Genetic variability and traits association in maize (*Zea mays* L.) genotypes

T.N. BHIUSAL[1], G.M. LAL, S. MARKER AND G.J. SYNREM

Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture Science and Technology (Deemed-to-be-university), Allahabad-211007 (U.P.), India

ABSTRACT

With the aim to estimate the extent of genetic variability and traits association in maize, fifty five genotypes available at Department of Genetics and Plant breeding, SHIATS, Allahabad were tested during rabi 2013-14 under irrigated condition in randomized block design with three replications. Analysis of variance revealed significant differences for 18 characters studied among the genotypes. High genotypic and phenotypic coefficient of variation was recorded for grain yield/plant, biological yield/plant and cob weight coupled with high heritability and genetic advance. Strong positive associations were exhibited to grain yield per plant with plant height, ear height, leaf area index, cobs/plant, cob weight, cob length, cob girth, grains/row and biological yield/plant both at genotypic and phenotypic levels. Thus, traits showing variability and strong positive correlation both at genotypic and phenotypic levels need to be paid attention while formulating breeding strategies for improvement of grain yield of maize.

INTRODUCTION

Maize (*Zea mays* L.) is an important staple crop of the world after wheat and rice. 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 biofuels (Khan and Dubey, 2015). Yield is a complex inherited character resulted from the interaction between the vital processes (Naushad *et al.,* 2007) and associated with various contributing characters, therefore, direct selection for yield *per se* may not be the most efficient method for its improvement, but indirect selection for other yield related characters, which are closely associated with yield and high heritability estimates will be more effective (Mohammadia *et al.,* 2003). For developing suitable selection strategies knowledge on presence of genetic variability on available germplasm for yield and its related components and heritable difference among cultivars, within population is always desirable in plant breeding programme. Also, study on association of various attributing characters to yield is essential, for accumulating the optimum contribution of such traits to yield. Genetic correlation analysis is a handy technique which elaborates the degree of association among important quantitative traits (Malik *et al.* 2005). Association studies could lead plant breeders in the selection of traits contributing towards the character(s) of concern, and ultimately their improvement through hybridization. The study of characters association along with heritability and genetic variability has been applied in major crops like rice (Allam *et al.* 2015), wheat (Singh *et al.,* 2014), barley (Yadav *et al.,* 2015), maize (Maruthi and Jhansi Rani, 2015), etc. so the objective of present investigation was to measure the genetic variability and correlation of morpho-physiological and yield traits in maize inbred lines.

MATERIALS AND METHODS

The experimental materials comprising of fifty five maize inbred lines were grown in a randomized block design with three replications at Field Experimentation Center, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture Science and Technology (Deemed-to-be-University), Allahabad, India during *rabi* 2013-14 under irrigated condition. Each plot consisted of single row plot of 3m length with a spacing of 70×30 cm where 2 seeds per hill were dropped manually. Later, one plant per hill was maintained after thinning. Nitrogen, Phosphorus and Potassium (120:60:40 kg ha^{-1}) in the form of urea, di-ammonium phosphate and muriate of potash, were applied

and split application of nitrogen (⅓ as basal, ⅓ at knee high stage and ⅓ at tasseling stage) was followed. Other standard agronomic operation and plant protection measures were adapted to raise healthy and uniform crops. Data were recorded on visual observations of plants on plot basis for traits like days to 50% tasseling, days to 50% silking, and days to 50% maturity while data for plant height, ear height, leaf area index (LAI), cobs/plant, cob weight, cob length, cob girth, grain rows/cob, grains/ row, 100 seed weight, grain yield/plant, biological yield/plant and harvest index (HI) were taken from five randomly selected plants from middle of row of each entry in each replication. The difference between days to 50% silking and tasseling of each entry was reported as anthesis-silking interval (ASI) (days) while seed fill duration (SFD) (days) was computed as the difference between days to 50% maturity and silking for each entry. The mean values over replications were subject to analysis of variance as suggested by Panse and Sukhatme (1964). The variability presence in the genotypes was estimated by phenotypic and genotypic variances and coefficient of variations using the procedure suggested by Burton and De Vane (1953). Heritability in broad sense (H^2_{bs}) was computed using the formula given by Lush (1949). The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Johnson *et al.* (1955) and the correlation coefficient by Al-Jibouri *et al.* (1958).

