

COMPARATIVE STUDY OF HYBRID MAIZE VARIETIES IN RELATION TO YIELD BASED ON MORPHOLOGY AND GENETIC PARAMETERS

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Abstract

An experiment was conducted to study on morphological characters for yield and its contributing characters among 15 genotypes of hybrid maize. The study was carried out at the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207 during the period of November, 2016 to May, 2017. The results indicated that the genotypes differed regarding all the characters studied. The phenotypic variance and coefficients of variation were higher than the genotypic variance and coefficients of variation in all the characters studied. Moderate to high heritability was observed for all characters except cob per plot and row per cob. High heritability coupled with high genetic advance in percent mean were observed for days to tasseling, days to pollen shedding, days to silking, plant height, ear height, cob length, cob breadth, kernel per row, thousands seed weight and seed yield. The characters days to silking, plant height, ear height, field weight, moisture percentage, kernel per row, row per kernel and thousand seed weight showed positive direct effect on yield. All the genotypes were grouped into five clusters having 5, 4, 3, 2 and 1 genotypes, respectively. Cluster V comprised the maximum number (5) of genotypes followed by cluster III (4) and II (3). The highest inter-cluster distance (33.06) was observed between the cluster IV and V and the highest distant genotypes were G6 (PAC-999 supper) and G15 (PAC-339). Among the characters studied days to tasseling, days to pollen shedding, days to silking, plant height, number of leaf, cob per plot, cob length, cob breadth, row per cob, thousands seed weight were the important component characters having higher contribution to the genetic divergence.

Key words: Evaluation, Hybrid, Phenotypic variance, Genotypic variance, Heritability

Introduction

Maize (*Zea mays* L.) is an annual plant belonging to the grass family (*Graminae* or *Poaceae*) (Sprague and Dudley, 1988). Though it has wider environmental plasticity in general, it is a warm season crop and most production takes place between temperatures of 21-27°C and in regions receiving rainfall of 500-700 mm per annum (Lafitte, 1994). Maize is believed to have originated in Mexico (Mangelsdorf *et al.*, 1964) about 6,000-7,000 years ago (Goodman 1988, Hallauer, 1994) and it does not survive in its wild form probably

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because of the highly cross pollinated nature. It is currently the third most traded cereal, after wheat and rice with a total production of 822 million tons in over 160 million hectares (FAOSTAT, 2010). Maize grain today is recognized worldwide as a strategic food and feed crop that provides an enormous amount of protein and energy for humans and livestock. Among all the crop plants, maize is the most versatile one as it has high nutritive value containing 66.2% starch 11.1% protein, 7.12% oil and 1.5% minerals. Moreover, 100 g maize grains contain 90 mg carotene, 1.8 mg niacin 0.8 mg thiamin and 0.1 mg riboflavin (Chowdhury and Islam, 1993). Crop improvement depends upon the magnitude of genetic variability and extent to which the desirable character are heritable. High heritability alone is not enough to make efficient selection in segregating generation, unless the information is accompanied for substantial amount of genetic advance.

Genetic improvement of a crop is pivoted on the strength of genetic diversity within the crop species. Adequate variability provides options from which selections are made for improvement and possible hybridization. Genotypic correlations had been used as an effective tool to determine the relationships among agronomic traits in genetically diverse population for enhanced progress in crop improvement (Bello *et al.*, 2006). Heritability and genetic advance help in determining the influence of environment expression of the characters and the extent to which improvement is possible after selection (Robinson *et al.*, 1949). Considering the above mention facts the study was undertaken with screen out the superior hybrid maize for yield and yield contributing characters comparing the morphophysiological and genetic parameters for knowing the nature of association of traits and identifying the genetically divergent parents for future breeding programme.

