Heritability and Genetic Advance Estimates from the Parental Lines of Hybrid Maize (*Zea Mays* L.)

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Abstract

Twenty-two genotypes of maize parental line were grown during 2017-2018 at the Research field of Plant Breeding Division, Regional Agricultural Research Station (RARS), Bangladesh Agricultural Research Institute (BARI), Rahmatpur, Barisal, Bangladesh. The experiment was laid out in randomized complete block design with three replications. Heritabilty, coefficients of variability and genetic advance values were computed for days to tasseling, days to silking, days to maturity, plant height (cm), ear height (cm), cob length (cm) and diameter (cm), number of seed rows per cob, number of seeds per row, number of seeds per cob, thousand grain weight (g) and yield (g/plant). Among all the traits higher phenotypic coefficient of variation (44.53) and genotypic coefficient of variation (44.18) were observed for yield/plant. The uppermost heritability was observed in case of yield per plant (98.41) followed by 1000 seed weight (96.91). Genetic advance was highest for seeds/cob (197.87) followed by 1000-kernel weight (176.86).Greater magnitude of heritability coupled with higher genetic advance in characters under study provided the evidence that these plant parameters were under the control of additive genetic effects. Indicating that selection should lead to a fast genetic improvement of the material.

Key words: Genetic advance, Genotypic variance, Heritability, Phenotypic variance

Introduction

Maize (*Zea mays L.*) is one of the most important cereal crops and has the highest production area worldwide followed by wheat and rice (FAO, 2012). It can be consumed as boiled, roasted, vegetable directly by humans as well as being used for livestock feed. Maize cultivation has changed along with the revolution in genetics and maize breeding programs depend on characterization and genetic diversity among breeding material (i.e. inbred lines, hybrids, populations, landraces and races). Identification of genetically distant parental combinations provides best crop improvements for breeders. Also, it is essential to assess genetic purity of hybrids before seed marketing. Genetic purity is one of the quality criteria required for successful hybrid seed production. Conventionally, purity of F_1 hybrids is assessed by grow-out test (GOT) at the field (Noor *et al.*, 2010; Roos and Wianer, 1991). This test is time consuming and resource intensive. Also, it depends on morphological differences which are usually affected by environmental conditions. Isozyme analysis is an alternative method for seed purity testing but it is limited also by environmental conditions and requires accurate selection of isozymes (Lucchese *et al.*, 1999). Genetic purity can be determined based on agronomical, morphological, biochemical, and molecular analysis (Wang *et al.,* 1994). However, before hybrid development, prospective parent (inbred line) selection is a pre-requisite. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from same variety (Bello *et al.*, 2012; Vasal, 1998). Saxena *et al.* (1998) also reported that manifestation of heterosis usually depends on the genetic divergence of the two parental lines. Knowledge of germplasm diversity among elite breeding materials has a significant impact on the improvement of crop plant (Hallauer *et al.*, 1988). Therefore, this study was conducted to measure the genetic diversity among some parental lines used in hybrid maize breeding programs.

Materials and Methods
Experimental site, genotypes and design

The field experiment was conducted at the Research field of Plant Breeding Division, Regional Agricultural Research Station (RARS), Bangladesh Agricultural Research Institute (BARI), Rahmatpur, Barisal, Bangladesh during the period from 2017 –2018. The experimental materials was consist of 22 diverse inbred lines of maize which were collected from plant breeding division, BARI, Rahmatpur, Barisal. The inbred lines were NS1 to NS22. The experiment was conducted following RCBD design with three replications. The soil of the experimental land belongs to the Non-calcareous Grey Floodplain soils under the Ganges Tidal Alluvium tract. The unit plot size was $4×4m^2$ maintaining a spacing of $60×40$ cm^2. Standard cultural practices were done accurately.

Data Collection
Data were recorded for all studied characters on yield contributing traits viz. Days to tasseling, days to silking, days to maturity, plant height (cm), ear height (cm), cob length (cm) and diameter (cm), number of seed rows per cob, number of seeds per row, number of seeds per cob, thousand grain weight (g) and yield (g/plant).

Estimation of genotypic and phenotypic variances
Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955). Genotypic variance, $a\frac{2}{g} = \frac{GMS-EMS}{r}$ Where, GMS = genotypic mean square, EMS = error mean square, r = replication no.
Phenotypic variance, $\sigma^2_{ph} = \sigma^2_g + EMS$

Estimation of genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV)
Genotypic and phenotypic co-efficient of variation were estimated according to Burton (1952) and Singh and Chaudhury (1985), respectively.

$$GCV\ (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100 \qquad and \qquad PCV\ (\%) = \frac{\sqrt{\sigma^2_{ph}}}{\bar{x}} \times 100$$

Where, σ^2_g= Genotypic variance, σ^2_{ph}= Phenotypic variance and $\bar{x}$= Population mean

Results

Genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance (GA) as percent of mean (GA %) for all the yield contributing traits are presented in Table 1. The Phenotypic variance (δ^2p) was greater than genotypic variance (δ^2g) for all the traits. Among the traits yield/plant exhibited high estimates of GCV (44.18%), PCV (44.53%), highest value of genetic advance in percentage (90.28%) and highest heritability (98.41%).On the other hand highest genetic advance (197.87) was observed in seeds/cob.