RESULT AND DISCUSSION

Analysis of variance

The analysis of variance (Table 1) reflected highly significant differences among the genotypes for all the characters studied indicating that the experimental materials were genetically divergent to each other. This shows that there is sufficient space for selection of promising lines amongst the available genotypes aimed to enhance the genetic yield potential of maize. Existence of significant genetic variability among the treatments for all the quantitative characters studied was also noticed by Vashistha *et al.* (2013) and Zaman and Alam (2013).

Table 1 Analysis of variance for yield related traits in maize inbred lines

Sources of variation	Replication (*df* = 2)	Genotypes (*df* = 54)	Error (*df* = 108)	CV (%)
Days to 50% tasseling	2.13	187.45**	1.36	1.29
Days to 50% silking	0.48	199.33**	1.75	1.40
ASI	0.92	1.86**	0.36	13.28
Days to 50% maturity	0.66	109.53**	3.69	1.45
SFD	0.70	63.22**	2.26	3.95
Plant height	27.89	2268.14**	142.80	7.40
Ear height	245.31	643.87**	82.44	15.15
LAI	0.27	1.62**	0.06	7.47
Cobs/plant	0.07	0.55**	0.08	20.60
Cob weight	532.88	3512.67**	106.64	10.21
Cob length	1.96	17.08**	0.79	5.95
Cob girth	7.12	6.59**	0.15	2.93
Grain rows/cob	3.57	5.13**	0.95	7.35
Grains/row	2.40	94.63**	3.68	9.27
100 Seed weight	0.03	78.56**	0.03	0.59
Grain yield/plant	293.18	6154.12**	487.33	20.28
Biological yield/plant	1065.77	40679.72**	981.82	10.10
Harvest index	20.21	115.29**	43.08	18.64

*ASI = Anthesis-Silking interval; SFD = Seed fill duration; LAI = Leaf area index; * = significant at 1%; ** = significant at 5%*

Mean performance of genotypes

Based on the *per se* performance of all genotypes, all traits studied showed a wide range of variation for most of the morpho-physiological and yield components (Table 2). However, more variation were found in the yield related traits like anthesis-silking interval (3.00-

5.67 days), days to 50% maturity (123.33-146.67 days), seed fill duration (25.67-45.67 days), leaf are index (2.02-5.22), cob weight (31.67-176.67 g), cob length (8.43-20.53 cm), cob girth (9.92-16.91 cm), no. of grain row/cob (9.33-16.67), no. of grains/row (7.67-32.33), 100 seed weight (17.03-40.00 g), grain yield/plant (21.74-224.73 g) etc. indicating sufficient variation on the aforesaid traits and provide good opportunity for grain yield improvement in maize.

Phenotypic and genotypic variation

The data on estimates of variability parameters for various morpho-physiological and yield traits are presented in Table 2. The phenotypic and genotypic variances ranged from 0.24 to 14214.45 and 0.09 to 13232.63 for the characters studied, respectively. Comparatively higher phenotypic variances values of 14214.45 for biological yield/plant, 2598.94 for grain yield/plant and 1241.99 for cob weight were recorded in this study. Similarly, higher genotypic variance values were observed for the same traits pointed out that genotype could be reflected by phenotype and the effectiveness of selection of genotypes based on phenotypic performance of these traits. The PCV values ranged between 4.71 for days to 50% maturity and 47.06 for grain yield/plant and GCV values were dispersed as 4.48 for days to 50% maturity and 37.09 for biological yield/plant (Table 2). According to Deshmukh *et al.* (1986), classification of PCV and GCV values (as high: >20%, medium: 10-20% and low: <10%) high PCV and GCV were reported for the traits like ear height, LAI, cobs/plant, cob weight, grains/row, grain yield/plant and biological yield/plant. The selection of promising genotypes based on these traits may be effective and their phenotypic expression would be concomitant with the genotypic potential (Singh *et al.*, 1994). Besides, nominal differences between PCV and GCV for the traits such as days to 50% tasseling (0.10), days to 50% silking (0.11), days to 50% maturity (0.23), seed fill duration (0.64), plant height (1.59), LAI (1.22), cob weight (1.53), cob length (1.10), cob girth (0.37), grains/row (1.57), 100 seed weight (0.01) and biological yield/plant (1.35) there is considerably low influence of environment on the expression of these traits. However, traits like anthesis-silking interval (4.87), ear height (4.57), cobs/plant (12.96),

grain yield/plant (10.11) and harvest index (14.72) showed wide differences in the PCV and GCV indicating considerably higher environmental influence over these traits. Therefore, it is valuable to consider the above traits depending on the objective of maize improvement programmes. Earlier findings of researchers (Vashistha *et al.* 2013, Zaman and Alam 2013, Synrem *et al.* 2015) support the results of present investigation.

