RESEARCH ARTICLE

Estimates of variability, heritability and genetic advance for elite germplasm accessions in maize

Mehran Khan and Muhammad Amin Khan

Faculty of Agriculture, Department of Genetics and Plant Breeding, Gomal University, D. I. Khan, KPK, Pakistan

Corresponding authors email Id: mehrankhanpbg@gmail.com

Manuscript received: Sept. 2, 2018; Decision on manuscript: Nov. 10, 2017; Manuscript accepted: December. 9, 2018

Abstract

Twenty four maize accessions evaluated at Agriculture research Institute Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan during winter 2016-2017. Highly significant genotypic differences were recorded for all the traits which implies that there is a considerable amount of variation among genotypes for each character except no of cobs plant-1. The estimates of GCV were moderate all most all the characters except for no of cob plant-1, days to 50% silking and high for kernel yield plant-1. The estimates of PCV was moderate all most all the characters while low for a days to 50% silking and high for kernel yield plant-1 and no. of cob plant-1. High heritability was recorded for all the characters except for no. of cob plant-1. Genetic Advance value low for all the traits while high for plant height (cm) and kernel yield plant-1(g) which implies that these traits could be used to select maize accession for a further improvement. Such information will help to recognize the promising maize accessions which could be used for breeding programme and to develop varieties and hybrids suitable for Dera Ismail Khan, KPK, Pakistan.

Key words: Genetic variability, heritability, genetic advance, maize, yield

Introduction

Maize has great importance for several countries include India France and Argentina Pakistan, America, China, Brazil, Mexico, Indonesia (Aziz et al., 1992). It is grown on more than 120 million hectares and is called the "king of grain crops" (Vara Prasad and Shivani, 2017). In Pakistan grain yield of maize is 5,200 MT which is really low as compared to other countries like United States 386,748.0 MT, China 216,000.0 MT, Brazil 83,500.0 MT, Argentina 36,500.0 MT and India 24,500.0 (Anonymous, 2016). Between crop species the success of any crop does not depend upon the quantity of genetic variability. The nature and significant of genetic variability, heritability present in a population of any crop species is play a vital role for the crop improvement program and it causes after crossing the transfer of morphological attributes to successive generation. Genetic variability of agronomic characters also plays a central role in breeding programs enhancing the gene pool of crops. Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects. Hence, in relevance to above discussion the objective of the present study was to find out genetic variability in twenty four accessions of maize.

Materials and methods

The present experiment were conducted in the area of agriculture research institute (ARI), Dera Ismail Khan (KPK) during spring season (2016-2017) to estimation of genetic variability and broad sense heritability in 24 elite maize germplasm which were coded from 1210 to 1233. The experiment were laid out by using RCBD design with row to row distance is 75cm and plant to plant distance is 25cm and each line 4m in length. All the standard agronomic cultural practice and recommended dose of NPK were applied at the time of silk production. Data on randomly selected five plants were taken on eight traits viz., days to 50% emergence, plant height (cm), days to 50 % tasseling, days to 50% silking, cob girth (cm), yield kernel plant⁻¹ (g) and no. of cob⁻¹. Analysis of variance was calculated as suggested by Singh and Chaudhary (1985). Broad sense heritability was calculated as suggested by Falconer (1989) and LSD test was utilized when ANOVA showed significant differences among the accessions.

Results and discussion

Analysis of variance is presented in table 1 and *per se* performance of the maize accessions is presented in table 2. Highly significant differences (p≤0.01) observed for almost all the quantities attributes. However, the non-significant differences were recorded for number of cobs plant-1.

