant for grain yield, the number of grains per row and cob girth while non-significant for the rest of the characters. Reciprocal mean squares were highly significant for grain yield, plant height, cob height, number of grains per row and cob girth while non-significant for the number of days to 50% tasseling, days to 50% silking and cob length. GCA, SCA mean squares indicated that grain yield, cob girth and number of grains per row were non-additive traits while for the rest of the characters both additive and non-additive gene actions were equally important. Kanagarasu *et al.* (2010); Kage *et al.* (2013); Asif *et al.* (2007) and Joshi *et al.* (2002) have also reported similar findings for almost all the traits.

The genotypes MIL2020-51, and MIL2020-52 were good general combiners for grain yield, number of grains per row, cob height and plant height (Table 3). These lines had non-significant negative GCA effects for days to tasseling and days to silking which suggested that these lines had genes for earliness. The parent MIL2020 -53 was good general combiner for grain yield only. The parent MIL2020 -55 was the poorest general combiner for most of the characters studied. Specific combining ability (SCA) estimates (Table 4) revealed that MIL2020-51 x MIL2020-54, MIL2020-52 x MIL2020-53, MIL2020-51 x MIL2020-55, MIL2020-53 x MIL2020-55, MIL2020-51 x MIL2020-52 and MIL2020-52 x MIL2020-55 were the best combinations for grain yield. All these combinations involved at least one good general combiner which highlighted the importance of good general combiners for the improvement of grain yield genetically (Kanagarasu *et al.*, 2010).

The reciprocal crosses MIL2020-55x MIL2020-53, MIL2020-52x MIL20220-51, MIL2020-54I x MIL2020-52, MIL2020-55x MIL2020-51, MIL2020-54x MIL2020-51 and MIL2020-55 x MIL2020-54 (Table 5) had large positive estimates for grain yield. This suggested that cytoplasmic inheritance also had a role in the expression of grain yield.

Variance components due to SCA (Table 6) were higher than GCA variances for grain yield, plant height, cob height, number of grains per row, cob girth and cob length which suggested that non-additive genes had a major role in the inheritance of these traits. GCA variances were higher than SCA variances for days to tasseling and days to silking which suggested that additive gene action had a major part in the expression of these parameters Kanagarasu *et al.* (2010).

Table 7 revealed that best-performing crosses also exhibited significant positive heterosis for grain yield and some of its attributes. MIL2020-51 x MILl2020-55 and MIL 2020-52 x MIL2020-55 were the most heterotic crosses for grain yield, number of days to 50% tasseling and number of days to 50% silking, cob height, cob length, cob girth and number of grains per row. These findings suggested that both GCA and SCA had contributed to their outstanding performance (Zeleke, 2015)

Table 1: Means square values for grain yield and yield components in 5x5 diallel cross in Maize.

Source of variation	**Degree of freedom**	**Days to 50% tasseling**	**Days to 50% silking**	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
Replications	1	0.18^{ns}	0.98^{ns}	50.00^{ns}	0.18^{ns}	3.38^{ns}	0.98^{ns}	1.98^{ns}	942.00^{ns}
Treatments	24	21.5**	23.22**	1380.76**	503.27**	9.64**	106.58**	52.67**	3313661.00**
Error	24	2.60	3.90	29.79	12.97	0.51	1.61	0.65	50371.00

* & ** significant at 5% & 1% level of probability respectively.

Table 2: Combining ability means square values for grain yield and yield components in 5x5 diallel cross in Maize

Source of variation	**Degree of freedom**	**days to 50% tasseling**	**days to 50% silking**	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
GCA	4	3.9875 ns	9.3325 ns	870.13 ns	253.2425 ns	7.355 ns	41.9575 ns	6.511903 ns	1507423.41 ns
SCA	10	11.08 ns	9.731 ns	483.3665 ns	174.954 ns	7.5865 ns	61.286 **	25.23131 **	1374735.6 **
Reciprocals	10	13.125 ns	14.4 ns	825.4875 **	327.675 **	1.0375 ns	49.825 **	35.26235 **	1999461.86 **
Error	48	20.77333	31.17333	238.3333	103.7667	4.04	12.84	5.23	402966.667

* & ** significant at 5% & 1% level of probability respectively.