Estimates of heritability (H^2_{bs}) in broad sense and expected genetic advance

In the present study, estimated heritability in broad sense ranged from 18.39% for harvest index to 99.89% for 100 seed weight (Table 2). The heritability estimates can be low (<40%), medium (40-59%), moderately high (60-79%) and very high (≥80%) as reported by Pramoda and Gangaprasad (2007). Accordingly, heritability estimates were higher (83.22-99.89%) for the traits *viz.*,days to 50% tasseling, silking and maturity, seed fill duration, plant height, LAI, cob weight, cob length, cob girth, grains/row, 100 seed weight and biological weight/plant, suggesting progress in selection. Moderately high heritability was recorded for ear height (69.42%) and grain yield/plant (61.64%) indicating that these characters respond effectively to selection pressure. Low heritability was also recorded for no. of cobs/plant (39.41%) and harvest index (18.39%) showing that the improvement of these traits through selection is difficult. The expected genetic advance as percentage of mean by selecting top 5% (high grain yielder) of maize inbred lines arranged between 8.78% for days and 50% maturity to 73.71% for biological yield (Table 2). According to Johnson *et al.* (1955), the estimate of genetic advance and genetic advance as percent of mean could be classified as low (<10%), moderate (10-20%) and high (>20%). Estimated of genetic advance and genetic advance as percentage of mean, respectively were higher for plant height (50.02 & 30.99), cob weight (66.36 & 65.63), grain yield/plant (64.73 & 59.76) and biological yield/plant (228.64 & 73.71). However, harvest index had low both genetic advance (3.42) and genetic advance as percentage of mean (9.77).

High genetic coefficient of variation coupled with high heritability estimates and high

genetic advance provide better information than each parameter alone (Johnson *et al.*, 1955; Johnson and Hermandez, 1980). The traits like grain yield/plant and biological yield/plant had

high genetic coefficient of variation, moderate high to very high heritability and high genetic advance suggesting a direct selection of these traits can be done for enhancing the grain yield.

Table 2 Estimate of range, mean and other genetic components of various characters for maize inbred lines

Characters	Range	Mean±SEd	σ^2_g	σ^2_p	GCV	PCV	H²(bs)	GA	GA as % of mean
Days to 50% tasseling	77.67-109.67	90.07±0.95	62.03	63.39	8.74	8.84	97.86	16.05	17.82
Days to 50% silking	81.33-114.67	94.59±1.08	65.86	67.61	8.58	8.69	97.41	16.50	17.44
ASI	3.00-5.67	4.52±0.49	0.50	0.86	15.67	20.54	58.21	1.11	24.63
Days to 50% maturity	123.33-146.67	132.61±1.57	35.28	38.98	4.48	4.71	90.51	11.64	8.78
SFD	25.67-45.67	38.02±1.23	20.32	22.58	11.86	12.50	90.00	8.81	23.17
Plant height	39.30-204.73	161.39±9.76	708.45	851.25	16.49	18.08	83.22	50.02	30.99
Ear height	17.10-97.27	59.94±7.41	187.15	269.58	22.82	27.39	69.42	23.48	39.17
LAI	2.02-5.22	3.26±0.19	0.52	0.58	22.15	23.37	89.76	1.41	43.22
Cobs/plant	1.00-2.00	1.36±0.30	0.09	0.24	21.85	34.81	39.41	0.40	28.26
Cob weight	31.67-176.67	101.12±0.43	1135.34	1241.99	33.32	34.85	91.41	66.36	65.63
Cob length	8.43-20.53	15.03±0.73	5.43	6.23	15.50	16.60	87.16	4.48	29.81
Cob girth	9.92-16.91	13.14±0.31	2.15	2.30	11.16	11.53	93.55	2.92	22.23
Grain rows/cob	9.33-16.67	13.24±0.79	1.39	2.34	8.92	11.55	59.57	1.88	14.18
Grains/row	7.67-32.33	20.68±1.57	30.32	33.99	26.63	28.20	89.18	10.71	51.80
100 Seed weight	17.03-40.00	28.51±0.14	26.18	26.21	17.95	17.96	99.89	10.54	36.95
Grain yield/plant	21.74-224.73	108.86±25.78	1602.01	2598.94	36.95	47.06	61.64	64.73	59.76
Biological yield/plant	80.00-540.17	310.19±25.58	13232.63	14214.45	37.09	38.44	93.09	228.64	73.71
Harvest index	20.15-42.06	35.22±6.66	15.00	81.52	11.06	25.78	18.39	3.42	9.77

