Genetic Diversity with Cluster Analysis of Maize Genotypes (*Zea mays* L.)

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Abstract

The research investigation was carried out in the experimental area of Sher-e-Bangla Agricultural university, Sher-e-Bangla Nagar, Dhaka-1207, during the late Rabi season Mid December to May 2018 to study the genetic diversity with cluster analysis for the 35 maize genotypes as experimental materials that were laid out in Randomized Complete Block Design (RCBD) with three replications. The research work was oriented to calculate and estimate the yield factor through analyzing genetic diversity involving the yield contributing characters. The maximum yield per plant (117.51 g) was estimated in the genotype G12 (Pacific) and the minimum yield per plant (51.89 g) was recorded in the genotype G17 (Dekalb Super). Due to the crossing among the 35 maize genotypes, a wide range of divergence was observed in this experiment. The highest genotypes were included in cluster number V with 12 genotypes: BHM-5, PAC-60, Pacific-98, HP-222, Khai Bhutta, AS-999, Pioneer, Duranta, Kaveri 218, Chamak-07 and Golden-984. Here, the intra cluster distance was observed in cluster I (1.23), II (0.00), III (0.76), IV (2.08) and V (1.89) respectively. The highest intra cluster was recorded in cluster IV (2.08) and the lowest in cluster III (0.76) that showed that the genotypes within the intra cluster distances were closely related and inter cluster distances were recorded higher and larger than intra cluster distances. Between inter and intra cluster mean values, inter cluster distances were recorded higher than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups involved. The maximum value for the cluster distance D2 was recorded in cluster III (18.740) followed by cluster II (15.470, 13.032). The farthest cluster distance was recorded in cluster III that means it represented the highest diversified genotypes than other clusters. The nearest cluster distance was recorded in cluster IV and cluster V with 3.441 values which denoted the less diversified genotypes. In this case, days to male flowering, number of rows per cob, number of seeds per cob and 100-seed weight contributed towards

cluster mean performance, the maximum in cluster number V.

Keywords

Genetic Diversity, Cluster Analysis, Inter and Intra Cluster, PCA

1. Introduction

Maize (*Zea mays* L.) is the 3rd most significant cereal crop after wheat and rice in the world [1]. It is also commonly known as Corn (mostly in North America) originates in the Andean region of Central America and is basically first domesticated by indigenous people in southern Mexico. After domestication, maize spread quickly through North and South America, reaching the northeastern US and southern Canada prior to European colonization. Maize spread rapidly throughout Europe and from Europe to other parts of the world after the European discovery of the Americas [2]. Maize (*Zea mays* L.) is an important staple crop of the world after wheat and rice. At the same time, it is a versatile crop due to its multifarious uses as feeds, food and industrial raw material. The 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 [3].

Bangladesh in the year 2013-14, 2014-15 and 2015-16, the production of maize was 2,123,572 MT, 2,271,998 MT and 2,445,578 MT, respectively [3]. The area under maize cultivation has quickly increased to 804 thousand acres of land in FY 2014-15 from 72 thousand acres in FY 2003-04 [4] [5]. So, the production of maize in Bangladesh is continuously increasing. Among the different districts in Bangladesh-Dinajpur, Chuadanga, Takurgaon, Lalmonirhat, Rajshahi, Kushtia, Rangpur and Bogra are noted to be more progressive in maize production with higher rates of growth. Both composite and hybrid maize are grown well in the loam and sandy-loam soils of the country (with three to four irrigations). Hybrid maize has a greater yield with 2.4 tons/acre (5.4 tons per ha), which is higher by one-third over composite maize (1.47 tons/acre or 3.63 tons/hectare) [6].

