RESEARCH ARTICLE

SABRAO Journal
of Breeding and Genetics
52 (4) 418-434, 2020

GENETIC DIVERSITY OF COMMERCIALLY CULTIVATED WATERMELON (*Citrullus lanatus*) HYBRIDS IN BANGLADESH

F. MOHOSINA[1], M.N.H. MEHEDI[2*], E. MAHMUD[3], M.K. HASAN[4],
M.M.A. NOOR[2], M.H.S. RAHMAN[2] and A.K. CHOWDHURY[1]

[1] Department of Genetics and Plant Breeding, Patuakhali Science and Technology University,
Dumki Patuakhali, Bangladesh
[2] Bangladesh Institute of Nuclear Agriculture (BINA), BAU campus, Mymensingh, Bangladesh
[3] Bangladesh Agricultural Research Institute (BARI), Bangladesh
[4] International Maize and Wheat Improvement Center (CIMMYT), Bangladesh
*Corresponding author email: nazmul02348@gmail.com
Email addresses of coauthors: mahipstu175@gmail.com, kashem@pstu.ac.bd,
eftekharmahmud@yahoo.com, alnoormahmud4@gmail.com, sofiur1988@gmail.com,
mk.hasan@cgiar.org

SUMMARY

This experiment was carried out to study the genetic variability of watermelon *(Citrulluslanatus)* genotypes in the southern region of Bangladesh at Regional Horticulture Research Station, BARI, Lebukhali, Patuakhali during Rabi season, 2017–18. Sixteen commercially cultivated hybrids collected from different seed companies as well as from farmers' collection were used. Significant variations were recorded among the watermelon accessions in terms of different parameters. The genotype World Queen (7.4) and Sugar Kis (4.5) showed the highest performance for fruit weight and fruits number/plant, respectively. The highest genotypic and phenotypic coefficients were recorded for fruit yield/plant (55.14% and 58.69%) followed by single fruit weight/plant (34.51% and 37.65%). The number of male flower, fruit weight, fruit length, fruit diameter, leaf shape, and fruit yield were found to be highly correlated characters among the watermelon genotypes. The number of female flower was negatively correlated with vine length. The number of fruit showed negative correlation with rind thickness and positive correlation with fruit yield. The results of principal component analysis revealed that the important characters responsible for genetic divergence in major axis of differentiations are days to first male flower opening, number of male flower per plant, fruit weight, fruit length, fruit diameter, fruit yield, and leaf shape. Cluster analysis grouped the genotypes into five classes. Larger intercluster distances in all cases than intracluster distances suggested wider genetic diversity where Cluster I had highest vine length with higher internodal length. Cluster II had the highest mean value for number of fruit and fruit yield. Cluster III has the highest number of male flower, highest number of branch, and fruit length. Cluster V produced the largest fruit with highest fruit diameter and rind thickness. It also required maximum days for male flowering and highest number of female flower. This study shows wide variability among the watermelon genotypes which could be used for future breeding program.

Keywords: Characterization, genetic diversity and variability, genotypes, *Citrullus lanatus*

Key findings: Wide variability existed among the watermelon accessions used in this experiment. That variability could be used for future breeding program to develop a recognized high-yielding watermelon variety in our country. To develop a high-yielding variety, selection should be done on the basis of desired characters , such as single fruit weight, number of fruits/plant, and weight of fruits/plant. Collection of watermelon germplasm should be continued for more variability and desired traits , as well as molecular techniques , such as RAPD, SSR should be used for proper identification of the accession at the molecular level.

Manuscript received: October 14, 2020; Decision on manuscript: October 24, 2020; Accepted: November 5, 2020.

Communicating Editor: Dr. Naqib Ullah Khan

INTRODUCTION

Watermelon (*Citrullus lanatus)* belongs to the Cucurbitaceae family and a member of the sub-family Cucurbitoidae (Dane and Liu, 2007). It is cultivated in 6.2% of the world area devoted to vegetable crops (FAOSTAT, 2019). China is the largest producer of watermelon with 52.3 million tons of the total world production. Other major producing countries are Turkey, Iran, Brazil, Uzbekistan, Alzeria, USA, Russia Egypt, and Mexico (FAOSTAT, 2019). In Bangladesh, watermelon production is not uniformly distributed in all of the regions due to the prevailing climatic and edaphic factors and most are produced in the southern parts of the country. In Bangladesh, watermelons are cultivated annually in approximately 15,740 hectares of land and 274,000 metric tons are produced with an average production of 23.3 Mt/ha. Only in the eight specific watermelon-growing regions of Patuakhali district with 13,718 hectares this fruit is usually cultivated (BBS, 2019). It is usually cultivated in the southern part of Bangladesh and it is one of the major crops grown here. Watermelons from this region have high demand due to their high quality and bigger size. Both hybrid and open-pollinated varieties are cultivated by Bangladeshi growers but the demand for hybrid varieties is much higher than the open-pollinated ones. Watermelon is an ideal health food because it doesn't contain any fat or cholesterol and is an excellent source of vitamins A, B6, and C. It is a popular summer fruit well known for many potential attributes. It contains appreciable amount of soluble solids, beta carotene, and high amount of potassium which make watermelon juice to posses' variable diuretic properties. Although watermelon is primarily eaten fresh, it is also eaten as a cooked vegetable in Africa. Another use of watermelon is as a source of drinking water during

Table 1. List of watermelon genotypes and their sources.

S.No.	Genotypes	Source
a.	Tropical Dragon	Golachipa (Patuakhali)
b.	Sonya	Golachipa (Patuakhali)
c.	Asian-2	Golachipa (Patuakhali)
d.	Dragon King	Golachipa (Patuakhali)
e.	Black Giant	Barguna (Patuakhali)
f.	Sweet Black	Barguna (Patuakhali)
g.	Red Sugar	Barguna (Patuakhali)
h.	World Queen	Dumki (Patuakhali)
i.	Kanya	Dumki (Patuakhali)
j.	Dragon-2	Dumki (Patuakhali)
k.	Big Badshah	Dumki (Patuakhali)
l.	Big Sweet	Bhola
m.	Anarkoli	Bhola
n.	Sugar Kis	Bhola
o.	Sweet Dragon	Bhola
p.	China Sugar	Bhola

summer seasons, which is well known in parts of Sudan and Nigeria (Van-der-Vossen *et al.,* 2007).