ASI = Anthesis-Silking interval; SFD = Seed fill duration; LAI = Leaf area index; SEd = Standard error of mean of differences; σ^2_g = Genotypic variance; σ^2_p = Phenotypic variance; h^2 (bs) = Heritability in broad sense; GA= Genetic advance or gain

Genotypic and phenotypic correlation

Association analyses for various morpho-physiological traits were done at both phenotypic and genotypic levels (Table3). In general, higher genotypic correlation coefficients were observed in present study than phenotypic values indicating that strong intrinsic association is reduced at phenotypic level due to significant environmental effects. Mahesh *et al.* (2013) also reported similar results. Significant negative phenotypic correlations were observed between grain yield with days to 50% tasseling and silking while negative one was reported for anthesis-silking interval and days to 50% maturity. In addition, negative correlation was shown by the same trait at genotypic level also. Traits like plant height (0.61**), ear height (0.57**), leaf area index (0.57**), cobs/plant (0.51**), cob weight (0.78**), cob length (0.58**), cob girth (0.68**), grains/row (0.71**) and biological yield/plant (0.90**) had significant and strong phenotypic correlation while significant positive correlation was recorded in other traits *viz.* seed

fill duration, grain rows/cob, 100 seed weight and harvest index at phenotypic level. Genotypic correlation coefficients followed a similar trend in magnitude and significance with that of phenotypic correlation coefficients. At genotypic level, plant height (0.67), ear height (0.65), leaf area index (0.60), cobs/plant (0.51), cob weight (0.81), cob length (0.62), cob girth (0.72), grains/row (0.75) and biological yield/plant (0.93) expressed strong association to grain yield/plant. There were significant negative phenotypic and genotypic correlation of days to 50% tasseling, silking and ASI with SFD, cob weight, rows/cob, grains/row and harvest index; cob length with grains/row and cob girth with rows/cob. Genetic association among grain yield and yield components observed in this study indicate that each character could be used to select indirectly for grain yield. These are the most economic traits usually targeted by maize breeders. Prime priorities therefore need to pay on these characters during the formulation of indirect selection indices for grain yield improvement in maize. Jayakumar *et al.* (2007) also reported significant and positive correlation of grain yield

Table 3: Phenotypic correlation (r_p, above diagonal) and genotypic correlation (r_g, below diagonal) for various morpho-physiological traits of maize