Yield is a complex inherited character resulted from the interaction between the vital processes [7] 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 [8]. In the year 2017/2018, the United States was the largest producer of corn with a production volume amounting to about 370.96 million metric tons. China and Brazil rounded off the top corn producing countries. Total maize production in Maize output increased the most, reaching a record in 2017, driven largely by higher production in several major exporting countries. Wheat output was

high but slightly below the record set in 2016, and other coarse grain output declined in 2017 due mainly to lower barley production in Australia and lower sorghum and barley production in the United States. Global maize production is expected to grow by 161 Mt to 1.2 billion ton over the next decade, with the largest increases in China (31 Mt), followed by Brazil (24 Mt), the United States (22 Mt), the European Union (11 Mt) and Argentina (10 Mt). Increased production in Brazil will be largely driven by higher second-crop maize following soybeans. Production growth in the United States is expected to slow to less than 1% p.a. over the next ten years, compared to 2.4% p.a. the decade before, due to slower growth in domestic demand, particularly for ethanol, and increased export competition [9].

A successful selection program depends not only on heritability of desirable characters but also on the information about the association among various yield component characters and their association with grain yield [10] [11]. Variability is the differences between individuals in a population due to genetic composition and growing environment [12]. The existence of variability is utmost role as success of any plant breeding program depends on the genetic variability and selection skill of plant breeder [13]. Selection is only effective if the parent population have significant amount of variability. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides insight information on magnitude of variability in a population and heritability shows the component of a character transmitted to future generations [14] [15]. Furthermore, heritability coupled with genetic advance shows the expected genetic gain in next generation [16]. In addition, correlation between yield and yield attributing traits are prime important for indirect selection for those traits which have high heritability and closely associated to contributes to improve yield [17]. This study was conducted to elaborately understand about the genetic parameters and character associated attributes to consider the yield and its components involving 35 Maize populations to achieve following objectives: to know the yield potentiality of different maize genotypes, to understand the nature of association of traits, direct and indirect relation between yield contributing characters of maize genotypes and to study genetic variability among the genotypes.

2. Materials and Methods

The research work was conducted in the experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, during Rabi season (Mid December to May 2018). Sher-e-Bangla Nagar Thana (Dhaka metropolitan) area 5.25 sq km, located in between 23°45' and 23°47' north latitudes and in between 90°22' and 90°23' east longitudes. The soils of this AEZ have been developed from the Madhupur Clay and occupy a large area of 4244 km^2 [18]. Madhupur Tract or Red Soil Tract is a forest-based land. The area is also known for the production of mango, banana, pomelo and pineapple. But deforestation

in the last few decades has made a great loss to the environment which will not be recovered in future [19]. The optimum soil pH is 6.6 - 7.3 [20]. 35 Maize genotypes were used to execute the experiment in 360msq of land in three replications during 2017-2018 (Rabi season) cropping season. The germination percentage of the genotypes was satisfactory, uniformed with 94% - 96% respectively. The experiment was designed and laid out in Randomized Complete Block Design (RCBD) with 3 replications. The supplied experimental land was 360 msq in total. The field was divided into 3 blocks and the individual block size was 3 m × 30 m. Spacing was maintained 60 cm × 20 cm, row to row distance was 60 cm, line to line distance was 20 cm, block to block distance was 1 m. The Genotypes were distributed randomly without biasness. Green manure and decomposed organic matter were used at the rate of 6 ton/ha before final land preparation. For land preparation chemical fertilizers were applied such as Urea (14 kg), TSP (8 kg), MOP (6 kg), Gypsum (6 kg), Zinc Sulphate (1 kg) and Boric Acid (1 kg) in 360 m^2 of the experimental land. The rest amount of Urea was applied 25 days after the first installment. The 35 maize genotypes were planted in lines each having a line-to-line distance 20 cm and row to row distance 60 cm under direct planting in well prepared plot on 20 December 2017. The data obtained for different characters were statistically analyzed to find out the significance of the difference among the maize genotypes. The mean values of all the characters were evaluated and analysis of variance was performed by the "F" test. The significance of the difference among the treatment means were estimated by the Duncan's Multiple Range Test (DMRT) test at 5% level of significance [21]. By applying following formulae for genotypic & phenotypic variance, genotypic and phenotypic coefficient of variation, estimation of genetic advance, heritability and multivariate analysis were estimated with GENSTATE 4.2 program.