Bangladesh is a country with diversified ecological conditions including climate, vegetation, and soil, which result in an enormous wealth of diversified indigenous genetic resources of crops of which watermelon is an example. The southern part of Bangladesh is an important region for the diversity of watermelon where different cultivars and uses are known, especially in the Patuakhali region (Nasim *et al.,* 2017). Despite the extent of its distribution, cultivation, and its importance, watermelon is a poorly described species as no standard descriptor list has been developed and published yet by the genetic resources community. Hence, available information on watermelon genetic diversity within the germplasm is very scarce. Successes in genetic improvement are largely attributed to the appropriate evaluation and use of genetic diversity.

Growing interest to this valuable crop was achieved through the studies on its constituents, but no systematic research on genetic variations has so far been done to evaluate the genetic potentialities of the available hybrids with a view to releasing modern varieties, and to meet up with increasing demands to come. Under such circumstances, this study was conducted to identify genetic variations within each of the watermelon germplasm, so that level of morphological variability and genetic distances among watermelon germplasm can be established using morphological marker.

MATERIALS AND METHODS

Sixteen commercially cultivated watermelon hybrids from different parts of southern regions of Bangladesh were used in this study (Table 1). The experiment was laid out in a randomized complete block design (RCBD) with three replications.

Each replication was divided into 16 unit plots where plot size was 4.5 m length by 1.5 m width with recommended spacing at 1.5 m from plant to plant and 1.5 m from row to row distance. Those 16 genotypes were allocated randomly on 16 unit plots. Recommended doses and application methods of manure and fertilizers were applied in the experimental field with NPK @ 110/312/83 kg/ha, respectively. The healthy single seedlings of 30 days old were transplanted in the pits of the experimental field. Necessary intercultural operations and irrigation were done during the experimental period to ensure normal growth and development of the plants. Control measures were taken against red pumpkin beetle at seedling stage and fruit fly at fruiting stage. Observations were recorded for days to first male and female flower opening, node number of first male and female flower, main vine length (cm), number of primary branches per vine, nodes on main vine, number of fruits per vine, average single fruit weight (g), fruit yield per vine (kg), fruit length (cm), fruit diameter (cm), thickness of the fruit flesh(mm), thickness of the rind (mm) etc. Genetic diversity was studied following Mahalanobis's (1936) D2 statistics extended by Rao (1952). Clustering of genotypes was done in accordance with Tocher's method (Rao, 1964) and principal component analysis (PCA), principal co-ordinate analysis (PCO), canonical vector analysis (CVA) were done with a computer by using GenStat 5.13 (Payne *et al.,* 1993). Intracluster distances were computed by using the values of intergenotype distance from distance matrix of PCO in accordance with Singh and Chaudhry (1985).

RESULTS

Results showed that days required to first male flowering, node order of first male flower, number of male flower plant^{-1}, days required to first female flower opening, node order first female flower, and number of female flower per plant were not significantly different among the accessions. The genotype Big Badshah required the minimum days to first male flowering (54.4 days). On the other hand, Tropical Dragon and Sonya took maximum days to first flowering (58 days). The lowest node order per vine was recorded (3) in accession World Queen and the highest node order (5) was recorded from Black Giant. Number of nodes per vine increased with increase in length of vine. Singh and Singh (1988) also reported the wide range of variability in pointed gourd for node order of first flowering and number of nodes per vine. Genotype World Queen produced the maximum number of male flowers per plant (37), whereas Big Sweet produced the minimum number (25) of male flowers. The accession Kanya required the minimum days to first female flowering (60 days), whereas Anarkoli took maximum days to first female flower opening (67 days). The lowest node order per vine was recorded (11) in China Sugar and the highest node order (18.0) was recorded from Sugar Kis. The plants of accession Kanya produced the maximum number of female flowers (22) and Black Giant produced the minimum number of female flowers (17). High amount of fixable variation in watermelon has been reported by Lalta *et al.* (2008).

The vine length, number of branching per plant, internode length, number of fruits per plant, single fruit weight, fruit length, fruit diameter, rind thickness, and fruit yield were significantly different among the accessions. Highest vine length was found in Dragon King (281.7 cm), whereas the germplasm Red Sugar get lowest (161.7) vine length (Table 2). Kumaran *et al.* (2005) also observed significant variation in plant height of three pointed gourd accessions. Vine length depends on genetic makeup of the vine. Highest branching per plant, maximum length of internode, maximum number of fruits per plant, longest fruit, highest fruit breadth, and rind thickness were recorded from the China Sugar (9), Dragon King (12 cm), Sugar Kis(4.5), China Sugar (27.3 cm), Dragon-2 (22.3 cm), and Sweet Dragon (2.0 mm) respectively. On the contrary, the lowest branching per plant, maximum length of internode, maximum number of fruits per plant, longest fruit, highest fruit breadth, and rind thickness were recorded from the genotype Red Sugar (3.5 cm), Sweet Black (8.9 cm), Dragon King (1.5 cm), Sonya (14.5 cm), and Kenya (0.6 mm), respectively. The accession World Queen had the highest fruit weight (7.4 kg) that was significantly different from other accessions. Sonya produced the lowest weight of fruits (2 kg) compared to other accessions. The variation of fruit weight could be due to the genetics, physiological, nutritional or environmental influences. The maximum yield of fruit (29.6 kg/plant) was obtained in World Queen, whereas the minimum yield of fruit yield (5.5 kg/plant) was obtained in Dragon king. Considerable differences between genotypic and phenotypic variances, as well as genotypic and phenotypic coefficient of variations, indicates the considerable environmental effect upon the expression of the above mentioned morphological characters of all the genotypes (Table 3). These results indicated that there were greater variations among the cultivated hybrids that might support the design of a breeding program for watermelon improvement. As stated, the PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) values are ranked as low, medium, and high with 0 to 10%, 10 to 20%, and > 20%, respectively. High GCV were recorded for fruit yield (55.1), fruit weight (34.5), number of fruit (29), node order of first male flower (25.2), number of male flower per plant (25), and rind thickness (23.1); while number of female flower per plant (18.9), branching (18), fruit length (14.7), and fruit diameter (10.6) showed medium GCV and vine length (10.0), node length (8.3), node order of first female flower (6.7), days to first female flower open (5), and days to first male flower open (4) exhibited low GCV. High phenotypic coefficients of variation (PCV) were also recorded for fruit yield (58.7), fruit weight (37.7), rind thickness (33), number of male flower per plant (33), and node order of first male flower (31.9), but moderate PCVs were recorded from branching (28.5), node order of first female flower (19.4), vine length (18.6), and fruit length (16.8); in contrast, remaining traits showed low PCV (Table 3). The estimated phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits indicating greater environmental influence on these traits for total variation.

Table 2. Mean values of 16 watermelon genotypes.

