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Assessment of genetic diversity of sweet corn (*Zea mays* conva. *Saccharata* var. rugosa) genotypes using D^2 statistics

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Abstract
The existence of a mutant form of one or more minor alleles in the endosperm that contributes in starch synthesis distinguished modern sweet corn from other maize. Current study was performed to identify diverse genotypes for developing good hybrid and exploit heterosis. This study also aimed to identify diverse material for prebreeding as an objective of maize improvement. In this experiment Mahalanobis D^2 multivariate technique was used to calculate diversity. Highest distance of 1546.34 was observed between 1820197/T1 and 1820196/T2 while lowest distance of 28.66 was observed between 1820193/T2 and 1820195/20 genotypes. Similarly, Cluster V had greater intra cluster distance indicated the highest diversity. Cluster II and Cluster VII had highest distance provide the genotypes for pre breeding and help to improve sweet corn.

Keywords: Horse, hindgut fermenter, race horse, pasture feeding, water, nutrition

Introduction
Sweet corn (*Zea mays* L. *saccharata*) is popular vegetable in some of the countries like USA and Canada and gaining popularity in India and Asian countries. This type of corn has sweet kernels because of naturally occurring recessive mutations in the genes controlling the conversion of endospermic sugar into starch. Corn having sugar content greater than 25 % in the milking stage is called as sweet corn. Sweet corn is a spontaneous mutation in maize that was formerly grown by various Native American tribes. In 1779, the Iroquois handed European settlers the first known sweet corn, called Papoon, which quickly became a favourite dish in the southern and central regions of the United States. Sweet corn, also known as sugar corn and pole corn, is harvested at the milking stage and eaten as a vegetable rather than a grain, as opposed to other corn varieties, which are harvested at the dent stage, or when mature. Processing of corn is utilised to extend its shelf life, however as a consequence, considerable nutritional loss may occur due to heat degradation or leaching (Scott and Eldridge, 2005) [2]. From pollination till harvest, the cob of sweet corn experiences numerous physical and chemical alterations that affect the flavour and quality of the kernels (Cherr *et al*., 2007) [3]. Sugar changes have a significant impact on flavour. Studying the variations present among the various genotypes of sweet corn can provide important information to the breeders which helps in crop improvement programmes for sweet corn.
Study of genetic diversity in germplasm can aid in the classification and identification of distinct heterotic groups with potential breeding values in a specific breeding programme. Progenies resulting from varied crosses, selected based on genetic divergence analyses are intended to show a broad range of genetic variability in a breeding programme. It also provides a greater opportunity for identifying transgressive segregants in advanced generations. D^2 statistics by Mahalanobis (1936) [4] is a strong technique for assessing the degree of genetic diversity between genotypes and relate clustering patterns to geographical origin. The genetic distance played a significant influence in the efficient selection of parents for the hybridization programme (Saha *et al*., 2018) [5]. As a result, the current experiment was designed to investigate the genetic divergence and clustering pattern of sweet corn genotypes in order to identify acceptable parents for use in a hybridization programme and to investigate the genetic characteristics associated with yield.

Material & Methods

The experimental material for present investigation was comprised of 45 genotypes of sweet corn (*Zea mays* L. *saccharata*) procured from ICAR-Indian Institute of Maize Research (IIMR), Ludhiana (Table 1). The crop was raised through dibbling of maize seed. The experiment was conducted at Experimental Farm, Department of Genetics and Plant Breeding, B. A. College of Agriculture, AAU, Anand during *Rabi*, 2020-21. The crop was raised through dibbling of maize seeds with spacing of 60 × 30 cm and surrounded by guard row to avoid damage and border effect. The recommended agronomical and plant protection practices were followed for the successful raising of the crop. The various characters such as days to 50 per cent tasseling, days to 50 per cent silking, plant height, ear height, ears per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per row, number of kernels per ear, protein content, total soluble sugar, β-carotene, lysine, and tryptophan were recorded.

