Evaluation of Baby Corn Genotypes on Productivity and Quality Traits in Bangladesh

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Abstract

Baby corn is very nutritious crop and the current demand is increasing in Bangladesh, but

lacking of promising and high yielding variety. Hence, the study was conducted during the winter season of 2015-16 to evaluate twenty baby corn genotypes on the basis of quality, yield and yield contributing traits, and to find out the suitable genotype for yield maximization and quality improvement of baby corn through proper agronomic management. Twenty baby corn genotypes were planted in a randomized complete block design with three replications. As per result, the Baby Star genotype got highest cob yield with husk (11.9 t ha^{-1}) and cob yield without husk (3.02 t ha^{-1}) followed by Dream Sweet 3 and MSC 001. Maximum protein (11.03%) and starch content (57.03%) were recorded in Baby Star. The most total soluble solid (9.51%) was recorded in Dream Sweet-3 genotype. Baby star genotype followed by Dream Sweet 3 and MSC 001 were better than other genotypes in terms of yield attributes. Grouping of genotypes through multivariate (cluster) analysis on yield, yield attributes and quality parameters indicated that the cluster II showed higher performance among other clusters that means Baby Star, Dream Sweet-3 and MSC No.001 were better among twenty genotypes. Results suggest that Baby star followed by Dream Sweet-3 and MSC No.001 genotype can be recommended as potential baby corn genotypes for cultivation in Bangladesh and release as a variety. Some genotypes with specific features might be potential used in genetic resources for the future improvement of breeding program useful for baby corn expansion.

Keywords: *Zea mays* L., yield, yield traits, protein, starch, TSS

1. Introduction

Present demand of baby corn (*Zea mays* L.) in Bangladesh is increasing rapidly for quick growing population (Barma, 2023). Baby corn is the young cob of maize harvested just after the silks has emerged within 3 to 5 days after flowering and is suitable for raw consumption (Uddin et al., 2023). Baby corn is a dual purpose crop grown round the year like 3 to 4 times for baby corn as well as fodder production. Baby corn is short duration (2 to 3 months) crop that can easily be matched in intensive cropping system (Barma, 2023; Uddin et al., 2023). Cultivation of baby corn generates employment opportunity for the rural poor of all age right from production, processing, packaging and marketing (Barma, 2023). Although the production and marketing started in 1992-93 in Bangladesh with the co-operation of IFDC (International Fertilizer Development Center) but its uses, area and marketing facility have not yet been increased considerably. Eventually to meet the demand of baby corn it is imported from foreign countries like Thailand, Taiwan etc. and costing about BDT (Bangladesh currency) 100 million per year (Asaduzzaman et al., 2014). The average yield of baby corn in Bangladesh is lower about 1.1 t ha^{-1} compared to other countries due to lack of high yielding varieties. Worldwide, baby corn markets and production are rising, especially in Asia, Africa, and South America (Shahi, 2017). Asian countries are the major consumers of the world's baby corn. In Asia, Thailand, China, and Taiwan are the major baby corn producers (Shahi, 2017). Due to its high demand, promising market, prospects for value addition, and high earning prospective, it is rising more popular among people of Bangladesh, much like in other Asian countries (Roy, 2015).

Baby corn is high nutritious vegetable. Previous several studies denoted that it contained 90.03, 17.96, 2.13, 5.30 and 5.89 percent moisture, protein, fat, ash and crude fiber, respectively. One hundred grams of baby corn contained 23.43 g total soluble sugars, 1.96 g reducing sugars, 8.10 g cellulose, 5.41 g lignin, 5.43 mg ascorbic acid, 670 µg β-carotene. 95 mg calcium, 345 mg magnesium, 898.62 mg phosphorus, 6.91 mg iron and 6.25 mg zinc (Hooda and Kawatra, 2013; Uddin et al., 2023). Baby corn is consumed as a fresh vegetable in curry, pickles, soup, pulao, salads, snacks, etc. and provides many food benefits to people (Barma, 2023). The baby corn is also considered as ideal fodder crop due to its succulence, palatability and digestibility (Singh et al., 2009; Barma, 2023).

Due to increasing demand of baby corn in Bangladesh, research should be needed to find out the high yielding nutritious genotypes suitable for Bangladesh environment. Few varieties of baby corn are cultivated in Bangladesh that yielded low compared to other baby corn producing countries. Hence effort should be taken up to find out the high yielding and nutritious appropriate advance genotypes through selection method for releasing as variety to fulfill the baby corn requirement in Bangladesh to ensure higher economic returns to the poor farmers.

Therefore, a study was undertaken to evaluate the different baby corn genotypes on the basis of quality, yield and yield contributing traits and to find out the suitable genotype through proper agronomic management for improvement of baby corn yield and quality in Bangladesh soil condition.

2. Materials and Methods

2.1 Site Description

Field experiment was conducted during winter season of 2015-16 at the research field of Bangladesh Agricultural Research Institute, Gazipur, Bangladesh. The experimental location was at $23^0$59' N latitude, $90^0$24' E longitude with an elevation of 8.4 m from sea level. The site was subtropical climatic condition strongly influenced by the southwestern monsoon. It belongs to Agro Ecological Zone (AEZ 28) known as Madhupur Tract. The soil was terrace to Orcrept suborder belongs to Chhiata soil series (Shaheed, 1984).The texture of soil was clay loam (sand 28.8%, silt 41.5 and clay 29.7%) having the pH 5.8, organic carbon 0.585%, total nitrogen 0.054%, exchangeable K 0.13 meq./100 g soil. The available P, S, Zn and B were 12.5, 12.0, 0.90 and 0.18 $\mu g\ g^{-1}$, respectively.

