DOI: http://doi.org/10.5281/zenodo.4131424
U.S. ISSN 2694 -4812

Variability studies of guava (*Psidium guajava* L.) genotypes for growth, yield and quality attributes in Chattogram region of Bangladesh

Md. Golam Azam[1]*, M Shalim Uddin[2], SM Kamrul Hasan Chowdhury[3], ASM Harunor Rashid[4], Haimonti Barua[1], Rozina Afroz Chhanda[2], Sajia Rahman[2], Shamim Ara Bagum[5], Mossammat Shamsunnahar[2] and Md. Nazirul Islam[6]
[1]Plant Breeding Division, Agricultural Research Station, BARI, Pahartali, Chattogram-4225, Bangladesh
[2]Plant Genetic Resource Center, BARI, Gazipur-1701, Bangladesh
[3]Plant Pathology Division, Agricultural Research Station, BARI, Pahartali, Chattogram-4225, Bangladesh
[4]Horticulture Division, Agricultural Research Station, BARI, Pahartali, Chattogram-4225, Bangladesh
[5]Seed Technology Division, BARI, Gazipur-1701, Bangladesh
[6]Horticulture Division, BARI, Gazipur-1701, Bangladesh
*Corresponding author's email: kbdrashedbari@gmail.com, kbdrashed@bari.gov.bd

Abstract— Guava (*Psidium guajava* L.) is considered as an important profitable fruit in Bangladesh. The study was conducted in the fruits orchard of Agriculture Research Station (ARS), Pahartali, Chattogram and Regional Agriculture Research Station (RARS), Hathazari, Chattogram during 2019-20 to assess the genetic diversity of the in situ guava germplasm. Twenty two guava lines were assessed in this investigation. A total of 21 traits (11 qualitative and 10 quantitative) enabled an assessment of the genetic variability and construction of this guava germplasm. The maximum variation was observed in pulp color and seediness in guava fruits. Plant height ranged from 2.38 to 6.20 m with an average 3.85 m. Based girth ranged from 28.00 to 81.00 cm with an average of 47.79 cm. Fruit weight ranged from 55.0-362.0 g with average 101.92 g and yield per plant ranged from 12.53 to 126.70 kg with average 26.54 kg. The morphological dendrograph generated from agglomeration hierarchical clustering grouped the 22 genotypes into 5 major clusters. Heatmap explaining the overall performance of the genotypes indicated that BARI Peyara 2 and BARI Peyara 4 had higher yield potentiality. BARI Peyara 2, BARI Peyara 4 , PG Pah 001, PG Pah 005, PG Pah 07, PG Hat 004, PG Hat 009, PG Hat 010, PG Hat 012, PG Hat 017, PG Hat 018 and PG Hat 020 can be selected for breeding program based on their desirable qualitative and quantitative traits.

***Keywords*— Morphological variability, qualitative characters, quantitative characters, heatmap and dendrograph**

I. INTRODUCTION

Guava (*Psidium guajava* L.) is one of the best essential fruit crops domesticated in Mesoamerica and widely cultivated in the tropics and some sub-tropical regions [1,2]. The family of guava is Myrtaceae contained about 150 genera and more than 5,000 species [3]. There are several secondary centers of diversity for common guava in the wet tropics, mainly in South America, Australia, and tropical Asia. It also occurs in Africa and even South Europe [4]. Preferential cross-fertilization of the species causes high genetic diversity in cultivated guava genotypes [5]. Seedlings are arisen from the seeds of heterogeneous parents also responsible for wider genetic diversity in guava. The fruits are usually consumed directly as fresh and processed products. Fresh fruit pulp contains high amount of vitamins specially vitamin C, potassium, and phosphorus as well as numerous antioxidants and dietary fibers [6, 7, 8].Furthermore, besides fruits, the leaves, roots, bark and flowers of guava are also used as medicine traditionally [9]. Recently the guava has gained reputation in the global market for its nutritional value as well as the diverse processed products including jam, jelly, and juice. There are possibly 400 guava cultivars across the world, but among them only few are commonly cultivated across the universe [10]. There are huge diversity in cultivated cultivars regarding tree appearance, bearing habit, fruit size, shape, nutrient composition, ripening season as well as yield [10,11]. Irrespective of the morphological and biochemical variability detected in these cultivars, several reports designate selection of genotype usually based on few important traits [12, 13, 14] and, therefore, huge variation of guava is left untouched. This is usually responsible for genetic vulnerability of the plant [15], especially with respect to climatic modification over time. The goals of this investigation were to assess the morphological variations through phenotypic study, to investigate the genetic variability and to select parents for better and more production.