Days to tasselling, silking and maturity
The days to tasselling of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 3.38.and 1.56. Whereas days to silking of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 3.31.and 1.56. Similarly, days to maturity of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 3.03.and 1.49. The heritability of days to tasselling was 21.13 and the genetic advance was 1.47, heritability of days to silking was 22.10 and the genetic advance was 1.51 and days to maturity of heritability was24.30 and the genetic advance was 2.26.

Plant height, ear height, cob length and diameter
The plant height of Phenotypic variance (δ^2p) and Genotypic variance (δ^2g) was 14.27and 13.62and ear height of Phenotypic variance (δ^2p) and Genotypic variance (δ^2g) was 22.55 and 22.05. The heritability of plant height was 91.09 and the genetic advance was 44.85 and ear height of heritability was 95.60 and the genetic advance was 33.02. The Phenotypic variance (δ^2p) was greater than genotypic variance (δ^2g). The cob length of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 13.10 and 12.07 and cob diameter of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 13.41 and 11.95. The heritability of cob length was 84.97 and the genetic advance was 3.42. On the other hand, cob diameter of heritability was 79.46 and the genetic advance was 0.85.

Number of rows/ cob and seeds/ cob
The number of rows/cob of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 13.54 and 12.12. In case of seeds/cob of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 30.06 and 28.87. The heritability of no. of rows/cob was 80.05 and the genetic advance was 2.91 seeds/cob heritability was 92.26 and the genetic advance was 197.87.

1000 seeds weight and yield/plant
The 1000 seeds weight of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was30.05 and 29.59. Likewise, the yield/plant of phenotypic variance (δ^2p) and genotypic variance (δ^2g) was 44.53 and 44.18. The Phenotypic variance (δ^2p) was also greater than genotypic variance (δ^2g). The heritability of1000 seeds weight was96.91 and the genetic advance was 176.86. On contrary, heritability of yield/plant was 98.41and the genetic advance was 80.84.

Table 1. Estimation of genetic parameters for yield attributes of 22 inbred maize lines

SL. No.	Characters	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV	GCV	Heritability	GA
1	Days to tasselling	10.92	2.31	3.38	1.56	21.13	1.44
2	Days to silking	10.96	2.42	3.31	1.56	22.10	1.51
3	Days to maturity	20.31	4.94	3.03	1.49	24.30	2.26
4	Plant height (cm)	571.30	520.39	14.27	13.62	91.09	44.85
5	Ear height (cm)	281.15	268.79	22.55	22.05	95.60	33.02
6	Cob length (cm)	3.81	3.24	13.10	12.07	84.97	3.42
7	Shelling	123.67	113.19	14.07	13.46	91.53	20.97
8	Cob diameter (cm)	0.27	0.22	13.41	11.95	79.46	0.85
9	No of rows/ cob	3.11	2.49	13.54	12.12	80.05	2.91
10	Seeds/ cob	10839.80	10000.35	30.06	28.87	92.26	197.87
11	1000 seeds wt(g)	7848.34	7606.10	30.05	29.59	96.91	176.86
12	Yield (g/ plant)	1590.25	1564.90	44.53	44.18	98.41	80.84

Discussion

The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability. Since most of the economic characters (grain yield) are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, the study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection. Table 1 indicated that for all traits PCV were higher than GCV. However, the differences between genotypic and phenotypic coefficient of variation indicated the environmental influence.

Heritability estimates was of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. Almost all traits studied here showed high heritability (Table 1). High heritability for ear length and 1000-kernel weight was also recorded by Noor *et al.* (2010). Aminu and Izge (2012) studied high heritability for plant height and yield/plant. Very high heritability (above 90%) was observed for plant height, ear height, number of kernels/ear, 1000-kernel weight and yield/plant by Bello *et al.* (2012) and Anshuman *et al.* (2013). Character exhibiting high heritability may not necessarily give high genetic advance. Johnson *et al.* (1955) showed high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. Bello *et al.* (2012) recorded higher genetic advance for plant height, number of kernels/ear and yield/plant. In the present study high heritability was found for the trait yield/ plant and high genetic advance was found seeds/cob which indicated the preponderance of additive gene action for the expression of these traits which was fixable in subsequent generations. The author

suggested that these parameters were under the control of additive genetic effects. Sumathi *et al.* (2005) also suggested that these parameters could be manipulated according to requirements, and worthwhile improvement could be achieved through selection. However, high heritability and low genetic advance were observed for ear height, ear length and ear diameter which may be attributed to non-additive gene action governing these traits, and these characters could be improved through the use of hybridization and hybrid vigor.