The minimum and maximum temperature during the crop growing season ranged between 10.2 ^{0}C to 33.5 ^{0}C, with an average of 21.9 ^{0}C at experimental site. The rainfall amount 118 mm was recorded in March. The relative humidity was varied from 66.2 to 83.3% during the crop growth period, while the highest relative humidity (83.3%) was recorded in March (Figure 1a). The sunshine and cloudy hours have been varied during experimental period between 4.76 to 7.94 hours day^{-1} and 2.96 to 5.93 hours day^{-1}, respectively. The solar radiation ranged between 233 to 352 $cal.cm^{-2}day^{-1}$ (Figure 1b).
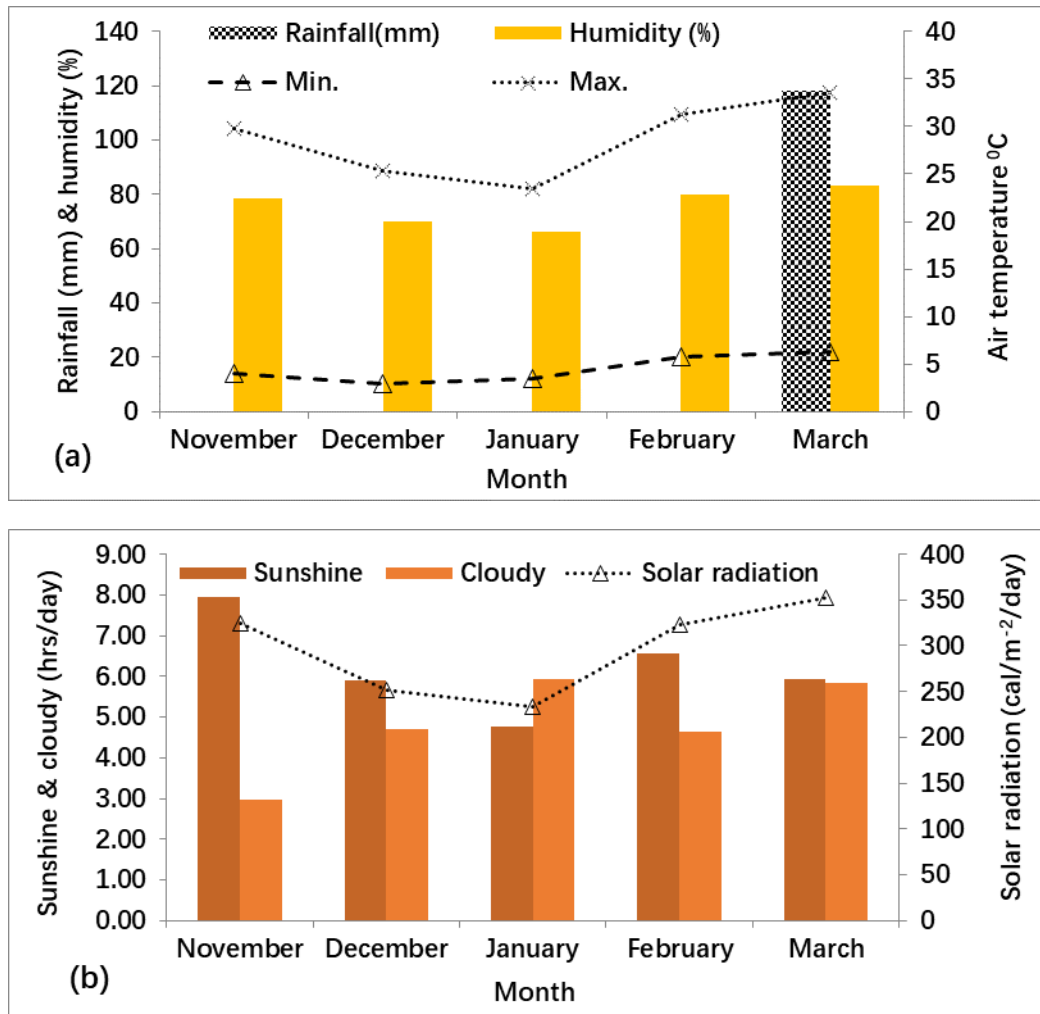
Figure 1. (a) Monthly air temperature, rainfall, relative humidity and (b) sunshine hours, cloudy hours and solar radiation during the experimental crop growth

2.2 Collection of Planting Materials

Seeds of twenty genotypes of baby corn were collected from different organization. Five genotypes were collected from Bangladesh Agricultural Research Institute, Joydebpur, Gazipur, Bangladesh. These genotypes were BARI Sweet Corn 1, BHM-07, BHM-06, BHM-05 and BHM-11. Five genotypes were collected from Thailand. These genotypes were Thai gold, Suwan 1, Pacific Thai 271, Thai Pop and Kamlai Thong. The rest ten genotypes were obtained from reputed company and open market in Bangladesh. The seeds germination percentages of all genotypes were more than 90%.

2.3 Land Preparation, Treatment, Layout and Fertilizer Application

The field was opened by tractor driven disc plough with 4 passes followed by leveling with tractor driven rotavator to obtain desirable tilth. The land was cleaned manually removing the weed and stubbles. The experiment was planned with 20 genotypes of baby corn according to the Randomized Complete Block Design with three replications. The genotypes were G_1= Dream Sweet-3, G_2= Hybrid Indian-900M, G_3= BARI Sweet Corn-01, G_4= Hybrid-09, G_5=

BHM-07, G_6= BHM-06, G_7= Baby Star, G_8= BHM-05, G_9= Thai gold, G_{10}= Suwan 1, G_{11}= Pacific Thai 271, G_{12}= Thai Pop, G_{13}= MSC No.001, G_{14}= Kamlai Thong, G_{15}= Hybrid NK-40, G_{16}= Super gold, G_{17}= Pioneer-07, G_{18}= Pacific-559, G_{19}= HM-987 and G_{20}= BHM-11. The unit plot size and plant spacing were 4.5 m × 3 m and 50 cm × 25 cm. Plot to plot and replication to replications distance were 1 m and 1.5 m. The blanket dose of Urea, triple super phosphate (TSP), muriate of potash (MoP), gypsum, zinc sulphate and boric acid were applied at 260, 177, 133, 97, 13.89, 5 kg ha^{-1} for composite genotypes and at 543, 266, 200, 208, 13.89, 5 kg ha^{-1}, respectively for hybrid genotypes (Chowdhury and Hasan, 2013). One-third urea and full dose of other fertilizers were applied as basal during final land preparation. The rest urea was top dressed in two equal splits at 15 and 35 days after sowing (DAS), respectively.

2.4 Seed Sowing and Agronomic Management

Healthy seeds were sown in every point with two seed in furrow prepared with a tine following the spacing of 50 cm x 25 cm and then the seeds were covered manually for proper germination. The seedlings were thinned for maintaining single plant in a point. Gap filling was completed within 7 to 10 days after completion of seedling emergence in each plot. This was done to maintain optimum stand that is 8 m^{-2} areas. Sometimes the seedlings were infested by cutworm at early stages. In such cases, seedlings grown separately in the same date were transplanted to maintain optimum plant population. Weddings were done twice at 20 and 40 DAE (days after emergence) for minimizing weed competition. Insects like stem borer and cut worm were control by application of Carbofuran 3G at 5 kg ha^{-1} after 30 days of seed emergence and Dursban was sprayed two times @ 2 ml L^{-1} at 45 and 55 DAE. Cupravit 50 WP was sprayed twice @ 1.5 g L^{-1} at 30 and 40 DAE controlling bacterial soft rot. Irrigations were applied at different stages viz, germination and establishment stage, pre vegetative, vegetative, tasseling and silking stage, respectively. Excess water was drained out immediately after the irrigation to overcome excess moisture stress. Earthing-up was done manually at 45 DAE after completion of second irrigation. Earthing-up was facilitated to protect the plant lodging as well as climatic hazards. Detasseling was done by removing the tassel of the plant after emergence of flag leaf due to maintain the baby corn quality. Harvesting was done when baby corn silk comes out 3.0 to 4.0 cm from the top end of ears, preferably in the morning. Five pickings were done for collecting the baby corn. The picking cobs of baby corn were weighed as per treatment and it was converted into t ha^{-1}.

2.5 Data Collection

Number of cobs per plant was recorded from the total number of ears harvested in each plot divided by the whole number of plants. Cob length (cm) was measured from randomly selected 5 cobs in each plot by using a meter scale from base up to top end of the cob and it was averaged. Cob diameter (cm) was measured by vernier caliper from randomly selected 5 cobs without husk in each plot and it was averaged. The 5 randomly selected cobs with husk of each plot were weighed and the average value of the weight was recorded in gram (g). The total number of cob obtained from individual plants of whole plot of each treatment was weighed and it was converted t ha^{-1} for yield estimation. The selected cobs were weighed without husk and the average values of the weight of cob without husk were recorded. The total number of

cob obtained from individual plants of each plot and it was weighed and converted in to t ha^{-1} for yield estimation.