II. MATERIALS AND METHODS

The study was conducted in the fruits orchard of Agriculture Research Station (ARS), Pahartali, Chattogram and Regional Agriculture Research Station (RARS), Hathazari, Chattogram during 2019-20. The experimental areas lie between 22.18^0N latitudes and 91.89^0E longitudes at an average elevation of 20 m above the sea level. The experimental unit belongs to Agroecological Zone 23 known as Chittagong Coastal Plains. The physiographic unit of these areas is low hills and valleys. The soils are predominantly moderately fine textured and the pH of soil is about 6.5. The organic matter ranges from 0.7 %-1.47 % in top soil and 0.38 % – 0.76 % in sub soil. About 22 diverse guava germplasm were included in the experiment. Among these genotypes, 20 were collected from "Kanchan nagor" area of Chattogram region. The genotypes of "Kanchan nagor" area are usually sweet in taste and have huge variability in maturity, fruit size and shape, skin color, flesh color and yield. The remaining two genotypes were Bangladesh Agricultural Research Institute (BARI) released guava variety namely BARI Peyara 2 and BARI Peyara 4. The data was recorded as per the descriptor of National Bureau of Plant

Genetic Resources (NBPGR), India. Shape and flesh color of fruit and mature leaves was assessed by eye estimation and stated in language on the basis of the descriptors for guava developed by NBPGR. Skin color of fruit was determined at full mature stage. Surface smoothness of fruit of all selected guava germplasm was determined by finger touch and eye estimation method. Texture of pulp, pulp flavor, seed hardness and sweetness/taste of fruit were determined by a panel of judges though organoleptic test. Data were recorded like plant height(m), base girth (cm), no. of branch, canopy (N-S), canopy(E-W), leaf shape, mature leaf color, fruit shape, fruit surface, fruit breadth(cm), fruit length(cm), fruit weight(g), fruit skin color, pulp color, pulp texture, pulp flavour, fruit taste, TSS, seediness, seed hardness and yield/ plant (kg).

Data analysis

Statistical analyses were performed using R-statistics software Version 4.0.2 for Windows (R Development Core Team, 2020). The hierarchical clustering was performed using the Spearman's rank correlation algorithm.

III. Results and Discussions

Analysis of variance

Analysis of variance (ANOVA) provided high significant variation among treatments for all the considered traits. The trait study in this experiment has influenced by genotypes. In descriptive statistics, a box plot is a suitable technique of graphically presenting sets of numerical data with the help of their quartiles. Box plot might also have lines expanding perpendicularly from the boxes (whiskers) representing variability outside the upper and lower quartiles. In the box plot, box edges show upper and lower quartiles and the median as shown in the middle of the box. Individuals falling outside of the rank of whisker are shown as circles. All the traits of this experiment fitted with normal distribution except some trait skewed left and some are right (Fig. 1).

Qualitative characters

Qualitative traits of guava presented in table 1. Leaf shape was varied from oblong lanceolate (2) to eliptical (3). Among the accession 50% was found oblong lanceolate and 50% was found eleptical leaf. Mature leaf color varied from pale green to green. In case fruit shape, 54.55% provided globose shape, 27.27 % provided pear shape and 18.18 % provided oblong shape. Fruit surface was found smooth to ridge among the studied genotypes. Smooth fruit surface was found from 31.82 % germplasm which is our one of the desired traits. Fruit skin color varied from yellow white to greenish white. The maximum variation was observed in pulp color and seediness in guava fruits. Four types of pulp color were found among the germplasm (Table 1). White pulp colored guava were found 31.81%, creamy white 45.45%, greenish white 18.18% and light red 4.54 %. Seed hardness varied from soft to hard. Fruit seediness was found four types among the germplasm. Seedless guava was found 4.54%, which our desired trait and high seed also found 4.54%, low seed was observed 36.36% and 54.54% was observed medium number of seed. If crossed low seeded or seedless guava genotypes with high seed containing genotypes will provide maximum variation in seediness which help in the selection good quality guava variety. Based pulp color, seed hardness and seediness, BARI Peyara 4, PG Pah 001, PG Pah 005, PG Hat 004, PG Hat 009, PG Hat 010, PG Hat 017, PG Hat 018 and PG Hat 020 can be selected as desired type genotypes of guava.

