



Genetic diversity analysis using morphological and biochemical traits in baby corn (*Zea mays*)

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ABSTRACT

The present investigation was conducted to examine the genetic diversity existing among 24 genotypes of babycorn (*Zea mays* L.). The experiment was conducted in three replications in randomized block design during *rabi* 2018–19 at research farm of Bihar Agricultural University, Sabour. Different morphological and biochemical observations were taken to identify diverse genotypes among them. Observations were taken for 10 morphological characters and nine biochemical traits. Analysis of variance showed significant variation in genotypes for all the traits. On the basis of mean performance genotypes Suwan and VQL1 were found to be the best genotypes for baby corn yield. Genotypes LM14 (203.44 q/ha), LM13 (208.73 q/ha), VQL1 (203.25 q/ha), 95IOWA (200.34 q/ha) and Suwan (230.11 q/ha) were found to be the best genotypes for fodder yield. On the basis of D² Mahalanobis statistical analysis, all the genotypes were grouped into seven clusters. Seven genotypes were found in the cluster III, followed by six genotypes in cluster II and minimum number of genotype was in cluster VI and VII (with one genotype in each cluster). The maximum intra cluster distance was found in cluster V (117.93) followed by cluster III (93.49) and minimum in cluster I (27.64). The maximum inter cluster distance was found in between cluster IV and VII (317.11) and minimum in between cluster I and VII (92.78). The present investigation revealed that cluster IV and VII were most diverse. Genotypes constituted in these clusters may be used as parents for future hybridization.

Keywords: Babycorn, D² analysis, Genetic diversity, Maize

Maize (*Zea mays* L.) is one of the most important cereal crops and has the highest production area worldwide followed by wheat and rice due to its diverse usage and being a staple food to large number of human population in the world. It plays a significant role in human and livestock nutrition worldwide and has greater nutritional value, as it contains about 72% starch, 10% proteins, 8.5% fibre, 4.8% oil, 3% sugar and 1.7% ash. It is the highest yielding grain crop having multiple uses and one of the most important cereal crops and occupies prominent position in global agriculture after wheat and rice. Early ripening, low height, flowering uniformity and prolificacy are considered the most important traits for the production of baby corn. In addition, agronomic practices such as population densities, nitrogen fertilization and detasseling can increase baby corn yield considerably. Information on genetic diversity and population structure are very important in any breeding programme for the improvement of traits of interest and the development of outstanding products for commercialization

(Adu *et al.* 2019). Classification of germplasm collection is a prerequisite for identifying genetically close and divergent types for various traits under study in plant breeding programmes. By using biometrical techniques such as multivariate analysis based on Mahalanobis D² statistics (1936), it has now become possible to quantify the degree of genetic divergence among biological populations and assessing the relative contribution of various desirable traits for breeding as well as agronomic values to the total divergence. D² statistics has been employed widely to resolve divergence at inter varietal, species and subspecies levels in classifying problems in crop plants. It is believed that genetically diverse parents are likely to produce high heterotic effects.

The identification of genetically distant parental combinations provides better crop improvement strategy for breeders. D² analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both in intra and inter-cluster level.

MATERIALS AND METHODS

The present study was conducted in the research farm of Department of Plant Breeding and Genetics, Bihar

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Agricultural University, Sabour. The experiment was carried out with 24 germplasm from different sources, including three checks (VL 145312, DHOLI 55 and CM 600) in randomized block design with three replications. Observations were recorded for days to 50% silking, plant height, ear height, number of leaves/plant, baby corn length, baby corn girth, baby corn weight, no. of cobs/plant, baby corn yield, fodder yield and biochemical traits such as TSS (refractometer), ascorbic acid (titration method), total sugar and reducing sugar (Lane and Eynon method), protein content (Micro Kjeldahl method), phosphorous content (spectrophotometer), iron content (atomic absorption spectrophotometer), calcium content (flame photometer) and copper (atomic absorption spectrophotometer). The data were analysed by using analysis of variance suggested by Panse and Sukhatme (1954), genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all 20 characters indicating the existence of genetic variability among the experimental material.

The 24 genotypes of maize were grouped into seven clusters (Table 1). Cluster III was the largest having seven genotypes indicating genetic similarity among them, whereas cluster VI and cluster VII had one genotype each. In cluster

VII, genotype ZL14501 grouped for no. of leaves/plant and Iron content (mg/100 g). In cluster I genotype such as 96ROHYO, HK I335 classified for characters such as TSS, ascorbic acid, total sugar, reducing sugar, protein content, plant height and earliness. Genotype Suwan, CM 600, CML 451 exhibited in cluster IV for characters such as baby corn girth, baby corn length, baby corn weight, no. of cobs/plant, baby corn yield, fodder yield, ear height and phosphorous content.