3. Results and Discussion

3.1. Genetic Diversity

Genetic diversity serves as a way for populations to adapt to changing environments. Thus, genetic diversity plays in important role in improvement of new breeding program through selection and introduction with diversified crop characters. The capability of the population to adapt to the changing environment will depend on the presence of the necessary genetic diversity [22]. The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

3.1.1. Non-Hierarchical Clustering

In this non-hierarchical clustering, 35 maize genotypes were used and grouped with the application of covariance matrix into five different clusters. The highest 35% genotypes were included in cluster number V (12; G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35); 30% genotypes in cluster number IV (11; G1, G2, G6, G7, G15, G16, G19, G23, G24, G25, G30), 20% genotypes in cluster

number I (7; G8, G9, G10, G20, G22, G28, G32) and 11% genotypes in cluster number III (4; G3, G17, G26, G33); the lowest 3% genotypes were included in cluster number II (1; G12). The composition of clusters with different genotypes is presented in Table 1.

3.1.2. Principal Component Analysis (PCA)

Here, principal component axes were estimated according to the Eigen values, percent variation and cumulative percent variation. The results showed the first principal axis for days to male flowering greatly accounted for the variation among the genotypes representing 31.51% of the total variation among the genotypes (Table 2).

The first seven characters of the principal component axes with eigen values was accumulated around 96.70% of the total variation among the eleven characters.

Table 1. Distribution of 35 genotypes of maize in different clusters (Mahalanobis' generalized distance D2).

Cluster no.	Accession No.	No. of populations
I	G8, G9, G10, G20, G22, G28, G32	7
II	G12	1
III	G3, G17, G26, G33	4
IV	G1, G2, G6, G7, G15, G16, G19, G23, G24, G25, G30	11
V	G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35	12
	Total	35

Table 2. Eigen values and yield percent contribution of 11 characters of 35 genotypes.

Principle component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.466	31.51	31.51
II	2.666	24.24	55.75
III	1.359	12.35	68.1
IV	1.098	9.99	78.09
V	0.908	8.25	86.34
VI	0.746	6.78	93.12
VII	0.394	3.58	96.7
VIII	0.298	2.71	99.41
IX	0.060	0.55	99.96
X	0.003	0.03	99.99
XI	0.001	0.01	100

The rest four characters were contributed around 3.3% of the total variation (Table 3). According to the principal component analysis, the principal component axis showed two-dimensional scatter diagram using 35 maize genotypes. The scatter diagram is represented in Figure 1.

3.1.3. Inter and Intra Cluster Distance

Through canonical variate analysis inter and intra cluster distance was analyzed and presented in Table 4 and nearest and farthest cluster distance are presented in Table 5. The maximum value for the cluster distance D2 were recorded in

Table 3. Cluster mean values of 11 different characters of 35 genotypes.

