International Journal of Chemical Studies

Arunkumar B
Assistant Professor, Department
Genetics & Plant Breeding,
College of Agriculture,
Bheemarayanagudi, UAS,
Raichur, Karnataka, India

Gangapp E
Professor, Department of
Genetics & Plant Breeding,
University of Agricultural
Sciences, GKVK, Bengaluru,
Karnataka, India

Ramesh S
Professor, Department of
Genetics & Plant Breeding,
University of Agricultural
Sciences, GKVK, Bengaluru,
Karnataka, India

Savithramma DL
Professor, Department of
Genetics & Plant Breeding,
University of Agricultural
Sciences, GKVK, Bengaluru,
Karnataka, India

Nagaraju N
Professor, Department of
Genetics & Plant Breeding,
University of Agricultural
Sciences, GKVK, Bengaluru,
Karnataka, India

Lokesha R
Professor and Head, Dept.
Genetics & Plant Breeding,
University of Agricultural
Sciences, Raichur, Karnataka,
India

Correspondence
Arunkumar B
Assistant Professor, Department
Genetics & Plant Breeding,
College of Agriculture,
Bheemarayanagudi, UAS,
Raichur, Karnataka, India

Genetic potential, variability, heritability and genetic advance of grain yield and its component traits in maize (*Zea mays* L.) inbreds

Arunkumar B, Gangapp E, Ramesh S, Savithramma DL, Nagaraju N and Lokesha R

Abstract
Studies were carried out to estimate the extent of genetic variability among 422 maize (*Zea mays* L.) inbreds during summer 2012 and *kharif* 2012. Pooled analysis of variance revealed genotypes differed significantly for all the traits except shelling %. Mean sum of squares due to inbreds × season differed significantly for days to anthesis, days to silking, anthesis silking interval, ear length, ear circumference kernel rows ear^{-1} and fodder yield plant^{-1}. Anthesis silking interval recorded larger variation as indicated by standardized range (3.43) and fodder yield plant^{1} (248.68) registered highest mean value. Estimates of PCV (78.84) and GCV (65.09) were highest for anthesis-silking interval. Days to anthesis, days to silking, ear length, ear circumference, kernel rows ear^{-1} and 100 grain weight recorded lower PCV and GCV estimates. Days to silking (0.88), days to anthesis (0.87) and kernel rows ear^{1} (0.72) registered higher estimates of heritability in broad sense. However, these traits recorded moderate values of genetic advance as Percent of mean (16.79, 16.63 and 21.95, respectively). Higher estimates of heritability in broad sense and GAM were reported for anthesis-silking interval, plant height, ear length, kernel row^{-1} and fodder yield plant^{-1}. Whereas, shelling Percent recorded lower estimates of heritability in broad sense and GAM. Higher estimates of heritability in broad sense and lower GAM was reported for grain yield plant^{-1}, indicated non-additive gene action and provides limited scope for improvement through selection.

Keywords: Genetic variability, heritability, genetic advance, maize (*Zea mays* L.)

Introduction
Maize is the most cultivated cereal crop in the world after wheat (FAO, 2013). It is grown throughout the world in a wide range of agro-ecological environments which include tropics, sub-tropics and temperate regions; from sea level to 3000 m above (Morris, 2002) [11] both under irrigated to semi-arid conditions. Though, originated in Mexico, now it is grown at least in 164 countries around the world. There is a tremendous choice is available for varieties maturing in 85 days to more than 200 days (Brink & Belay, 2006) [4] with variability in grain colour, size and texture and other characters. Maize crop serves as a source of basic raw material for a number of industries *viz.*, starch, protein, oil, alcoholic beverages, food, sweeteners, cosmetics and bio fuels (Khan and Dubey, 2015) [10]. Many countries rely on maize as a primary staple as it meets the protein and calorie requirements of the human beings (Vasal, 2002) [18].

It is well established fact that the progress in improvement of a crop depends on the degree of variability in the desired character in the base material. The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. Among the various traits, grain yield in maize is the most important and complex quantitative traits controlled by numerous genes (Zdunic *et al.*, 2008) [19]. Yield is a complex inherited character resulted from the interaction between the vital processes (Naushad *et al.*, 2007) [13]. Grain yield is related with diverse physiological, morphological and agronomic traits of maize.

By improving these traits the production of maize genotypes may be improved. Heritability, genetic advance and genotypic correlation provide a great prospect to a plant breeder to select genotypes on the basis of strong correlation among grain yield and its contributing traits

(Ali *et al*., 2013a, b) [1, 2]. Therefore, quantifying the genetic variability among maize cultivars grown in an area is important before initiation of breeding programme. Keeping this back ground in view, the present study was undertaken to analyze the variance, genetic variability, heritability and genetic gain among 422 inbreds of maize.