The intra and inter-cluster values among the seven clusters are presented in Table 2. The intra-cluster distances were lower than the inter cluster distances. Thus, the genotypes included within a cluster had less diversity among themselves. The maximum intra cluster distance was found in cluster V (117.93) followed by cluster III (93.49), cluster IV (88.55), cluster II (77.09) and minimum in cluster I (27.64). The highest inter-cluster distance (317.11) was observed between clusters IV and VII followed by clusters IV and VI (310.34), clusters III and IV (264.68), and minimum in between cluster I and VII (92.78), suggesting more diversity in genetic make-up of the genotypes included in these clusters. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Genotypes of these clusters can be utilized in further breeding programme.

The lowest cluster mean value for days to 50% silking, no. of leaves/plant, baby corn weight, baby corn length, baby corn yield and plant height were recorded in cluster I and for baby corn girth and number of cobs/plant found in cluster VII. The lowest mean value for ear height was recorded in cluster IV. The lowest mean value for fodder yield was recorded in cluster V. The highest mean value for baby corn girth, baby corn length, baby corn weight, number of cobs/plant, baby corn yield, fodder yield, ear height and phosphorous content were recorded in cluster VII. The higher mean value for days to 50% silking found in cluster VII. In cluster VI, higher mean value for plant height, ear height and calcium content were observed. The highest mean value for number of leaves/plant and iron content found in cluster VII. The highest mean value for TSS, ascorbic acid, total sugar, reducing sugar, protein content was recorded in cluster I. In cluster IV, higher mean value for phosphorous content was observed. In cluster II, highest mean value for copper content was observed (Table

Table 1 Grouping of 24 genotypes into different clusters

Cluster	Number of genotypes	Name of genotypes
Cluster I	2	96 ROHYO, HKI 335
Cluster II	6	VQL 1, HKI1532, DHOLI 55, CM 400, BML 7, LM 14
Cluster III	7	LM 13, VL 1055, VL 145312, CM 501, 95 IOWA, CML 425, VL 1010762
Cluster IV	3	SUWAN, CM 600, CML451
Cluster V	4	SML 1, BML 6, CLO 2450, HKI 1105
Cluster VI	1	CLQRCY 44
Cluster VII	1	ZL 14501

Table 2 Average intra and inter cluster distances

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	27.64	192.93	123.38	242.96	191.11	199.33	92.78
Cluster II		77.09	134.18	223.31	126.07	120.56	212.03
Cluster III			93.49	264.68	171.36	117.10	116.49
Cluster IV				88.55	157.04	310.34	317.11
Cluster V					117.93	195.32	237.95
Cluster VI						0.00	171.72
Cluster VII							0.00

Table 3 Mean performance of different clusters for different quantitative characters

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50% Silking	82.30	98.50	103.38	98.33	97.67	100.00	112.33
Plant height (cm)	96.46	109.16	111.73	100.42	111.58	134.42	121.03
Ear height (cm)	50.89	49.00	48.63	44.77	54.09	55.02	52.42
No. of leaves/plant	8.24	9.37	9.67	9.72	9.76	9.72	10.6
Baby corn length (cm)	5.93	7.49	7.53	7.82	7.24	6.93	6.87
Baby corn girth (cm)	1.25	1.27	1.27	1.34	1.33	1.30	1.22
Baby corn weight (g)	5.88	6.46	6.71	7.18	6.45	6.73	6.53
No. of cobs/plant	1.90	2.13	1.76	2.14	2.10	2.20	1.60
Baby corn Yield (q/ha)	9.65	11.44	10.75	12.03	12.14	12.71	10.88
Fodder yield (q/ha)	181.56	181.22	184.94	199.11	166.87	189.61	174.97
TSS (°Brix)	11.03	10.68	8.83	10.38	10.43	10.07	6.52
Total protein (%)	4.42	3.13	3.19	3.97	3.46	4.26	4.14
Total sugar (%)	8.05	6.66	5.48	6.60	6.75	5.60	4.25
Reducing sugar (%)	5.33	4.12	4.19	4.15	4.36	4.27	4.19
Ascorbic acid (mg/100 g)	10.11	8.07	8.21	8.98	6.50	5.32	9.40
Calcium content (mg/100 g)	29.75	100.02	66.92	70.98	88.14	110.48	35.38
Phosphorous content (mg/100 g)	129.74	127.92	106.59	236.08	174.04	80.50	88.17
Iron content (mg/100 g)	2.97	2.72	3.63	2.29	3.56	3.24	3.76
Copper content (mg/100 g)	2.70	7.32	4.66	6.34	6.48	4.84	2.25

3). Similar finding was suggested by Marker and Krupakar (2008).