Materials and Methods

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during the period from November 2016 to June 2017 to study on the genetic diversity, correlation and path coefficient analysis in Maize (*Zea mays* L). Fifteen (15) genotypes were used in the study. These are G1 = BHM-5, G2 = BHM-6, G3 = BHM-7, G4 = BHM-9, G5 = Prince, G6 = PAC-999, G7 = Kaveri 25 k 60, G8 = 9120 (Palomoni), G9 = Elit, G10 = Pioneer, P-3396, G11 = Sun shine, G12 = CP- 808, G13 = HP- 701, G14 = 981 and G15 = PAC-339. The experiment was laid in Randomized Complete Block Design (RCBD) with three replications. Each entry was sown in single row of 4 m length with a spacing of 20 cm between rows and 60 cm between plants. The experimental plots were ploughed and raised the bed, applied the recommended dose of fertilizers and farm yard manures (FYM). Five plants in each entry were selected randomly and were tagged. These tagged plants were used for recording observations for the characters. Mean data of the characters was subjected to multivariate analysis. Univariate analyses of the individual character were done for all characters under study using the mean values (Singh and Chaudhury, 1985) and were estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were estimated using MSTAT-C.

Results and Discussion

The highest moisture percentage was found 22.64 in BARI hybrid maize-6 and lowest moisture percentage was found 17.27 in PAC-3339 genotype. The maximum cob length was found 20.67 cm in HP-701 whereas minimum cob length was found 15.17 cm in CP-808. The lowest cob breadth was recorded 15.00 cm in BARI hybrid maize-5 whereas the highest cob breadth was recorded 18.50 cm in CP-808. The maximum kernel per row was found 46.33 in elit whereas prince showed minimum kernel per row 34.00. The lowest row per cob was found 13.00 in prince whereas maximum row per cob was found 16.00 in elit. The maximum thousand seed weight was recorded 370.00g in PAC-999 super whereas the minimum thousands seed weight was 320.00g in 981 genotype. The maximum seed yield was recorded 11.1 ton/ha Palmoni-9120 whereas minimum seed yield was 6.46 ton/ha in BARI hybrid maize-5. (Table 1)

The phenotypic coefficients of variation were higher than genotypic coefficients of variation in all the characters under study showed in table-1. Phenotypic coefficients of variation were also near to genotypic coefficients of variation for all the characters under study. High heritability (>50%) was observed for all the characters under study except cob per plot, moisture percentage, and row per cob. The highest heritability was found for thousand seed weight (99.25%). The high heritability coupled with high genetic advance in percent of mean observed in days to tasseling, days to pollen shedding, days to silking, plant height, ear height, cob length, kernel per row, 1000 seed weight and seed yield which would be selected for future breeding program. High heritability coupled with low genetic advance in percent of mean was observed in number of leaf, cob per plot, field weight, moisture percentage, cob breadth, row per cob.

The characters which had positive direct effects are days to silking (0.612), plant height (0.155), ear hight (0.735), field weight (2.048), moisture percentage (0.168), kernel per row (0.940), row per cob (0.114) and thousand seed weight (0.812) . However characters viz., days to tasseling (-0.265), days to pollen shedding (-0.775) and number of leaf (-0.374), cob per plot (-0.359), cob length (-1.771), cob breadth (-0.375) had negative direct effect on seed yield per plant (Table 5). Path coefficient analyses revealed that seed yield per plant was directly influenced by days to silking, plant height, ear hight, field weight, moisture percentage, kernel per row, row per kernel, and thousand seed weight. Hence selection of any of these traits can be done for the improvement of genotypes. Wright (1921) and Dewey and Lu (1959) observed direct and indirect contribution of various characters on yield by path coefficient analysis.

Days to tasseling showed a indirect positive effect on seed yield through days to silking, plant height, ear hight, cob per plot, moisture percentage, kernel per row, row per cob, thousand seed weight . However it had indirect negative effect on seed yield through days to pollen shedding, leaf number, field weight, cob length, cob breadth.

Days to pollen shedding showed a positive indirect effect on seed yield through days to silking, plant height, cob per plot, moisture percentage, cob length, kernel per row, row per cob, and thousand seed weight. Though it showed a negative indirect effect on seed yield through days to tasseling, ear height, number of leaf, field weight, cob breadth, day to silking showed a positive indirect effect on seed yield through plant height, ear height, cob per plot, moisture percentage, cob breadth, kernel per row, row per cob, thousand seed weight. Though it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, number of leaf, field weight, and cob length.

