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## Genetic Divergence In Baby Corn (*Zea Mays L.*)

**S. Madhusudhan Reddy**

Department Of Genetics And Plant Breeding

Acharya N. G. Ranga Agricultural University, College Of Agriculture, Rajendra Nagar, Hyderabad, India

**S. Sudheer Kumar**

Department Of Genetics And Plant Breeding

Acharya N. G. Ranga Agricultural University, College Of Agriculture, Rajendra Nagar, Hyderabad, India

**M. R. Sudharshan**

Maize Research Center, Ari, Rajendra Nagar, Hyderabad, India

**K. Vijay Kumar**

Department Of Genetics And Plant Breeding

Acharya N. G. Ranga Agricultural University, College Of Agriculture, Rajendra Nagar, Hyderabad, India

### **Abstract:**

A field experiment was conducted with 80 genotypes in three replications in randomized block design at College Farm, College of Agriculture, ANGRAU, Rajendranagar during Kharif 2011-2012. The data on baby corn yield and other traits were results indicated that the varieties were distributed in eight clusters of which cluster VI had maximum intra- cluster distance (3.09) followed by cluster III (3.01) cluster I (2.99) and cluster V (2.85) and remaining clusters are having minimum cluster distances with the zero. The inter- cluster distance ranged from 2.32 (clusters V and IV) to 9.32 (clusters VII and VI). Among the clusters variations were planted height, ear height, baby corn length, cob weight, number of cobs per plant, cob yield per plant, cob yield and green fodder yield. The contribution of each character towards total genetic diversity. In 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.

**Key words:** Baby corn, clusters, genetic diversity, inter cluster distances

### **1.Introduction**

For diversification and value addition of maize as well as the growth of food industries, maize researches made a significant head way through breeding and identifying suitable cultivars, specially corns viz., baby corn, popcorn, sweet corn, QPM etc. assumes tremendous market potential not only in India but also in the international market. Spatiality corns in particular baby corn and sweet corn with their high market value, is perfectly suitable either as sole crop or intercrop with other remunerative crops like cutflowers and spices. Thus they promise higher income to maize growers. Baby corn is delicious, decorative and nutritious vegetable rich in fiber and low calorific vegetable. Keeping in view the increasing importance of baby corn in India and looking to present and expected future needs for its improvement, the present investigation was carried out.

### **2.Material And Methods**

The experimental material comprising 80 genotypes was evaluated in randomized block design with three replications. Each Replication of 4 m length with inter – and intra row spacing 60 and 20 cm, respectively. The data on the days to tasseling, days to sailing, plant height, ear height, baby corn length, baby corn girth, baby corn weight, number of cobs per plant, cob yield per plant, cob yield, green fodder yield, TSS and moisture percentage were recorded. These data were subjected to divergence analysis (Mahalaonobis, 1936). Inter –cluster and intra cluster variances were estimated. Contributed to total divergence were evaluated.

### **3.Results**

The data were subjected to RBD analysis. The results given in Table 1 indicate that the treatment differences were found significant for eleven characters out of thirteen characters. Non significant found in a number of cobs per plant and moisture percentage. Similar results were reported by Vaghela (2008). This indicated sufficient variability existing in the genotypes of baby corn. The data were further subjected to D<sup>2</sup> analysis (Mahalanobis, 1936).

This indicates that grouping of baby corn genotypes in different clusters Table-2.

The inter – and intra – cluster distances were worked out and presented in Table 3. These results indicated that genotypes of VI had highest intra- cluster distance (3.09) followed by cluster III (3.01) cluster I (2.99) and cluster V (2.85) and remaining clusters are having minimum cluster distances with the zero. The inter- cluster distance ranged from 2.32 (clusters V and IV) to 9.32 (clusters VII and VI).

Statistical analysis using completely randomized design considering eight clusters as treatments and genotypes of clusters as observations were carried out. The mean values for different clusters are given in Table 4. The results indicated that on average genotypes of clusters VIII, VI, III and I had a higher baby corn yield per ha. The green fodder yield per ha was highest in VII cluster followed by VI and III cluster. The plant height was highest in VI followed by III, and VIII cluster. The ear height was highest in VI followed by III and VIII cluster, while the baby corn length was highest in VIII followed by VI and III. Genotypes of these clusters can be utilized for further breeding programme (Datta and Mukherjee, 2004).

Based on the  $R^2$  and F values, it was observed that the contribution of each character towards total genetic diversity in Table -5. In 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 the baby corn yield.

#### 4. Discussion

Genetic diversity present in the available genotypes has immense value of crop improvement in character of interest. From the point of selecting the parents for hybridization, which are divergent enough for the character of interest, estimation of the genetic distance is most important. The analysis variance revealed highly significant differences among the genotypes for eleven characters. Indicating the existence of genetic variability among the experimental material. Cluster I was the largest having 38 genotypes followed by Cluster III having 26 genotypes. The genotypes within the same cluster originated from the different geographical regions of the world.

