



Inheritance of Yield Related Traits in a Half Diallel Crosses of Some Maize (*Zea mays* L.) Genotypes

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Abstract

Inheritance of grain yield, heterosis and combining ability were investigated in maize populations obtained from half-diallel crossing among six inbred parental lines. General (GCA) and specific (SCA) combining ability effects were significantly different among parental lines. The grain yield was under the partial gene effect. The parents P_1 , P_3 and P_5 were considered suitable according to their yield contributing attributes couple with general combining ability effects. The midparent heterosis values ranged from -27.246 ($P_2 \times P_5$) to 15.209% ($P_1 \times P_2$) whereas the better parent heterosis values varied between 22.375 ($P_2 \times P_3$) to 40.363% ($P_2 \times P_5$) only seven crosses had higher grain yields. Of those crosses, $P_1 \times P_2$, $P_2 \times P_5$ and $P_1 \times P_3$ were considered most promising hybrids yielding heterosis as 15.880%, 20.363% and 40.363 respectively over their parents.

Keywords: Maize, diallel analysis, combining ability, heterotic effect

1. Introduction

Maize (*Zea mays* L.) is one of the major cereal crops for providing raw material of the food industry and animal feed. The production area of maize is gradually increasing in Bangladesh (Zekele, 2015). Maize is the third most important cereal crop after rice and wheat contributing to agricultural economy of Bangladesh in various ways. Maize is gaining importance in recent years as a promising crop aimed in boosting agricultural growth in Bangladesh. The area and production of maize in 2017-18 was 4.4 lac hectares and 3.3 million tons, respectively (USDA, 2018). It has already been popularized as poultry feed in Bangladesh. Due to recent establishment of some poultry and dairy industries in the country, the demand of maize is increasing day by day. Hybrid maize can play an

important role in fulfilling the increasing demand through its high yield potentiality (Haddadi *et al.*, 2012).

New maize hybrids thus need to be developed with high yield capacity to meet the demands of maize producers. Several breeding procedures have been established to increase the grain yields of the maize populations and their hybrids. In order to choose the best hybrid combinations a large number of subjectively chosen inbred lines are crossed. It would be a considerable advantage to be able to estimate the combining ability of parents, gene effects and heterotic effects of crosses before making crosses among inbred lines (Xu and Crouch., 2008).

To develop better hybrids, two types of combining ability i.e. general (GCA) and

specific (SCA) have been recognized in genetic studies. General combining ability relates to additive gene effects, while specific combining ability reflects the non-additive gene actions (Sprague and Tatum, 1942). GCA is average performance of a parent in a series of crosses and SCA designates those cases in which certain combinations perform relatively better or worse than would be expected on the basis of average performance of parents. In specific combining ability; dominance or epistatic effects of genes are commonly involved in maize (Rahman, 2013). Selection of parents on the basis of *per se* performance with good GCA effect is the best approach to assess the nature of gene action involved in the inheritance of character. Combining ability analysis is one of the powerful tools in identifying the better combiners which may be hybridized to exploit heterosis as well as to select better crosses for direct use or further breeding work (Nigussie and Zelleke, 2001). One of the most informative methodologies in this concern is diallel analysis system which is widely and extensively used for estimating the types of gene action. Information on the heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development (Beck *et al.*, 1990). Breeder's objectives are to select hybrids on the basis of expected level of heterosis as well as specific combining ability (Amiruzzaman *et al.*, 2013). Genetic components of variation, D (additive effects of genes), H_1 , H_2 (dominance effects of genes) and F were computed from estimates of variances and covariances. These parameters provide estimates of the relative frequency of dominant to recessive alleles in the parental lines. The information on gene action and presence of dominant and recessive genes in the parents was also inferred by plotting the covariance (W_r) of each array against its variance (V_r).

The objectives of this study were to estimate the genetic parameters and heterotic effects as well as to determine suitable parents and promising

crosses for grain yield in a 6 × 6 half-diallel maize population.

2. Materials and Methods

Six inbred lines, P_1 , P_2 , P_3 , P_4 , P_5 and P_6 obtained from the Biometrical Genetics Lab. Department of Botany, University of Rajshahi, Bangladesh were crossed in a 6x6 half-diallel mating scheme in the 2018 growing season. The parents, their 15 F_1 populations and a commercial hybrid, 21 entries in total, were grown at the Botanical Research Field, Rajshahi University, in the 20 December 2019 growing season. The plots were represented by 4 rows; 5 m long and spaced 0.7 m apart with 25 plants per row after thinning. The soil of the experimental site was clay loam in texture. The experiment design was a randomized complete block design (RCBD) with 3 replications. Cultural practices were consistent with the production of maize at this location. Grain yields of each genotype were obtained from each row of the plots and were corrected according to 15% of kernel moisture. Data were collected on number of grains/cob and grain yield/plant.

