RESEARCH ARTICLE

GENETIC VARIABILITY AND SELECTION PARAMETERS FOR YIELD AND QUALITY TRAITS IN MAIZE

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ABSTRACT

$45F_1$ maize hybrids produced through a line x tester mating and 15 inbred lines and 3 testers were evaluated with three replication at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur to determine the genetic parameters governing the inheritance of grain yield and quantitative traits. The genetic parameters studied among the traits included the mean performance, genotypic variances, phenotypic variances, genotype by environment variances, broad sense heritability and phenotypic and genotypic correlation coefficients. Significant differences were recorded for all traits studied thereby revealing the diversity of the maize genotypes. The grain yield and biological yield which showed high heritability had high genotypic variances suggesting the involvement of additive gene action. Germination %, seedling length (cm) and protein content (%) showed the highest heritability and low genotypic variance suggesting the preponderance of non-additive gene action. Grain yield was positively and strongly correlated with biological yield, germination%, harvest index and seed vigour index. The positive relationships observed in this study imply that the desirable traits in these hybrids could be exploited in further breeding activities for the development of composites and synthetics for the resource constrained maize farmers who cannot access hybrid seeds every year.

INTRODUCTION

Maize is the third most important food crop of the world, after wheat and rice, providing 15% of the protein and 19% of the calories for the developing countries (Shakoor *et al.,* 2007; Nzuve *et al.,* 2014). The maize yield character is influenced by several genes which also interact with various environmental conditions (Bocanski *et al.*, 2009). Thus, the yield has a multiplicative effect on the end product of many factors otherwise referred to as yield components (Zeeshan *et al.*, 2013). The assessment of performance of parental lines based on the yield components could aid in the selection of superior parents for the production of better yielding hybrids (Bocanski *et al.,* 2009). This can successfully be achieved if the genetic parameters which govern inheritance of important traits are established. In addition, the proper characterization of the quantitative traits and their relationship with maize yield and yield component coupled with utilization of the revealed genetic variability could be lead to improvement and broadening of the diversity of the maize gene pool (Alake *et al.,* 2008; Al-Tabbal *et al.,* 2012). The mean values, genotypic and phenotypic variances, heritability and the correlation

coefficients of the traits are some of the key parameters which determine the efficiency of a breeding program. The phenotypic variance explicates the total variance among phenotypes tested in different environments of interest to the plant breeder, while, the total genotypic variance explains the portion of phenotypic variance attributable to the failure of homogeneity among genotypes in different environments (Sujiprihati *et al.,* 2003). The heritability measures the value of selection for a particular trait in various types pf progenies (Al-Tabbal *et al.,* 2012; Lule *et al.,* 2012). It encompasses the phenotypic variance attributable to genetic causes which have a predictive function in plant breeding leading to permanent genetic improvement. This is because a genotype could be selected based on the phenotype given that the environmental effect is separated from the total variability (Bello *et al.,* 2012). The knowledge of heritability establishes appropriate selection method coupled with the prediction of any gains from selection, while, also helping to establish the magnitude of the genetic effects. Larger genotypic variance is most preferred given that high heritability value can be obtained with genotypes with either small or large genetic progress. High heritability is associated with additive gene effect whereas low heritability is due to dominance and epistasis. The coefficient of variance shows that extent of variability represented by the different characters but it excludes the heritable portion.

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Table 1. Analysis of variance for quantitative and qualitative characters in F_1 of maize

	Traits	df	Germination (%)	Seedling length (cm.)	Seed vigour index	Protein content (%)	Oil content (%)	Harvest index (%)	Biological yield	Grain yield/ plant (g)
Mean	Source Replication		23.31	0.71	10094.88	0.02	0.06	0.39	42.85	5.26
sum of	Treatment	63	197.94**	6.99**	204048.34**	0.78**	0.16**	34.87**	7434.74**	770.58**
Squares	Error	126	6.18	0.41	5824.77	0.05	0.05	0.36	78.36	5.81

Table 2. Estimates of mean, phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficient of variation, heritability in broad sense (H^2 %) and genetic advance (GA) in per cent of mean for eight characters in F_1 generation of maize