Genotypes	DMF	NOMF	NMF	DFF	NOFF	NFF	VL(cm)	BN	NL (cm)	NF	FW (kg)	FD (cm)	FL (cm)	RT(cm)	FY
Tropical Dragon	56.5	3.78	29.11	64.28	11.94	17.22	266.7 ab	5.0 b	10.78 abc	3.0 bcd	3.5 efg	16.0 bcd	22.0 abc	1.07 ab	10.50 cde
Sonya	58.0	3.33	25.67	66.89	12.78	21.83	191.7 ab	4.0 b	9.0 c	3.67 ab	2.0 g	13.33 d	14.58 d	1.0 ab	7.33 de
Asian-2	55.0	4.22	35.28	66.28	13.5	19.72	220.0 ab	6.33 ab	11.0 abc	2.0 de	4.07 def	17.33 bc	22.33 abc	1.8 a	8.13 de
Dragon King	58.0	4.33	27.56	64.5	14.17	18.5	281.67 a	6.0 ab	12.0 a	1.5 e	3.63 d–g	16.33 bcd	19.67 bcd	1.33 ab	5.45 e
Black Giant	57.6	4.83	30.61	66.44	15.78	16.33	245.0 ab	5.67 ab	11.0 abc	3.0 bcd	2.31 fg	15.33 cd	16.33 d	1.4 ab	6.94 de
Sweet Black	57.6	3.72	30.17	65.78	15.5	17.28	251.7 ab	5.83 ab	8.89 c	2.5 cde	4.2 def	17.67 bc	22.83 abc	1.33 ab	10.5 cde
Red Sugar	57.1	4.39	32.44	64.11	13.72	20.89	161.7 b	3.5 b	10.5 abc	2.0 de	6.4 abc	19.0 abc	22.0 abc	2.0 a	12.8 cde
World Queen	54.8	3.11	36.11	66.89	16.89	17.67	222.5 ab	5.5 ab	11.16 abc	4.0 ab	7.4 a	19.0 abc	25.33 a	1.7 a	29.6 a
Kanya	55.4	3.89	31.33	60.44	13.11	21.89	240.0 ab	5.33 ab	12.0 a	3.5 abc	4.17 def	19.67 ab	23.0 abc	0.6 b	14.58 cd
Dragon-2	55.4	3.56	34.78	66.22	15.22	18.66	251.7 ab	5.67 ab	11.75 ab	4.0 ab	6.65 ab	22.33 a	23.83 ab	1.37 ab	26.59 a
Big Badshah	54.4	3.67	28.39	66.94	14.89	17.22	276.7 a	6.33 ab	10.33 abc	3.0 bcd	2.2 fg	17.0 bcd	18.0 cd	1.5 ab	6.70 de
Big Sweet	57.3	3.78	24.72	65.67	13.5	20.44	231.0 ab	4.33 b	10.0 abc	3.0 bcd	4.8 b–e	18.33 bc	24.0 ab	1.33 ab	14.4 cd
Anarkoli	56.0	4.44	28.45	67	13.89	17.39	230.0 ab	5.0 b	10.5 abc	2.17 de	4.0 d–g	17.33 bc	23.0 abc	1.53 ab	8.67 cde
Sugar Kis	55.0	3.83	34.5	65.67	18	18.33	199.7 ab	5.33 ab	9.91 abc	4.5 a	5.15 b–e	18.0 bc	25.33 a	1.0 ab	23.18 ab
Sweet Dragon	54.6	3.78	35.67	66.11	16.11	19.44	221.7 ab	5.5 ab	9.33 bc	1.83 e	4.44 cde	17.33 bc	24.5 ab	2.0 a	8.35 de
China Sugar	56.2	4.22	35.9	65.3	11.3	17.7	226.7 ab	9.0 a	11.65 ab	3.0 bcd	5.57a–d	18.67 abc	27.25 a	1.67 a	16.7 bc
Level of Significance	NS	NS	NS	NS	NS	NS	*	***	***	***	***	***	***	***	***
CV (%)	4.05	25.15	24.9	4.56	18.2	20.04	15.78	22.11	7.8	12.79	15.05	7.15	7.02	23.55	20.08

*NS = Not Significant, * = Significant at 5% level of significance, *** = Significant at 0.1% level of significance*

DMF = Days to first male flower opening, NOMF = Node order of first male flower, NMF = Number of male flower per plant, DFF = Days to first female flowering, NOFF = Node order of first female flower, NFF = No. of female flower plant^{-1}, VL = Vine length, NL = Nodal length, BN = Branching, NL = Node length, NF = Number of fruits plant^{-1}, FW = Fruit weight, FD = Fruit diameter, FL = Fruit length, RT = Rind thickness, FY = Fruit yield

Table 3. Minimum, maximum, mean value genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of different parameters of 16 watermelon genotypes.

Variable	Minimum	Maximum	Mean	GV	PV	GCV	PCV
Days to first male flower open	54.39	58.00	56.19	4.97	7.84	3.97	4.98
Node order of first male flower	3.110	4.830	3.930	0.98	1.57	25.19	31.88
Number of male flower per plant	24.72	36.11	31.30	61.0	104.1	24.96	32.60
Days to first female flower open	60.44	67.00	65.53	8.92	13.5	4.56	5.60
Node order of first female flower	11.33	18.00	14.40	0.94	7.77	6.73	19.36
Number of female flower per plant	16.33	21.89	18.78	12.1	20.5	18.87	24.33
Vine length (cm)	161.7	281.7	232.3	529.3	1873	9.90	18.63
Branching	3.500	9.000	5.520	0.98	2.47	17.97	28.49
Node length (cm)	8.890	12.00	10.61	0.78	1.46	8.30	11.39
Number of fruit	1.500	4.500	2.917	0.71	0.85	28.95	31.65
Fruit weight (kg)	2.000	7.400	4.406	2.31	2.75	34.51	37.65
Fruit diameter (cm)	13.33	22.33	17.67	3.50	5.09	10.59	12.78
Fruit length (cm)	14.58	27.25	22.12	10.6	13.73	14.70	16.75
Rind thickness (mm)	0.600	2.000	1.414	0.11	0.22	23.06	32.96
Fruit yield (kg/plant)	5.445	29.60	17.52	52.6	59.57	55.14	58.69

Correlation among morphological traits

Correlation coefficient and factor loadings of the morphological traits were measured in 16 watermelon genotypes were shown in Table 4 and 10. Days to first male flowering was found negatively correlated with number of male flower. This trait also has correlation with fruit skin color. Node order of male flowering was found negatively correlated with number of fruit. Number of male flower, fruit weight, fruit length, fruit diameter, leaf shape, and fruit yield were found to be highly correlated characters. Number of female flower was negatively correlated with vine length. Number of fruit showed negative correlation with rind thickness and positive correlation with fruit yield. Fruit yield showed very poor correlation with days to first female flowering, number of female flower, vine length, branch number, node length, rind thickness, fruit shape, skin color, and flesh color.