Plant height showed a positive indirect effect on seed yield through days to silking, ear height, number of leaf, cob per plot, field weight, moisture percentage, kernel per row. However it showed negative indirect effect days to tasseling, days to pollen shedding, cob length, cob breadth, row per cob, thousand seed weight. Ear height showed a positive indirect effect on seed yield through days to pollen shedding, days to silking, plant height, cob per plot, moisture percentage. Saidaiah *et al.* (2008) and Shinde *et al.* (2009) reported almost similar result. Though it showed negative indirect effect days to tasseling, number of leaf, field weight, cob length, cob breadth, kernel per row, row per cob, thousand seed weight. Number of leaf showed a positive indirect effect on seed yield through days to silking, ear height, moisture percentage, cob length whereas it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, plant height, cob per plot, field weight, cob breadth, kernel per row, row per cob, thousand seed weight. Cob per plot showed a positive indirect effect on seed yield through days to tasseling, days to pollen shedding, field weight, and cob length. Though it showed a negative indirect effect on seed yield through days to silking, plant height, ear height, number of leaf, moisture percentage, cob breadth, kernel per row, row per cob, and thousand seed weight (-0.148).

Field weight showed a positive indirect effect on seed yield through days to tasseling, days to pollen shedding, plant height, number of leaf, moisture percentage, kernel per row, row per kernel. Though it showed a negative indirect effect on seed yield through days to silking, ear height, cob per plot, cob length, cob breadth and thousand seed weight. Moisture percentage showed a positive indirect effect on seed yield through days to silking, plant height, ear height, cob per plot, field weight, kernel per row, and row per cob. Though it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, number of leaf, cob length, cob breadth, thousand seed weight. Cob length showed a positive indirect effect on seed yield through days to pollen shedding, days to silking, plant height, ear height, number of leaf, cob per plot, field weight, moisture percentage, cob breadth, kernel per row, row per cob, thousand seed weight. Though it showed a negative indirect effect on seed yield through days to tasseling. Cob breadth showed a positive indirect effect on seed yield through plant height, ear height, field weight, moisture percentage, cob length and row per cob. Though it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, days to silking, number of leaf, cob per plot, kernel per row, and thousand seed weight.

Kernel per row showed a positive indirect effect on seed yield through days to silking, plant height, number of leaf, cob per plot, field weight, moisture percentage, cob breadth, row per cob. Though it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, ear height, cob length and thousand seed weight. Row per cob showed a positive indirect effect on seed yield through days to silking, number of leaf, cob per plot, field weight, moisture percentage, kernel per row, Though it showed a negative indirect effect on seed yield through days to tasseling, days to pollen shedding, plant height, ear height, cob length, cob breadth, thousand seed weight. Thousand seed weight showed a positive indirect effect on seed yield through showed a positive indirect effect on seed yield through days to silking, number of leaf, cob per plot, cob breadth. Though it showed a negative indirect effect on seed yield days to tasseling, days to pollen shedding, plant height, ear hight, field weight, moisture percentage, cob length, kernel per row, row per cob. Similar result was observed by Kumar *et al.* (2015) and Huda (2015).

Genetic diversity of fifteen maize hybrid genotypes based on fourteen characters was measured through multivariate analysis. The 15 genotypes clustered into five distant clusters. The cluster V comprised the maximum number 5 of genotypes followed by cluster III 4. The cluster III, II, I AND IV comprised 4, 3, 2 and 1 genotypes, respectively. The highest inter-cluster distance (33.06) was observed between the cluster I and V and the highest distant genotypes were G6 (PAC-999 supper) and G15 (PAC-339). The lowest inter-cluster distance (5.11) was observed between the cluster V and II and the lowest distance genotypes were G8 (Palmoni-9120) and G2 (BARI hybrid maize-6).

The inter-cluster distances were larger than the intra-cluster distances. The intra cluster distances in the entire five clusters were more or less low indicating that the genotypes within the same cluster were closely related. Days to tasseling, days to pollen shedding, days to silking, plant height, number of leaf, cob per plot, cob length, cob breadth, row per cob, thousands seed weight were the important component characters having higher contribution to the genetic divergence. Beyene *et al.* (2005) also reported that the first principal component cluster analysis revealed that 40.4% of the total variation was due to days to tasseling and silking, plant and ear height, leaf length and days to maturity.

The result of the present study exposed that a wide variability exists among the studied and collected hybrid maize genotypes. In addition, there was also genotype of different yield contributing characters with yield of maize.

