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Research Note

Genetic variability analysis in diverse maize genotypes (*Zea mays* L.)

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Abstract

The present study was carried out to assess the genetic variability, heritability, genetic advance for yield and kernel quality traits in twenty diverse maize genotypes. The crop was raised at Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan) during *kharif* 2012. The trials were set up in randomized block design with three replications. Highly significant differences were observed for all the traits studied. Genetic variability parameters showed that phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV) and heritability is high for most of the traits. High genetic advance as percent of mean (genetic gain) along with high estimate of heritability and GCV are also observed for most of the traits. Test weight, grain yield per plant, grains per cob, cob length, grains per row and harvest index are important in selection programms aiming to maize yield improvement and the breeder may consider these traits as the main selection criteria.

Keywords:
Maize, Genetic advance, Heritability, Genotypic and phenotypic coefficient of variation.

Maize (*Zea mays* L.), with a remarkable productive potential among the cereals, is the third important grain crop after wheat and rice and belongs to the tribe Maydeae, of the grass family, Poaceae. Maize is widely cultivated in tropics, sub-tropics and temperate regions of the world. In India, this crop is cultivated in an area of 8.55 million hectares with a total net production of 21.73 million tonnes and an average productivity of 26.81 quintals per hectare during 2011-12, but the yield level was low at 2.06 tonnes per hectare compared to world average 5.12t/ha (Anonymous., 2012). Presence of high amount of carbohydrates, fats, proteins, vitamins and minerals maize acquired a well deserved reputation as a poor man's nutria-cereal. Several million people, in the developing countries, derive their protein and calorie requirements from maize. Protein from cereals including normal maize, have poor nutritional value because of reduced content of essential amino-acids such as lysine and tryptophan leading to harmful consequences such as growth retardation, protein energy malnutrition, anemia, pellagra, free radical damage etc. Normal maize varieties are deficient to two essential amino acids, lysine and tryptophan (Azevedo and Arruda, 2010; Mbuya *et al*., 2011). Maize mutants for high lysine and tryptophan have been reported in several studies. Likewise, lysine metabolism and endosperm protein synthesis in maize mutants are well documented in various reports (Azevedo *et al*., 2004). The lysine and tryptophan content in normal maize varieties is less than a half of the recommended rate for human nutrition (FAO/WHO-Expert consultation, 1990). This problem has been addressed through research breakthroughs at CIMMYT in the late 1990's that lead to the development of quality protein maize (QPM) that content twice the amount of lysine and tryptophan (Krivanek *et al*., 2007).

Genetic improvement in traits of economic importance along with maintaining sufficient amount of variability is always the desired objective in maize breeding programme (Hallauer and Scobs, 1973). To improve genetic diversity of local germplasm, it is important to know the extent of already existing genetic variability in the material. Genetic variability, which is a heritable difference among cultivars, is required in an appreciable level within a population to facilitate and sustain an effective long term plant breeding programme. Thus analysis of genetic component of variability is essential for improvement of a trait. Among several traits, grain yield is a complex trait conditioned by interaction of various growth and physiological process throughout the life cycle. The nature of association between grain yield and its components determine the appropriate traits to be used in indirect selection for improvement in grain yield. Direct selection for yield based on *per se* only might not be the most efficient method for traits improvement, but indirect selection for other yield related traits, which are closely associated with yield and their components *viz.*, cob length, cob girth and grain per cob**.** Estimates of heritability was extensively used by plant breeders in selection of promising genotypes and in prediction of percent heritability of desirable traits Morakinyo (1996). Keeping this back ground in view, the present study was undertaken to analyze the variance, genetic variability, heritability, genetic gain among 20 elite genotypes of maize.