Material and Methods
Location
The study was undertaken during summer, 2012 and *Kharif* 2012 at K-block (experimental block), Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. Geographically, the study location is situated at 13° 05' N latitude and 77° 34' E longitude and at an altitude of 924 meters above mean sea level. The average annual rainfall is about 915 mm.

Experimental material
The experimental material consisted of 422 inbred / breeding lines, collected from AICRP on Maize, ZARS, VC Farm, Mandya, AICRP on Maize, ARS, Arabhavi, College of Agriculture, Bheemarayanagudi and CYMMIT, c/o. ICRISAT Campus, Hyderabad and three checks *viz*., MAI 105, NAI 137 and SKV 50

Field Design
The material was evaluated in augmented block design (Federrer, 1956) [6]. The design consisted of 15 blocks containing 32 genotypes in each with 29 test inbred / breeding lines and three check entries. Each line was sown in a single row of 3 m length with row to row and plant to plant spacing of 0.60 m and 0.30 m, respectively. In each block the checks were allotted randomly. All the recommended packages of practices were followed to raise a healthy crop.

Recording of observations
Data on the 12 quantitative traits were recorded on five randomly selected competitive plants from each line. Mean values of two seasons was calculated and average values of the two season was used for statistical analysis.

Statistical analysis
The statistical analysis was carried out using the computer software system of SAS (SAS Institute, 2002).

Results and Discussion
Analysis of variance
The development of new cultivars depends mainly on the magnitude of genetic variability in the base material for the desired character. Genetic variability is of greatest interest to the plant breeder as it plays a vital role in framing successful breeding programme. Most characters of breeder's interest are complex and are the result of a number of components. Grain yield is one such dependent trait which is influenced by many independent characters. The knowledge of genetic variability, heritability, genetic advance and relationship between yield and its contributing characters in a given crop species is of paramount importance for the success of any plant breeding programme.

Analysis of variance for 12 quantitative traits is presented in Table 1. Analysis of variance (ANOVA) helps in detecting the genetic variability among the inbreds or breeding lines. It is evident from the pooled analysis of variance that means sum of squares for genotypes differed significantly for all the characters except for shelling % indicating the existence of ample variability among the inbreds for traits of economic importance. The mean sum of squares for seasons was also differed significantly for all the characters studied. Significantly different mean sum of squares for inbreds × season for days to anthesis, days to silking, anthesis silking interval, ear length, ear circumference kernel rows ear^{-1} and fodder yield plant^{-1} is an indication of the influence of season in the expression of these traits. Earlier workers such as Saleem *et al*. (2011) [15], Kashiani *et al*. (2014) [9], Praveen Kumar *et al*. (2014) [14] and Mushtaq *et al*. (2016) have reported similar results in maize. However, non-significant inbreds × season interaction for plant height, kernel rows^{-1}, 100 grain weight, shelling Percent and grain yield plant^{-1} was noticed which is in line with results of Idris and Abuali (2011) [7].

Table 1: Pooled Analysis of variance for grain yield and its component traits in maize inbreds across two seasons

Source of variation	df	Days to anthesis	Days to silking	Anthesis silking Interval (Days)	Plant height (cm)	Ear length (cm)	Ear circumference (cm)
Season	1	19.17*	349.70**	216.99**	75839.95**	529.93**	40.12**
Block	14	2.50	2.88	1.30	233.15	2.46	1.72
Inbreds	434	32.71**	35.16**	3.58**	940.49**	9.24**	3.25**
Check	2	92.84**	92.78**	1.88	463.63	12.08*	84.45**
Season × Inbreds	435	7.57**	9.02**	2.23**	419.25	4.27*	1.48*
Error	72	4.22	4.18	1.14	333.12	2.72	1.04
Source of variation	df	Kernel rows Ear^{-1}	Kernels row^{-1}	100 grain weight (g)	Shelling percent	Grain yield plant^{-1}(g)	Fodder yield Plant^{-1} (g)
Season	1	21.14**	149.77*	254.80**	3025.06**	21167.85**	2710859.05**
Block	14	0.88	24.31	14.78	46.78	529.66	3711.86
Inbreds	434	4.26**	56.14**	36.70**	50.18	2251.77**	12880.68**
Check	2	243.98**	778.47**	13.34	230.15**	13554.74**	527449.34**
Season × Inbreds	435	1.77*	24.43	17.58	30.10	1201.68	7012.52*
Error	72	1.21	24.68	14.03	44.04	942.98	4906.37

*Significant at P = 0.05   ** Significant at P = 0.01   *** Significant at P = 0.001