Table 1. Mean performance of different morphological characters of 15 hybrid Maize genotypes

Genotypes	DT	DPS	DS	PH	EH	LN	Cob	FW
BHM-5	86.00F	88.00G	90.00DE	200A	106AB	14.67AB	24AB	3.12D
BHM-6	88.00D	90.00E	92.00BC	192AB	121A	14.67AB	27AB	4.30C
BHM-7	90.00B	92.00C	93.00B	180A-D	114A	14.67AB	25AB	4.47BC
BHM-9	85.00G	89.00F	92.33B	180A-D	91BC	14.00A-C	27AB	4.50BC
Prince	82.33I	85.33I	89.00EF	155E	83CD	15.00A	30A	5.28A-C
PAC-999	93.00A	95.00A	97.00A	172B-E	79CD	14.00A-C	29A	4.98A-C
Kaveri 25 k 60	88.00D	92.00C	92.00BC	180A-D	81CD	12.67BC	25AB	5.40AB
9120 (Palomoni)	87.00E	91.00D	90.00DE	166C-E	71D	12.00C	26AB	5.75A
Elit	86.00F	89.00F	91.00CD	175B-E	86CD	14.00A-C	24AB	5.15A-C
Pioneer,P-3396	83.00I	86.00H	88.00F	158DE	84CD	12.00C	30A	5.19A-C
Sun shine	84.00H	90.00E	91.00CD	172BC-E	91BC	14.00A-C	30A	5.33AB
CP- 808	90.00B	93.00B	92.00BC	169B-E	88B-D	15.00A	29A	5.22A-C
HP- 701	89.00C	91.00D	92.00BC	188A-C	85CD	13.00A-C	25AB	5.07A-C
981	83.00I	85.00I	89.00EF	162DE	89B-D	13.67A-C	28AB	4.95A-C
PAC- 339	89.00C	92.00C	92.67B	1250F	78CD	14.33AB	22B	3.05D

DT= days to tasseling, DPS= days to pollen shedding, DS= days to silking, PH= plant height (cm), EH= Ear height (cm), LN= Leaf no., Cob= Cob per plot, FW= Field weight (g).

Table 1. Continued.

Genotypes	M (%)	CL	CB	KPR	RPC	TSW	YTH
BHM-5	19.90A-D	17.67CD	15.00F	39.00C-E	14.00AB	344.0G	6.46F
BHM-6	22.64A	20.00AB	16.83BC	41.00A-D	15.00AB	341.3H	8.22DE
BHM-7	20.57A-C	18.33B-D	16.17CDE	38.67C-E	15.00AB	365.7B	9.01CD
BHM-9	20.33A-D	18.67B-D	15.50EF	43.00A-C	15.33AB	324.7J	9.26CD
Prince	18.13CD	18.00CD	16.17C-E	34.00E	13.00B	354.7E	9.50A-D
PAC-999	18.87B-D	18.50B-D	15.50EF	41.67A-C	15.00AB	370.0A	9.35B-D
Kaveri 25 k 60	19.58A-D	19.33A-C	16.00CD-F	40.67A-D	15.00AB	344.3G	11.0AB
9120 (Palomoni)	19.63A-D	20.00AB	16.17CDE	45.00AB	15.00AB	360.3D	11.1A
Elit	21.13A-C	20.00AB	17.33B	46.33A	16.00A	346.0G	10.7A-C
Pioneer,P-3396	18.70B-D	18.33B-D	15.67D-F	39.67B-E	13.67AB	352.0F	9.63A-D
Sun shine	18.75B-D	17.67CD	15.83C-F	34.67E	15.00AB	353.3EF	9.65A-D
CP- 808	19.13B-D	15.17E	18.50A	35.33DE	16.00A	330.3I	9.45A-D
HP- 701	21.47AB	20.67A	16.83BC	41.33A-C	16.00A	353.3EF	9.90A-D
981	19.20B-D	17.67CD	16.67B-D	41.00A-D	15.00AB	320.7K	9.02CD
PAC- 339	17.27D	17.00D	15.67D-F	37.67C-E	16.00A	363.0C	6.90EF

M (%) = Moisture, CL = Cob length (cm), CB = Cob breadth (cm), KPR = Kernel per row, RPC = Row per cob, TSW = 1000 Seed weight (g), YTH = Yield (t/ha).