Euclidean distance among accessions

Estimation of phenotypic distance was obtained from qualitative and quantitative data measured from the total samples. This assumes that the differences between the characters reflect the genetic divergence of the accessions being compared. Distance coefficients between pairs of the varieties using Euclidean geometry are shown in Table 5. Euclidean distance in pair wise comparison ranges from 5.97 to 120.53 from a total of 120 pair. Lowest distance was exhibited by genotype 3 and genotype 15, whereas maximum distance was exhibited by genotype 4 and genotype7.

Association among the genotypes revealed by cluster analysis with UPGMA method and Euclidean distance coefficient are presented in Figure 1. Dendrogram grouped the genotypes into two major classes. There were thirteen genotypes in the first group and only three in the second group. The dendrogram then sub-divided the first group into two sub-classes. There were 10 genotypes in one class and three in other class. After the cutting of point accomplishment with multivariate analysis of variance, hybrids were categorized into five groups in , which these groups revealed noticeable difference.

The distribution pattern indicated that the highest number of genotypes (7) was included in Cluster III and the lowest were in Cluster V. Interand intracluster distances are presented in Table 4. The intercluster distances in all cases were larger than intracluster distances suggesting wider genetic diversity among the accessions of different groups. The highest intercluster distance was observed between I and V while the lowest distance was observed between the Cluster III and IV. Cluster I exhibited the highest intracluster distance while the lowest distance was observed in Cluster II. The cluster mean of 16 accessions are presented in Table 6. The results revealed that Cluster I had the highest vine length with higher internodal length. Cluster II had the highest mean value for number of fruit and fruit yield. Cluster III had the highest number of male flower, highest number of branch, and fruit length. Fruit shape was almost oblong. Cluster V produced the largest fruit with the highest fruit diameter

Table 4. Correlation matrix (Pearson's)among different morphological traits of 16 genotypes of watermelon**.**

Variables	DMF	NOMF	NMF	DFF	NOFF	NFF	VL	BN	NL	NF	FW	FD	FL	RT	FY	LS	FS	SC	StC	FC
DMF	1	0.308	−0.632	−0.086	−0.365	0.103	−0.008	−0.274	−0.139	−0.252	−0.310	−0.448	−0.460	−0.219	−0.396	−0.321	−0.008	0.579	0.076	−0.157
NOMF	0.308	1	−0.042	−0.153	−0.198	−0.210	0.007	0.155	0.301	−0.559	−0.235	−0.146	−0.134	0.215	−0.491	−0.253	0.230	0.088	0.031	−0.024
NMF	−0.632	−0.042	1	0.008	0.336	−0.149	−0.260	0.451	0.270	0.154	0.630	0.529	0.613	0.432	0.546	0.499	0.035	−0.481	−0.153	0.002
DFF	−0.086	−0.153	0.008	1	0.350	−0.451	−0.040	0.071	−0.434	0.038	−0.087	−0.274	−0.178	0.467	0.000	−0.220	−0.391	−0.469	−0.318	−0.824
NOFF	−0.365	−0.198	0.336	0.350	1	−0.300	−0.053	−0.138	−0.248	0.289	0.229	0.166	0.106	0.117	0.378	0.303	−0.230	−0.488	−0.344	−0.191
NFF	0.103	−0.210	−0.149	−0.451	−0.300	1	−0.533	−0.474	−0.088	0.009	0.059	0.064	−0.080	−0.195	−0.032	−0.031	0.049	0.238	0.427	0.477
VL	−0.008	0.007	−0.260	−0.040	−0.053	−0.533	1	0.412	0.343	−0.120	−0.347	−0.018	−0.132	−0.268	−0.214	−0.072	0.148	0.109	−0.005	0.065
BN	−0.274	0.155	0.451	0.071	−0.138	−0.474	0.412	1	0.401	−0.030	0.044	0.166	0.342	0.156	0.066	0.324	0.234	−0.109	−0.384	−0.042
NL	−0.139	0.301	0.270	−0.434	−0.248	−0.088	0.343	0.401	1	0.026	0.288	0.449	0.199	−0.086	0.264	−0.020	0.027	0.202	0.079	0.370
NF	−0.252	−0.559	0.154	0.038	0.289	0.009	−0.120	−0.030	0.026	1	0.221	0.239	0.109	−0.535	0.716	0.233	−0.350	0.189	−0.394	0.178
FW	−0.310	−0.235	0.630	−0.087	0.229	0.059	−0.347	0.044	0.288	0.221	1	0.802	0.785	0.353	0.825	0.447	0.049	−0.126	−0.136	−0.040
FD	−0.448	−0.146	0.529	−0.274	0.166	0.064	−0.018	0.166	0.449	0.239	0.802	1	0.707	0.130	0.708	0.489	0.107	0.038	−0.032	0.266
FL	−0.460	−0.134	0.613	−0.178	0.106	−0.080	−0.132	0.342	0.199	0.109	0.785	0.707	1	0.232	0.624	0.511	0.550	−0.217	−0.228	0.069
RT	−0.219	0.215	0.432	0.467	0.117	−0.195	−0.268	0.156	−0.086	−0.535	0.353	0.130	0.232	1	−0.054	0.123	−0.132	−0.533	−0.060	−0.573
FY	−0.396	−0.491	0.546	0.000	0.378	−0.032	−0.214	0.066	0.264	0.716	0.825	0.708	0.624	−0.054	1	0.433	−0.150	−0.039	−0.336	0.052
LS	−0.321	−0.253	0.499	−0.220	0.303	−0.031	−0.072	0.324	−0.020	0.233	0.447	0.489	0.511	0.123	0.433	1	0.000	−0.138	−0.411	0.327
FS	−0.008	0.230	0.035	−0.391	−0.230	0.049	0.148	0.234	0.027	−0.350	0.049	0.107	0.550	−0.132	−0.150	0.000	1	−0.019	0.116	0.197
SC	0.579	0.088	−0.481	−0.469	−0.488	0.238	0.109	−0.109	0.202	0.189	−0.126	0.038	−0.217	−0.533	−0.039	−0.138	−0.019	1	0.132	0.212
StC	0.076	0.031	−0.153	−0.318	−0.344	0.427	−0.005	−0.384	0.079	−0.394	−0.136	−0.032	−0.228	−0.060	−0.336	−0.411	0.116	0.132	1	0.240
FC	−0.157	−0.024	0.002	−0.824	−0.191	0.477	0.065	−0.042	0.370	0.178	−0.040	0.266	0.069	−0.573	0.052	0.327	0.197	0.212	0.240	1