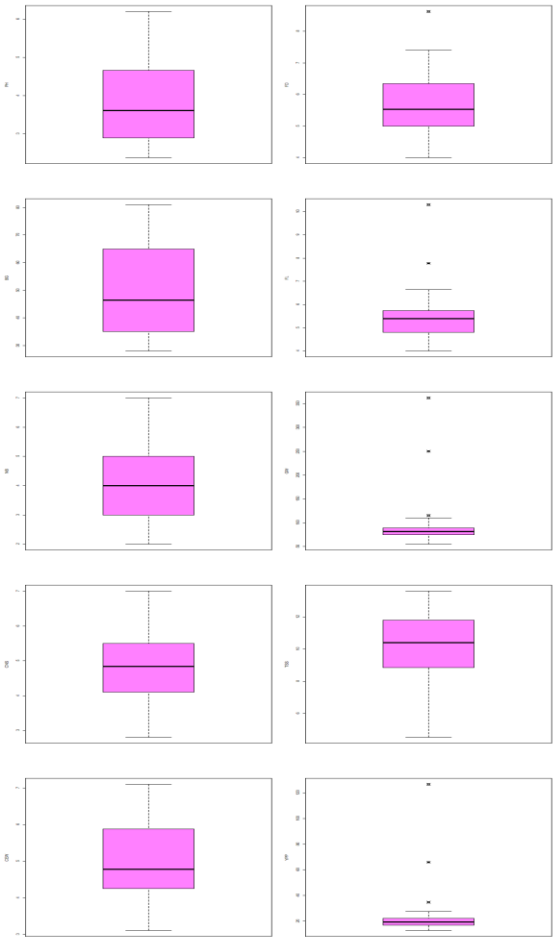


Fig. 1. Box plots showing the pattern of the measured traits of germplasm. Box edges show upper and lower quantile and the median as shown in the middle of the box.

Dendro graph analysis

Dendo Graph based on genetic distance using 21 agro-morphological parameters of 22 guava germplasm grouped into five major clusters (Fig. 2). Cluster D contain the maximum (9) number of germplasm (PG Pah 07, PG Hat 009, PG Hat 010, PG Hat 011, PG Hat 012, PG Hat 013, PG Hat 017, PG Hat 018 and PG Hat 020) flowed by Cluster B (PG Pah 01, PG Pah 02, PG Pah 03, PG Pah 04, PG Pah 06 and PG Hat 004). The cophenetic correlation coefficient was found 0.741, which indicating that the cluster is quite fit.

Table 1. Qualitative characteristic of twenty two guava genotypes

Accession	Leaf shape	Mature leaf Color	Fruit shape	Fruit surface	Fruit skin color	Pulp color	Pulp texture	Fruit taste	Pulp flavor	Seed hardness	Seediness
BARI Peyara 2	2	1	2	1	4	1	5	3	3	7	5
BARI Peyara 4	2	1	4	2	4	1	5	3	3	0	0
PG Pah 01	3	2	2	1	3	3	3	3	5	3	3
PG Pah 02	3	2	2	1	3	2	1	5	5	7	5
PG Pah 03	2	1	2	1	3	2	3	3	5	7	3
PG Pah 04	2	1	2	2	4	2	3	3	3	5	5
PG Pah 05	3	2	3	2	4	6	5	3	5	7	7
PG Pah 06	2	1	2	2	4	2	3	3	5	5	5
PG Pah 07	2	1	3	3	4	1	3	3	5	5	5
PG Hat 004	2	1	3	1	3	1	3	3	5	3	3
PG Hat 009	2	2	2	2	4	2	3	3	7	3	5
PG Hat 010	3	2	3	3	3	1	3	3	5	3	5
PG Hat 011	2	1	2	2	3	1	5	3	7	5	5
PG Hat 012	2	1	2	2	3	1	5	3	7	5	5
PG Hat 013	3	2	2	2	3	2	5	3	7	5	5
PG Hat 014	3	1	4	3	4	2	3	3	7	5	3
PG Hat 015	3	2	3	2	4	2	3	3	7	5	3
PG Hat 016	3	2	4	1	4	2	3	3	7	7	3
PG Hat 017	3	2	2	1	4	3	5	3	7	3	5
PG Hat 018	3	2	3	2	3	3	3	3	5	3	5
PG Hat 019	2	1	4	2	3	2	5	5	7	5	3
PG Hat 020	3	1	2	3	4	3	3	3	7	3	3