Table 2. Estimation of genetic parameters in fifteen characters of 15 hybrid maize genotypes

Parameters	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to tasseling	9.57	9.42	0.16	3.56	3.53	0.45	98.38	6.27	7.22
Days to Pollen Shedding	8.39	8.30	0.09	3.22	3.20	0.33	98.94	5.90	6.57
Days to Silking	4.96	4.50	0.46	2.44	2.32	0.74	90.78	4.16	4.56
Plant height (cm)	431.49	265.77	165.72	12.11	9.50	7.50	61.59	26.36	15.37
Ear height (cm)	248.07	155.10	92.97	17.52	13.85	10.73	62.52	20.29	22.57
Leaf no.	1.73	0.63	1.10	9.50	5.74	7.57	36.51	0.99	7.15
Cob per plot	12.70	2.31	10.38	13.31	5.68	12.03	18.20	1.34	4.99
Field weight (g)	0.80	0.53	0.27	18.64	15.20	10.77	66.57	1.22	25.55
Moisture (%)	3.65	1.02	2.63	9.70	5.14	8.23	28.05	1.10	5.61
Cob length (cm)	2.65	1.66	0.99	8.82	6.98	5.39	62.70	2.10	11.39
Cob breadth (cm)	0.98	0.66	0.33	6.10	4.98	3.52	66.65	1.36	8.38
Kernel per row	18.66	9.48	9.18	10.82	7.71	7.59	50.81	4.52	11.32
Row per cob	2.02	0.16	1.86	9.47	2.64	9.10	7.78	0.23	1.52
1000 Seed weight (g)	213.29	211.70	1.59	4.19	4.18	0.36	99.25	29.86	8.57
Yield (t/ha)	2.25	1.46	0.79	16.15	12.99	9.59	64.75	2.00	21.54

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance and σ^2_e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

Table 3. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of maize

	DT	DPS	DS	PH	EH	LN	Cob	FW	M (%)	CL	CB	KPR	RPC	TSW
DPS	0.931**													
DS	0.878**	0.869**												
PH	0.148	0.083	0.118											
EH	0.051	-0.101	0.030	0.549**										
LN	0.206	0.090	0.340*	-0.045	0.608**									
Cob	-0.50**	-0.39**	-0.242	-0.134	-0.253	0.173								
FW	-0.185	-0.031	-0.180	0.048	-0.553**	-0.594**	0.697**							
M (%)	0.254	0.091	0.163	1.385**	1.064**	0.042	-0.199	0.096						
CL	0.012	-0.020	0.030	0.526**	0.012	-0.757**	-0.395**	0.276	0.908**					
CB	0.168	0.127	-0.068	0.027	0.009	0.179	0.346*	0.458**	0.404**	-0.197				
KPR	0.155	0.094	0.149	0.348*	-0.213	-0.817**	-0.765**	0.080	0.791**	0.757**	-0.068			
RPC	1.201**	1.302**	1.09**	-0.106	-0.295*	-0.285	-1.050**	0.155	0.418**	0.065	0.869**	1.026**		
TSW	0.419**	0.437**	0.366*	-0.260	-0.206	-0.147	-0.183	-0.028	-0.308*	0.239	-0.386**	-0.084	-0.238	
YTH	-0.080	0.087	-0.098	0.086	-0.613**	-0.768**	0.632**	1.009**	0.162	0.482**	0.337*	0.428**	0.428**	0.021

Table 4. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of maize

	DT	DPS	DS	PH	EH	LN	Cob	FW	M (%)	CL	CB	KPR	RPC	TSW
DPS	0.928**													
DS	0.850**	0.844**												
PH	0.130	0.073	0.118											
EH	0.059	-0.061	0.052	0.611**										
LN	0.108	0.046	0.205	0.170	0.463**									
Cob	-0.216	-0.182	-0.103	0.011	-0.015	-0.113								
FW	-0.133	-0.017	-0.118	0.026	-0.253	-0.364*	0.532**							
M (%)	0.118	0.050	0.068	0.311*	0.250	0.006	-0.263	0.006						
CL	0.022	-0.009	0.030	0.258	0.035	-0.250	-0.172	0.239	0.456**					
CB	0.168	0.128	0.000	0.037	0.097	0.223	-0.115	0.300*	0.240	-0.027				
KPR	0.127	0.064	0.091	0.200	-0.034	-0.216	-0.173	0.194	0.330*	0.644**	0.064			
RPC	0.359*	0.388**	0.304*	0.019	-0.014	0.134	-0.366*	-0.174	0.246	0.059	0.407**	0.119		
TSW	0.413**	0.431**	0.347*	-0.200	-0.164	-0.099	-0.084	-0.027	-0.169	0.175	-0.312*	-0.069	-0.093	
YTH	-0.048	0.087	-0.019	0.027	-0.300*	-0.382**	0.044	0.830**	0.132	0.373*	0.354*	0.290	-0.013	0.021