The present investigation was carried out at the Instructional Farm, Rajasthan College of

Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan) during *kharif* 2012. The nucleus seed of five genotypes of high quality protein maize were obtained from CCHAU, Hisar, five hybrids and seven composites and remaining three local land cultivars were obtained from NAIP, Biodiversity, PBG, Rajasthan College of Agriculture (Table-1). Twenty diverse genotypes were raised in randomized block design with three replications. All the recommended package of practices were applied to raise a good and healthy crop. The data were recorded on five randomly selected plant samples from each replication for eleven characters, *viz.* plant height, days to 50% flowering, cob length, cob girth, number of kernel rows per cob, number of kernels per row, hundred grain weight, biological yield per plant (after removing cobs from plant, plant are dried and weighted on digital electrical balance), grain yield per plant, harvest index and days to maturity. Data from average mean values from each replication was utilized for following statistical analysis of all the characters. The data recorded on different characters were statistically analyzed using software WINDOSTAT version 7.0 developed by Indostat Services Ltd., Hyderabad, India. The analysis of variance for Randomized Block Design was carried out on the basis of the model described by Panse and Sukhatme (1985) for individual characters. To estimate the extant of magnitude of variation among examined traits, all data were analyzed according to Singh and Chaudhary (1985). Variance genotypic and phenotypic variance were estimated using the formula (Wricke and Weber, 1986).

Success of a breeding programme largely depends on the extent of genetic variability present in the material, greater the diversity in the material better the chances for evolving promising and desired types. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic components being the heritable part of the total variability, its magnitude for yield and related characters influence the selection strategies to be adopted by the breeders. Morphological markers differ among species, genus and varieties of plants. It is the easiest and quickest way to identify or detect the variation in morphological traits for improvement (Bagali *et al*., 2010). However, these traits are largely affected by environmental variations until and unless these are studied minutely over locations and variable environmental conditions *viz.*, temperature and climate.

Aanlysis of variance: The average mean squares for different characters (Table 2) revealed that the mean squares due to genotypes were highly significant for all the characters, including grain protein content, indicated the presence of significant genetic variability in the material providing sufficient scope for further selection. Similar, kind of genotypic variation is also observed in their material of maize for one or other aforesaid traits by Ahmad *et al*. (2011) and Atif and Mohammed (2012).

Mean Performance: Mean value of all characters indicate the normal distribution of genotypes in the present study and hence, representing wide spectrum of variability (Table 3). The coefficient of variation for traits studied being in the range of 2.88 to 13.52 indicated the adequacy of the material and characters studied for further estimation of genetic variability parameter in present investigation (Table 3). Genotypes classified according to their high *per se* performance for all the characters are listed in Table 4. HQPM-5 showed superiority for cob characters *viz*., cob length, cob girth and grain per cob. Lines HQPM-1, EQH-16, HQPM-7, BIO-9637 and EQH-16 were also superior for grain yield contributing characters *viz.*, cob length, cob girth and grain per cob, thereby indicating that grain yield is the end product of its component. The total soluble protein of maize genotypes were estimated by Lowry’s method and it was varied in all the genotypes. High soluble protein (ranged from 6.4 to 10.2) was recorded in HQPM-5, HQPM-1, EQH-63, HQPM-7, EQH-16 and Navjot over average protein (8.3 mg/g). Genotypes, EQH-63 HQPM-5, HQPM-7 and HQPM-1 exhibited high performance for grain yield per plant. Based on the mean performance, HQPM-5, HQPM-1 and EQH63 displayed superiority for grain yield, biological yield as well as for grain protein content. Therefore, these genotypes could be utilized in breeding programmes.

Genetic Variability: Environment has great influence on many quantitative and qualitative traits of plants. This influence showed heritable and non-heritable variation, which can be estimated by the parameters like genotypic coefficient of variation (GCV), heritability and genetic gain. Mean standard error, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic gain as percentage of mean were given in Table-5. It revealed that phenotypic coefficient of variation (PCV) was higher than respective genotypic coefficient of variation (GCV) for all traits, but a relatively marginal difference was observed between PCV and GCV for leaf number, plant height, days to maturity, cob girth, grains yield per plant, harvest index and grain protein content revealed that variability was due to genotypic differences. On the other hand, environmental influences were predominant for the characters *viz.*, days of 50% flowering, cob length, grain per cob, grains per row, test weight and biological yield per plant. Therefore, selection based on the above characters is expected to be effective while for other characters selection must be performed carefully considering environmental factors. High GCV was recorded for test weight, grains per cob, grains per row and harvest index. Similar results were also reported by Kabdal *et al.* (2003) for grain yield, ear length and harvest index in maize genotypes. Moderate GCV was recorded for grain yield per plant, cob length, cob girth, days to 50 percent flowering, leaf number and days to maturity. However, characters like plant height and biological yield per plant showed comparatively low estimates of GCV and PCV indicating that these characters were highly influenced by the environment.