Leaf shape	**Mature leaf Color**	**Fruit shape**	**Fruit surface**	**Fruit skin color**	**Pulp color**
2=Oblong lanceolate	1= Pale green	2=Globose	1=Smooth	3=Yellow white	1=White
3=Eliptical	2=Green	3=Pear shape	2= Bumpy	4= Greenish white	2= Creamy white
		4=Oblong	3= Ridge		3=Greenish white
					6=Light red

Pulp texture	**Pulp flavour**	**Fruit taste**	**Seediness**	**Seed hardness**
1= Very soft	3=Mild	3= Less sweet	0= Seedless	3=Soft
3= Soft	5=Moderate	5=Medium sweet	3=Low	5=Intermediate
5=Medium hard		7=Highly sweet	5=Medium	7=Hard
			7=High	

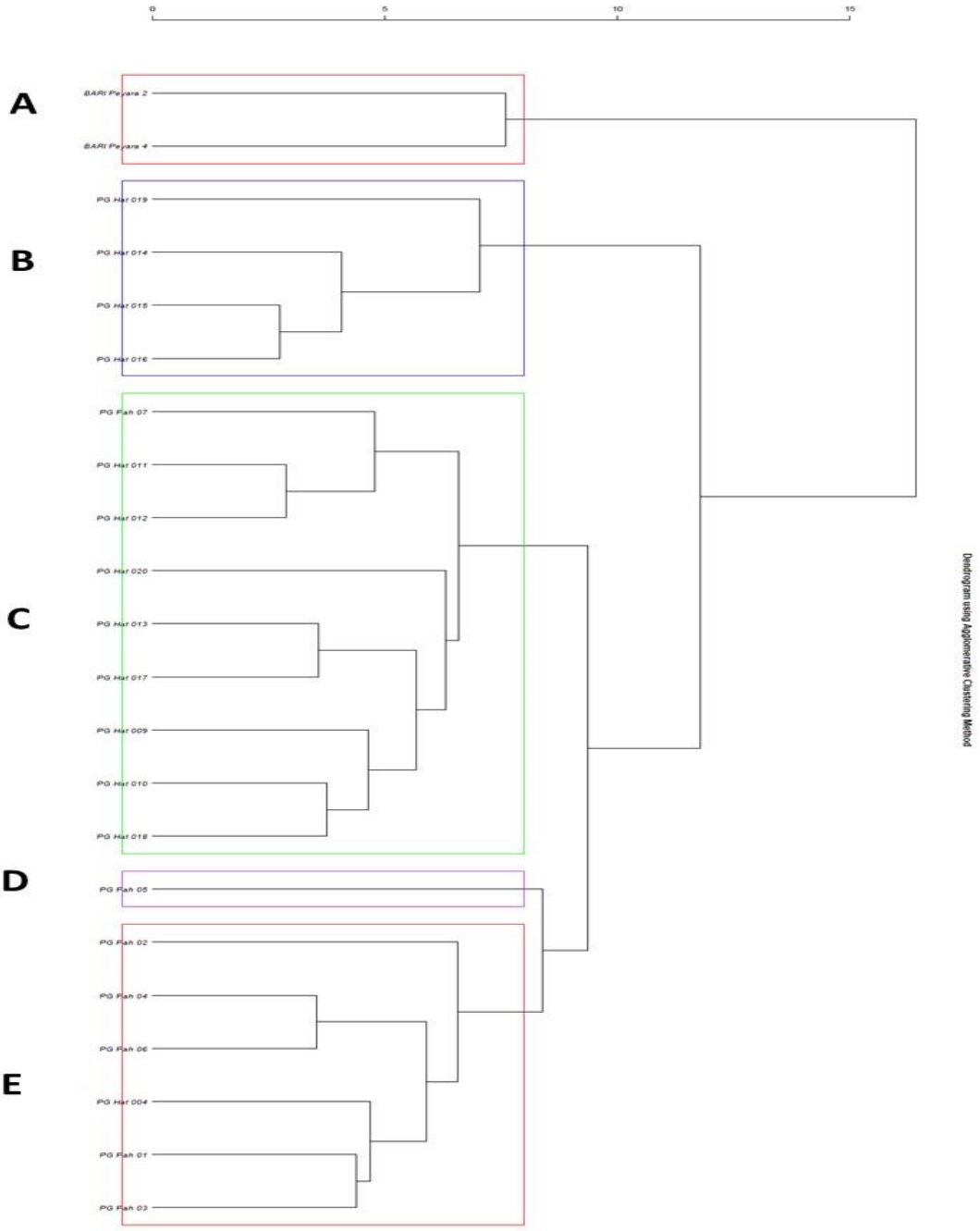
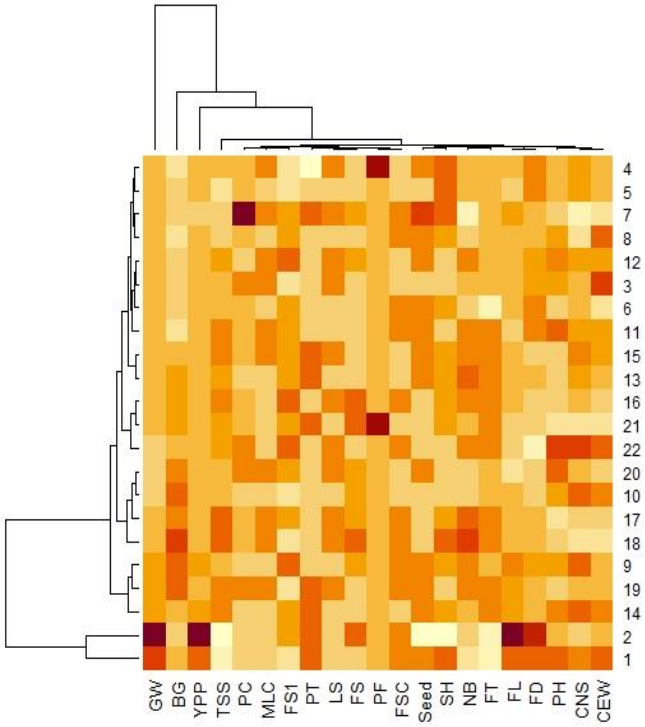