Table 1: List of sweet corn genotypes and their sources

Sr. No.	Genotypes	Source	26	1820166/T2	IIMR, Ludhiana
1	I-07-62-42-2	AAU, Godhra	27	1820162/T2	IIMR, Ludhiana
2	1820161/20-5	IIMR, Ludhiana	28	1820162/T1	IIMR, Ludhiana
3	1820164/20	IIMR, Ludhiana	29	1820212/T2	IIMR, Ludhiana
4	1820168/T1	IIMR, Ludhiana	30	1820214/C1-20	IIMR, Ludhiana
5	1820213/9-20	IIMR, Ludhiana	31	1820228/T1	IIMR, Ludhiana
6	1820215/C1-20	IIMR, Ludhiana	32	1820229/T1	IIMR, Ludhiana
7	1820228/T2	IIMR, Ludhiana	33	1820230/T1	IIMR, Ludhiana
8	11820211/T2	IIMR, Ludhiana	34	1820230/T2	IIMR, Ludhiana
9	1820211/T1	IIMR, Ludhiana	35	1820231/T1	IIMR, Ludhiana
10	1820200/C1-20	IIMR, Ludhiana	36	1820199/20-5	IIMR, Ludhiana
11	1820198/C1-20	IIMR, Ludhiana	37	1820194/T2	IIMR, Ludhiana
12	1820197/T2	IIMR, Ludhiana	38	1820196/T2	IIMR, Ludhiana
13	1820197/T1	IIMR, Ludhiana	39	1820193/T2	IIMR, Ludhiana
14	1820167/C4-20	IIMR, Ludhiana	40	1820195/20	IIMR, Ludhiana
15	1820194/T1	IIMR, Ludhiana	41	1820166/T1	IIMR, Ludhiana
16	1820192/4-20	IIMR, Ludhiana	42	1820231/T3	IIMR, Ludhiana
17	1820229/T2	IIMR, Ludhiana	43	1820196/T1	IIMR, Ludhiana
18	I-07-33-04	AAU, Godhra	44	1820212/T1	IIMR, Ludhiana
19	I-07-34-3-1	AAU, Godhra	45	I-07-62-3-2	AAU, Godhra
20	I-07-36-1-4	AAU, Godhra			
21	I-07-36-2	AAU, Godhra			
22	I-07-37-6-1	AAU, Godhra			
23	I-07-40-4-2	AAU, Godhra			
24	I-07-62-22-5	AAU, Godhra			
25	1820162/T3	IIMR, Ludhiana			

Genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936) [4]. Grouping of the genotypes in different clusters was done by following Tocher's method (Rao, 1952) [6]. The per cent contribution of characters towards genetic divergence was calculated as per Singh and Choudhary (1985) [11].

Result and Discussion

While trying to improve a complicated trait like yield, understanding the level of variability and genetic variation present in the population is critical. As a result, when enhancing seed yield, selecting parents with large genetic divergence for a number of traits as measured by Mahalanobis' D^2-statistics (1936) [4] is important. The D^2 values between all 990 pairs ranged from 28.66 (between 1820193/T2 and 1820195/20) to 1546.34 (between 1820197/T1 and 1820196/T2), which indicated the presence of high genetic diversity among the genotypes for all the traits (these D^2 values were taken from matrix table, which is not provided here).

The clustering pattern might be used in a hybridization algorithm to determine which cross combinations will produce the most variability for specific traits. Superior genotypes for breeding programmes could be chosen based on cluster mean and inter-cluster distance.

Composition of Clusters

The genotypes were grouped using Tocher's approach (Rao, 1952), with the assumption that genotypes within a cluster have lower D^2-values among themselves than genotypes from different clusters. Overall, 8 clusters were formed from 45 genotypes. The composition of clusters is given in Table 2. Cluster I was the largest cluster with 30 genotypes most of them were from IIMR, Ludhiana. Cluster II was the second largest cluster with five genotypes and all of them except I-07-40-4-2 were from IIMR, Ludhiana. The cluster III had the genotypes sourced from IIMR, Ludhiana with three genotypes, while clusters IV and V both had two-two genotypes. Among them, cluster IV had both the genotypes of IIMR, Ludhiana and cluster V had the genotypes from both sources. Clusters VI, VII and VIII were solitary clusters with a single genotype in each. The mono-genotypic cluster indicated that genotypes belonging to these clusters had wide diversity from the rest as well as from each other. Thus, these genotypes have entirely different genetic makeup from the others.