Values in bold are different from 0 with a significance level alpha = 0.05

DMF = Days tofirstmale flower opening, NOMF = Node order of first male flower, NMF = Number of male flower per plant, DFF = Days to first female flowering, NOFF = Node order of firstfemale flower, NFF = No. of female flower plant^{-1}, VL = Vine length, NL = Nodal length, BN = Branching, NL = Node length, NF = Number of fruits plant^{-1}, FW = Fruit weight, FD = Fruit diameter, FL = Fruit length, RT = Rind thickness, FY = Fruit yield, LS = Leaf shape, FS = Fruit shape, SC = Skin color, Stripe color, FC = Flesh color

Table 5. Proximity matrix (Euclidean distance) among different morphological traits of 16 genotypes of watermelon.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.00	75.91	47.46	16.50	23.91	16.48	105.32	49.87	28.45	24.56	13.49	36.71	36.99	68.96	46.28	42.05
2		0.00	32.09	90.54	54.21	61.59	33.24	42.64	51.30	65.43	85.52	41.89	40.27	24.97	34.61	41.47
3			0.00	62.48	27.28	32.84	59.01	23.42	23.20	37.56	57.62	17.48	12.59	26.35	5.97	13.97
4				0.00	37.62	31.33	120.53	65.53	43.79	38.64	9.17	52.04	52.08	84.72	61.24	57.77
5					0.00	11.71	84.22	34.55	16.32	24.44	32.07	20.10	17.97	49.67	26.54	25.67
6						0.00	90.36	36.19	15.46	18.56	26.57	22.32	22.53	53.99	31.02	27.56
7							0.00	63.83	78.68	91.30	115.60	70.00	68.94	40.39	60.75	65.98
8								0.00	26.18	30.07	60.20	22.42	25.11	24.52	22.63	16.31
9									0.00	19.30	39.44	13.56	15.57	42.51	21.85	17.24
10										0.00	34.08	27.03	29.85	52.63	36.16	28.33
11											0.00	47.43	47.35	79.61	56.27	53.00
12												0.00	9.06	34.51	17.00	14.27
13													0.00	34.86	12.48	14.52
14														0.00	27.28	29.12
15															0.00	13.27
16																0.00

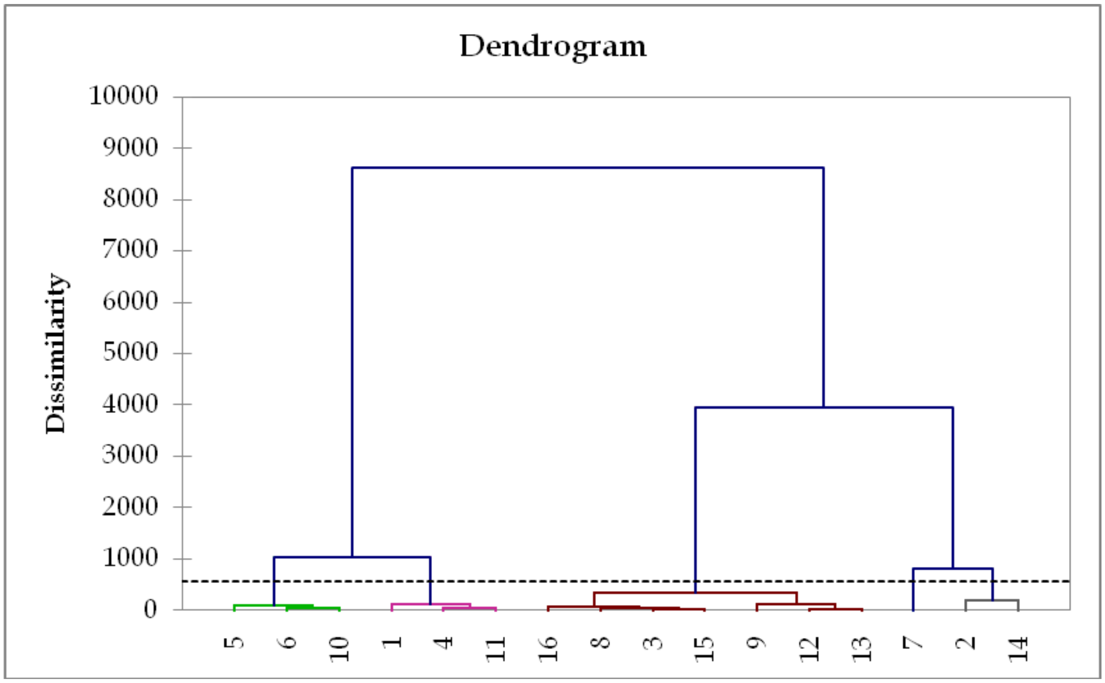

Figure 1. Dendogram showing clustering of 16 watermelon genotypes.

Table 6. . Results by class wise distribution of genotypes.

Class	1	2	3	4	5
Objects	3	2	7	3	1
Sum of weights	3	2	7	3	1
Within-class variance	82.732	186.393	101.493	70.007	0.000
Minimum distance to centroid	5.296	9.654	6.554	4.818	0.000
Average distance to centroid	7.262	9.654	9.005	6.693	0.000
Maximum distance to centroid	9.096	9.654	14.477	8.057	0.000
Genotypes	1.Tropical dragon, 4.Dragon king, 11.Big Badshah	2.Sonya 14.Sugar Kis	3.Asian – 2 8.World queen 9.Kanya 12.Big sweet 13.Anarkoli 15.Sweet dragon 16.China sugar	5.Black giant 6.Sweet black 10.Dragon–2	7.Red sugar