Large variation is present among the maize accessions based on *per se* performance which indicates good amount of variability among the accessions. The days to 50% emergence varied

from 9.33 to 15.00. Maximum days (15.00) were recorded in accession code 1212 while minimum days (9.33) were recorded in 1216. Days to 50% tesseling ranged from 42.00-62.66. Early flowering was observed in accession code 1228 sparkly early maturing accession while late flowering was observed in accession code 1214. Abdurakhmonov and Abdukarimov (2008) reported similar results for days to 50% emergence and days to 50% flowering. The plant height ranged from 153.33-228.00 cm among the maize accession. Maximum height (228.00 cm) was recorded in accession 1222 while minimum plant height was recorded in accession 1216. For parameter 100 grain weight along with maximum 100-grain weight was found in accession code 1217 while minimum was found in accession 1230. The cob length (cm) varied from 16.66 to 24.33 among the maize accession. Maximum length (24.33) was recorded in accession code 1229 while minimum length (16.66) was recorded in accession code 1210. The Kernel yield plant-1 (g) ranged from 50 to 662.00 among the maize accession. Maximum the kernel yield plant-1 (g) (662.00) was recorded in accession 1230 while minimum the kernel yield plant-1(g) was recorded in accession 1210. Highly significant differences for kernel yield plant-1 were obtained by reported by Alvi et al., (2003) as well. Therefore, it is seen from the mean presentation that variable range was there among all the elite maize accessions.

Variability parameters for various studied traits in 24 maize accessions are presented in table 3. For days to 50% emergence the genetic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) vales ranges between 14 and 16 the value of genetic variance (GV) and phenotypic variance (pv) between 2.62 and 3.51 respectively. The values PCV were larger than GCV which indicates the interaction of environment for the trait. The heritability value for days to 50% emergence is 75 and the

value of genetic advance is 4. The variation among high heritability and low genetic advance depicts that there is a more role of non additive gene. Similar result is recorded by earlier researchers such as Reif et al., (2005). The values GV and PV were 28 and 31 for days to 50% teaseling. Low values of GCV i.e. 10.15 and PCV was i.e.10.73 recorded. Heritability value was noted as 90.00 and expected genetic advance was 10.39. Very high values for heritability and moderate genetic advance are depicted according to the present find. The results for heritability and genetic advance for this parameter were encouraged by Rajesh et al., (2013). High heritability values along with moderate genetic advance indicate that the character is under the control of non additive gene action and selection may be effective during early generations. The value of genotypic variance, phenotypic variance is 3.28 and 5.37 for days to 50% silking. Small differences between PV and GV suggest that there is small influence of environment in the expression of character. For silking the values of GCV and PCV was 3.21 and 4.10 respectively. The heritability value of this parameter was 61.00 and the value of expected genetic advance recorded was 3.00. Singh et al., (2017) also reported high heritability along with low value of genetic advance. For plant height gcv and pcv recorded in between 10.65 and 11.90 but from analysis in variance the value of GV and PV ranged between 378.25 and 472.55 respectively. The values of PCV were larger than GCV which means the huge interaction of environment with plant height. Similar results were reported by and Khan et al., (2017). Heritability for plant height is 80.00 but the value of genetic advance is 36.00. The variation among high heritability and high genetic advance shows that there is a more role of additive gene. Tengan et al., (2012) found similar high values of heritability and high value of genetic advance for plant height in maize. For cob length (cm) genetic coefficient of

variation and phenotypic coefficient of variation ranged from 11.09 and 13.67 but the value of genetic variance and phenotypic ranged between 5.64 and 8.58 (Table 3). The values of PCV were larger than GCV which means the interaction of environment for cob length. Similar results were reported by Khan et al., (2017). The value of heritability for cob length is 66 and genetic advance is 4.00. The variation among high heritability low genetic advance appears that there is a more role of non-additive gene. Same results were reported by Tengan et al., (2012). For 100-grains weight the value of genotypic variance (GV) was 10.35 and phenotypic variance was 13.81. The values of GCV and PCV were 10.32 and 11.92 respectively. Heritability estimates was 75 and expected genetic advance was 6 (Table 4). The variation among high heritability low genetic advance appears that there is a more role of non additive gene. An estimate of GV and PV for kernel yield plant-1 (g) was 14746.53 and 14797. Value of the GCV was 58.13 while the value of PCV was 58.53. The value PCV was larger than GCV which indicates the interaction of environment with kernel yield plant-1 (g) similar observations was reported by Abirami et al., (2005). The heritability value for this parameter was 99.65 and expected genetic advance was 250.0. The deviation among high heritability high genetic advance implies that there is a more role of additive gene. Khan et al., (2017) reported similar results for PCV, GCV, heritability, and genetic advance which encouraged the current findings. Such information will help to recognize the promising maize accessions which could be used for breeding programme and to develop varieties and hybrids suitable for Dera Ismail Khan, KPK, Pakistan.