Fig.2. Dendrograph showing the clustering pattern of 22 guava germplasm based on measured traits.

Quantitative characters

The pattern of 10 quantitative traits of guava presented in Fig. 3 and Table 2. The highest quantitative coefficient variation (%) was observed in yield per plant (94.04%) followed by TSS (68.59%). Plant height ranged from 2.38 to 6.20 m with an average 3.85 m. Based girth ranged from 28.00 cm to 81.00 cm with an average of 47.79 cm. Canopy spread in north south direction ranged from 2.80 to 7.00 m and canopy spread in east-west direction ranged from 3.10 m to 7.10 m. The maximum fruit breadth (8.6 cm) was recorded from BARI Peyara 4 followed by BARI Peyara 2 (7.4 cm). In contrary, the minimum fruit breadth was obtained from PG Hat 020 (4.0 cm) followed by PG Hat 004 and PG hat 014 which was recorded as 4.8 cm. BARI peyara 4 provided the the maximum fruit length (10.3 cm) whereas PG Hat 018 provided the minimum fruit length (4.0). Babu *et al*. [16] reported the fruit breadth was maximal in hybrid-8 (6.27 cm) while it was minimum in hybrid-5 (5.32 cm). He also reported that the maximum fruit length (7.04 cm) was found in hybrid-3 whereas Hybrid-5 had the minimum fruit length (4.91 cm). Singh *et al*. [17] reported the highest fruit length was observed in Hisar surkha (6 cm) followed by L-49 (5.57 cm) whereas the fruit breadth (6.79 cm) was found in Latil. The highest TSS was attained from PG Hat 016 (13.6 %) followed by PG hat 015 (13 %). While the minimum TSS was obtained from BARI Peyara 4 (4.5 %). Some researchers reported that TSS (13.83%) in L-49 [17], TSS (13.5 %) in Hybrid Red Supreme [11], TSS (10.83%) in RCGH 1 [18]. Fruit weight ranged from 55.0-362.0 g with average 101.92 g. BARI Peyara 4 provided the maximum fruit weight (362 g) followed by BARI peyara 2 (250 g). On the other hand, the minimum fruit weight was attained from PG Hat 020 (55 g). The highest fruit weight (133.04 g) was found in in L-49 [19], selection 11 (144.20 g), Sardar guava (140.50 g) [16]. Yield per plant ranged from 12.53 to 126.70 kg with average 26.54 kg (Table 2). The genotypes BARI Peyara 4 (126.70 kg per plant), BARI Peyara 2 (66.00 kg per plant), PG Pah 07 (34.7 kg per plant), PG Hat 012 (27.50 kg per plant) and PG Hat 017 (26.3 kg per plant) selected as a higher yielder than other genotypes. The highest yield (24.27 kg per plant) was in latil followed by Sangam (24.07 kg per plant) [20]. The variation in fruit yield due to cultivar was also reported by various workers [21, 22, 23, 24].Heatmap also expressed the same result of this experiment. Heatmap explaining the overall performance of the genotypes indicated that BARI Peyara and BARI Peyara 2 4 had higher yield potentiality.



Here, CEW-Canopy direction (East-West), CNS-Canopy direction (North-South), PH-Plant height, FD-Fruit diameter, FL-Fruit length, FT-Fruit taste, NB-No. of branch, SH-Seed hardness, Seed- Seediness, FSC-Fruit skin color, PF- Pulp flavor, FS- Fruit surface, LS-Leaf Shape, PT-Pulp texture, MLC-Mature leaf color, PC-Pulp color, YPP-Yield/ plant, BG-Base girth, GW-Fruit weight

Fig.3: Heatmap showing the variability in the characters of studied genotypes.

IV. CONCLUSION

A wide variation was observed in the guava germplasm in this study. The maximum variation was observed in pulp colour and seedness in guava fruits. The morphological dendrogram created from agglomeration hierarchical clustering grouped the 22 genotypes into 5 major clusters. Based on the qualitative and quantitative characters BARI Peyara 2 , BARI Peyara 4 , PG Pah 001, PG Pah 005, PG Pah 07, PG Hat 004, PG Hat 009, PG Hat 010, PG Hat 012, PG Hat 017, PG Hat 018 and PG Hat 020 can be identified as desired type of guava genotypes. Therefore, selection of these genotypes might play a significant role for future guava improvement program.