2.6 Estimation of Protein (%)

The nitrogen content was determined by micro kjeldhal method outlined by Page et al. (1982). 0.1 g plant sample was digested with 10 ml concentrated H_2SO_4 in presence of K_2SO_4 catalyst mixture (K_2SO_4: CuSO .$5H_2O$: Se = 10: 1: 0.1). Then heating at 380 (^{0}C) was continued for about 3 hours until the digest becomes clear and colorless, then the digestion tube was allowed to cool and the contents were taken into 100 ml volumetric flasks and the volumes were made up to the mark with distilled water. The solution is then transferred quantitatively to a distillation apparatus, 15 ml of 40% of NaOH was added and the liberating ammonia was collected in a flask containing 10 ml of 4% boric acid (H_3BO_3) with 5 drops of mixed indicator of Bromocressol green ($C_{21}H_{14}O_5Br_4S$) and methyl red ($C_{10}H_{10}N_3O_3$) solution. Distillation was continued for 5 minutes' appearance of green color to ensure the complete evaluation of ammonia. After distillation solution was titrated with 0.1 N H_2SO_4 until the color changed from green to pink. Nitrogen and protein percent was calculated by the following formula:

$$\text{Nitrogen (\%)} = \frac{14 \text{ x Normality of } H_2SO_4 \text{ x (TV - TB) x Vol. of } H_2SO_4 \text{ x } 100}{\text{Weight of sample x } 100}$$

Protein content was estimated multiplying nitrogen percent of sample by factor 6.25. (Hiller et al., 1948)

Protein (%) = Nitrogen (%) x 6.25.

2.7 Estimation of Starch (%) and Total Soluble Solid (TSS)

Starch was estimated by anthrone reagent method. The test sample was treated with 80% alcohol to remove sugars and then starch is extracted with perchloric acid. In hot acidic medium starch was hydrolyzed to glucose and dehydrated to hydroxymethyl furfural. This compound forms a green colored product with anthrone. Glucose content in the sample was taken using the standard graph by the help of spectrophotometer (Model-JASCO V-750) at 630 nm. Starch content was calculated multiply the glucose content value by a factor 0.9 (Anon., 1984). Total soluble solid (^{0}Brix) was measured by Digital Refractometer (Model-NR 151).

2.8 Multivariate (cluster) and Statistical Analysis of Yield, Yield Traits and Quality Traits of Baby Corn Genotypes

The genetic divergence of 20 baby corn genotypes was estimated following Mahalanobis (1936) generalized distance (D^2) extended by Rao (1952). Tocher's method (Rao, 1952) was followed for determining the group constellations. Canonical analysis was also done according to Rao (1986) to confirm the results of cluster and D^2 analysis. Mean data for each character were subjected to multivariate analysis techniques for principal component analysis (PCA) using the R software with the package "AgroR" (Shimizu et al., 2023) and canonical

vector analysis (CVA). Cluster analysis (CLSA) was done by computer using GENSTAT 5.52 software program. The collected data were subjected to statistical analyzed using the analysis of variance (ANOVA) procedure according to Statistix 10 software (www.statistix.com). The means of each treatment were compared using the least significant difference (LSD) at significant level $p \leq 0.05$ (Statistix-10, 1985).

3. Results

3.1 Yield and Yield Attributes of Baby Corn Genotypes

The Table 1 exhibited that number of cobs per plant, cob length and diameter, cob weight with and without husk, yield with husk and without husk were significantly different among baby corn genotypes. Significantly differences were observed in number of cob per plant where the highest number (2.65) was obtained by Baby Star genotype and the lowest (1.00) was in Kamlai Thong genotype. The performance of baby corn genotypes was statistically significant in cob length. The longest cobs were found in Baby Star (11.0 cm), BHM-07 (10.9 cm), BARI Sweet Corn-01 (10.4 cm), Dream Sweet-3 (10.2 cm), MSC No.001 and BHM-11 (10.1 cm) genotypes, while the shortest cob was recorded in Kamlai Thong genotype (7.39 cm). The highest cob diameter (0.95 cm) was found in Baby Star genotype statistically similar with most of the genotypes (genotypes number 3, 4, 5, 6, 8, 12, 15, 17, 18 and 20), whereas minimum cob diameter (0.80 cm) was found in Kamlai Thong (Table 1). The highest cob weight with husk (60.6 g) was registered in Baby Star, while the minimum (35.4 g) was in Kamlai Thong genotype. The maximum cob weight without husk (13.7 g) was obtained in Baby Star, whereas the minimum (7.93 g) was observed in Kamlai Thong genotype. The cob yield with husk was statistically significant among baby corn genotypes. The highest cob yield with husk (11.9 t ha^{-1}) was produced in Baby Star genotype followed by Dream Sweet-3 (10.8 t ha^{-1}) and MSC No. 001 (9.93 t ha^{-1}), while the minimum (5.32 t ha^{-1}) was in Kamlai Thong genotype. Similarly the highest cob yield without husk (3.02 t ha^{-1}) was obtained from Baby Star followed in second place by Dream Sweet-3 (2.59 t ha^{-1}) and third place by MSC No.001 (2.41 t ha^{-1}). The minimum cob yield without husk (1.03 t ha^{-1}) was recorded in Kamlai Thong genotype (Table1).

Table 1. Yield traits of different baby corn genotypes

Genotypes (G) serial number	Genotypes (G)	No. of cob plant^{-1}	Cob length (cm)	Cob diameter (cm)	Cob wt. with husk (g)	Cob wt. without husk (g)	Yield with husk (t ha^{-1})	Yield without husk (t ha^{-1})
1	Dream Sweet-3	2.33b	10.2ab	0.90a-e	55.9b	12.4b	10.8b	2.59b
2	Hybrid Indian-900M	1.08hi	8.11d-f	0.87b-g	50.2c-e	10.3fg	5.64lm	1.18f-k
3	BARI Sweet Corn-01	1.63d	10.4a	0.93a-c	51.4cd	11.4cd	8.90ef	1.63d
4	Hybrid-09	1.3f	8.49c-e	0.94ab	51.8cd	10.8d-g	7.72e	1.30e-g
5	BHM-07	1.16gh	10.9a	0.93a-c	50.5cd	10.5e-g	6.30ij	1.25e-i
6	BHM-06	1.12gh	7.93d-f	0.91a-d	51.4cd	10.4e-g	6.10jk	1.22e-j
7	Baby Star	2.65a	11.0a	0.95a	60.6a	13.7a	11.9a	3.02a
8	BHM-05	1.21e-g	8.86cd	0.88a-f	50.0c-e	10.3fg	6.45mg	1.20f-k
9	Thai gold	1.06i	7.99d-f	0.85d-g	43.7gh	8.70h	5.68m-l	1.09i-k
10	Suwan 1	1.03i	8.02d-f	0.83c-g	45.1f-g	8.36hi	5.8lm	1.12n-k
11	Pacific Thai 271	1.03i	8.45c-e	0.86c-g	40.4h	8.03hi	5.52ef	1.05jk
12	Thai Pop	1.18f-h	8.28d-f	0.88a-f	50.6cd	10.9c-f	7.45e	1.35ef
13	MSC No.001	2.06c	10.1ab	0.86c-g	52.9bc	11.4c	9.93c	2.41c
14	Kamlai Thong	1.00i	7.39f	0.80g	35.4i	7.93i	5.32m	1.03k
15	Hybrid NK-40	1.21e-g	9.33bc	0.93a-c	49.0de	10.7e-g	6.83gh	1.30e-g
16	Super gold	1.19f-h	8.43c-e	0.82fg	50.7cd	10.4e-g	6.40ij	1.23e-i
17	Pioneer-07	1.16gh	7.89d-f	0.90a-e	52.4c	10.5e-g	6.55hi	1.27e-h
18	Pacific-559	1.18f-h	8.09ef	0.92a-d	51.4cd	10.8c-f	7.18fg	1.33e-g
19	HM-987	1.11g-h	7.58ef	0.82fg	47.1ef	10.1g	6.40ij	1.16g-k
20	BHM-11	1.33e	10.1ab	0.92a-d	50.8cd	11.1c-e	7.33d	1.38e
-	Level of significance	**	**	*	*	**	*	**
-	CV (%)	5.76	6.98	6.80	7.10	8.92	5.37	7.23

Values in a column followed by uncommon letter differed significantly at 5% level by LSD test. CV=Coefficient of variation, **Significant at 1% level of probability, *Significant at 5% level of probability.