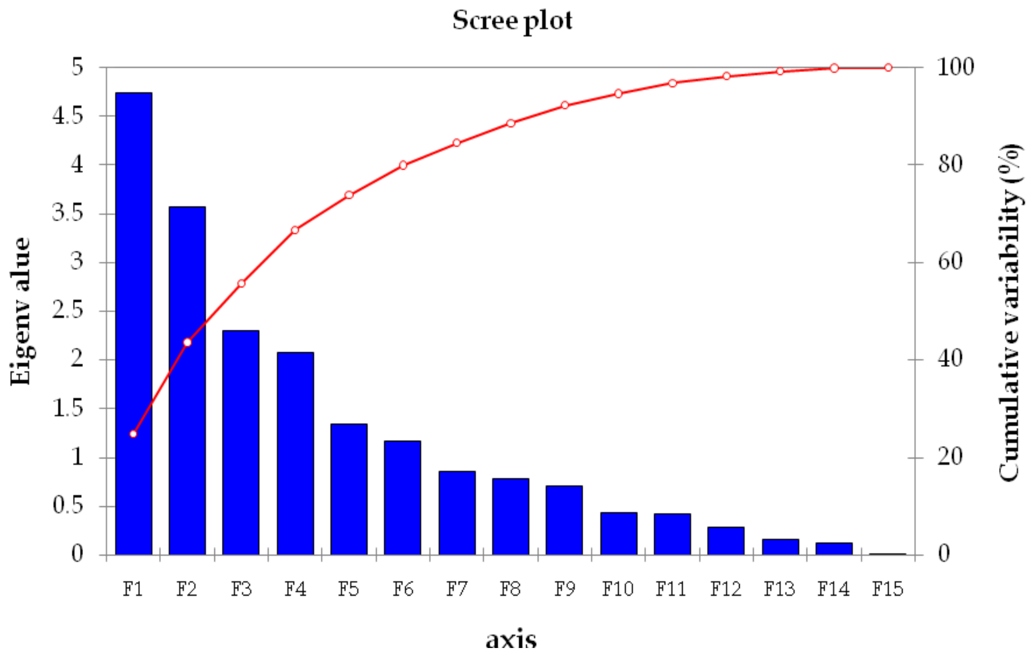

Figure 2. Screen plot indicting factors distribution along with Eigen values. Cumulative variability (Red line) indicating F1 and F2 as the most effective components of variability.

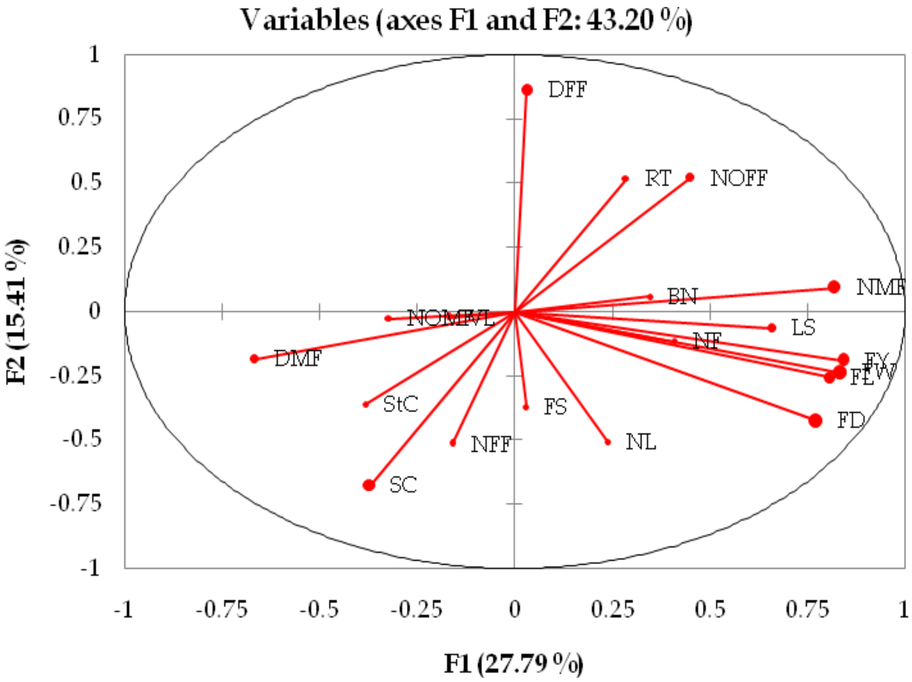

Figure 3. Bi-plot of the 14 quantitative characters along the first and second principal component vectors based 16 accession of watermelon.

and rind thickness. It also required maximum days for male flowering and highest number of female flower (Table 7 and Table 8).

PCA

PCA was used to identify the most significant variables in the data set (Table 4). The screen plot of the PCA (Figure 2) shows that the first six eigen values correspond to the whole percentage of the variance in the dataset. The first six main PCAs were extracted from the complicated components, the total cumulative variance of these six factors amounted to 81.7% and these components had eigen values > 1 (Table 9). The PCA simplifies the complex data by transforming the number of associated traits into a smaller number of variables as PCAs. The first PCA accounts for maximum variability in the data with respect to succeeding components. The PCA grouped the estimated watermelon variables into six main components of , which PCA1 accounted for approximately 27.8% of the variation; PCA2 for 15.4%, PCA3 for 14.1%, PCA4 for 11.4%, PCA5 for 6.7%, and PCA6 for 6.3%. The first PCA was related to days to first male flower opening, number of male flower per plant, fruit weight, fruit length, fruit diameter, fruit yield, and leaf shape, whereas the second PCA was related to days to first female flower opening, node order of first female flower per plant, node length, and fruit skin color (Table 4).

The third PCA contrasts variables that were related to number of fruit, node order of first male flower, and branch number. The forth PCA was related to vine length, number of female flower and, rind thickness. By contrast, the fifth PCA was related to fruit shape and the sixth PCA was related to stripe color. The first two principal components contributing approximately half of the variance were plotted to observe the relationships between the measured traits of watermelon (Figure 2). The correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors. The correlation coefficients among the traits indicate that the plot currently shows the relationship among the traits that had relatively large loading on both PCA1 and PCA2 axes.

The most prominent relations shown in Figure 3 are a strong positive association among NMF, FW, FD, FL, FY, and LS, between DMF–SC, between NF–FY as indicated by the small obtuse angles between their vectors (r = cos0 = +1). There was a negative correlation between DMF – NMF, between NOMF–NF, between NFF–VL, and between NF–RT (Figure 3) as indicated by the angle of approximately 180° (r = cos180 = –1). Some discrepancies of the plot predictions and original data were expected because the first two PCAs accounted for <100% of the total variation.

DISCUSSION

Correlation between the traits like number of male flower, fruit weight, fruit length, fruit diameter, leaf shape, and fruit yield indicated that positive change for one of them will be positive for others and these are the important trait to increase yield. Number of fruit

Table 7. Class centroids of watermelon genotypes based on different morphological traits.