Table 2. Quantitative characteristic of twenty two guava genotypes

Accession	Plant height (m)	Base girth (cm)	N0. of branch	Canopy (N-S)	Canopy (E-W)	Friut breadth (cm)	Fruit length (cm)	TSS (%)	Individual Fruit weight (g)	Yield/ plant (kg)
BARI Peyara 2	5.3	44.0	2.3	6.1	6.6	7.4	7.8	5.4	250.0	66.0
BARI Peyara 4	3.6	37.3	3.0	4.1	4.6	8.6	10.3	4.5	362.0	126.7
PG Pah 01	4.0	35.0	4.0	4.7	7.1	6.1	4.9	8.9	79.0	15.8
PG Pah 02	3.5	28.0	4.0	5.1	4.9	6.6	5.5	9.4	89.0	22.3
PG Pah 03	3.6	35.0	4.0	5.3	4.9	6.8	4.8	6.5	87.0	21.8
PG Pah 04	2.9	38.0	3.0	4.2	3.6	6.4	5.3	9.9	84.0	16.8
PG Pah 05	2.9	30.0	2.0	2.8	3.4	5.5	6.0	8.7	89.5	12.5
PG Pah 06	4.2	28.0	3.0	3.1	6.3	5.2	5.5	8.7	83.3	16.7
PG Pah 07	3.9	70.0	5.0	6.1	4.6	6.0	6.7	10.0	115.5	34.7
PG Hat 004	4.2	67.0	3.0	6.2	5.9	4.8	5.5	10.1	60.0	15.0
PG Hat 009	5.2	28.0	5.0	5.0	5.1	6.5	4.5	12.4	75.0	18.8
PG Hat 010	4.7	35.0	5.0	5.2	5.0	6.0	5.0	10.7	80.0	20.0
PG Hat 011	3.3	49.0	6.0	5.0	4.7	5.3	5.0	10.9	80.0	20.0
PG Hat 012	4.9	48.0	4.0	6.1	5.9	5.7	5.9	11.6	110.0	27.5
PG Hat 013	3.2	45.0	5.0	5.5	5.2	5.0	5.5	12.3	85.0	21.3
PG Hat 014	2.9	55.0	5.0	4.2	4.0	4.8	5.5	12.0	70.0	17.5
PG Hat 015	2.6	65.0	6.0	4.0	4.3	5.2	4.8	13.0	75.0	18.8
PG Hat 016	2.9	81.0	7.0	3.3	3.5	5.3	5.2	13.6	80.0	20.0
PG Hat 017	3.1	70.0	5.0	4.2	4.4	5.6	5.8	11.8	105.0	26.3
PG Hat 018	5.2	65.0	3.0	4.5	4.3	4.9	4.0	10.1	60.0	15.0
PG Hat 019	2.4	50.0	4.0	3.0	3.1	5.0	4.3	11.1	68.0	17.0
PG Hat 020	6.2	48.0	5.0	7.0	6.5	4.0	4.4	11.4	55.0	13.8
Mean	3.85	47.79	4.24	4.75	4.89	5.75	5.54	10.13	101.92	26.54
S. Error	0.22	3.39	0.27	0.24	0.24	0.22	0.29	0.50	14.90	5.32
Minimum	2.38	28.00	2.00	2.80	3.10	4.00	4.00	4.52	55.00	12.53
Maximum	6.20	81.00	7.00	7.00	7.10	8.63	10.30	13.60	362.00	126.70
CV (%)	26.82	33.30	30.21	24.15	22.55	17.72	24.33	68.59	23.21	94.04

ACKNOWLEDGMENT

We are indebted to Director General, Bangladesh Agricultural Research Institute (BARI), Bangladesh for providing the all types of logistic support to conduct the experiment. We also extend our gratitude to project no. PBRG-128, NATP-II, Bangladesh Agricultural Research Council (BARC) for the financial support to conduct the experiment.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCES

[1] NN Gautam, K Singh, B Singh, S Seal, A Goel, VL Goel. Studies on Clonal Multiplication of Guava (*'Psidium guajava'L.*) through Cutting under Controlled Conditions. Australian Journal of Crop Science. 2010; 4(9):666.

[2] NN Rodríguez, J Valdés, JA Rodríguez, JB Velásquez, D Rivero, F Martínez, G González, DG Sourd, L González, J Cañizares. Genetic resources and breeding of guava (*Psidium guajava* L.) in Cuba. Biotecnología Aplicada. 2010; 27(3):238-40.

[3] R Govaerts, M Sobral, P Ashton, F Barrie, BK Holst, LL Landrum, K Matsumoto, FF Mazine, EN Lughadha, C Proneça, LH Soares-Silva. World checklist of Myrtaceae. Royal Botanic Gardens; 2008.

[4] D Grattapaglia, RE Vaillancourt, M Shepherd, BR Thumma, W Foley, C Külheim, BM Potts, AA Myburg. Progress in Myrtaceae genetics and genomics: Eucalyptus as the pivotal genus. Tree Genetics & Genomes. 2012; 8(3):463-508.

[5] JE Alves, BM Freitas. Requerimentos de polinização da goiabeira. Ciência Rural. 2007; 37(5):1281-6.

[6] A Jiménez-Escrig, M Rincón, R Pulido, F Saura-Calixto. Guava fruit (*Psidium guajava* L.) as a new source of antioxidant dietary fiber. Journal of Agricultural and food Chemistry. 2001; 49(11):5489-93.

[7] Z Lukmanji, E Hertzmark, N Mlingi, V Assey, G Ndossi, W Fawzi. Tanzania food composition Tables. 2008. Dar-es-Salaam: Muhimbili University of Health and Allied Sciences, Tanzania Food and Nutrition Centre and Harvard School of Public Health. 2008.