3.2 Quality Traits of Baby Corn Genotypes

The protein content (%), starch content (%) and total soluble solid (TSS) of baby corn revealed significant differences among genotypes (Table 2). The highest protein content (11.0%) was achieved in Baby Star followed by Dream Sweet-3 (10.0%), while the minimum protein content (6.30%) was in Kamlai Thong. The highest starch content (57.0%) was recorded in Baby Star followed by Dream Sweet-3 (53.0%), whereas the lowest starch content (41.2%) was in Kamlai Thong. The highest TSS (9.51%) was noted in Dream Sweet-3 which was significantly different over the other genotypes, while the lowest TSS content (5.11%) was in Kamlai Thong.

Table 2. Protein content, starch content and total soluble solid (TSS) of baby corn genotypes

Genotypes (G) serial number	Genotypes (G)	Protein (%)	Starch (%)	TSS (%)
1	Dream Sweet-3	10.0b	53.0b	9.51a
2	Hybrid Indian-900M	7.23d	46.4cd	5.95e
3	BARI Sweet Corn-01	7.05de	47.9cd	8.33b
4	Hybrid-09	7.35d	47.5cd	6.11c-e
5	BHM-07	7.28d	45.8de	5.98de
6	BHM-06	7.21d	45.6d-f	5.95e
7	Baby Star	11.0a	57.0a	6.58c
8	BHM-05	7.19d	45.5d-f	5.88e
9	Thai gold	6.66ef	42.3fg	6.53c
10	Suwan 1	6.48f	42.9e-g	6.48cd
11	Pacific Thai 271	6.33f	42.6e-g	6.36c-e
12	Thai Pop	7.18d	47.3cd	5.98de
13	MSC No.001	9.15c	49.5c	7.96b
14	Kamlai Thong	6.30f	41.2g	5.11f
15	Hybrid NK-40	7.16d	48.2cd	5.23f
16	Super gold	7.20d	48.3cd	5.19f
17	Pioneer-07	7.24d	46.5cd	5.12f
18	Pacific-559	7.21d	47.6cd	5.21f
19	HM-987	7.16d	45.4d-f	5.18f
20	BHM-11	7.17d	45.3d-f	5.36f
-	Level of Significance	**	**	**
-	CV (%)	5.62	8.36	6.49

Values in a column followed by uncommon letter differed significantly at 5% level by LSD test. CV=Coefficient of variation, **Significant at 1% level of probability.

3.3 Multivariate (Cluster) Analysis of Yield and Yield Attributes of Baby corn (genotypes grouping)

The multivariate approaches of analysis of variation among the genotypes were done under the present investigation to identify genetically diverse genotypes for identifying higher yield and yield attributes. The results of genetic variability and divergence of baby corn genotypes have been presented simultaneously in the Tables 3 to 7 and in Figures 2 to 3.

3.3.1 Principal Component Analysis (PCA)

Seven yield and yield contributing characters such as number of cob plant^{-1}, cob length, cob diameter, cob weight with husk and cob weight without husk, yield with husk and yield without husk of 20 baby corn genotypes were considered for principal components analysis (Figure 2). The results of PCA revealed that leading of two principal components (PCs) were accounted for 89.66% of the total variation. PC1 and PC2 were considered for constructing the PCA-biplot. The first factor (PC1) characters like cob length (cm), cob weight without husk (g) and cob weight with husk (g) were contributed most 76.99% of the total variance, however the second factor (PC2) characters such as yield without husk (t ha^{-1}) and cob diameter (cm) contributed about 12.67%. The PCA biplot exhibited the variations and correlation among the genotypes. The traits cob length (cm), cob weight without husk (g) and cob weight with husk (g) were nearly located in the same, which indicated a strong positive correlation. The yield without husk (t ha^{-1}), number of cob plant^{-1} and yield with husk (t ha^{-1}) were also nearly located in the same that indicated a strong positive correlation with each other.
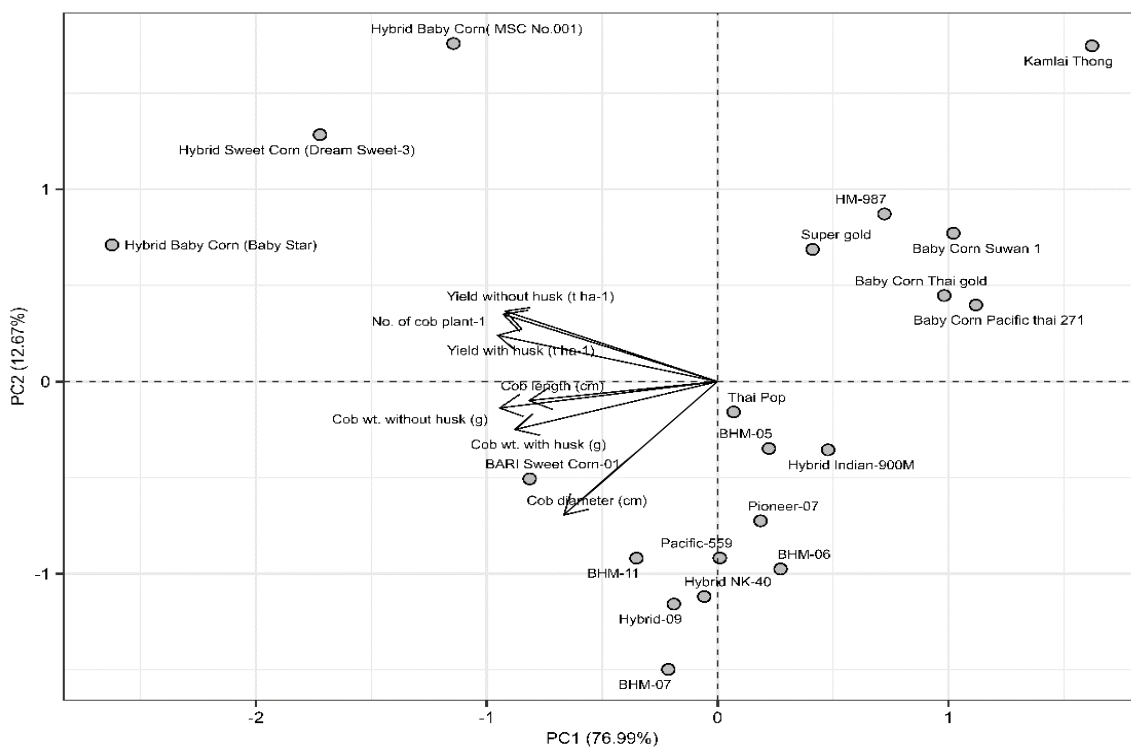