Table 2: Estimates of parameters specifying variability for grain yield and its component traits in maize inbreds across two seasons

Characters	Range		Standardized Range	Mean	Coefficient of variation		h² (Broad sense)	Expected genetic. advance as Percent of mean
	Minimum	Maximum			PCV %	GCV %		
Days to anthesis	33.88	75.96	0.68	61.70	9.27	8.65	0.87	16.63
Days to silking	34.13	76.30	0.66	64.09	9.25	8.68	0.88	16.79
Anthesis silking interval (Days)	0.01	08.25	3.43	02.40	78.84	65.09	0.68	110.69
Plant height (cm)	88.30	294.17	1.26	163.90	18.71	15.04	0.65	24.89
Ear length (cm)	10.08	24.83	0.9	16.36	18.58	15.61	0.71	27.01
Ear circumference (cm)	09.17	17.83	0.64	13.54	13.31	10.98	0.68	18.65
Kernel rows ear^{-1}	09.67	19.17	0.68	13.87	14.88	12.59	0.72	21.95
Kernels row^{-1}	13.83	43.83	1.01	29.67	25.25	18.90	0.56	29.15
Grain yield plant^{-1} (g)	18.00	237.50	2.17	101.23	58.39	44.51	0.58	69.91
100 grain weight (g)	14.00	41.00	0.95	28.34	5.98	4.70	0.62	7.62
Shelling Percent	45.69	93.45	0.59	81.27	25.00	8.74	0.12	6.30
Fodder weight plant^{-1} (g)	57.50	655.00	2.40	248.68	45.64	35.91	0.62	58.20

Components of variability, heritability and genetic advance

A survey of genetic variability with the help of suitable parameters such as coefficients of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme. The extent of observed variability, which is a combined estimate of genetic and environmental causes was assessed in terms of standardized range, broad sense heritability (h²$_{bs}$), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and expected genetic advance as Percent mean (GAM).

The variability parameters such as mean, range, standardized range, PCV, GCV, h2 (bs) and expected genetic advance as Percent of mean (GAM) in maize inbreds estimated for pooled data (Table 2) is presented below. Among all characters studied anthesis silking interval recorded larger variation as indicated by standardized range (3.43) followed by fodder yield plant^1(2.4) and grain yield plant^1(2.17) the presence of larger variation for these characters. The characters *viz,* shelling Percent, cob girth, days to silking, days to anthesis and kernel rows ear^{1}recorded smaller variation. The character fodder yield plant^1 (248.68) registered highest mean value followed by plant height (163.90) and grain yield plant^1 (101.23).

The estimates of PCV and GCV, indicates variation in a character at genotypic and phenotypic levels. The estimates of PCV were larger than the GCV estimates. The estimates of PCV for anthesis-silking interval (78.84) was highest followed by grain yield plant^1 (58.39) and fodder yield plant^1 (45.64) and the lowest estimates were recorded by 100 grain weight (5.98) followed by days to silking (9.25) and days to anthesis (9.27). Similarly the estimates of GCV were highest for anthesis-silking interval (65.09) followed by grain yield plant^1 (44.51) and fodder yield plant^1 (35.91) indicating the larger variation for these traits among the maize inbreds. However, lower estimates of PCV and GCV for flowering traits days to anthesis, days to silking and ear related traits such as ear length, ear circumference, kernel rows ear^{-1} and 100 grain weight indicated the need to explore for variability or create variability for these traits. Inbreds with narrow anthesis-silking interval is considered as a selection criterion for breeding cultivars for moisture stress tolerance. Hence, it is necessary to identify inbreds with narrow anthesis-silking interval so as to employ them in developing drought tolerant hybrids.

Heritability is expressed as the ratio of genetic variance to the total variance and it denotes the proportion of phenotypic variance that is due to genotypic variance. Heritability alone provides little indication on the amount of genetic improvement that would result from selection of individual genotypes. Hence, knowledge of heritability estimates along with genetic advance is more helpful in predicting the gain under selection than heritability estimates alone. The character with high heritability may not necessarily give high genetic advance; it should be accompanied with high genetic advance to arrive at more reliable conclusion.

In the present investigation, days to silking (0.88), days to anthesis (0.87) and kernel rows ear^1 (0.72) registered higher estimates of heritability in broad sense indicating lesser environmental effects. These finding is in line with the reports of Chen *et al*. (1996) [5]. However, these characters recorded moderate values of genetic advance as Percent of mean 16.79, 16.63 and 21.95, respectively, for expected genetic advance as Percent of mean. Moderate heritability coupled with high estimates of GAM was noticed for characters anthesis-silking interval (110.69), grain yield plant^1 (69.91) and fodder yield plant^1 (58.20).