Data obtained from the 15 F_1 progeny and 6 parents were analyzed by Jinks-Hayman type diallel analysis for genetic parameters (Jinks and Hayman, 1953). The methods were calculated by Mather and Jinks (1971) and using the software of GANTAT.

3. Results and Discussion

The analysis of variance showed highly significant differences between the lines for gain yield and combining ability of variance indicated that genotypes were significantly different for grain yields (Table 1). The general combining ability (GCA) and specific combining ability (SCA) effects of genotypes and crosses were also significantly different for number of grains/cob and grain yields.

The genetic parameters for grain yield estimated from the 6 x 6 half-diallel cross population are

given in Table 2. The value of (H_1) was higher than that of (D), revealing that non-additive gene effects were more important than additive gene effects for those traits. The significant value of additive component (D) and the non-significant values of dominance components (H_1) and (H_2) for grain yield/plant indicated stability in the additive variance of this trait; it can thus be improved through simple selection procedures. The estimate of genetic components of variation indicated from significant D and H components which displayed that both additive and dominance effects of gene were important. Unequal value of H_1 and H_2 revealed the different distribution of dominant genes for grain yield/plant. The component F was found significant showed greater frequency of dominant alleles. The significant h^2 component showed important effect of heterozygous loci for number of grains/cob. The overall dominance effect was determined by h^2 estimates, which gave the total sum over all the loci in a

heterozygous state. This was positive and significant for no. of grains/cob and grain yield/plant, indicating that dominance is largely unidirectional. Environmental variation (E) was found non significant. Degree of dominance was less than one which indicated additive gene action for number of grains/cob. The results were in agreement with those of Haq *et al.*, (2010), Afshar *et al.*, (2012) and Amiruzzaman *et al.* (2013).

The positive value of F indicated that dominant allele were more frequent than recessive one, the F value will be equal to zero (Crumpacker and Allard, 1962). As an indicator of the relative frequency of dominant and recessive alleles in the parents, the F value was found to be positive but non-significant for grain yield, which means either that no allele's exhibit dominance or else that the dominant and recessive alleles are distributed equally among the parents (Verhalen and Murray, 1967).

Table 1. Analysis of variance for genotypic difference and combining ability for different characters in maize

Sources of variation	df	NGC	GYP
		MS	MS
Line/Genotype	24	947.161**	68.778**
GCA	5	12916.598**	1035.173**
SCA	15	3571.143**	286.216**
Crosses	20	5907.507**	473.455**
Error	40	3376.707	270.629
GCA/SCA		3.6169	3.6167

NGC=Number of grains/cob, GYP = Grain yield/plant, *, ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

Table 2. Components of variation and their proportions for number of grains/cob

Notation	Components of Variation	Proportional Values	
	Estimated Values	Proportion	Estimated Values
D	77.847±29.919	$\sqrt{H_1/D}$	1.4743
F	37.384±73.0943	$H_2/4H_1$	0.2243
H1	169.2121±75.954	$[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$	1.3890
H2	151.8614±67.8519	h^2/H_2	1.1937
h2	181.288±45.668	V_{1L1}/W_{oLo1}	1.8398
E	7.2261633±11.308	h^2NS	0.3901

Table 3. Components of variation and their proportions for grain yield/plant

Notation	Components of Variation		Proportional Values	
	Estimated Values	Proportion	Estimated Values	
D	16.3356±10.529	$\sqrt{H_1/D}$	1.9605	
F	1.5754±25.724	$H_2/4H_1$	0.2319	
H1	62.793±26.730	$[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$	1.051	
H2	58.269±23.879	h^2/H_2	1.024	
h2	63.071±16.072	V1L1/WoLo1	2.533	
E	9.4061±3.979	h^2NS	0.318	