** = Significant at 1%; * = Significant at 5%.

DT= days to tasseling, DPS= days to pollen shedding, D = days to silking, PH= plant height (cm), EH = Ear height (cm), LN = Leaf no., Cob = cob per plot, FW = Field weight (g). M (%)= Moisture, C= Cob length (cm), C= Cob breadth (cm), KPR= Kernel per row, RPC= Row per cob, TSW= 1000 Seed weight (g), YTH= Yield (t ha⁻¹).

Table 5. Partitioning of genotypic correlations into direct (bold) and indirect effects of ten important characters by path analysis of Maize

	DT	DPS	DS	PH	EH	LN	Cob	FW	M (%)	CL	CB	KPR	RPC	TSW	Genotypic correlation with yield
DT	-0.265	-0.721	0.537	0.023	0.037	-0.077	0.181	-0.378	0.043	-0.021	-0.063	0.145	0.137	0.340	-0.08
DPS	-0.247	-0.775	0.532	0.013	-0.074	-0.034	0.140	-0.064	0.015	0.035	-0.048	0.089	0.149	0.355	0.087
DS	-0.233	-0.673	0.612	0.018	0.022	-0.127	0.087	-0.369	0.027	-0.052	0.026	0.140	0.126	0.297	-0.098
PH	-0.039	-0.064	0.072	0.155	0.403	0.017	0.048	0.098	0.233	-0.932	-0.010	0.328	-0.012	-0.211	0.086
EH	-0.013	0.078	0.018	0.085	0.735	-0.227	0.091	-1.133	0.179	-0.022	-0.003	-0.201	-0.034	-0.167	-0.613**
LN	-0.055	-0.070	0.208	-0.007	0.447	-0.374	-0.062	-1.216	0.007	1.341	-0.067	-0.768	-0.033	-0.120	-0.768**
Cob	0.134	0.302	-0.148	-0.021	-0.186	-0.065	-0.359	1.426	-0.034	0.700	-0.130	-0.720	-0.120	-0.148	0.632**
FW	0.049	0.024	-0.110	0.007	-0.407	0.222	-0.250	2.048	0.016	-0.489	-0.172	0.075	0.018	-0.023	1.009**
M (%)	-0.067	-0.071	0.100	0.215	0.782	-0.016	0.071	0.197	0.168	-1.608	-0.151	0.744	0.048	-0.250	0.162
CL	-0.003	0.015	0.018	0.082	0.009	0.283	0.142	0.566	0.153	-1.771	0.074	0.712	0.007	0.194	0.482**
CB	-0.045	-0.099	-0.042	0.004	0.006	-0.067	-0.124	0.939	0.068	0.349	-0.375	-0.064	0.099	-0.314	0.337*
KPR	-0.041	-0.073	0.091	0.054	-0.157	0.306	0.275	0.164	0.133	-1.340	0.026	0.940	0.117	-0.068	0.428**
RPC	-0.318	-1.009	0.672	-0.017	-0.217	0.106	0.377	0.318	0.070	-0.115	-0.326	0.965	0.114	-0.193	0.428**
TSW	-0.111	-0.338	0.224	-0.040	-0.152	0.055	0.066	-0.057	-0.052	-0.424	0.145	-0.079	-0.027	0.812	0.021

Residual effect: 0.131 ** = Significant at 1%; * = Significant at 5%.

DT = days to tasseling, DPS = days to pollen shedding, DS = days to silking, PH = plant height (cm), EH = Ear height (cm), LN = Leaf no., Cob = cob per plot, FW = Field weight (g). M (%) = Moisture, CL = Cob length (cm), CB = Cob breadth (cm), KPR = Kernel per row, RPC = Row per cob, TSW = 1000 Seed weight (g), YTH = Yield (t/ha).