Figure 2. PCA – Biplot for yield and yield attributes of Baby corn genotypes

The genotypic variance and correlations with seven characters of yield and yield attributes were also clarified by forming three distinct groups. The first group was formed by the genotypes Hybrid Baby Corn (Baby Star), Hybrid Sweet Corn (Dream Sweet-3) and Hybrid Baby Corn (MSC No.001), while the second group was formed by BARI Sweet Corn-01, BHM-11, Hybrid NK-40, Hybrid-09 and BHM-07 genotypes. The rest genotypes were formed the last group. Genotype Hybrid Baby Corn (Baby Star) and Hybrid Sweet Corn (Dream Sweet-3) followed by Hybrid Baby Corn (MSC No.001) was best suited for yield without husk (t ha^{-1}), yield with husk (t ha^{-1}) and number of cob plant^{-1}. Whereas the genotype BARI Sweet Corn-01 followed by BHM-11, Hybrid NK-40, Hybrid-09 and BHM-07 was for Cob length (cm), Cob weight with husk (g), Cob weight without husk (g) and Cob diameter (cm).

3.3.2 Mean Performances of 20 Baby Corn Genotypes

Range, mean, standard deviation and co-efficient of variation of different characters of the studied genotypes are presented in Table 3. Number of cob plant^{-1} ranged from 1 to 2.65, cob length (cm) ranged from 7.39 to 11.03, cob diameter (cm) ranged from 0.80 to 0.95, cob wt. with husk (g) ranged from 35.38 to 60.58, cob wt. without husk (g) ranged from 7.93 to 13.65, yield with husk (t ha^{-1}) ranged from, 5.32 to 11.90 and yield without husk (t ha^{-1}) ranged from 1.03 to 3.02. Cob wt. with husk and yield with husk showed a wide range of variability accounting for 35.38 to 60.58 (g) and 5.32 to 11.90 (t ha^{-1}), respectively.

Table 3. Mean performance of 20 genotypes of baby corn

Characteristics	Mean	Range		Standard deviation	CV%
		Min.	Max.		
No. of cob plant^{-1}	1.351	1.00	2.65	0.460	34.07
Cob length (cm)	8.884	7.39	11.03	1.164	13.10
Cob diameter (cm)	0.885	0.80	0.95	0.044	4.97
Cob wt. with husk (g)	49.56	35.38	60.58	5.369	10.83
Cob wt. without husk (g)	10.441	7.93	13.65	1.388	0.01
Yield with husk (t ha^{-1})	7.2106	5.32	11.90	1.823	25.28
Yield without husk (t ha^{-1})	1.455	1.03	3.02	0.550	37.80

3.3.3 Cluster Analysis

The analysis of variance revealed highly significant differences among the genotypes for all the seven characters indicating the existence of genetic variability. The twenty genotypes (serial number of genotypes are described in Table 2) were grouped into four clusters using the non-hierarchical clustering method by Genstat Version 5.52 software program, where the genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 4).

Table 4. Distribution of 20 baby corn genotypes in four clusters

Cluster	Number of genotypes	Genotypes (G) in different clusters
I	12	2, 3, 4, 5, 6, 8, 12, 15, 16, 17, 18, 20
II	03	1, 7, 13
III	02	11, 14
IV	03	9, 10, 19

3.3.4 Average Intra and Inter Cluster Distance

The intra and inter cluster distance (D2) values worked out from divergence analysis are presented in Table 5. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the same cluster. The inter cluster distances in all cases were larger than the intra cluster distance which indicated that wider diversity was present among the genotypes of distant group. The genotypes included within a cluster had less diversity among themselves. The highest inter cluster distance of 13.47 was observed between cluster II and III followed by 9.911 between cluster II and IV, 9.213 between cluster I and III suggesting wide diversity between them and the genotypes in these cluster could be used as genotypes for conducting experiment on level of fertilizer and irrigation. The highest intra cluster distance was computed for cluster II (0.249) followed by cluster I (0.221). The cluster IV showed the least intra cluster distance (0.154) which indicated that the genotypes in this cluster were more or less homogeneous.

Table 5. Intra (bold) and inter-cluster distances of seven characters of baby corn

Clusters	I	II	III	IV
I	**0.221**			
II	6.697	**0.249**		
III	9.213	13.470	**0.1818**	
IV	4.278	9.911	5.135	**0.154**

3.3.5 Construction of Scatter Diagram

Based on these values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1 -Z_2) using component scores 1 as X axis and component scores 2 as Y axis was constructed which has been presented in Figure 3. The positions of the genotypes in the scatter diagram were apparently distributed into three groups which indicated the existence of considerable diversity among the genotypes.
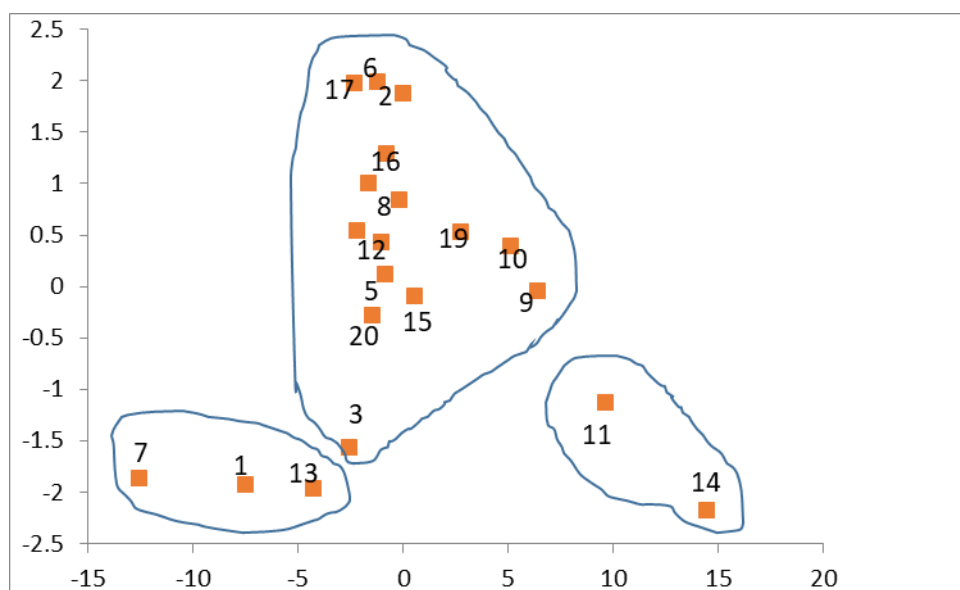
Figure 3. Scatter distribution of 20 baby corn genotypes based on their principal component scores superimposed with clustering (1….. 20 = serial no. of baby corn genotypes)

3.3.6 Cluster Mean

Mean values of cluster for yield and its different contributing characters are presented in the Table 6. It appeared that the maximum number of cobs plant^{-1} was included in the cluster II (2.49) followed by cluster I (1.29). The highest cob length was recorded in cluster II (10.64 cm) followed by cluster I (9.00 cm) and the smallest in cluster IV (7.86 cm). The uppermost cob diameter was included in the cluster II (0.93 cm) followed by cluster I (0.90 cm) and the lowermost included in the cluster III (0.83 cm) that was identical in cluster IV. The highest cob weight with husk was obtained in cluster II (58.22 g) followed by cluster I (51.01 g) and the lowest cob weight with husk was found in cluster III (37.87 g). The biggest cob weight without husk was found in cluster II (13.03 g) followed by cluster I (10.74 g) and the smallest in cluster III (7.98 g). The maximum yield with husk was found by the cluster II (11.35 t ha^{-1}) followed by cluster I (7.14 t ha^{-1}) and the minimum yield with husk was obtained in the genotypes of the cluster III (5.42 t ha^{-1}). The highest yield without husk was produced by the cluster II (2.80 t ha^{-1}) followed by cluster I (1.39 t ha^{-1}) and that of the lowest yield without husk was recorded in the genotypes of the cluster III (1.04 t ha^{-1}).