References

1. Abdurakhmonov, I. and A. Abdukarimov 2008. Application of association mapping to

- understanding the genetic diversity of plant germplasm resources. Int J of Plant Genomics, 1-18.
- Alvi M.B.M., Rafique, M., Tariq, S., Hussain, A., Mahmood, T., Sarwar, M. 2003. Character association and path coefficient analysis of grain yield and yield components maize (*Zea mays L.*). *Pak J Biol. Sci.*, 6(2):136-138.
- Anonymous. 2016. Agriculture Statistics of Pakistan. Ministry of Food, Agriculture and Livestock, Federal Bureau of Statistics, Islamabad.
- 4. Abirami, S., Vanniarajan, C. and Armugachamy, S. 2005. Genetic variability Studies in maize (*Zea mays* L.) germplasm. *Plant Archi.*, 5 (1): 105-108.
- Aziz, A., Saleem, M., Rahman, H. and Mohammad, F. 1992. Genetic variability for yield and disease resistance in full and short season varieties of maize. *Sarhad J Agri.*, (8): 195-198.
- Falconer, D.S. 1989. Introduction to Quantitative Genetics. Third Edition. Longman Scientific and Technical. Copublised in the United States with John Wiley and Sons. P.163.
- Khan, B., Nawab, N.N., Qamar, M., Abbas, M., Haroon, M., Intikhab, A, Ahmed, H., Ahmed, I., Khan, K. and Afreen, M. 2017. Genetic variability in different maize (*Zea mays L.*) genotypes for comparative yield performance under local conditions of Rawalakot, Azad Jammu and Kashmir. *Int J. Bio. Sci.*,11(3):102-107.
- 8. Rajesh, V., Kumar, S. S., Reddy, V. N. and Sankar, A. S. 2013. Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). *Int. J. Applied Biology Pharmc. Techn.*, 4(4): 0976-4550.
- 9. Reif, J.C., Hallauer, A.R. and Melchinger, A.E. 2005. Heterosis and heterotic patterns in maize. *Maydica*, 50: 215-223.

- Singh, R. K. and Chaudhary, B. D. 1985.
 Biometrical methods in quantitative genetic analysis. Kalyani Publishers New Delhi India.
- 11. Tengan, K.M.L., Obeng-Antwi, K. Akromah, R. 2012. Genetic variances, heritability, and correlation studies on selected phenotypic traits in a backcross breeding program involving normal and opaque-2 maize. Agric. Biol. J. N. America., 3(7): 287-291.
- 12. Vara Prasad, B.V.V. and Shivani, D. 2017. Correlation and path analysis in maize (*Zea mays* L.). *J. Genet., Genomics, Plant Breed.*, 1(2): 1-7.