Traits	50%T	50%S	ASI	50%M	SFD	PH	EH	LAI	CP	CW	CL	CG	RC	GR	100SW	BY	HI	GY
50%T	**1.00**	0.99**	0.27*	0.84**	-0.67**	-0.32*	-0.15	-0.10	0.16	-0.39**	-0.08	-0.33*	-0.42**	-0.34*	-0.19	-0.23	-0.28*	-0.33*
50%S	0.99	**1.00**	0.36**	0.83**	-0.68**	-0.32*	-0.15	-0.09	0.18	-0.39**	-0.08	-0.32*	-0.41**	-0.35**	-0.19	-0.22	-0.28*	-0.32*
ASI	0.30	0.38	**1.00**	0.20	-0.36**	-0.13	-0.13	0.08	0.17	-0.18	-0.02	-0.03	-0.03	-0.19	-0.11	0.04	-0.09	-0.01
50%M	0.84	0.84	0.21	**1.00**	-0.16	-0.17	-0.01	0.00	0.08	-0.20	0.06	-0.01	-0.29*	-0.22	-0.02	-0.09	-0.29*	-0.21
SFD	-0.68	-0.70	-0.40	-0.19	**1.00**	0.34*	0.26	0.17	-0.21	0.44**	0.22	0.56**	0.35**	0.33*	0.32*	0.27*	0.12	0.30*
PH	-0.33	-0.33	-0.14	-0.18	0.36	**1.00**	0.84**	0.64**	0.20	0.59**	0.44**	0.55**	0.17	0.61**	0.27*	0.64**	0.11	0.61**
EH	-0.15	-0.16	-0.13	-0.00	0.29	0.93	**1.00**	0.63**	0.22	0.56**	0.48**	0.46**	0.15	0.62**	0.19	0.61**	0.06	0.57**
LAI	-0.10	-0.10	0.10	0.01	0.18	0.67	0.69	**1.00**	0.29*	0.51**	0.33*	0.43**	0.05	0.53**	0.22	0.66**	-0.01	0.57**
CP	0.18	0.19	0.20	0.07	-0.25	0.23	0.27	0.30	**1.00**	-0.04	0.21	0.01	-0.18	0.09	-0.19	0.54**	0.03	0.51**
CW	-0.39	-0.40	-0.20	-0.20	0.46	0.62	0.61	0.53	-0.04	**1.00**	0.54**	0.76**	0.44**	0.82**	0.59**	0.64**	0.47**	0.78**
CL	-0.08	-0.08	-0.04	0.06	0.22	0.47	0.53	0.35	0.24	0.57	**1.00**	0.51**	0.24	0.57**	0.13	0.59**	0.15	0.58**
CG	-0.33	-0.33	-0.05	-0.01	0.57	0.58	0.49	0.44	0.00	0.77	0.52	**1.00**	0.43**	0.57**	0.49**	0.61**	0.28**	0.68**
RC	-0.46	-0.45	-0.04	-0.30	0.40	0.22	0.18	0.06	-0.19	0.44	0.27	0.48	**1..00**	0.19	0.16	0.20	0.30*	0.29*
GR	-0.35	-0.35	-0.22	-0.22	0.35	0.64	0.66	0.55	0.11	0.83	0.60	0.58	0.22	**1.00**	0.13	0.61**	0.39**	0.71**
100SW	-0.19	-0.20	-0.12	-0.02	0.33	0.28	0.20	0.22	-0.21	0.59	0.13	0.50	0.18	0.13	**1.00**	0.26*	0.32*	0.38**
BY	-0.23	-0.22	0.04	-0.10	0.27	0.67	0.67	0.68	0.57	0.66	0.61	0.62	0.22	0.63	0.27	**1.00**	-0.02**	0.90**
HI	-0.35	-0.35	-0.11	-0.36	0.16	0.16	0.09	-0.02	-0.07	0.57	0.20	0.34	0.38	0.48	0.41	-0.00	**1.00**	0.40**
GY	-0.35	-0.34	-0.00	-0.23	0.31	0.67	0.65	0.60	0.51	0.81	0.62	0.72	0.31	0.75	0.40	0.93	0.34	**1.00**

** = Significant at 1%, * = Significant at 5%
50%T = Days to 50% tasseling; 50%S = Days to 50% silking; ASI = Anthesis-Silking interval; 50%M = Days to 50% maturity; SFD = Seed fill duration; PH = Plant height; EH = Ear height; LAI = Leaf area index; CP = Cobs/plant; CW = Cob weight; CL = Cob length; CG = Cob girth; RC = Rows/cob; GR = Grains/row; 100SW = 100 Seed weight; BY = Biological yield/plant; HI = Harvest index and GY = Grain yield/plant

with ear girth, kernel rows, grains/rows, ear length, grain weight and plant height while days to tasseling, silking and maturity were negatively and significantly correlated with grain yield. These results were supported by the findings of Knife and Tsehaye (2015) who observed positive and strong association of grain yield with ear length, ear diameter, plant height and ear height both at phenotypic and genotypic levels. Brown and Caligari (2008) reported that high and positive association between characters such as plant height and ear height as well days to tasseling and silking indicated that each of two character pairs could be controlled by closely linked genes, same or similar genes or by genes with pleiotropic effects on these characters.

Significant positive association between grain yield and its component characters augmenting yield are most desirable in plant breeding as it facilitates selection process and gains from selection.

It may be concluded that genotypes depicted existence of sufficient variability for the characters studied. Similarly, most of the yield attributing characters namely plant height, ear height, leaf area index, cobs/plant, cob weight, cob length, cob girth, grains/row and biological yield/plant has strong and positive correlation with grain yield at both phenotypic and genotypic level. So that grain yield of maize could be increased through selection process by considering such traits.