Table 6. Cluster means for seven different characters of baby corn genotypes

Characters	Clusters			
	I	II	III	IV
No. of cob plant[-1]	1.29	2.49	1.02	1.07
Cob length (cm)	9.00	10.64	7.92	7.86
Cob diameter (cm)	0.90	0.93	0.83	0.83
Cob wt. with husk (g)	51.01	58.22	37.87	45.30
Cob wt. without husk (g)	10.74	13.03	7.98	9.06
Yield with husk (t ha^{-1})	7.14	11.35	5.42	5.96
Without husk Yield (t ha^{-1})	1.39	2.80	1.04	1.12

3.3.7 Contributions of Characters Towards Divergence

Contributions of characters towards divergence were estimated through canonical variate analysis. In this method, vectors of canonical roots were calculated to represent the genotypes in the graphical form (Rao, 1952). The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 7. The positive absolute values of the two vectors revealed that C_1 (number of cob plant[-1]), C_3 (cob diameter) and C_5 (cob weight without husk) had the greatest contribution to genetic divergence.

Table 7. Relative contributions of the seven characters to the total divergence in baby corn genotypes

Sl. No.	Characters	Vector i	Vector ii
i	No. of cob plant[-1]	2.868	13.769
ii	Cob length (cm)	0.055	-0.834
iii	Cob diameter (cm)	1.486	17.562
iv	Cob wt. with husk (g)	0.470	-0.387
v	Cob wt. without husk (g)	1.159	0.419
vi	Yield with husk (t ha^{-1})	-1.145	-1.018
vii	Yield without husk (t ha^{-1})	-0.764	-1.800

3.4 Grouping of Genotypes through Multivariate (Cluster) Analysis on Quality Parameters

The multivariate approaches of analysis of variation among the genotypes were done under the present investigation to identify genetically diverse genotypes for identifying quality of baby corn. The results of genetic variability and divergence of baby corn genotypes for identifying quality of baby corn are presented simultaneously in the Tables 8 to 12 and in Figures 4 to 5.

3.4.1 Principal Component Analysis (PCA) for Quality Parameters

Three quality parameters viz. protein, starch and total soluble solid (TSS) of 20 baby corn genotypes were considered for principal components analysis (Figure 4). The results of PCA exhibited that leading of two principal components (PCs) were accounted for 97.54% of the total dissimilarity among three quality characters. PC1 and PC2 were considered for constructing the PCA-biplot. The first factor (PC1) parameters like starch and protein contributed most 76.11% of the total variance, while the second factor (PC2) only TSS contributed about 21.43%. The first biplot displayed the variations and correlation between the genotypes. The traits starch and protein were located nearly in the same that indicated a strong positive correlation with each other, but TSS exhibited a weak positive correlation to starch and protein.
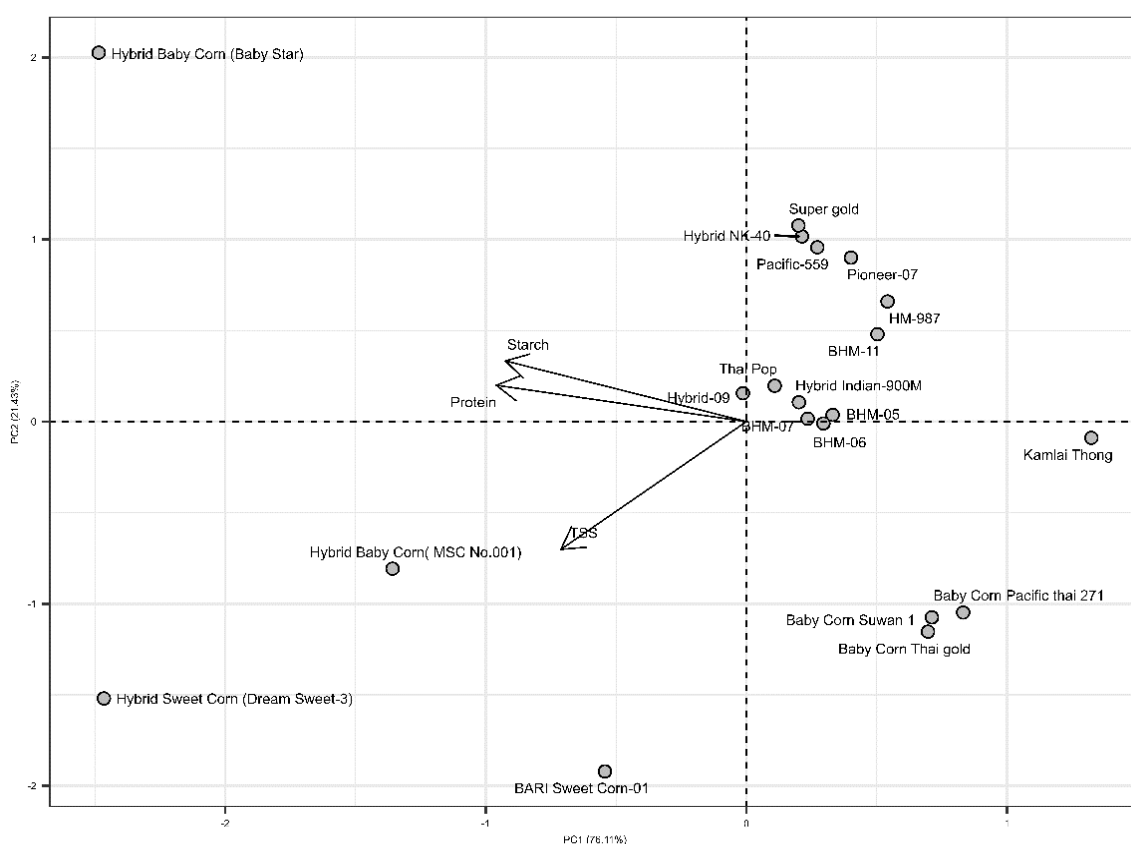
Figure 4. PCA – Biplot for quality parameters of Baby corn genotypes

The genotypic variance and correlations with three quality traits were also clarified by making three distinct groups. The Hybrid Baby Corn (Baby Star) genotype formed a single group, while the second group was formed by Hybrid Baby Corn (MSC No.001), Hybrid Sweet Corn (Dream Sweet-3) and BARI Sweet Corn-01 genotypes. The rest genotypes were formed the last group. The Hybrid Baby Corn (Baby Star) genotype was best suited for starch and protein. While Hybrid Baby Corn (MSC No.001) followed by Hybrid Sweet Corn (Dream Sweet-3) and BARI Sweet Corn-01 genotypes were suited high for TSS.