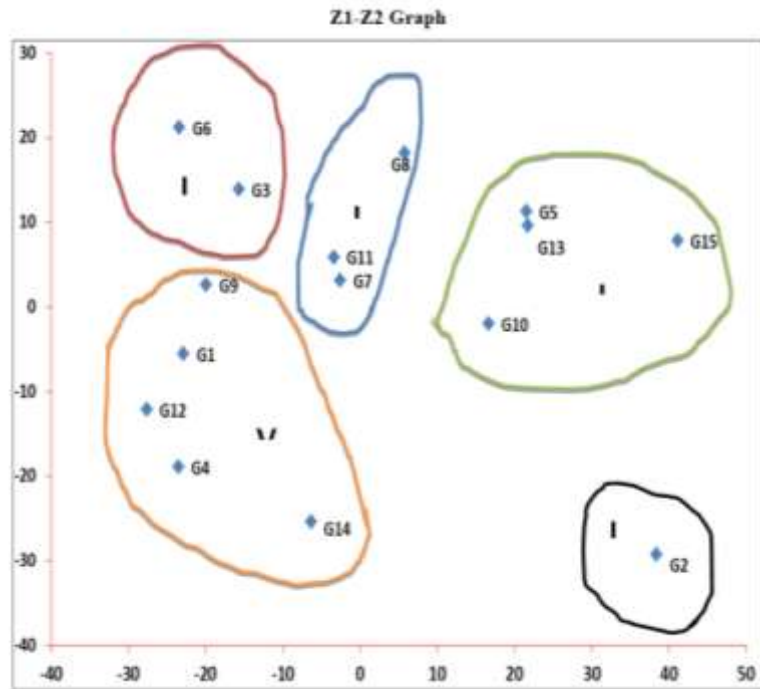


Fig. 1. Scatter diagram of 15 maize genotypes based on their principal component scores.

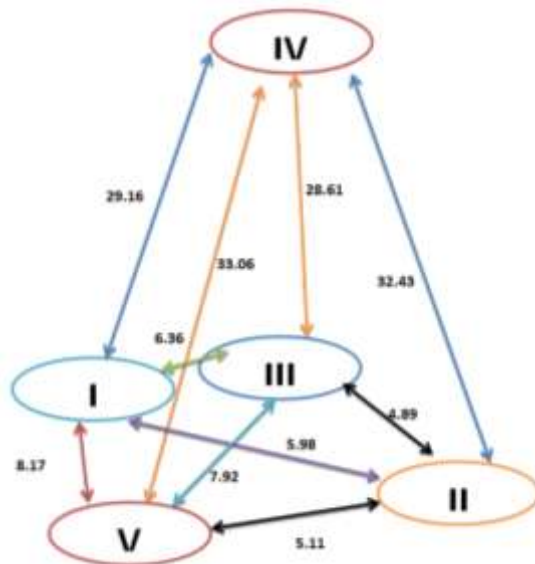


Fig. 2. Intra and inter cluster distances of 15 genotypes in maize

Conclusions

The genotype of clusters I was more diverse from the genotypes of cluster V. Wide range of genetic diversity present among the maize genotypes. Wide genetic diversity was found in 15 genotypes of maize, which were grouped into five clusters and most diverse genotypes were G6 (PAC-999 supper) and G15 (PAC-339). That variability could be used for future breeding program of maize in Bangladesh. Field weight, cob length, cob breadth, kernel per row, row per cob showed highly significant and positive correlation with seed yield at both genotypic and phenotypic levels. This results suggested that seed yield per plant can be increased by improving these characters. High heritability coupled with high genetic advance in percent of mean was observed in days to tasseling, days to pollen shedding, days to silking, plant height, ear height, cob length, cob breadth, kernel per row, thousands seed weight and seed yield. Hence, yield improvement in maize would be achieved through selection of these characters. Days to silking, plant height, ear height, field weight, moisture percentage, kernel per row, row per kernel, thousand seed weight showed positive direct effect on seed yield. So yield improvement was associated with these characters. Days to pollen shedding, days to silking, plant height, ear height, cob length, cob breadth, kernel per row, thousands seed weight were found responsible for the maximum diversity. On the other hand, days to tasselling, moisture percentage, and cob per plot have the least responsibility of both the primary and secondary differentiation of genotypes. Further collection of maize hybrid genotypes would be continued for getting more variability and desired qualities and higher yield in Maize in Bangladesh.

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