Characters/Parameters	Mean	H^2 (%)	GA (%)	PCV	GCV	ECV
Germination (%)	86.04	91.00	18.28	9.73	9.29	2.89
Seedling length (cm.)	22.20	84.00	12.62	7.28	6.68	2.89
Seed vigour index	1914.97	92.00	26.51	14.00	13.42	3.99
Protein content (%)	9.85	83.00	9.41	5.51	5.02	2.27
Oil content (%)	4.28	42.00	5.92	6.81	4.42	5.18
Harvest index (%)	30.95	97.00	22.23	11.13	10.96	1.93
Biological yield	229.11	97.00	43.83	21.96	21.61	3.86
Grain yield/ plant (g)	70.62	98.00	46.05	22.87	22.61	3.41

Table 3. Genotypic (G) and phenotypic (P) correlation coefficients among yield and quantitative traits in maize

Characters	Correlation coefficients	Germination (%)	Seedling length (cm.)	Seed vigour index	Protein content (%)	Oil content (%)	Harvest index (%)	Biological yield	Grain yield/ plant (g)
Germination	G	1	0.454**	0.896**	-0.346	-0.186	0.252**	0.275**	0.373**
(%)	P	1	0.387**	0.876**	-0.300	-0.127	0.236**	0.257**	0.351**
Seedling	G		1	0.801**	0.087	-0.013	0.391**	-0.111*	0.094
length (cm.)	P		1	0.781**	0.081	0.022	0.349**	-0.095*	0.089
Seed vigour	G			1	-0.197*	-0.140	0.363**	0.129	0.295**
index	P			1	-0.167*	-0.079	0.340**	0.124	0.282**
Protein	G				1	0.930**	-0.286**	-0.398**	-0.507**
content (%)	P				1	0.605**	-0.248**	-0.358**	-0.454**
Oil content	G					1	-0.318**	-0.112	-0.244*
(%)	P					1	-0.196*	-0.075	-0.156*
Harvest index	G						1	-0.165	0.329**
(%)	P						1	-0.172*	0.323**
Biological	G							1	0.875**
yield	P							1	0.874**
Grain yield/	G								1
plant (g)	P								1

Conversely, the coefficient of correlations help to measure the level of relationships between the traits and also establish the level at which these traits are mutually different (Bocanski *et al.,* 2009; Nagabhushan *et al.,* 2011). The correlations also give reliable and useful information on nature, extent and direction of selection (Zeeshan *et al.,* 2013). This study aimed at understanding the genetic parameters which govern the inheritance of maize yield and other qualitative traits.

MATERIALS AND METHODS

A set of fifteen diverse inbred lines were crossed with three testers in line x tester mating design during rabi, 2013 and F_1 seeds of all the resultant crosses were procured. All the 45 F_1s and their parents (15 lines and 3 testers) were grown in a randomized complete block design with three replications during Kharif, 2015 with one standard check (31Y45) at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh.

The observation were taken for grain yield per plant, biological yield, harvest index, germination%, seedling length (cm), seed vigour index, protein content (%) and oil content(%) on five randomly selected competitive plants of each entry in each replication. Analysis of variance (ANOVA) was carried out to establish the level of significance among genotypes using the Panse and Sukhatme (1967) method. The phenotypic and genotypic coefficient of variability according to Burton and de Vane (1953), heritability in broad sense (Burton, 1952), genetic advance according to Robinson *et al.* (1951) and correlation (Al-Jibouri *et al*, 1958).

RESULTS AND DISCUSSION

Analysis of variance indicated significant differences among the genotypes for all the traits evaluated (Table-1). It indicated that experimental genotypes had sufficient genetic variability for all the characters evaluated (Vishasth *et al.,* 2013; Nzuve *et al.,* 2014). Genetic parameters of yield and their components are given in table-2. In the present study, the highest genotypic coefficient of variances were found for grain yield per plant (22.61), biological yield (21.61) and seed vigour index (13.42), while, lowest genotypic coefficient of variances was found for oil content (4.42) and protein content (5.02). The highest phenotypic coefficient of variances was found for grain yield per plant (22.87) and biological yield (21.96), while, lowest phenotypic coefficient of variance was found for protein content (5.51) and oil content (6.81). The highest environmental coefficient of variances was found for oil content (5.18) and seed vigour index (3.99), while, lowest was found for harvest index (1.93) and protein content (2.27). Similar findings were reported by Satyanarayana *et al.* (2003); Kanagarasu *et al.* (2013); Sharma *et al.* (2014). The higher values of genetic advance were found for grain yield per plant (46.05%), biological yield (43.83%) and seed vigour index (26.51%) and lowest for oil content (5.92%). The greater values of genetic advance indicated that biological yield and seed vigour index can be used for selecting higher yielding genotypes (Nayak *et al.* 2013; Maruthi and Rani, 2015). The highest heritability (98%) was found for grain yield per plant. The range of heritability from 42 to 98%.