3.4.2 Mean Performances of Quality Traits of 20 Baby Corn Genotypes

Range, mean, standard deviation and co-efficient of variation of different characters of the studied genotypes are presented in Table 8. Protein content (%) ranged from 6.3 to 11.03, starch content (%) ranged from 41.21 to 57.03 and TSS content (%) ranged from 5.11 to 9.51. Hence, there is enough scope for selection of potential genotypes for agronomic management.

Table 8. Mean performance of quality traits of 20 genotypes of baby corn

Characteristics	Mean	Range		Standard deviation	CV (%)
		Min.	Max.		
Protein (%)	7.480	6.3	11.03	1.199	16.02
Starch (%)	46.78	41.21	57.03	3.636	7.77
TSS (%)	6.20	5.11	9.51	1.177	18.98

3.4.3 Cluster Analysis

The analysis of variance revealed highly significant differences among the genotypes for all the three characters indicating the existence of genetic variability among the experimental genotypes. The twenty genotypes were grouped into four clusters using the non-hierarchical clustering method by Genstat Version 5.52 software program in such a way that the genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 9). Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The maximum number of genotypes (12) was comprised into cluster IV indicating overall genetic similarity among them which was followed by cluster III (4) and II (3) respectively. The minimum genotypes (1) comprised into cluster I.

Table 9. Distribution of 20 baby corn genotypes in four clusters

Cluster	Number of genotypes	Genotypes (G) in different clusters
I	1	3
II	3	1, 7, 13
III	4	9, 10, 11, 14
IV	12	2, 4, 5, 6, 8, 12, 15, 16, 17, 18, 19, 20

3.4.4 Average Intra and Inter Cluster Distance

The intra and inter cluster distance (D2) values worked out from divergence analysis are presented in Table 10. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the same cluster. The inter cluster distances in all cases were larger than the intra cluster distance which indicated that wider diversity was present among the genotypes of distant group. The genotypes included within a cluster had less diversity among themselves. The highest inter cluster distance of 14.739 was observed

between cluster II and III followed by 11.845 between cluster II and IV, 8.203 between cluster I and III suggesting wide diversity between them and the genotypes in these cluster could be used as genotypes for conducting experiment on level of fertilizer and timing of irrigation. The highest intra cluster distance was computed for cluster II (0.3456) followed by cluster I (0.2375). The cluster IV showed the least intra cluster distance (0.0814) which indicated that the genotypes in this cluster were more or less homogeneous.

Table 10. Intra (bold) and inter-cluster distances of 20 genotypes of baby corn

Clusters	I	II	III	IV
I	**0.2375**			
II	6.989	**0.3456**		
III	8.203	14.739	**0.1194**	
IV	5.699	11.845	3.615	**0.0814**

3.4.5 Construction of Scatter Diagram

Based on these values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1 - Z_2) using component scores 1 as X axis and component scores 2 as Y axis was constructed which has been presented in Figure 5. The positions of the genotypes in the scatter diagram were apparently distributed into four groups which indicated the existence of considerable diversity among the genotypes.
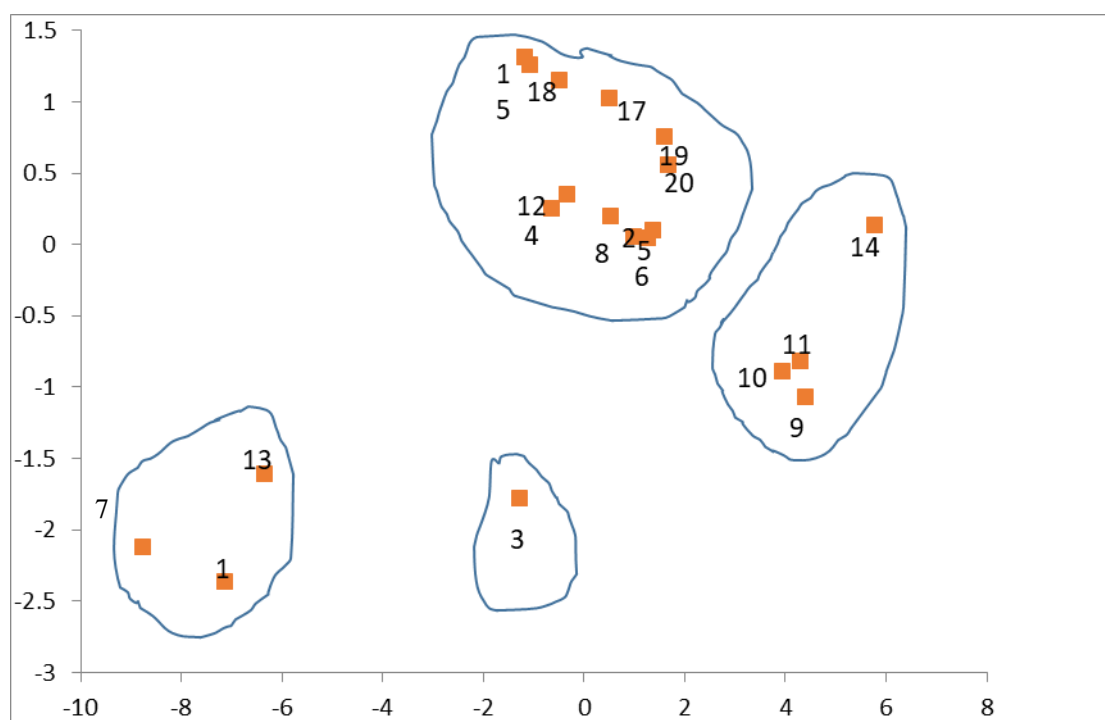

Figure 5. Scatter distribution of 20 baby corn genotypes based on their principal component scores superimposed with clustering (1….. 20= serial number of baby corn genotypes)

3.4.6 Cluster Mean

Mean values of cluster for quality parameters are presented in the Table 11. It appeared that the maximum Protein (%) were included in the cluster II (10.53%) followed by cluster I (8.10%). The highest Starch (%) was recorded in cluster II (55.03%) followed by cluster I (48.75%) and the smallest in cluster III (42.25%). The highest TSS (%) were included in the cluster II (8.15%) followed by cluster I (8.05%) and the lowest included in the cluster IV (5.59%) that was identical in cluster III.

Table 11. Cluster means for 3 different characters of 20 baby corn genotypes

Characters	Clusters			
	I	II	III	IV
Protein (%)	8.10	10.53	6.44	7.12
Starch (%)	48.75	55.03	42.25	46.60
TSS (%)	8.05	8.15	6.12	5.59

3.4.7 Contributions of Characters Towards Divergence

Contributions of characters towards divergence were estimated through canonical variate analysis. In this method, vectors of canonical roots were calculated to represent the genotypes in the graphical form. The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 12. The positive absolute values of the two vectors revealed that C_1 (Protein (%), and C_3 (TSS (%) had the greatest contribution to genetic divergence. However the positive absolute values of vector-1 and negative absolute value for vector-2 for the characters like Starch (%) indicated the responsibility of primary differentiation.