The significant values of D, H₁, H₂ and h² showed that both additive non additive gene effects were important in controlling this character (Table 3). The higher value of H₁ and D revealed that non additive effects were more pronounced as compared to additive gene effects. The value of (H₁/D)^{1/2} being greater than unity (1.96) indicated the involvement of over dominance. The proportion of genes with positive and negative effects (H₂/4H₁) in the parents was found to be less than 0.25 denoting asymmetry at the loci showing dominance. Since the mean dominance effect of the heterozygote locus (h²) was significant, high heterotic effect values would be expected for grain yield among crosses. The h²/H₂ ratio denotes an approximate number of genes or groups of genes controlling the traits, i.e., exhibiting dominance, and was more than one for those traits which most likely was underestimated. This may be attributed to the differences in the intensity of dominant genes effects as well as dependence on their direction and cancellation effects. Over dominance types of gene action for grain yield/plant in maize was also reported by Irshad *et al.* (2010) and Afshar *et al.* (2012). As the H₂/4H₁ did not deviate from its expected value of 0.232, it indicated that the positive and negative alleles were distributed equally at the loci exhibiting dominance in the parental genotypes. The ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ suggested that dominant and recessive alleles controlling the character were equal. The ratio of h²/H₂ indicated that probably six groups of genes were controlling the grain yield/plant. The results were in agreement with Irshad *et al.* (2010), who demonstrated that positive and negative alleles were distributed

equally at the loci, indicating dominance in the parental genotypes for grain yield.

The regression line for number of grains/cob cut the Wr axis over the origin in the positive zone, suggesting the partial-dominance type of gene action (Fig. 1), this is also supported by the greater than unity ratio (Table 2). The (V_r=variances of arrays, W_r=covariances between parents and their offspring) regression line for grain yield/plant intercepted the Wr axis above the origin, indicating the importance of additive gene action with partial dominance (Fig. 2). Zare *et al.* (2011) reported a similar type of gene action for grain yield. With regard to grain yield, the parents P₃ and P₅ had more dominant genes whereas P₁, P₂, P₄ and P₆ carried more recessive genes. This result was also supported by the GCA/SCA ratio (0.65). Similarly, Kalla *et al.* (2001) and Zeleke (2015) estimated that a non-additive gene effect was involved in maize grain yield.

The estimated heritability degree of yield (narrow sense; 0.318) is consistent with other researchers results (Kalla *et al.*, 2001; Muhammad and Muhammad, 2002 and Zeleke, 2015). Since the K value was 3.929, approximately 4 genes will control grain yield.

Grain yield and GCA effects of parents are given in Table 4. Significant differences were found for grain yield among parents. P₆ While P₁ and P₃ can be considered high yielding parents, P₂ and P₄ had medium yield capacity. Two parents, P₁ and P₅, had high yield and statistically significant and positive GCA effects. Grain

yield, SCA effects, mid parent and useful heterosis values of the crosses are given in Table 4. Three crosses that had highest grain yields were $P_1 \times P_5$, $P_2 \times P_5$ and $P_3 \times P_6$. These crosses also

had high and positive SCA effects. Significantly, the better performing crosses usually had at least one parent with high GCA effects (Aydin *et al.*, 2004; Chaudhary *et al.*, 2000).

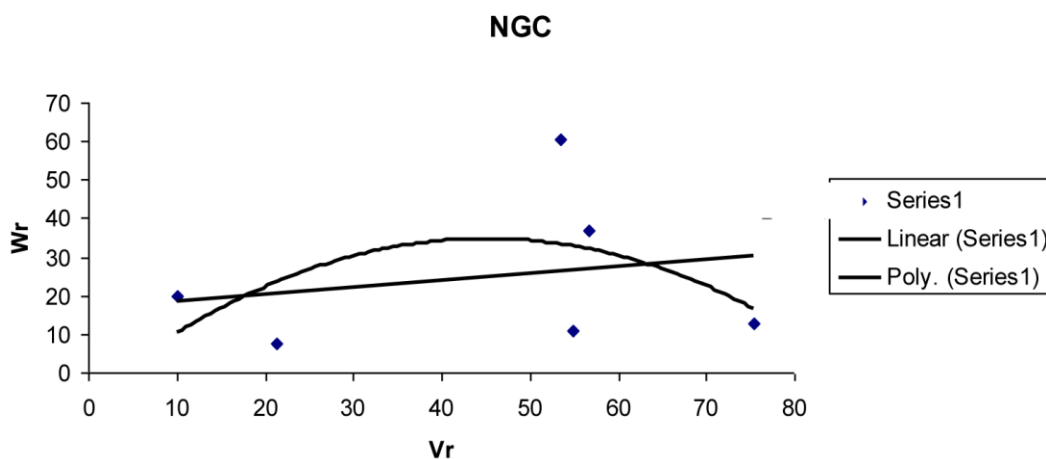


Figure 1. Vr–Wr graph for number of grains/cob in 6x6 diallel cross in maize (Vr = variances of arrays, Wr = covariances between parents and their offspring)