REFERENCES

Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958) Genetic and environmental variances and covariances in upland cotton cross of inter-specific origin, *Agronomy Journal* **50** (10): 633-637.

Allam, C.R., Jaiswal, H. K. and Qamar, A. (2015) Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.) *The Bioscan* **9** (4): 1733-1737.

Brown, K. and Caligari, P. (2008) *An introduction to plant breeding*. Blackwell Publishing Ltd, Oxford, UK.

Burton, G.W. and DeVane, E.H. (1953) Estimation of heritability in Tall Festuca (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* **45**: 478-481.

Deshmukh, S.N.N., Basu, M.S. and Reddy, P.S. (1986) Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. *Indian Journal of Agriculture Science* **56**: 516-521.

Jayakumar, J., Sundaram, T., Arun Prabu, D. and Ragu Rama Rajan, A. (2007) Correlation studies in maize (*Zea mays* L.) evaluated for grain yield and other yield attributes *International Journal of Agriculture Science* **3** (2): 57-60

Johnson, C.E. and Hernandez, T.P. (1980) Heritability studies of early and total yield in tomatoes. *Horticulture Science* **15**: 280-285.

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

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

Kinfe, H., and Tsehaye, Y. (2015) Studies of heritability, genetic parameters, correlation and path coefficient in elite maize hybrids *Academic Research Journal of Agriculture Science Research* **3** (10): 296-303

Lush, J. L. (1949) Intra-site, correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proceeding of American Society of Animal Production* **33**: 293-301.

Mahesh, N., Wali, M. C., Gowda, M. V. C., Motagi, B. N. and Uppinal, N. F. (2013) Correlation and path analysis of yield and kernel components in maize. *Karnataka Journal of Agriculture Science* **26** (2): 306-307

Malik, H.N., Malik, S.I., Hussain, M., Chughtai, S. U. R. and Javed, H. I. (2005) Genetic correlation among various quantitative characters inmaize (*Zea mays* L.) hybrids. *Journal of Agriculture and Social Science* **1** (3): 262–265.

Maruthi, R. T. and Jhansi Rani, K. (2015) Genetic variability, heritability and genetic

advance estimates in maize (*Zea mays* L.) inbred lines. *Journal of Applied Natural Science* **7** (1): 149 – 154

Mohammadia, S.A., Prasanna, B. M. and Singh, N.N. (2003) Sequential path model for determining interrelationship among grain yield and related characters in maize. *Crop Science* **43**: 1690-1697.

Naushad, A., Turi, S., Shah, S., Ali, S., Rahman, H., Ali, T. and Sajjad, M. (2007) Genetic variability for yield parameters in maize (*Zea mays* L.) genotypes. *Journal of Agriculture and Biology Science* **2** (4-5): 1-3.

Panse, V.G and Sukhatme, P.V. (1985) *Statistical methodology for agricultural workers*. ICAR Publications, New Delhi.

Pramoda, H.P. and Gangaprasad, S. (2007) Biometrical basis of handling segregation population for improving productivity in onion (*Allium cepa* L.). *Journal of Asian Horticulture 3* (4): 278-280.

Singh, A.K., Singh, S.K., Garg, H.S., Kumar, R. and Choudhary, R. (2014) Assessment of relationships and variability of morpho-physiological characters in bread wheat (*Triticum aestivum* L.) under drought stress and irrigated conditions. *The Bioscan.* **8** (2): 473-484.

Singh, G.P., Maurya, K.R., Prasad, B. and Singh, A.K. (1994) Genetic variability in *Capsicum annuum* L. *Journal of Applied Biology* **4**: 19-22.

Synrem, G.J., Marker, S., Bhusal, T. N. and Kumar, L. N. (2015) Genetic diversity for grain yield and physiological traits in maize (*Zea mays* L.) *Geobios* **42**: 22-32.

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**: 165-168.

Yadav, S. K., Singh, A. K., Pandey, P. and Singh, S. (2015) Genetic variability and direct selection criterion for seed yield in segregating generations of barley (*Hordeum vulgare* L.). *American Journal of Plant Science* **6**: 1543-1549

Zaman, M. A. and Alam, M. A. (2013) Genetic diversity in exotic maize (*Zea mays* L.) hybrids. *Bangladesh Journal of Agriculture Research* **38** (2): 335-341.