The greater values of heritability were found for all the characters except oil content (42%). The higher value of heritability for grain yield per plant, biological yield and harvest index indicates that these characters can be used as the genetic parameters for the improvement and selection of higher yielding genotypes. These results were in accordance with the findings of Sasidharan *et al.* (2012), Maruthi and Rani (2015). The grain yield per plant and biological yield indicated high heritability coupled with genotypic variation by using Mather and Jinks (1982) model of heritability. Crop improvement could be possible by simple selection because high heritability coupled with high genotypic variation revealed the presence of an additive gene effect (Noor *et al.* 2003). On the other hand, low heritability coupled with low heritability coupled with low genotypic variation was observed for oil content. The result indicated that these traits were greatly influenced by the environment (Satyanarayana *et al.,* 2003). A study of table-3 shows that the genotypic and phenotypic correlations coefficients of grain yield per plant with biological yield (0.875), germination% (0.373), harvest

index (0.329) and seed vigour index were positive and significant but negative and significant relation observed with protein content (-0.507) and oil content (-0.244). Also, biological yield showed positive and significant correlation with germination% (0.257) but negative correlation with seedling length (-0.095), protein content (-0.358) and harvest index (-0.172). Similar results have been obtained by Srivastava *et al.* (2002) and Kote *et al.* (2014). Harvest index correlation significant and positively with germination% (0.236), seedling length (0.349) and seed vigour index (0.340). Oil content correlated significant and positively only with protein content (Mahesh *et al.,* 2013). Seed vigour index positively significant correlated with germination% (0.876) and seedling length (0.781). Seedling length significant and positively correlation with germination% (0.876). Similar finding have also been reported by Mahesh *et al.,* (2013).

REFERENCES

Alake, C.O., Oje, D.K., Oduwaye, O.A. and Adekoya, M.A. 2008. Genetic variability and correlation studies in yield and yield related characters of tropical maize (*Zea mays L.) Asset Series A,* 8(1), 14-27.

Al-Jibouri, H.A., Miller, P. A. and Robinson, H. F. 1958. Genotypic and environmental variances in upland cotton of inter-specific origin. *Agronomy Journal*, 50:633-636.

Al-Tabbal, J.A. and Al-Fraihat, A.H. 2012. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotyper. *Journal of Agricultural Science,* 4(3), 193.

Bello, O.B., Ige, S.A., Azeez, M.A., Afolabi, M.S., Abdulmaliq, S.Y. and Mohamood, J. 2012. Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays L.) International journal of plant research,* 2(5), 138-145.

Bocanski, J., Sreckov, Z. and Nastasic, A. 2009. Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays L.) Genetika,* 41(2), 145-154.

Burton, G.W. 1952. Quantitative inheritance in grasses. Proceeding of 6th International. Grassland Congress, 1 : 227-283.

Burton, G.W. and De vane, E.H. 1953. Estimating heritability in tall fescue (*Festuca aruntanaceae*) from replicated clonal material. *Agronomy Journal*, 45: 478-481.

Fisher, R.A. and Yates, F. 1938. Statistical tables for Biological, Agricultural and Medicinal Research. Published by Oliver and Boyd, Edinburgh.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating population of Korean lespedeza. *Agronomy Journal,* 48 : 262-272.

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

Kanagarasu, S., Nallathambi, G., Kannan, S. and Ganesan, K. N. 2013. Genetic variability and association analysis for yield and its components in single cross hybrids of maize (*Zea mays L.) Electronic Journal of Plant Breeding;* 4(4):1319-1324.