| Characters	I	II	III	IV	V
Days to male flowering	65.4	62.0	65.5	65.2	64.6
Days to female flowering	61.0	63.3	61.7	60.9	61.6
Days to maturity	128.9	129.7	128.3	128.8	128.9
Plant height (cm)	247.4	209.4	238.1	236.9	238.0
Cob length (cm)	17.6	15.8	16.8	17.1	16.7
Cob breadth (cm)	15.9	14.4	15.1	15.3	15.1
No. of rows per cob	15.1	22.4	13.5	13.7	13.4
No. of grains per row	41.6	35.5	27.1	38.8	34.2
Number of grains per cob	626.7	799.0	364.5	530.7	457.8
100 grain weight (g)	31.8	28.7	32.3	32.3	31.4
Grain yield per plant (g)	100.0	117.5	58.9	86.0	71.9
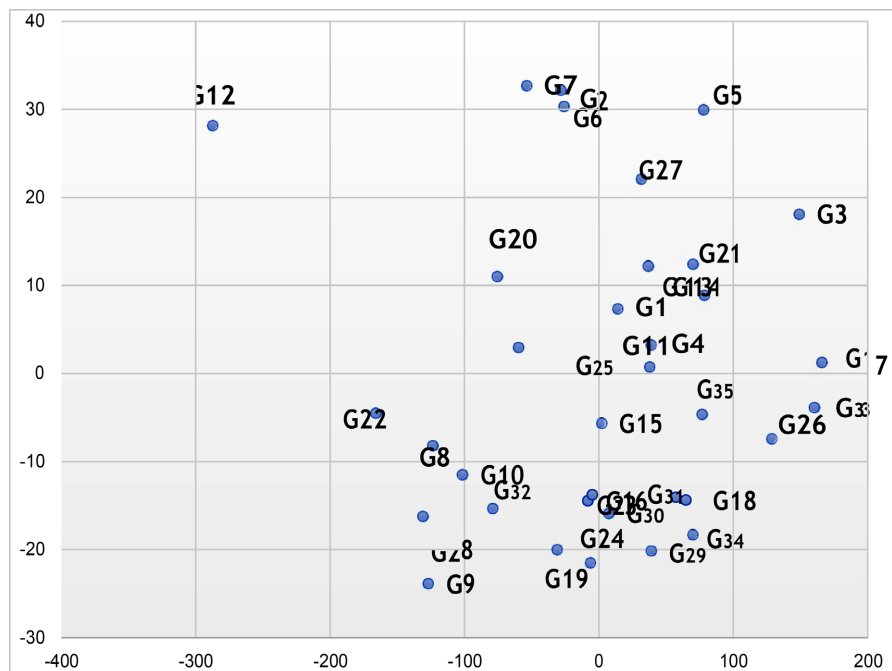
Figure 1. Scattered diagram of 35 maize genotypes.

Table 4. Intra (Bold) and inter cluster distances (D2) for 35 genotypes.

Cluster	I	II	III	IV	V
I	**1.23**	9.779	11.689	4.526	7.662
II		**0.00**	18.740	13.032	15.470
III			**0.76**	7.633	4.388
IV				**2.08**	3.441
V					**1.89**

Table 5. The nearest and the farthest cluster distances.

Cluster	Nearest cluster distance	Farthest cluster distance
I	IV (4.526)	III (11.689)
II	I (9.779)	III (18.740)
III	V (4.388)	II (18.740)
IV	V (3.441)	II (13.032)
V	IV (3.441)	II (15.470)

cluster III (18.740) followed by cluster II (15.470, 13.032). The intra and inter cluster distances (D2) values clearly showed in Table 4. The farthest cluster distance was recorded in cluster III that means it represented the highest diversified genotypes than other clusters. The nearest cluster distance was recorded in cluster IV and cluster V with 3.441 values which denoted the less diversified genotypes (Table 5).

Here, the intra cluster distance was observed in cluster I (1.23), II (0.00), III (0.76), IV (2.08) and V (1.89) respectively. The highest intra cluster was recorded in cluster IV (2.08) and lowest in cluster III (0.76) that showed that the genotypes within the intra cluster distances were closely related and inter cluster distances were recorded higher and larger than intra cluster distances that indicated the genotypes had wider genetic diversity among the genotypes in different groups (Table 4 and Table 5).

3.1.4. Cluster Diagram
The cluster diagram showed the distribution of the 35 maize genotypes grouped into five sections. The positioning nature of the genotypes were remarkably diversified among the genotypes (Figure 2).