Heritability (broad sense) estimates were high (>70%) for all the traits except leaf number, plant height, grains per row, biological yield and grain protein content. The estimates of heritability in broad sense were moderate to high for most of the characters *viz*., grains per cob, test weight, grain yield per plant and harvest index. Mahmood *et al.* (2004) reported broad-sense heritability, for days taken to tasseling, number of days taken to silking, plant height, ear length, number of kernel rows per ear, number of kernels per row, 100-grain weight and grain yield per plant in maize. Vashistha *et al*. (2013) revealed high broad-sense heritability were observed for plant height, ear length and ear girth in maize. While assessing the overall position, the present study revealed high genetic advance as percentage of mean (genetic gain) along with high estimate of heritability and GCV for test weight, grain yield per plant, grains per cob, cob length, grains per row and harvest index. Kabdal *et al.* (2003) reported high heritability and genetic advance for grain yield, ear height, plant height and ear length. However, high heritability with moderate genetic advance was recorded for days to 50 percent flowering, cob length, cob girth, grain yield per plant and days to maturity indicating involvement of both additive and non-additive gene action and hence selection for these characters based on phenotypic observations alone may not be effective. Bello *et al*. (2012) revealed high heritability along with high genetic advance recorded for grain yield, grains per ear, ear weight, plant and ear heights providing evidence that these parameters were under the control of additive gene effects and effective selection could be possible for improvement of these characters.

This study exhibited high significant difference for analysis of variance in all the traits. The variability parameters showed that phenotypic coefficient of variation (PCV) was higher than respective genotypic coefficient of variation (GCV) and high estimates of broad-sense heritability within the traits revealing that variation were transmitted to the progeny. High to moderate heritability indicated considerable potential for development of high yielding varieties through selection of desirable plants in succeeding generation. High genetic advance as percentage of mean (genetic gain) along with estimate of heritability and GCV are also present for most of the traits. Test weight, grain yield per plant, grains per cob, cob length, grains per row and harvest index are important in selection programms aiming to maize yield improvement and the breeder may consider these traits as the main selection criteria.

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Table 1. Pedigree and source of 20 genotypes of maize used for study

Genotype	Pedigree	Source
QPM		
HQPM-1	HKI-193-1 X HKI-163	CCS HAU, Hisar
HQPM-5	HKI-163 X HKI-161	CCS HAU, Hisar
HQPM-7	HKI-193-1 X HKI-161	CCS HAU, Hisar
EQH-16	Unknown	CCS HAU, Hisar
EQH-63	Unknown	CCS HAU, Hisar
Hybrids		
PHM-1	EI-116 X EI-634	MPUAT, Udaipur
PHEM-2	CM-137 X CM-138	IARI, New Delhi
PHM-2	EI-472 X EI-460	RCA (MPUAT) Udaipur
BIO-9637	Unknown	Bioseed Company
HM-8	HKI-163 X HKI-163	CCS HAU, Hisar
Composites		
Arawali	Bulk of early and stress tolerant HS families from X-2 W pool	RCA (MPUAT) Udaipur
PM-3	Bulk of CEW- 8 pool	RCA (MPUAT) Udaipur
PM-4	Bulk of material pool-2	RCA (MPUAT) Udaipur
PM-5	Bulk of II HS progenies selected from C3 cycle of material pool-2	RCA (MPUAT) Udaipur
Navjot	Pratap x Tarun	PAU, Ludhiana
PM-6	Compositing of 11 early to medium white seeded entries	RCA (MPUAT) Udaipur
EC-3161	Unknown	RCA (MPUAT) Udaipur
Local land races		
Black Sathi	Local land race	RCA (MPUAT) Udaipur
Kumbhalgarh Malan	Local land race	RCA (MPUAT) Udaipur
Chanawada Sathi	Local land race	RCA (MPUAT) Udaipur

Table 2. ANOVA for various characters in maize.