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 maximum contribution percentage towards divergence was by phosphorous content (46.01%) followed by copper content (30.07%) and calcium content (18.48%). Iron content, ascorbic acid and reducing sugar has comparatively low contributions towards divergence. Rest of the traits had no contribution towards diversity. Reddy *et al.* (2013) observed that out of 13 characters plant height (42.31%), ear height (16.84%), baby corn length (17.22%) and cob yield (7.97%) contributed high for divergence. These characters may be utilized for further breeding programme to improve baby corn yield.

Genetic diversity present in the available genotypes has immense value of crop improvement in character of interest. From the point of selecting the

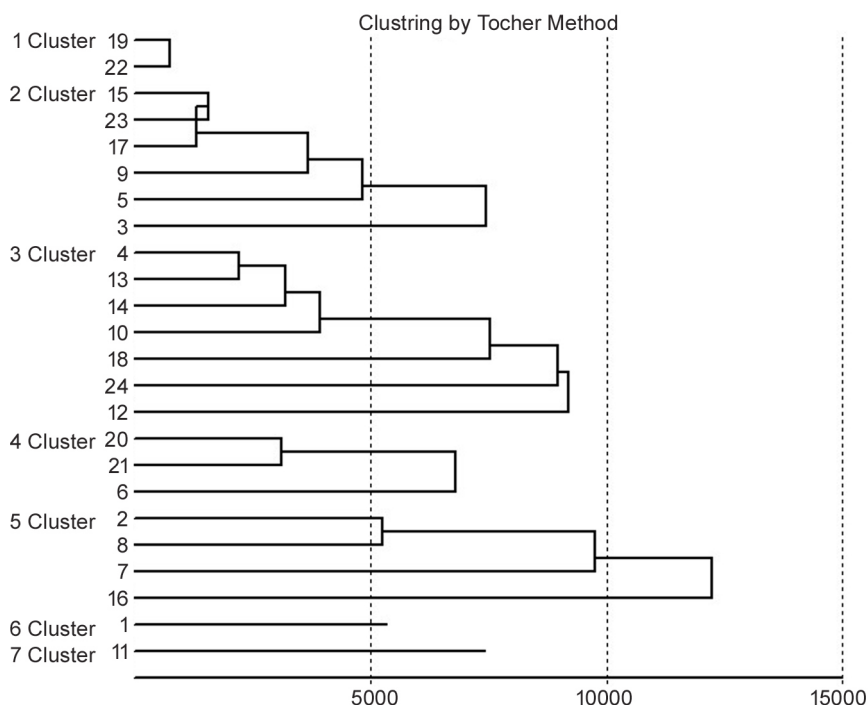


Fig 1 Dendrogram showing clustering of 24 maize genotypes by Tocher's method.

1-CLQRCY44	2-SML1	3-LM14	4-LM13	5-BML7	6-CML451
7-CLO2450	8-BML6	9-CM400	10-CM501	11-ZL14501	12-VL1010762
13-VL1055	14-VL145312	15-VQL1	16-HKI1105	17-DHOLI55	18-95IOWA
19-96ROHYO	20-SUWAN	21-CM600	22-HKI335	23-HKI1532	24-CML425

parents for hybridization, which are divergent enough for the character of interest, estimation of the genetic distance is most important. The clustering pattern could be utilized for identifying the best cross combination for generating variability with respect to various traits. Selection of superior genotypes on the basis of inter cluster distance, cluster means and per se performance would be effective to employ in hybridization programme as better recombinants may be obtained in the segregating generations and as the most of the characters are showing the adequate gene action. Genetic divergence is related to the degree of distance between populations in the set of genetic characters that differ between the populations. Distantly related parents within the same species when utilized in a crossing programme are likely to produce a wide spectrum of variability.

In the present investigation, such type of studies would be helpful in identifying the hybrids clearly distinct from each other that can be further grown under varying environmental conditions for identifying hybrids for a specific environment.

Cluster analysis provides grouping of genotypes on the basis of their genetic diversity that clears the interrelationship between the genotypes. The dendrogram construction of 24 genotypes using Tocher's method is shown in Fig 1. The genotypes belonging to the clusters separated by high statistical distance could be used in the hybridization programme for a broad spectrum of variation among the segregants. These findings are in conformity with the findings of Singh *et al.* (2007), Ganesan *et al.* (2010), Azad *et al.* (2012), Chakraborty and Sah (2012), Kumar *et al.* (2016), Chauhan *et al.* (2017), Kumari *et al.* (2018) and Adu *et al.* (2019). Wide genetic variability existed among the inbred lines making them unique with the potential to contribute new beneficial alleles to maize breeding programmes.

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