Table 3: General combining ability estimates for grain yield and yield components in 5x5 diallel cross in Maize

Parents	days to 50% tasseling	days to 50% silking	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
MIL2020 -51	-0.20	-1.27	12.61	6.16**	0.71ns	2.62 **	0.76ns	299.47**
MIL2020 -52	-0.85	-0.62	4.01	3.36 **	-0.19 ns	1.27*	0.37 ns	349.92 **
MIL2020 -53	0.90	1.23	-0.69	-6.99 **	0.91ns	0.02ns	0.44 ns	168.47 **
MIL2020 -54	0.00	0.28	-12.74	-1.24*	-0.19ns	-2.53**	-0.32 ns	-290.58 **
MIL2020 -55	0.15	0.38	-3.19	-1.29*	-1.24ns	-1.38*	-1.26 ns	-527.28 **
SE	**1.61**	**1.29**	**0.37**	**0.45**	**0.52**	**0.39**	**0.63**	**0.36**

* & ** significant at 5% & 1% level of probability respectively.

Table 4: Specific combining ability estimates for grain yield and yield components in 5x5 diallel cross in Maize

Crosses	**days to 50% tasseling**	**days to 50% silking**	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
MIL2020-51 x MIL2020-52	-2.25	-3.23	9.39	8.59	0.79	1.18	-1.47	198.63
MIL2020-51 x MIL2020-53	3.50	3.17	-20.41	-5.56	-2.06	-5.82	-2.96	-718.67
MIL2020-51 x MIL2020-54	-0.10	-0.38	15.14	0.19	0.54	2.73	4.36	975.13
MIL2020-51 x MIL2020-55	1.25	1.52	-1.16	0.24	2.59	1.33	-2.51	630.83
MIL2020-52 x MIL2020-53	-1.85	-1.73	-9.31	-8.76	-0.41	4.78	0.12	752.13
MIL2020-52 x MIL2020-54	1.30	1.47	-1.26	7.74	-1.81	-8.67	-2.58	-1136.82
MIL2020-52 x MIL2020-55	3.40	2.37	-2.06	0.29	0.99	-0.57	3.02	126.88
MIL2020-53 x MIL2020-54	2.30	1.12	17.44	16.34	-0.16	0.08	-0.52	-576.87
MIL2020-53 x MIL2020-55	-1.35	0.52	12.14	8.64	0.39	-3.82	1.24	325.33
MIL2020-54 x MIL2020-55	-1.20	-1.03	-30.06	-7.61	1.49	-5.52	-6.46	-859.62
SE	**0.97**	**1.26**	**0.50**	**0.54**	**0.52**	**0.32**	**0.32**	**0.38**

* & ** significant at 5% & 1% level of probability respectively.

Table 5: Reciprocal combining ability estimates for grain yield and yield components in 5x5 diallel cross in Maize

Crosses	days to 50% tasseling	days to 50% silking	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
MIL2020 -52x MIL2020 -51	0.00	0.50	-5.25	-7.25	-0.25	-1.75	2.61	1145.00
MIL2020 -53x MIL2020 -51	-0.50	0.75	-34.25	-23.75	-1.00	-8.00	-2.95	-1555.75
MIL2020 -53x MIL2020 -52	-3.50	-4.25	15.25	-2.25	-0.50	-1.00	-6.11	-842.00
MIL2020 -54x MIL2020 -51	3.50	2.25	14.00	13.25	0.50	6.25	5.06	560.00
MIL2020 -54Ix MIL2020 -52	-0.50	-1.50	11.25	-3.25	-0.75	-1.25	-0.48	807.50
MIL2020 -54x MIL2020 -53	-4.75	-5.25	-43.75	-47.00	-1.25	-7.25	-7.56	-1200.50
MIL2020 -55x MIL2020 -51	-0.50	-0.75	18.50	9.00	0.00	2.00	3.17	719.50
MIL2020 -55x MIL2020 -52	0.50	0.75	9.75	3.25	0.50	5.25	0.41	-278.00
MIL2020 -55x MIL2020 -53	-4.00	-3.75	1.50	-3.00	-0.50	7.50	5.51	1524.50
MIL2020 -55x MIL2020 -54	1.25	1.75	4.25	-1.00	1.00	-0.25	0.15	479.50
SE	**0.89**	**1.04**	**0.38**	**0.40**	**1.39**	**0.36**	**0.27**	**0.32**

Table-6: Variance components for grain yield and yield components in 5x5 diallel cross in Maize.