Characters	Source of variation		
	Replications	**Treatments**	**Error**
Degree of freedom	**2**	**19**	**38**
Leaf number	0.82	1.70**	0.32
Plant height	263.20**	237.16**	31.19
Days of 50% flowering	88.35**	61.24**	6.68
Days of maturity	21.80	186.18**	14.94
Cob length	4.08*	14.29**	1.11
Cob girth	0.27	2.81**	0.23
Grain/ cob	2119.21	34052.91**	2561.28
Grain/row	12.11	93.92**	19.45
Test weight	0.57	41.35**	2.25
Grain yield /plant	144.48**	400.30**	10.20
Biological yield/ plant	57.43	114.65*	61.32
Harvest index	61.14**	98.63**	4.58
Grain protein content	0.42	2.42**	0.54

* Significant at 5 per cent and **Significant at 1 per cent probability level

Table 3. Mean performance of different genotypes for various characters in maize.

S. No.	**Variety**	**Leaf number**	**Plant height (cm)**	**Days of 50% flowering**	**Days of maturity**	**Cob length (cm)**	**Cob girth**	**No. of grain/ cob**	**No. of grain/row**	100 grain weight (g)	**Grain yield/ plant**	**Biological yield (g)**	**Harvest index (%)**
1	HQPM-1	13.44	191.57	59.33	112.66	17.74	12.50	577.66	39.00	18.91	93.90	201.23	46.29
2	HQPM-5	13.77	189.21	57.00	109.67	18.53	13.10	653.66	43.00	17.48	98.10	207.43	46.81
3	HQPM-7	12.41	183.03	56.01	108.00	15.76	12.63	551.67	34.00	15.81	95.23	216.90	45.17
4	EQH-16	13.30	187.87	54.02	105.00	16.86	12.30	570.00	39.67	16.45	88.26	216.80	38.91
5	EQH-63	13.98	192.49	54.01	106.00	18.16	13.93	639.33	31.33	19.11	98.86	210.86	47.00
6	PHM-1	12.20	183.68	48.66	97.33	18.00	11.76	335.33	35.00	19.54	69.23	211.70	32.82
7	PHM-2	11.75	192.17	51.01	99.66	15.23	13.06	440.33	35.67	18.93	83.30	212.96	37.99
8	PHEM-2	12.19	184.34	49.66	92.33	17.30	12.90	346.33	32.33	22.18	83.76	211.16	38.67
9	BIO-9637	11.45	198.47	53.00	108.66	16.50	14.23	469.66	36.00	25.45	93.60	201.53	46.45
10	HM-8	12.38	185.18	51.33	102.33	15.10	11.46	291.34	31.33	16.95	70.60	212.93	33.22
11	Navjot	13.39	189.78	47.66	100.66	14.16	10.70	389.34	22.66	21.04	69.50	212.60	33.33
12	PM-3	12.56	190.63	45.67	103.00	15.10	11.23	438.00	25.33	20.63	70.50	215.10	33.32
13	PM-5	13.01	197.71	53.33	105.34	13.03	13.00	507.67	28.00	22.01	69.30	214.50	32.41
14	PM-4	13.05	184.72	53.33	105.00	14.93	12.00	426.09	25.33	16.35	77.80	206.13	38.31
15	Arawali	13.13	198.56	48.67	100.67	15.00	11.06	458.67	37.67	17.10	67.36	215.76	31.77
16	B.Sathi	13.60	210.78	42.34	80.68	18.20	11.76	360.67	34.67	26.13	86.90	201.23	41.25
17	EC-3161	12.95	187.83	46.67	97.67	11.06	13.23	410.34	35.33	20.94	65.56	213.16	31.18
18	PM-6	14.48	213.26	50.66	105.67	15.60	12.10	430.00	27.00	23.04	77.06	217.26	38.82
19	K. Malan	13.37	206.12	44.00	93.01	11.20	11.13	319.66	25.00	14.55	66.73	216.93	30.94
20	C. Sathi	13.33	199.72	44.67	87.76	13.90	11.73	355.33	29.00	25.23	75.11	207.98	36.57
Mean		**13.03**	**193.36**	**50.60**	**101.05**	**15.57**	**12.29**	**447.56**	**32.36**	**20.14**	**80.03**	**211.91**	**38.06**
C.V.		4.34	2.88	5.10	3.82	6.78	3.94	11.30	13.62	7.45	3.99	3.69	5.62
S.E.		0.32	3.22	1.49	2.23	0.60	0.27	29.21	2.54	0.86	1.84	4.52	1.23
C.D. 5%		0.93	9.23	4.27	6.38	1.74	0.80	83.65	7.28	2.48	5.28	12.94	3.53
C.D. 1%		1.23	12.36	5.72	8.55	2.33	1.07	112.04	9.76	3.32	7.07	17.37	4.74