[8] G Flores, SB Wu, A Negrin, EJ Kennelly. Chemical composition and antioxidant activity of seven cultivars of guava (*Psidium guajava*) fruits. Food Chemistry. 2015; 170:327-35.

[9] RM Gutiérrez, S Mitchell, RV Solis. *Psidium guajava*: a review of its traditional uses, phytochemistry and pharmacology. Journal of ethnopharmacology. 2008; 117(1):1-27.

[10] CV Pommer, KR Murakami. Breeding guava (*Psidium guajava* L.). InBreeding plantation tree crops: Tropical species .Springer, New York, NY; 2009; 83-120.

[11] A Sharma, SK Sehrawat, RS Singhrot, TE Ajinath. Morphological and chemical characterization of Psidium species. Notulae Botanicae Horti Agrobotanici Cluj-Napoca. 2010; 38(1):28-32.

[12] A Mehmood, MJ Jaskani, S Ahmad, R Ahmad. Evaluation of genetic diversity in open pollinated guava by iPBS primers. Pakistan Journal of Agricultural Sciences. 2013; 50(4): 591-97.

[13] A Mehmood, S Luo, NM Ahmad, C Dong, T Mahmood, Y Sajjad, MJ Jaskani, P Sharp. Molecular variability and phylogenetic relationships of guava (*Psidium guajava* L.) cultivars using inter-primer binding site (iPBS) and microsatellite (SSR) markers. Genetic Resources and Crop Evolution. 2016; 63(8):1345-61.

[14] LL Valera-Montero, PJ Muñoz-Rodríguez, H Silos-Espino, S Flores-Benítez. Genetic diversity of guava (*Psidium guajava* L.) from Central Mexico revealed by morphological and RAPD markers. Phyton, International Journal of Experimental Botany. 2016; 85:176-83.

[15] AM Nogueira, MF Ferreira, JH Guilhen, A Ferreira. Multivariate analysis in a genetic divergence study of *Psidium guajava*. Genetics and Molecular Research. 2014; 13:10657-68.

[16] KD Babu, A Singh, DS Yadav. Performance evaluation of red and white flesh guava hybrids under midhill altitude of Meghalaya. InI International Guava Symposium 735 2005; 95-8.

[17] BK Singh, S Singh, AK Pal. Morphological-Chemical Attributes of Guava (*Psidium guajava* L) Cultivars. Indian Horticulture Journal. 2014; 4(3and4):152-5.

[18] NA Deshmukh, P Lyngdoh, AK Jha, RK Patel, BC Deka. Comparative study on newly developed guava hybrids with commercial cultivars under mid hills of NE India. The Bioscan. 2013; 8(4):1467-70.

[19] D Dolkar, P Bakshi, VK Wali, B Bhushan, A Sharma. Growth and yield attributes of commercial guava (*Psidium guajava* L.) cultivars under sub-tropical condition. Indian Journal of Plant Physiology. 2014; 19(1):79-82.

[20] SK Pandey, JE Joshua. Influence of gamma-irradiation, growth retardants and coatings on the shelf life of winter guava fruits (*Psidium guajava* L.). Journal of food science and technology. 2010; 47(1):124-7.

[21] KD Babu, AK Dubey, DS Yadav. Evaluation of guava cultivars for their performance under mid hill altitude of Meghalaya. Indian Journal of Hill Farming. 2002; 15:119-21.

[22] PS Aulakh. Effect of seasonal variation on yield and fruit quality of some promising guava cultivars under arid irrigated region of Punjab. Haryana Journal of Horticultural Science. 2004; 33(3-4):170-1.

[23] RC Yadav, AK Nagar, D Pandey, SK Shukla. Promising guava (*Psidium guajava* L.) cultivars for North Indian conditions. InI International Guava Symposium 735.2005; 91-4.

[24] RK Patel, CS Maiti, BC Deka, NA Deshmukh, D Roy. Variability studies in guava (*Psidium guajava* L.) genotypes for growth, yield and quality attributes at mid-hills of Meghalaya. Indian Journal of Hill Farming. 2011; 24(1):24-8.