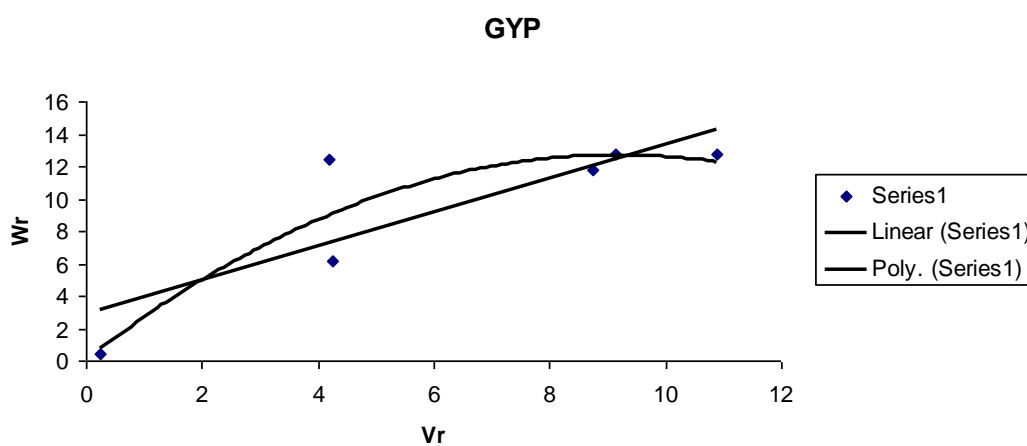


Figure 2. Vr–Wr graph for grain yield/plant in 6x6 diallel cross in maize (Vr=variances of arrays, Wr=covariances between parents and their offspring)

Table 4. Mean of parents and GCA effects for different characters in maize

Parents	Number of grains/cob		Grain yield/plant	
	Mean	GCA	Mean	GCA
P ₁	177.098	18.422**	84.904	-8.301**
P ₂	160.468	7.419**	69.478	-7.018**
P ₃	165.48	19.055**	74.863	0.358
P ₄	173.615	-15.88**	65.523	3.178**
P ₅	108.161	2.703**	72.057	8.877**
P ₆	178.432	-2.880**	71.326	2.906**

Table 5. Mean yields, specific combining ability effects and heterosis value of crosses

Crosses	Grain yield/plant	SCA	Mid parent heterosis (%)	Better parents heterosis (%)
P ₁ ×P ₂	108.617	15.880**	15.209**	4.936**
P ₁ ×P ₃	96.962	-3.150**	-5.590**	25.008**
P ₁ ×P ₄	103.853	0.920	3.372**	-13.973**
P ₁ ×P ₅	113.245	4.613**	6.721**	-16.669**
P ₁ ×P ₆	101.034	-1.626	1.732*	-14.435**
P ₂ ×P ₃	99.595	-1.800	-13.23**	-22.375**
P ₂ ×P ₄	95.011	-9.205**	-15.742**	-15.742**
P ₂ ×P ₅	89.551	20.363**	-27.246**	40.363**
P ₂ ×P ₆	100.109	3.834**	-9.466**	-15.360**
P ₃ ×P ₄	-15.360	-7.585**	-15.891**	-17.963**
P ₃ ×P ₅	110.664	-6.627**	-15.278**	-19.250**
P ₃ ×P ₆	104.089	-7.231**	-14.630**	-17.881**
P ₄ ×P ₅	126.973	6.861**	3.103**	-2.941**
P ₄ ×P ₆	116.321	2.181**	-0.327	-1.505*
P ₅ ×P ₆	127.150	7.309**	4.457**	-2.764**

The mid parent heterosis ranged from -27.25% to 15.209% where magnitude of heterosis of nine crosses combination were in negative direction. The remaining six crosses were in positive direction among which only one cross combination (P₁×P₂) performed more than 10% heterosis revealing its potentiality for future use. Generally high heterosis values showed parallelism with the h² parameter, indicating the mean dominance effect of the heterozygote locus. Moreover, better parent heterosis ranged from -22.315% to 40.363% and only three crosses elucidated heterosis in positive direction. The cross combination P₁×P₅, P₁×P₃ and P₂×P₅

revealing heterosis as 4.936%, 25.008% and 40.363% could be subjected for further evaluation. These results are in agreement with the results of Uddin *et al.* (2008), Alam (2009) and Afshar *et al.*, (2012).

4. Conclusions

The of both additive and non-additive gene effects for number of grains/cob and grain yield/plant suggested that reciprocal recurrent selection would be an effective approach for improving those traits.