Kote, U. B., Kumar, P. V. R., Ahamed, M. L., Rani, Y. A., Rao, V. S. and Adilakshmi, D (2014. Correlation and path analyses in maize (*Zea mays L.) Electronic Journal of Plant Breeding;* 5(3):538-544.

Lule, D., Tesfaye, K., Fetene, M. and De Villiers, S. 2012. Inheritance and association of quantitative traits in finger millet (*Eleusine coracana* Subsp. *Coracana*) landraces collected from eastern and south eastern Africa. *International journal of genetics,* 2(2); 12-21.

Mahesh, N., Wali, M. C., Gowda, M.V.C., Motagi, B. N. and Uppinal N.T. 2013) Genetic analysis of grain yield, starch, protein and oil content in single cross hybrids of maize. *Karnataka J. Agric. Sci.,* 26(2) : 185-189

Maruthi, R. T. and Rani, K. J. 2015) Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *Journal of Applied and Natural Science;* 7(1):149-154.

Mather, K. and Jilks, J.L. 1982. The study of continuous variation. 3rd ed. London: Chapman and Hall; *Biometrical genetics*.

Nagabhushan, N. M., Mallikarjuna, C. H., Shashibhaskar, M. S. and Prahalada, G. D. 2011. Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays L.) Current Biotica*, 5, 157-163.

Nayak, V. H. Rajesh Singh Potla, K. R.(2013) Genetic variability analysis of yield and yield related traits in inbred lines of maize(*Zea mays* L.) *Environment and Ecology*; 31(4):1669-1671.

Noon, F., Ashaf, M. and Ghafoor, A. 2003. Path analysis and relationship among quantitative traits in chickpea. *Pak. J. Biol. Sci.,* : 551-555.

Nzuve, F., Githiri, S., Mukunya, D. M. and Gethi, J. 2014. Genetic variability and correlation studies of grain yield and related agronomic traits in maize. *Journal of Agricultural Science,* 6(9), 166-176.

Panse, V.G. and Sukhatme, D.V. 1967. Statistical methods for agricultural workers, ICAR, New Delhi, Second England Edition.

Robinson, H., Comstock, R.F. and Harvey, P.H. 1951. Genotypic and phenotypic correlations in corn and their importance in selection. *Agron. J.,* 43 : 282-287.

Sasidharan, N., Chakraborty, S., Patel, J.N., Trivedi, R., Panwar, B.S. and Vala, A. 2012. Genetic analysis and character association studies for yield and different phenotypic characters in maize (Zea mays L.) *International Journal of Planr Sciences*, 7(2); 341-350.

Satyanarayana, E., Shanthi, P., Rekha, P. M. and Kumar, R. S.(2003. Studies on the identification of suitable parents from high-oil maize (*Zea mays* L.) germplasm for making potential single cross hybrids *Research on Crops;* 4(3): 348-354.

Shakoor, M. S., Akber, M. and Hussain, A. 2007. Correlation and path coefficients studies of some morphophysiological traits in maize double crosses. *Pak. J. Agri. Sci.,* 44(2), 213-216.

Sharma,R., Maloo, S. R. and Joshi, A. 2014. Genetic variability analysis in diverse maize genotypes (*Zea mays* L.) *Electronic Journal of Plant Breeding;* 5(3): 545-551.

Srivastava, A. and Singh, I.S. 2002. Heterosis and combining ability for yield and maturity involving exotic and indigenous inbred lines of maize (*Zea mays L.) Indian Journal of Genetics and Plant Breeding*, 63(4): 345-346.

Sujiprihati, S., Saleh, G. B. and Ali, E. S. 2003. Heritability, performance and correlation studies on single cross hybrids of tropical maize. *Asian Journal of Plant Science*,2(1); 51-57.

Vashistha, A., Dixit, N. N., Dipika, Sharma, S.K. and Marker, S. 2013. Studies on heritability and genetic advance estimates in maize genotypes. *Bioscience Discovery*, 4(2); 165-168.

Zeeshan, M., Ahsan, M., Arshad, W., Ali, S., Hussain, M. and Khan, M.I. 2013. Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. *International Journal of Adnanced Research,* 1(5); 24-29.

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