Table 4. Genotypes classified as per their high *per se* performance in maize.

Character	Best Genotypes	Genotypes showing high *per se* performance
Leaf number	PM-6	EQH-63, HQPM-5, B.Sathi, HQPM-1
Plant height(cm)	PM-6	B.Sathi, K.Malan, C.Sathi, Arawali
Days of 50% flowering	HQPM-1	HQPM-5, HQPM-7, EQH-16, EQH-63,
Days of maturity	HQPM-1	HQPM-5, BIO-9637, HQPM-7, EQH-63
Cob length (cm)	HQPM-5	B.Shathi, EQH-63, PHM-1, HQPM-1
Cob girth (cm)	BIO-9637	EQH-63, EC-3161, HQPM-5, PHM-2
Grain/cob	HQPM-5	EQH-63, HQPM-1, EQH-16, HQPM-7
Grain/row	HQPM-5	EQH-16, HQPM-1, Arawali, BIO-9637
Test weight (g)	B.Sathi	BIO-9637, C.Sathi, PM-6, PHEM-2
Grain yield/plant (g)	EQH-63	HQPM-5, HQPM-7, HQPM-1, BIO-9637
Biological yield (g)	PM-6	K.Malan, HQPM-7, EQH-16, Arawali
Harvest index (%)	HQPM-1	HQPM-5, EQH-63, BIO-9637, HQPM-7
Protein content	EQH-63	HQPM-5, BIO-9637, HQPM-1, EQH-16

Table 5. Genetic variability parameters for various characters in 20 genotypes of maize.

Characters	Mean and Standard error	Range	PCV %	GCV %	Heritability (broad sense) %	Genetic gain (%)
Leaf number	13.03 ± 0.32	11.45-14.48	6.77	5.20	58.97	8.23
Plant height(cm)	193.36 ± 3.22	183.03-213.26	5.16	4.28	68.76	7.31
Days of 50% flowering	50.60 ± 1.49	42.33-59.33	9.85	8.42	73.13	14.84
Days of maturity	101.05 ± 2.23	80.66-112.66	8.39	7.47	79.26	13.71
Cob length (cm)	15.57 ± 0.60	11.06-18.53	15.07	13.45	79.74	24.75
Cob girth	12.29 ± 0.27	10.70-14.23	8.50	7.53	78.51	13.75
Grains/ cob	447.56 ± 29.21	291.33-653.66	25.53	22.89	80.39	42.28
Grains/row	32.36 ± 2.54	22.66-43.00	20.55	15.39	56.07	23.74
Test weight	20.14 ± 0.86	14.55-27.18	19.40	17.92	85.25	34.04
Grain yield /plant	80.03 ± 1.84	65.56-98.86	14.79	14.24	92.72	28.26
Biological yield/plant (g)	211.91 ± 4.52	201.33-223.80	4.19	1.98	22.47	1.94
Harvest index (%)	38.06 ± 1.23	30.94-47.00	15.74	14.70	87.24	28.30
Grain protein content	8.13 ± 0.32	6.12-10.70	6.17	5.87	54.93	8.11