References

- Afshar E., Heidari B. 2012. Combining ability and gene action for maturity and agronomic traits in different heterosis groups of maize inbred lines and their diallel crosses. *Journal of Crop Science and Biotechnology*, 15(3):219-229.
- Amiruzzaman M., Islam MA., Hasan L., Kadir M., Rohman MM. 2013. Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea mays* L.). *Emirate Journal of Food Agriculture*, 25 (2): 132-137.
- Beck DL., Vaal SK., Carossa J. 1990. Heterosis and combining ability of CIMMYT's tropical early and intermediate maturity maize (*Zea mays* L.) germplasm. *Maydica*, 35:279-285.
- Chaudhary AK., Chaudhary LB., Sharma KC. 2000. Combining ability estimates of early generation inbred lines derived from two maize populations. *Indian Journal Genetics and Plant Breeding*, 60: 55-61.
- Crumpacker DW., Allard RW. 1962. A diallel cross analysis of heading date in wheat. *Hilgardia*, 32: 275-318.
- Davis DD. 1978. Hybrid cotton: Specific problems and potentials. *Advance Agronomy*, 30: 129-147.
- Dehghanpour Z., Ehdaie B., Moghaddam M. 1996. Diallel analysis of agronomic characters in white endosperm maize. *Journal of Genetics and Breeding*, 50: 357-365.
- Griffing B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Science*, 9: 463-493.
- Haddadi MH., Eesmaeil M., Choukan R., Ramech V. 2003. Combining ability analysis of days to silking, plant height, yield components and kernel yield in maize breeding lines. *African Journal of Agricultural Research*, 7(33): 4685-4691.
- Hallauer AR., Miranda JB. 1981. Quantitative genetics in maize breeding. Iowa State University Press, Ames, USA.
- Irshad HM., Ajmal SU., Munir M., Gulfaraz M. 2010. Gene action Studies of different quantitative traits in Maize. *Pakistan Journal of Botany*, 42(2):1021-1030.
- Jinks JL., Hayman I. 1953. The analysis of diallel crosses. *Maize Genetics Cooperation, Newsletter*, 27: 48-54.
- Kalla V., Kumar R., Basandrai AK. 2001. Combining ability analysis and gene action estimates of yield and yield contributing characters in maize. *Crop Research. Hisar*, 22: 102-106.
- Mather K., Jinks JK. 1971. *Biometrical Genetics*. Second Edition. Chapman and Hall Ltd. London.
- Muhammad Y., Muhammad S. 2002. Estimates of heritability for some quantitative characters in maize. *International Journal of Agriculture and Biology*, 4: 103-104.
- Nigussie M., Zelleke H. 2001. Heterosis and combining ability in a diallel among eight elite maize populations. *African Crop Science Journal*, 9:471-479.
- Rahman H., Arifuddin Z., Shah S., Shah A., Iqbal M., Khalil IH. 2013. Evaluations of maize S² lines in test cross combinations I: flowering and morphological traits. *Pakistan Journal of Botany*, 42(3): 1619-1627.
- Singh AK., Shai JP., Singh JK., Singh RN. 1998. Heritability and genetic advance for maturity and yield attributes in maize. *Journal of Applied Biology*, 8: 42-45.
- Sprague GF., Tatum LA. 1942. General vs. specific combining ability in single

- crosses of corn. *Journal of American Society in Agronomy*, 34: 923-932.
- Uddin MS., Amiruzzaman M., Begum SA., Hakim MA., Ali MR. 2008. Combining ability and heterosis in maize (*Zea mays* L.). *Bangladesh Journal of Genetics and Plant Breeding*, 21(1):21-28.
- USDA. 2018. Foreign Agricultural Service, Grain and Feed Annual, Dhaka, Bangladesh.
- Verhalen LM., Murray JC. 1967. A diallel analysis of several fiber property traits in upland cotton. *Crop Science*, 7: 501-505.
- Xu JL., Crouch H. 2008. Genomics of tropical a stable food and feed across the world. pp.333-370. In *Genomics of Tropical Crop Plants*, Springer, London. UK.
- Zare M., Choukn R., Bihamta MR., Heravan EM., Kamelmanesh MM. 2011. Gene action for some agronomic traits in maize (*Zea mays* L.). *Crop Breeding Journal*, 1(2):133-141.
- Zekele H. 2015. Heterosis and combining ability for grain yield and yield component traits of maize in Eastern Ethiopia. *Science Technology and Research Journal*, 4(3):32-37.