Table 1: Analysis of variance in 24 maize accessions

Parameters	Mean	MS	CV
Days to 50% emergence	11.81	8.75**	7.55
Days to 50% tasseling	52.181	87.74**	3.32
Days to 50% silking	56.33	11.44**	2.57
Plant height (cm)	182.47	1229.07**	5.32
Cob Length (cm)	21.36	19.88**	8.33
100-grain weight(g)	31.15	34.52**	5.98
Kernel yield plant ⁻¹ (g)	208.90	44290**	3.40
No of cobs	2.20	2.20 ^{N.S}	4.94

^{*, **} Significant at p≤0.05 and p≤0.01, N.S. = Non-significant,

Table 2: Per se performance for quantitative traits in 24 maize accession

Accessions	Days to	D ays to	Days to	Plant	100-grian	Cob	Yield	No. of
codes	50	50%	50%	height	weight (g)	length	plant ⁻¹	cob ⁻¹
	emergence	tasseling	silking	(cm)	8 (8)	(cm)	(g)	
1210	11.66	52.66	56.00	178.3	28.00	16.66	50.00	2.33
1211	11.66	54.00	57.33	176.67	34.33	21.33	64.33	2.56
1212	15.000	48.66	60.00	171.33	30.33	30.00	54.00	2.00
1213	11.00	45.00	52.00	171.00	30.00	19.00	160.67	2.53
1214	11.66	62.66	55.00	165.33	31.00	21.66	200.33	3.33
1215	10.66	48.00	57.33	155.00	32.33	22.00	232.00	2.10
1216	9.33	57.00	58.00	153.33	33.00	24.00	216.00	2.60
1217	10.33	54.33	57.33	218.00	37.00	23.00	261.00	2.28
1218	11.0	54.00	54.66	160.00	34.00	18.66	294.60	3.06
1219	11.00	46.66	55.66	188.33	30.3	21.00	122.33	2.40
1220	13.66	51.33	56.00	208.67	33.66	22.66	222.00	3.00
1221	13.00	58.66	55.00	174.33	36.00	20.33	236.67	2.53
1222	10.00	58.00	57.00	228.00	34.00	23.33	141.00	2.33
1223	10.33	48.33	55.33	185.67	32.00	21.00	140.00	2.60
1224	11.33	49.66	59.00	186.00	29.00	20.00	157.00	1.90
1225	12.66	45.00	56.66	168.00	32.33	20.66	155.00	1.90
1226	13.66	56.00	55.33	180.00	29.66	22.00	218.33	2.26
1227	13.66	59.33	58.66	172.00	33.00	20.33	207.00	2.53
1228	14.66	42.00	60.00	168.67	30.66	19.33	243.6	2.50
1229	14.66	45.00	53.33	180.00	23.33	24.33	330.6	3.36
1230	12.66	58.33	56.00	192.67	22.33	19.33	662.6	11.0
1231	10.00	50.66	56.66	220.00	30.00	22.00	134.00	2.20
1232	9.66	53.66	54.33	204.00	32.00	19.33	232.33	2.66
1233	10.33	11.000	55.33	174.00	29.33	20.667	278.00	2.00
Range	9.33-	42.00-	52.00-	153.33-	16.66-	22.13-	50.00-	1.90-
	15.00	62.66	60.00	228.00	24.33	37.00	662	11.00

CV = Coefficient of variation

Journal of Genetics, Genomics & Plant Breeding 3(1) 11-16 (January, 2019) ISSN (Online): 2581-3293

Table 3: Variability parameters for various studied traits in 24 maize accessions

Parameters	GV	PV	GCV	PCV	$h^2_{BS}\%$	GA
Days to 50% emergence	2.62	3.51	14	16	75	4
Days to 50% tasseling	28	31	10.15	10.73	90	10.39
Days to 50% silking	3.28	5.37	3.21	4.10	61	3
Plant height (cm)	378.25	472.55	10.65	11.90	80.00	36.00
Cob Length (cm)	5.64	8.58	11.09	13.67	66	4
100-grain weight	10.35	13.81	10.32	11.92	75	6
Kernel yield plant ⁻¹ (g)	14746.53	14797	58.13	58.23	99.65	250.00
No of cobs	0.01	2.09	0.49	65.45	0.71	2.10

Where, Vg: genotypic variance; Vp: phenotypic variance; GCV: genotypic coefficients of variation; PCV: phenotypic coefficients of variation H2BS: broad sense heritability; GA: genetic advance as percent of mean