Class	DMF	NOMF	NMF	DFF	NOFF	NFF	VL	BN	NL	NF	FW	FD	FL	RT	FY	LS	FS	SC	StC
1.00	56.32	3.93	28.35	65.24	13.67	17.65	275.00	5.78	11.04	2.50	3.11	16.44	19.89	1.30	7.52	3.67	4.67	3.67	2.33
2.00	56.50	3.58	30.09	66.28	15.39	20.08	195.67	4.67	9.46	4.09	3.58	15.67	19.96	1.00	15.26	4.00	4.00	3.50	1.50
3.00	55.63	3.92	32.50	65.38	14.05	19.18	227.41	5.86	10.81	2.79	4.92	18.24	24.20	1.52	14.32	5.57	5.43	2.43	1.57
4.00	56.87	4.04	31.85	66.15	15.50	17.42	249.45	5.72	10.55	3.17	4.39	18.44	21.00	1.37	14.68	5.67	3.67	3.33	1.33
5.00	57.05	4.39	32.44	64.11	13.72	20.89	161.67	3.50	10.50	2.00	6.40	19.00	22.00	2.00	12.80	5.00	3.00	4.00	3.00

DMF = Days to first male flower opening, NOMF = Node order of first male flower, NMF = Number of male flower per plant, DFF = Days to first female flowering, NOFF = Node order of first female flower, NFF = No. of female flower plant^{-1}, VL = Vine length, NL = Nodal length, BN = Branching, NL = Node length, NF = Number of fruits plant^{-1}, FW = Fruit weight, FD = Fruit diameter, FL = Fruit length, RT = Rind thickness, FY = Fruit yield, LS = Leaf shape, FS = Fruit shape, SC = Skin color, StC = Stripe color

Table 8. Distances between the class centroids of watermelon genotypes based on different morphological traits.

	1	2	3	4	5
1	0	79.845	48.617	27.109	113.731
2	79.845	0	32.488	54.023	34.818
3	48.617	32.488	0	22.551	65.994
4	27.109	54.023	22.551	0	88.002
5	113.731	34.818	65.994	88.002	0

Table 9. Eigen values, variability (%) and cumulative (%) for the principal component axes.

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15
Eigen value	5.28	2.93	2.68	2.16	1.27	1.20	0.87	0.81	0.72	0.35	0.30	0.22	0.12	0.06	0.03
Variability (%)	27.79	15.41	14.09	11.37	6.68	6.33	4.57	4.25	3.79	1.84	1.59	1.18	0.64	0.31	0.15
Cumulative (%)	27.79	43.20	57.29	68.66	75.35	81.68	86.25	90.50	94.29	96.13	97.72	98.90	99.54	99.85	100.00

Table 10. Factor loadings of the morphological traits of watermelon genotypes.

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15
DMF	−0.668	−0.183	0.069	0.038	−0.221	−0.533	−0.203	0.018	0.147	0.175	0.260	0.097	−0.092	0.044	−0.007
NOMF	−0.322	−0.026	−0.653	−0.111	−0.327	−0.270	0.047	0.414	−0.253	−0.023	−0.167	−0.001	−0.097	−0.020	−0.030
NMF	0.822	0.093	−0.234	−0.180	−0.090	0.103	0.260	0.036	−0.176	0.297	0.052	0.034	0.044	0.120	−0.045
DFF	0.031	0.865	0.110	0.050	−0.157	−0.020	−0.246	−0.313	−0.053	−0.005	−0.083	0.162	−0.110	−0.050	−0.044
NOFF	0.450	0.520	0.283	0.072	0.104	0.077	−0.141	0.587	0.047	0.058	0.032	0.204	0.102	−0.055	0.011
NFF	−0.160	−0.514	0.413	−0.567	0.100	0.049	0.283	−0.089	−0.028	−0.208	0.069	0.259	0.002	0.003	−0.043
VL	−0.169	−0.023	−0.410	0.698	0.147	0.356	−0.197	0.019	0.336	−0.059	0.055	0.035	0.010	0.058	−0.065
BN	0.346	0.060	−0.636	0.467	0.039	−0.079	0.295	−0.313	−0.065	0.108	0.003	0.199	0.007	−0.047	0.066
NL	0.240	−0.508	−0.424	0.284	−0.493	0.297	0.054	0.078	−0.127	−0.150	0.199	0.012	0.003	−0.070	−0.024
NF	0.409	−0.116	0.691	0.489	−0.018	0.012	0.068	−0.049	−0.277	0.055	−0.081	−0.036	−0.060	0.003	−0.055
FW	0.834	−0.235	0.053	−0.277	−0.234	−0.125	−0.269	−0.052	0.085	0.017	0.116	−0.027	0.033	−0.016	0.038
FD	0.771	−0.423	−0.063	−0.055	−0.158	0.097	−0.169	0.071	0.211	−0.106	−0.238	0.121	−0.119	0.093	0.044
FL	0.807	−0.255	−0.267	−0.147	0.262	−0.185	−0.241	−0.115	−0.065	−0.024	−0.028	−0.078	0.006	−0.063	−0.029
RT	0.286	0.517	−0.403	−0.533	−0.311	−0.091	−0.003	−0.170	0.221	−0.067	−0.035	−0.022	0.110	0.005	−0.053
FY	0.843	−0.190	0.381	0.147	−0.164	−0.020	−0.198	−0.047	−0.092	0.031	0.085	−0.009	−0.019	−0.017	−0.011
LS	0.660	−0.063	0.021	0.081	0.229	−0.301	0.414	0.138	0.445	0.039	0.009	−0.060	−0.105	−0.069	−0.036
FS	0.028	−0.370	−0.521	−0.139	0.642	−0.160	−0.285	0.008	−0.212	0.015	0.018	0.077	0.009	0.006	−0.029
SC	−0.372	−0.674	0.193	0.303	−0.240	−0.284	−0.056	−0.080	0.127	0.133	−0.245	0.067	0.176	−0.032	−0.027
StC	−0.382	−0.358	−0.052	−0.485	−0.016	0.584	−0.097	−0.025	0.125	0.325	−0.051	0.008	−0.080	−0.080	−0.007

DMF = Days tofirstmale flower opening, NOMF = Node order of first male flower, NMF = Number of male flower per plant, DFF = Days to first female flowering, NOFF = Node order of first female flower, NFF = No. of female flower plant^{-1}, VL = Vine length, NL = Nodal length, BN = Branching, NL = Node length, NF = Number of fruits plant^{-1}, FW = Fruit weight, FD = Fruit diameter, FL = Fruit length, RT = Rind thickness, FY = Fruit yield, LS = Leaf shape, FS = Fruit shape, SC = Skin color, StC = Stripe color also showed positive correlation, i.e., if the fruit number increase, yield will also increase. Poor correlation of days to first female flowering, number of female flower, vine length, branch number, node length, rind thickness, fruit shape, and fruit yield indicated that these characters had little effect on yield. Strong and highly significant for fruit weight, fruit length, and fruit width were also described by El-Madidi and Hakimi (2005). Similar high positive correlation of fruit size and number of fruit with fruit yield was described by Rakesh Kumar and Todd C. Wehner (2011). In qualitative parameters , such as leaf shape, fruit shape, fruit skin color, fruit stripe color, flesh color, etc. have showed significant frequencies in different categories among the genotypes due to their inherent genetic diversity. The high percentage of heterogeneity was calculated for fruit and seed characters and consequently some descriptor state disappeared in the homogeneity's level even though they were recorded when characterization was based on individual plants. All traits showed greater values for PCV than GCV indicating high contribution of genotypic effects for phenotypic expression of , such characters. High and moderate values of PCV and GCV indicated the existence of substantial variability for , such characters and selection may be effective based on these characters.