3.1.5. Cluster Mean Analysis
The cluster mean analysis was estimated using 35 maize genotypes grouped into five cluster with eleven characters involvement (Table 3). Here, within the clusters compared the considerable differences among the clusters for all the character studied. The maximum cluster mean value for days to male flowering was observed in cluster III (65.5) and the minimum was in cluster II (62.0). In case of days to female flowering, the maximum mean value was observed in cluster II
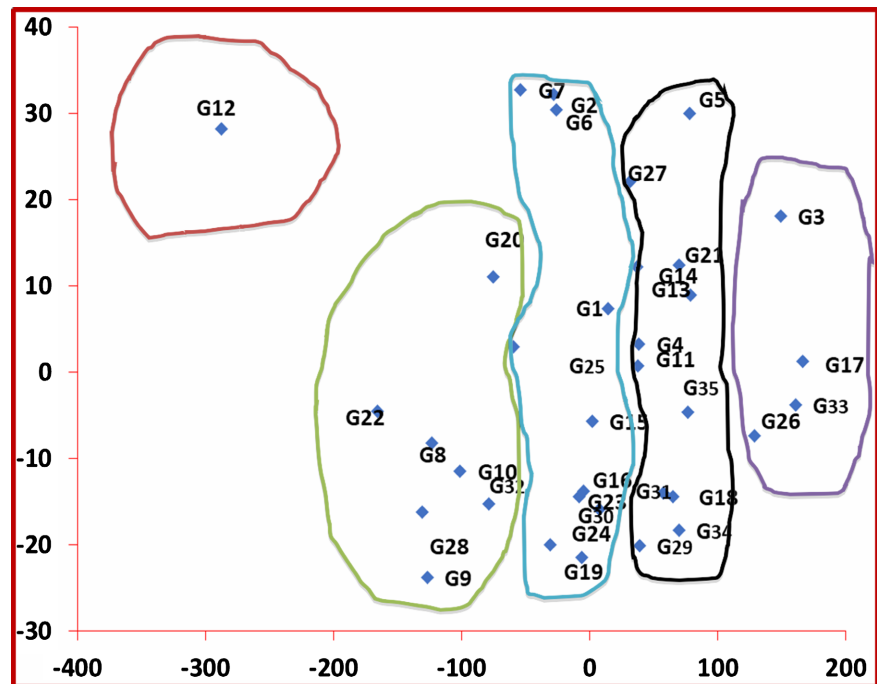
Figure 2. Cluster diagram of Maize genotypes of based on their principal component scores

(63.3) and the minimum was recorded in cluster IV (60.9). Days to maturity showed highest in cluster II (129.7) and lowest value in cluster III (128.3). The maximum mean value for plant height was observed in cluster I (247.4) and the minimum were recorded in cluster II (209.4). Cob length showed the highest value in cluster I (17.6) and the lowest value in cluster II (15.8). Cob breadth was observed the highest value in cluster I (15.9); whereas the lowest was observed in cluster II (14.4). The maximum mean value for number of rows per cob was estimated in cluster II (22.4) and the minimum was estimated in cluster V (13.4). Number of seeds per row showed the highest mean value in cluster I (41.6) and the lowest value in cluster III (27.1). The maximum value for number of seeds per cob was observed in cluster II (799.0) and the minimum was in cluster III (364.5). The maximum value for 100-seed weight was calculated in cluster III and IV (32.3); however, the minimum was calculated in cluster II (28.7). Total yield per plant shoed the highest in cluster II (117.5) and the lowest value in cluster III (58.9).

3.1.6. Contribution of Characters towards Divergence of the Genotypes

Relative contribution of characters towards divergence of the genotypes was observed and presented in Table 6. The character involved in high absolute magnitude for vector 1; considered to be responsible for primary differentiation and the character involved in high absolute magnitude in vector 2 was considered to be responsible for secondary differentiation. If the same character was obtained equal magnitude for the both vectors than the character was considered responsible for primary at the same time secondary differentiation.

Table 6. Relative contributions of the ten characters of 35 varieties to the total divergence.