Higher estimates of heritability in broad sense and GAM for anthesis-silking interval, plant height, ear length, kernel row^{-1} and fodder yield plant^{-1} indicated that selection is effective in improving these traits. Lower estimates of heritability in broad sense and GAM for shelling Percent and higher estimates of heritability in broad sense and lower GAM for grain yield plant^{-1}, indicated non-additive gene action and provides limited scope for improvement through selection. Similar results were reported by Thanga Hemavathy *et al.* (2008) [17], Jawaharlal *et al.* (2011) [8] and Anshuman *et al.* (2013) [3].

References
1. Ali Q, Ahsan M, Mustafa HSB, Hasan EU. Genetic variability and correlation among morphological traits of maize (*Zea mays* L.) seedling. Albanian Journal of Agricultural Science. 2013a; 12(3):405-410.
2. Ali Q, Ahsan M, Ali F, Muhammad S, Manzoor M, Khan NH, *et al*. Genetic advance, heritability, correlation, heterosis and heterobeltiosis for morphological traits of maize (*Zea mays* L). Albanian Journal of Agricultural Science. 2013a; 12 (4):689-698.
3. Anshuman Vashistha, Dixit NN, Dipika, Sharma SK, Marker S. Studies on heritability and genetic advance estimates in Maize genotypes. Bioscience Discovery. 2013; 4(2):165-168.
4. Brink M, Belay G. Plant Resources of Tropical Africa 1. Cereals and pulses. PROTA Foundation, Wageningen, Netherlands / Backhuys Publishers, Leiden, Netherland / CTA, Wageningen, Netherland, 2006, 233.

5. Chen Ling, Cuishaoping, Chen L, Cui AP, Sun YB. Analysis of the gene effect on ear characters in maize. Acta Agricultural Bareli Sinica. 1996; 11(2):28-32.

6. Federer W. Augmented designs. Hawaiian Planter Recorder. 1956; 55:191-208

7. Idris AE, Abuali AI. Genetic variability for vegetative and yield traits in maize (*Zea mays* L.) genotypes. International Research Journal of Agricultural Science and Soil Science. 2011; 1(10):408-411.

8. Jawaharlal J, Lakshmikantha Reddy G, Sai Kumar R. Genetic variability and character association studies in maize. Agricultural Science Digest. 2011; 31(3):173-177.

9. Kashiani P, Saleh G, Abdulla NAP, Sin MA. Evaluation of genetic variation and relationships among tropical sweet corn inbred lines using agronomic traits. Maydica. 2014; 59:275-282.

10. Khan R, Dubey RB. Combining ability analysis for nutritional quality and yield in maize (*Zea mays* L.). The Bioscan. 2015; 10(2):785-788.

11. Morris ML. Impacts of International Maize Breeding Research in Developing Countries. Mexico, DF. CIMMYT 1966-98, 2002, 4.

12. Mushtaq M, Bhat MA, Bhat JA, Mukhtar S, Shah AA. Comparative analysis of genetic diversity of maize inbred lines from Kashmir valley using agro-morphological and SSR markers. SABRAO Journal of Breeding and Genetics. 2016; 48(4):518-527.

13. Naushad A, Turi S, Shah S, Ali S, Rahman H, Ali T, *et al*. Genetic variability for yield parameters in maize (*Zea mays* L.) genotypes. Journal of Agricultural and Biological Science. 2007; 2(4-5):1-3.

14. Praveen Kumar G, Prashanth Y, Narsimha Reddy V, Sudheer Kumar S, Venkateshwara Rao P. Heterosis for grain yield and its component traits in maize (*Zea mays* L.) International Journal of Pure and Applied Bioscience. 2014; 2(1):106-111.

15. Saleem S, Tahir HM, Saleem U. Study of genetic variability in maize inbred lines under irrigated and drought conditions. International Journal of Agriculture and Applied Sciences. 2011; 3(2):80-85.

16. SAS Institute. SAS user's guide: statistics. SAS Institute, Inc., Cary, NC, 1982.

17. Thanga Hemavathy A, Balaji K, Ibrahim SM, Anand G, Deepa Sankar. Genetic variability and correlation studies in Maize (*Zea mays* L.). Agricultural Science Digest. 2008; 28(2):112-114.

18. Vasal SK. Quality protein maize: Overcoming the hurdles. Journal of Crop Production. 2002; 6:193-227.

19. Zdunic Z, Mijic A, Dugalic K, Simic D, Brkic J, Marjanovic-Jeromela A. Genetic Analysis of grain yield and starch content in nine maize populations. Turkish Journal of Agriculture and Forestry. 2008; 32:495-500.