Maize plant height, yield/plant, number of seeds/cob, 1000 seed weight can be improved by selection, as these characters exhibited high genotypic and phenotypic coefficient of variations along with high heritability and genetic advance. Cob length, ear height and cob diameter had high heritability but the genetic coefficient of variations was low. This indicated that though, the character was highly heritable, its improvement through early generation selection may not give the desired results. Effective selection for superior genotypes was possible considering yield/plant, number of seeds/cob, 1000 seed weight, plant height and ear height can be used as target traits to improve maize grain yield.

In the present study high heritability was found for the trait yield/ plant and high genetic advance was found seeds/cob which indicated the preponderance of additive gene action for the expression of these traits which was fixable in subsequent generations. However, high heritability and low genetic advance were observed for ear height, ear length and ear diameter which may be attributed to non-additive gene action governing these traits, and these characters could be improved through the use of hybridization and hybrid vigor.

Conclusion

Above all the circumstances it can be concluded that among all the traits higher phenotypic coefficient of variation and genotypic coefficient of variation were

observed for yield/plant. Maximum heritability was also estimated in yield per plant followed by 1000 seed weight. Genetic advance was highest for seeds/cob followed by 1000-kernel weight. These diversities could be used for future breeding program to develop a recognized high yielding maize variety in our country. Furthermore, to develop a high yielding variety of maize selection should be done on the basis of desired characters such as yield, no. of seeds/cob and 1000 seeds weight.

References

Aminu, D. and A.U. Izge.2012. Heritability and correlation estimates in maize (*Zea mays* L.) under drought conditions in Northern Guinea and Sudan Savannas of Nigeria. *World Journal of Agricultural Sciences,* 8: 598-602.

Anshuman, V., N.N. Dixit, Dipika, S.K. Sharma and S. Marker.2013. Studies on heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery,* 4: 165-168.

Burton, G.W. 1952. Quantitative inheritance in grass pea. *Proceedings of the 6th International Grassland Congress*, 1: 277-283.

Bello, O.B., S.A. Ige, M.A. Azeez, M.S. Afolabi, S.Y. AbdulmaliqandJ.Mahamood.2012. Heritability and genetic advance for grain yield and its component characters in maize (*Zea Mays* L.). *International Journal of Plant Research,* 2: 138-145.

FAO (Food and Agriculture Organisation). 2012. Statistical database. Available at: http://www.fao.org.

Hallauer, A.R., W.A. Russell and K.R. Lamkey.1988. Corn Breeding. In: Corn and Corn Improvement, 3rd edn. Agron Monogr 18, ASA-CSSA-SSSA, Madison, Wisconsin, USA. pp.469-564.

Johnson, H.W., H.F. Robinson and R.E. Comstock.1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal,* 47: 314-318.

Lucchese, C., G. Dinelli, A. Miggiano and Lovato. 1999. Identification of pepper (*Capsicum spp*) cultivars by field and electrophoresis tests. *Seed Science andTechnology,*27: 37-47.

Noor, M., H. Rahman, Durrishahwar, M. Iqbal, S.M.A. ShahandI.Ullah.2010. Evaluation of maize half sib families for maturity and grain yield attributes. *Sarhad Journal Agriculture,* 26: 545-549.

Roos, E.E. and L.E. Wiener. 1991. Seed testing and quality assurance. *Hort Technology,*11: 65-69.

Saxena, V.K., N.S. Mathi, N.N. Singhand S.K. Vasal.1998. Heterosis in maize: Grouping and patterns. *Proc. of 7th Asian Regional Maize Workshop.* Los Banos, Philippines. February23-27. pp.124-133.

Singh, R.K. and B.D. Chaudhury.1985. Biometrical Methods in Quantitative Genetic Analysis (rev. edition). Kalyani Publisher, New Delhi, India.

Sumathi, P., A. Nirmalakumari and K. Mohanraj.2005. Genetic variability and traits interrelationship studies in industrially utilized oil rich CIMMYT lines of maize (*Zea mays* L.), *Madras Agricultural Journal,* 92: 612-617.

Vasal, S.K. 1998. Hybrid maize technology: Challenges and expanding possibilities for research in the next century. *Proc. of 7thAsian Regional Maize Workshop.* Los Banos, Philippines. February 23-27. pp.58-62.

Wang, C., K. Bian, H. Zhang, Z. ZhouandJ.Wang.1994. Polyacrylamide gelelectrophoresis of salt soluble proteins for maize variety identification and genetic purity assessment. *Seed Science and Technology,* 22: 51-57.