In a similar study, 50 inbreds of sweet corn were grouped into ten clusters by Gopi *et al*. (2018) [8]. Singh *et al*. (2018) [5] also grouped 54 maize genotypes into four different clusters based on genetic divergence. Islam *et al*. (2020) [10] also conducted the experiment and classified 30 maize genotypes into seven

different clusters after mahalanobis's D2 analysis. Thirteen diverse genotypes of maize were grouped into three different clusters by Suman *et al.* (2020) [9]. Peer *et al.* (2022) [1] carried out similar type of genetic divergence study in 70 genotypes of maize and grouped them into 14 clusters using Tocher's method.

The clustering pattern indicated that there was no formal relationship between the source of genotypes and genetic diversity. This could be because there may be some other forces such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation responsible for genetic diversity.

Table 2: Grouping of 45 genotypes of sweet corn in various clusters on the basis of D^2 statistics

Name of cluster	Number of genotypes	Name of genotypes	Source
Cluster I	30	1820193/T2, 1820195/20, 1820197/T2, 1820231/T3, 1820215/C1-20, 1820196/T1, 1820211/T1, 1820162/T2, 1820166/T1, 1820199/20-5, 1820192/4-20, 1820200/C1-20, 1820212/T1, 1820214/C1-20, 1820230/T1, 1820166/T2, 1820194/T2, 11820211/T2, 1820229/T1, 1820212/T2, 1820164/20, 1820230/T2, 1820162/T1	IIMR, Ludhiana
		I-07-34-3-1, I-07-33-04, I-07-62-3-2, I-07-62-42-2, I-07-36-2, I-07-62-22-5, I-07-36-1-4	AAU, Godhra
Cluster II	5	1820228/T1, 1820194/T1, 1820167/C4-20, 1820162/T3	IIMR, Ludhiana
		I-07-40-4-2	AAU, Godhra
Cluster III	3	1820229/T2, 1820231/T1, 1820213/9-20	IIMR, Ludhiana
Cluster IV	2	1820168/T1, 1820228/T2	IIMR, Ludhiana
Cluster V	2	1820161/20-5	IIMR, Ludhiana
		I-07-37-6-1	AAU, Godhra
Cluster VI	1	1820198/C1-20	IIMR, Ludhiana
Cluster VII	1	1820197/T1	IIMR, Ludhiana
Cluster VIII	1	1820196/T2	IIMR, Ludhiana

Inter and intra-cluster distances

The inter-cluster and intra-cluster distances are shown in Table 3. The maximum inter-cluster distance (D = 1546.34) was found between cluster VII and VIII, followed by that between II and VII (D = 1375.05) and V and VII (1221.44). The minimum inter-cluster distance was observed between cluster II and VIII (D = 271.05). The intra-cluster distance (D) ranged from 140.22 (cluster-II) to 210.15 (cluster-V). The three clusters *viz.*, VI, VII and VIII contained a single genotype and therefore, their intra-cluster distance was zero. In general, intra-cluster distances were lower than inter-cluster distances. Thus, the genotypes included within a cluster tended to be diverge less from each other. The various genotypes belonging to the clusters separated by high genetic distance could be used in the hybridization programme for obtaining a wide spectrum of variation among the segregants. The clustering pattern could be used in the selection of parents for crossing and determining the optimum cross combinations that produce the highest possible variability for certain attributes

Table 3: Average intra-cluster and inter-cluster distance for 45 genotypes of sweet corn

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	208.97							
Cluster II	384.67	140.22						
Cluster III	333.91	834.93	158.97					
Cluster IV	320.15	389.14	447.59	205.92				
Cluster V	295.53	405.41	372.92	316.86	210.15			
Cluster VI	382.66	553.70	574.17	316.44	521.65	0		
Cluster VII	879.91	1375.05	959.41	1082.15	1221.44	362.89	0	
Cluster VIII	390.19	271.05	700.68	461.15	437.72	808.46	1546.34	0

Conclusion

According to D2 analysis cluster V had highest intra cluster distance indicated that genotypes of this clusters were enough diverse for creating good amount of variability by hybridization as well as this cluster contribute genotypes for developing good hybrids and biparental mapping population. Similarly, Cluster II and VII had highest distance include highly diverse genotypes and they are distantly related with each other help to exploit heterosis.

Conflicts of interest

There is no conflict of interest.

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