The results of the PCA revealed that in PCA1 the important characters responsible for genetic divergence in major axis of differentiations were days to first male flower opening, number of male flower per plant, fruit weight, fruit length, fruit diameter, fruit yield, and leaf shape. In PCA2, days to first female flower opening, node order of first female flower per plant, node length, and fruit skin color played a major role while the rest of the characters played minor role in second axis of differentiation. Alam *et al.* (2006) reported days to heading, 1000 grain weight, and yield per plant were the major contributors toward divergence in hull-less barley. Mondol *et al.* (1989) found that number of fruits per plant and yield per plant were important contributors towards divergence of pumpkin. Moreover, Habib *et al.* (2007) reported same for grains per panicle, grain length, and harvest index for rice.

In cluster analysis, the distribution pattern indicated that the highest number of genotypes (7) was included in Cluster III and the lowest were in Cluster V. Larger intercluster distances in all cases than intracluster distances suggests wider genetic diversity among the genotypes of different groups. The highest intercluster distance was observed between I and V while the lowest distance was observed between the Cluster III and IV. Cluster I exhibited the highest intracluster distance while the lowest distance was observed in Cluster II. Somayajullu *et al. (*2011) reported the clustering revealed instability due to relatively lesser divergence. Whereas, widely divergent clusters remain distinct in different environments. The result was also supported by Raut *et al. (2005)*. In this study, it was observed that Cluster II was highly diverged. So those would be more stable. The genotypes of the distant clusters could be used in crossing programs for obtaining wide range of variation among the segregates. Jagadev and Samal *(2001)* obtained segregants with wider variations among the genotypes in Niger from the crossing between the clusters involving the parents, which belonged to distant clusters. The crosses between the clusters-I and V were expected to exhibit higher heterosis and also likely to produce new recombinants with desired traits.

CONCLUSION

The results of this study revealed that a wide variability existed among the collected commercially cultivated watermelon hybrids. Also, there was correlation of different yield contributing characters with the yield of watermelon genotypes. From the correlation coefficient analysis, it was observed that the number of fruits per plant had maximum direct and positive effects on yield of fruit. This character contributes indirectly to yield per plant via days to first flower, number of node at first flower, fruit length, and weight of fruit per plant. Cluster analysis revealed that there was wider genetic diversity among the accessions. In cluster analysis, the intercluster distances in all cases were larger than intracluster distances suggesting wider genetic diversity among the accessions of different groups. In PCA, the first PC accounts for maximum variability in the data with respect to succeeding components. These results could be used for generation of a core collection of watermelon accessions by elimination of redundant ones and for watermelon breeding programs by helping to identify useful, genetically distinct lines.

REFERENCES

Alam AKM, Nahar N, Begum M (2006). Genetic divergence for quantitative characters for hull-less burley. *Bangladesh J. Agric. Res.* 31(3): 347-351.

BBS (2019). Year book of agricultural statistics of Bangladesh. Bangladesh Bureau of Statistics. pp. 119.

Dane F, Liu J (2007). Diversity and origin of cultivated and citron type watermelon (*Citrullus lanatus*). *Genet. Resour. Crop. Evol.*54: 1255-1265.

El-Madidi S, Hakimi F (2005). Genotypic variation in fruit characters in some genotypes of watermelon cultivated in Morocco. *Int. J. Agron. Agric. Res.* 6(4): 130-137.

FAOSTAT (2019). http://www.fao.org/faostat/en/#data/QC/visualize.

Habib SH, Akter K, Basher MK, Khalequzzaman M (2007). Multivariate analysis of divergence in advanced line and local rice accessions. *Bangladesh J. Agric. Res.* 32(1): 29-36.

Jagadev PN, Samal KM (2001). Multivariate analysis in Niger. *Indian J. Genet.* 51(4): 392-394.

Kumaran SS, Natarajan S, Thamburoj S (2005). Correlation and path analysis studies in pumpkin (*Cucurbita moschata* Poin.). *South Indian Hort.* 46(3-6): 138-142.

Lalta P, Gautan NC, Singh SP (2008). Studies on genetic variability and character association in watermelon. *Veg. Sci.* 15(l): 86-94.

Mahalanobis PC (1936). On the generalized distance in statistics. Proceedings of the National Institute of Science of India. pp. 49-55.

Mondal SN, Rashid A, Inove K, Hossain AKMA, Hossain MA (1989). Genetic variability, correlation and path coefficient analysis in watermelon. *Bangladesh J. Plant Breed. Genet.* 2(1): 31 -35.

Nasim M, Shahidullah SM, Saha A, Muttaleb MA, Aditya TL, Ali MA, Kabir MS (2017). Distribution of crops and cropping patterns in Bangladesh. *Bangladesh Rice J.* 21(2):1-55.

Payne RW, Lane PW, Baird DB, Gilmour AR, Harding SA, Morgan GW, Murray DA, Thompson R, Todd AD, Tunnicliffe G, Wilson, Webster R, Welham SJ (1993). Genstat 5.13. Statistics Department, IACR-Rothamsted, Harpenden, Hertfordshire AL52JQ, United Kingdom.

Rakesh K, Todd C (2011). Inheritance of fruit yield in two watermelon populations in North Carolina. *Euphytica* 182: 275–283.

Rao CR (1952). Advanced statistical methods in biometrical research. John Willy and Sons. New York.

Rao CR (1964). The use and interception of principal analysis in applied research. *Sankhya* 22: 317-318.

Raut VM, Rao VSP, Patil VP, Deodicar GB (2005). Genetic divergence in *Triticum durum*. *Indian J. Genet.* 31: 86-93.

Singh NK, Singh RK (1988). Correlation and path co-efficient analysis in watermelon. *Veg. Sci.* 15(1):95-100.

Singh RK, Chaudhury BD (1985). Biometrical methods in quantitative genetic analysis, rev. edition, Kalyani Publisher, New Delhi, India.

Somayajullu PLN, Joshi AB, Murty BR (2011). Genetic diversity in wheat. *Cereal Res. Commun.* 5(1): 47-58.

Van-der-Vossen HAM, Denton OA, El Tahir IM (2007). *Citrullus lanatus* (Thunb.) Matsum and Nakai, In: Grubben, GJH and Denton OA, eds., Plant resources of tropical Africa.