Characters	Principal Component	
	Vector-1	Vector-2
Days to male flowering	0.1387	−0.0764
Days to female flowering	−0.0793	0.1317
Days to maturity	−0.0196	−0.0754
Plant height (cm)	0.0249	−0.0064
Cob length (cm)	−0.5781	0.3700
Cob breadth (cm)	0.0439	−0.3695
No. of rows per cob	0.4963	1.0200
No. of grains per row	0.2522	−0.0446
Number of grains per cob	0.0083	0.0378
100 grain weight (g)	−0.4010	0.7554
Grain yield per plant (g)	0.1354	−0.3057

In vector 1, days to male flowering (0.1387), plant height (0.0249), cob breadth (0.0439), number of seed rows per cob (0.4963), number of seeds per row (0.2522), number of seeds per cob (0.0083) and seed yield per plant (0.1354) had positive value responsible for the genetic divergence in this axis. On the other hand, days to female flowering (−0.0793), days to maturity (−0.0196), cob length (−0.5781), 100-seed weight (−0.4010) had negative value towards the divergence of the genotypes.

In vector 2, days to female flowering (0.1317), cob length (0.3700), number of rows per cob (1.0200), number of seeds per cob (0.7554) and 100-seed weight (0.7554) was observed positive divergence value; whereas, days to male flowering (−0.0764), days to maturity (−0.0754), plant height (−0.0064), cob breadth (−0.3695), number of seed per row (−0.0446) and seed yield per plant (−0.3057) was observed negative value for the divergence of the genotypes.

Number of rows per cob and number of seeds per cob both had positive value; thus, these two characters are important towards the divergence of the genotypes investigated (Table 6).

4. Conclusions

To investigate the genetic diversity different analysis had been performed to find out the suitable relation among the genotypes. Principal component analysis, cluster mean analysis, canonical variate analysis and D2 statistics had been performed to observe the genetical divergence and that was shown in the Tables and Figures. Cluster mean values of 11 different characters of 35 genotypes were grouped into five categories; among them the highest 35% genotypes were included in cluster number V with 12 genotypes: BHM-5, PAC-60, Pacific-98, HP-222, KhaiBhutta, AS-999, Pioneer, Duranta, Kaveri 218, Chamak-07 and

Golden-984; (12; G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35) and the lowest were 3% genotypes were included in cluster number II (1; Pacific G12). Between inter and intra cluster mean values, inter cluster distances were recorded higher than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups involved. The maximum value for the cluster distance D2 was recorded in cluster III (18.740) followed by cluster II (15.470, 13.032). The farthest cluster distance was recorded in cluster III that means it represented the highest diversified genotypes than other clusters. The nearest cluster distance was recorded in cluster IV and cluster V with 3.441 values which denoted the less diversified genotypes. In this case, days to male flowering, number of rows per cob, number of seeds per cob and 100-seed weight contributed towards cluster mean performance; the maximum in cluster number V.

From this experimental study, the eleven characters such as days to male flowering, days to female flowering, days to maturity, plant height, cob length, cob breadth, number of rows per cob, number of grains per row, number of grains per cob and 100-seed weight had positive and significant combination and relation in total yield effect per plant. At the same time, among the 35 maize genotypes some (PAC-60, Pacific-98, HP-222, Khai Bhutta, AS-999, Pioneer, Duranta, Kaveri 218, Chamak-07 and Golden-984) showed diversified genotypic representation for the understanding of excellent selection and preservation in future experimentation as well as breeding (hybridization) program.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1]   FAO (2016) World Agriculture: Towards 2015/2030 Summary Report. FAO, Rome.

[2]   Tollenaar, M. and Dwyer, L.M. (1999) Physiology of Maize. In: Smith, D.L. and Hamel, C., Eds., *Crop Yield*, Springer, Berlin, 169-204.
      https://doi.org/10.1007/978-3-642-58554-8_5

[3]   Khan, R. and Dubey, R.B. (2015) Combining Ability Analysis for Nutritional Quality and Yield in Maize (*Zea mays* L.). *The Bioscan*, **10**, 785-788.