Table 12. Relative contributions of the three characters to the total divergence in baby corn genotypes

Sl. No.	Characters	Vector I	Vector II
I	Protein (%)	1.319	0.7949
II	Starch (%)	0.560	-0.5093
III	TSS (%)	1.102	0.9942

4. Discussion

The knowledge about the economic and nutritional importance of baby corn in Bangladesh coupled with non-availability of appropriate variety and production technology is the major constraints for baby corn cultivation. The yield of baby corn in Bangladesh is about 0.99 to 1.1 t ha^{-1} that means is very poor compared to other countries in Asia (Asaduzzaman et al., 2014). Superior cultivars (genotypes) need to be evaluated on the basis of multiple traits and genetic divergence to ensure the appropriate cultivars for Bangladesh environment through

selection method (Jahan, 2018; Yan et al., 2008). Genotype plays a vital role in achieving the maximum benefit from a crop in terms of yield and quality as each genotype has its unique optimum potential for a particular character under a given environment (Mahmood et al., 2022). It behaves differently under different environments for the expression of characters of interest. It means a particular genotype may not exhibit the same phenotypic performance or expression under different environments or different genotypes may respond differently to a specific environment (Mahmood et al., 2022).

In the present study, twenty genotypes were evaluated to identify the highest yielding and improved quality genotypes. It was found that yield contributing characters viz. number of cob plant^{-1}, cob length, and cob diameter and cob weight without husk varied significantly among the genotypes. The number of cob plant^{-1} in Baby Star was about 62% greater than Kamlai Thong. Similar results were also reported by Chauhan et al. (2010) that higher number of cob plant^{-1} could be attributed to its genetic constitution and potential. A significant variation was observed due to genotypes at the cob length of the baby corn genotypes. Cob length of Baby Star was around 33% higher than Kamlai Thong. These differences were mostly due to the genetic variation and high genetic advance to get higher cob length in Baby star among the genotypes. This result was consistent to Sravanti et al. (2017) who used forty two maize genotypes as an experimental material to study the heritability and genetic advance for yield and its contributing traits. The performance of baby corn genotypes was statistically significant in case of cob diameter. The highest cob diameter was found in Baby Star while the lowest cob diameter was observed in Kamlai Thong. Cob diameter of Baby Star was around 16% higher than Kamlai Thong. Cob diameter of Baby Star was higher than Kamlai Thong could be attributed to its genetic constitution and potential. Kheibari *et al*. (2012) noticed that cob diameter was very important parameter for selecting baby corn variety due to contribute higher yield and it was differed among the genotypes. Patil et al. (2016) stated that highest genetic advance assisted to get higher ear height and diameter. Cob weight without husk was significantly influenced by genotypes. Cob weight without husk in Baby Star was around 41% higher than Kamlai Thong. Kumar et al. (2015) and Chauhan et al. (2010) reported that cob weight without husk of baby corn genotypes was higher due to genetic make-up and potential characteristics of genotypes. Cob weight with husk is a manifestation of yield contributing characters and significant variation was found in cob weight with husk due to differential of genetically constitution. Kumar et al. (2015) reported that cob weight with husk differed among the genotypes. Young cob yield with husk as well as the cob weight with husk of Baby Star was around 65% and 41% higher, respectively than Kamlai Thong. The significant variation of young cob yield with husk might be due to production potential of genotypes along with their genetic characteristics. Young cob yield with husk differed due to differences of genetic constitution was also supported by Chauhan et al. (2010). Regarding economic young cob yield without husk, a significant difference was found among the genotypes. The highest economic young cob yield without husk was found in Baby Star while the lowest was produced in Kamlai Thong. Young cob yield without husk of Baby Star was around 65% greater than Kamlai Thong. The highest economic young cob yield without husk was found in Baby Star due to the higher number of cob plant^{-1}, cob length, and cob diameter and cob weight. Variation of economic young cob yield without husk might be due to the production potential of genotypes and for

their genetic characteristics making differences in the partitioning of photosynthates between them. Javier (2002) also observed significant differential young cob yield in different baby corn genotypes. The above result was consistent with the findings of Kumar et al. (2015) and Fahrurrozi et al., (2016).

The protein content obtained significant variations under the effect of genotypes. The genotype Baby Star recorded significantly highest protein content while the lowest protein content was found in Kamlai Thong which might be due to the better genetic potential of the genotypes as well as significantly higher differences in above parameters was supported by Sripriya and Sneha (2020). Significant variation was found in starch content under the effect of genotypes. The highest starch content was found in Baby Star while the lowest was produced in Kamlai Thong. The significant variation in starch content might be due to production potential of genotypes along with their genetic characteristics. This result was supported by Kidist (2018) and Danupol et al. (2015). In our study, the total soluble solid (TSS) in Dream Sweet-3 genotype was around 46% higher than Kamlai Thong. Similar observation was verified by Chauhan et al. (2010) and Dipika et al. (2014) that TSS varied due to differences in genetic constitution.

Principal Component Analysis (PCA) typically trusts on correlations between various traits and assistances in depicting individual differences and identifying potential groupings (Sagar et al., 2023; Sapna et al., 2020). In our study, the yield traits such as cob length, cob weight without husk, and cob weight with husk were closely located, indicating a strong positive correlation. Similarly, yield without husk, number of cobs per plant, and yield with husk were closely grouped, indicating a strong positive correlation. The PCA analysis also revealed strong correlations between specific genotypes both yield attributes and quality parameters. This information serves as a valuable guide for grouping genotypes and understanding the variability for genotypic selection of crop improvement. Similar observation reported by Sapna et al. (2020). Grouping of genotypes through multivariate (cluster) analysis on yield, yield attributes and quality parameters indicated that the cluster II showed higher performance among other clusters that means Baby Star, Dream Sweet-3 and MSC No.001 were better among twenty genotypes. Kumar et al. (2013) reported similar that grouping of genotypes through multivariate analysis widely used in plant sciences for the reduction of variables and grouping of genotypes. Cuevas et al. (2018) stated that the clustering pattern could be utilized in choosing genotypes for agronomic management.

5. Conclusion

The aforesaid results and discussion indicated that Baby Star genotype followed by Dream Sweet 3 and MSC 001 genotypes were better based on yield, yield traits and quality. Multivariate (cluster) analysis on yield, yield attributes and quality attributes also revealed that the Baby Star followed by Dream Sweet-3 and MSC No.001 are superior to other genotypes. Hence recommendation can be made that Baby star followed by Dream Sweet-3 and MSC No.001 genotypes support to obtain maximum yield and quality of baby corn and also potential to fit in cropping system in Bangladesh. These three genotypes (Baby Star, Dream Sweet-3 and MSC No.001) may release as a variety after on-farm trial with existing

variety. Some genotypes with specific features might be potential used in genetic resources for the future improvement of breeding program beneficial for baby corn expansion.

Author's contributions

Study design and revising, M.H.S, M.A.Q., M.A.S., M.R.K, M.A.I. and M.T.I.; Data collection, analysis and software, M.H.S., M.A.Q., M.M.A. and R.A.; Methodology, M.H.S., M.A.Q., M.A.S. and K.M.F.H.; Visualization and Validation, M.H.S., M.A.Q., and M.A.S.; drafted the manuscript, M.A.Q., M.H.S. and M.A.S.; revised and editing, M.A.Q., M.H.S. and M.M.A.; All authors have read and approved the final manuscript.

Competing interests

The authors are declared that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Informed consent

Obtained.

Ethics approval

The Publication Ethics Committee of the Macrothink Institute.

The journal's policies adhere to the Core Practices established by the Committee on Publication Ethics (COPE).

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Data availability statement

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

Data sharing statement

No additional data are available.

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