Variances	**days to 50% tasseling**	**days to 50% silking**	**Plant height (cm)**	**Cob height (cm)**	**Cob length (cm)**	**No of Gr per row**	**Cob Girth (mm)**	**Grain yield (Kg/ha)**
Vg	-1.09	-1.24	6.86	-0.69	-0.16	-1.17	-0.91	-8192.61
Vs	-5.77	-12.76	145.85	42.37	2.11	28.84	11.91	578433.89
Vr	-3.82	-8.39	293.58	111.95	-1.50	18.49	15.02	798247.60
Ve	20.77	31.17	238.33	103.77	4.04	12.84	5.23	402966.67

Table 7: Most heterotic crosses, their mean performance, GCA/SCA effects for grain yield and yield components in 5x5 diallel cross in Maize

Crosses	**Grain yield (Kg/ha)**	**%Heterosis over**		**SCA**	**GCA**		**Other traits showing heterosis**
		MP	**BP**		**P-I**	**P-II**	
MIL2020 -52 x MIL2020 -53	6858	26.14	23.81	752.13	G(349.9)	G(168.5)	PH, CH
MIL2020 -51 x MIL2020 -52	6773	37.77	22.28	198.63	G(299.5)	G(349.2)	CH, CL
MIL2020 -53 x MIL2020 -55	6271	41.94	17.54	325.33	G(168.5)	P(527.3)	CH, CG
MIL2020 -51 x MIL2020 -55	5744	47.39	33.80	630.83	G(299.5)	P(527.3)	DT, DS, CH, CL, Gr
MIL2020 -52 x MIL2020 -55	5449	20.55	-1.62	126.88	G(349.9)	P(527.3)	DT, DS, PH, CH, CL, CG

* & ** significant at 5% & 1% level of probability respectively.

Similar findings have been reported by Malik *et al.* (2004); Sharma *et al.* (2004); Muraya *et al.* (2006) and Seyoum *et al.* (2016). However, higher values of SCA mean squares pointed out that non-additive genes had a larger proportion in controlling these characters. Furthermore, comparatively higher SCA variances indicated that non-additive genes were more important than additive ones for most of these traits. The present finding agrees with (Kage *et al.*, 2013). Similar results were also reported by Amer (2005); El-Hosary *et al.* (2005); El-Hosary *et al.* (2006) and Sedhom *et al.* (2007). On the other hand, Akbar *et al.* (2008); AM Iqbal *et al.* (2007) and Hefny *et al.* (2008) reported that both additive and non-additive were important in the genetic expression of most of the traits studied in maize. The interaction between both types of combining abilities and environmental changes were reported to be significant for earliness and grain yield (Abbas *et al.*, 2021; Dadheech *et al.*, 2007; EL-Badawy *et al.*, 2010; MA Iqbal *et al.*, 2022; E Mosa *et al.*, 2005; H Mosa, 2003; Sedhom *et al.*, 2007).

Several investigators reported high heterosis for the yield of maize, i.e. (Alamnie *et al.*, 2006; EL-Badawy *et al.*, 2010; El-Hosary *et al.*, 2006; Hefny, 2007; Kanta *et al.*, 2005; Shafey *et al.*, 2003; Singh *et al.*, 2004). The observations were correlation values between the predicted genotypic values and the observed means of 0.55 to 0.70 and 0.61 to 0.70 for SCA values, with relationship coefficients obtained from microsatellite molecular markers, increasing the technique precision (Balestre *et al.*, 2010). Based on a large data set of molecular markers, single hybrid performance can be predicted efficiently for traits controlled by additive effects, as well as for traits with large heterosis participation, like grain yield. Thus, the prediction of untested single crosses can be a good alternative for breeding programs with a vast number of inbred lines, enhancing the chances for selecting superior genotypes, when pedigree information or relationship matrices through molecular markers are available for use in the model (Schrag *et al.*, 2009).

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