[4]   BBS (2017) Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka, 9-190.

[5]   BBS (2012) Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka.

[6]   BBS (2015) Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka.

[7]   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 Agricultural and Biological Science, **2**, 1-3.

[8] Muhammad, B.A., Muhammad, R., Hussain, A., Tariq, M. and Sarwar, M. (2003) Character Association and Path Coefficient Analysis of Grain Yield Components Maize (*Zea mays* L.). *Pakistan Journal of Biological Sciences*, **6**, 136-138. https://doi.org/10.3923/pjbs.2003.136.138

[9] OECD-FAO (2018) Agricultural Outlook 2018-2027.

[10] Abdurakhmonov, I.Y. and Abdukarimov, A. (2008) Application of Association Mapping to Understanding the Genetic Diversity of Plant Germplasm Resources. *International Journal of Plant Genomics*, **2008**, Article ID: 574927. https://doi.org/10.1155/2008/574927

[11] Singh, P., Singh, P. and Mukul, K. (2013) Genetic Variability and Analysis of Yield Components in Linseed Germplasm. *Annals of Agricultural Research*, **16**, 164-167.

[12] Sumanth, V., Suresh, B.G., Ram, B.J. and Srujana, G. (2017) Estimation of Genetic Variability, Heritability and Genetic Advance for Grain Yield Components in Rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, **6**, 1437-1439.

[13] Adhikari, B.N., Pokhrel, B.B. and Shrestha, J. (2018) Evaluation and Development of Fingermillet (*Eleusine coracana* L.) Genotypes for Cultivation in High Hills of Nepal. *Farming & Management*, **3**, 37-46. https://doi.org/10.31830/2456-8724.2018.0001.7

[14] Pal, S., Sharma, H.R., Rai, A.K. and Bhardwaj, R.K. (2016) Genetic Variability, Heritability and Genetic Gain for Yield and Quality Traits in Cucumber (*Cucumis sativus* L.) Genotypes. *The Bioscan*, **11**, 1985-1990.

[15] Girma, B.T., Kitil, M.A., Banje, D.G., Biru, H.M. and Serbessa, T.B. (2018) Genetic Variability Study of Yield and Yield Related Traits in Rice (*Oryza sativa* L.) Genotypes. *Advances in Crop Science and Technology*, **6**, Article No. 381.

[16] Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, A. and Singh, S.P. (2006) Genotypic Variability in Vegetable Amaranth (*Amaranthus tricolor* L.) for Foliage and Its Contributing Traits over Successive Cuttings and Years. *Euphytica*, **151**, 103-110. https://doi.org/10.1007/s10681-006-9134-3

[17] Aditya, J.P. and Bhartiya, A. (2013) Genetic Variability, Correlation and Path Analysis for Quantitative Characters in Rainfed Upland Rice of Uttarakhand Hills. *Journal of Rice Research*, **6**, 24-34.

[18] FAO-UNDP (1988) Land Resources Appraisal of Bangladesh for Agricultural Development. Report 2. Agroecological Regions of Bangladesh. FAO, Rome.

[19] Rahman, M.M. and Alam, M. (2010) Disappearing Forest Tree Species Diversity in Tropical Moist Deciduous Forest and Its Implications: A Case Study in the Madhupur Tract of Central Bangladesh. *Journal of Forest Science*, **26**, 161-170.

[20] SRDI (2001) Land and Soil Resources Utilization Guide (In Bengali) Upazila Nirdeshica Series-Madhupur Upazila, Soil Resources Development Institute, Dhaka.

[21] Gomez, K.A. and Gomez, A.A. (1984) Statistical Procedure for Agricultural Research. 2nd Edition, John Willey & Sons, Singapore, 28-192.

[22] Pullin, A.S. (2002) Conservation Biology. 1st Edition, Cambridge University Press, Cambridge. https://doi.org/10.1017/CBO9781139051927