These results indicated that genotypes of VI had highest intra- cluster distance (3.09) followed by cluster III (3.01) cluster I (2.99) and cluster V (2.85) and remaining clusters are having minimum cluster distances with the zero. The inter- cluster distance ranged from 2.32 (clusters V and IV) to 9.32 (clusters VII and VI) 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 sergeants. These findings are in conformity with the findings of Hemavathy *et al.* (2006), Singh *et al* (2007), Ganesan *et al.* (2010) and Azad *et al.* (2012).

Character	Mean Sum of Squares		
	Replications (d.f =2)	Treatments (d.f =79)	Error (d.f =158)
Days to 50% tasseling	2 2.06	8.23 **	1.83
Days to 50% silking	5.63 *	10.12 **	1.79
Plant height (cm)	1060.23**	1710.75 **	56.06
Ear height (cm)	245.71 **	853.50**	25.59
Baby corn length (cm)	0.27	1.71 **	0.10
Baby corn girth (cm)	0.01	0.03 **	0.02
Cob weight (g)	0.36	1.06 **	0.36
Number of cobs per plant	0.01	0.13	0.11
Cob yield per plant (g)	9.95	12.92**	5.50
Cob yield (kg/ha)	9608.83	36840.260 **	7138.16
Green fodder yield (q/ha)	477.08	9858.45 **	739.87
TSS	0.40	0.49 **	0.29
Moisture percentage (%)	4.39	5.84	6.89

Table 1: Analysis Of Variance For Cob Yield And Other Traits In Baby Corn

\* Significant At 5% Level; \*\* Significant At 1% Level

Cluster	Number of genotypes	Genotypes
Cluster I	38	5319, QPM-38, QPM-116, 5168, 5202, CM-118, CM-202, 5018, 5204-1-8, QPM-49, 5348, 5333, 92-60, CML-163, 5122-3, QPM-63-1, 5204-9, 5163, 5287, 5289, 5284, 5300, 5321, CM-201, QPM-62, 5204-5-2-1, 5317, 5223, 5207-2, 5228, 5341, 5216, CM-132, CM-133, 5263-1, 5277, 3001, 3003
Cluster II	1	92-5
Cluster III	26	5232, 5204-9, 5217, QPM-33, 5248, QPM-69-2, 5265-2, 5319, CM-104, 5175-1, 5017, 5160, CM-119, 5016, 5219, 5161, 5063-1, 5212, 5164, 5121, 5347-2, 400-6-2, 5287, CM-115, 5204-3, OPM-57-1
Cluster IV	1	5367
Cluster V	7	5200, 5095-2, 5072, 5021, PC-101, 5222, PC-14-2
Cluster VI	5	5134, 5118-3, 5150, 5157, 5119
Cluster VII	1	5111
Cluster VIII	1	5342

Table 2: Grouping Of Eighty Genotypes Into Different Clusters  
 \*Values In Bold Are Accession Numbers Of Selected Parents

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	2.99	3.46	4.47	3.45	3.99	7.86	3.56	5.36
Cluster II		0.00	5.82	2.50	2.75	9.00	3.54	7.47
Cluster III			3.01	6.10	6.34	5.78	4.40	4.63
Cluster IV				0.00	2.32	9.31	4.27	6.84
Cluster V					2.85	9.32	4.34	7.54
Cluster VI						3.09	8.43	7.89
Cluster VII							0.00	6.05
Cluster VIII								0.00

Table 3: Average Intra And Inter Cluster Distances  
 Note: Bold Values Are Intra Cluster Distances

Cluster	Days to 50% tasseling	Days to 50% Silking	Plant Height (cm)	Ear height (cm)	Baby corn length (cm)	Baby corn girth	Cob weight (g)	Number of cobs per plant	Cob yield per plant (g)	Cob yield (Kg/ha)	Green fodder yield (q/ha)	TSS	Moist ure percentage (%)
Cluster I	50.03	52.48	128.97	52.69	7.26	1.31	7.63	1.82	13.77	449.82	247.76	8.21	83.38
Cluster II	51.00	53.11	114.67	45.57	6.32	1.36	6.60	1.88	11.18	344.67	233.17	7.03	82.67
Cluster III	50.42	52.96	163.53	69.66	7.83	1.31	7.83	1.89	14.85	570.04	334.59	8.00	83.12
Cluster IV	52.00	54.22	109.67	45.00	6.48	1.12	7.57	1.82	12.31	330.00	185.00	8.57	83.00
Cluster V	51.43	54.33	109.56	46.79	6.15	1.20	6.83	1.72	11.08	372.82	203.99	8.29	84.59
Cluster VI	49.80	52.09	185.27	111.75	8.17	1.36	8.29	1.83	15.07	574.60	353.07	8.05	82.73
Cluster VII	50.67	53.11	133.17	44.78	6.52	1.29	6.70	1.47	9.89	461.67	341.67	8.14	81.00
Cluster VIII	52.00	54.67	150.33	57.00	9.48	1.23	8.46	1.93	16.29	588.33	298.67	9.33	83.00

Table 4. Mean Performance Of Different Clusters For Different Quantitative Characters In Baby Corn

S.No.	Source	Times Ranked First	Contribution percentage
1	Days to 50% tasseling	213	6.74 %
2	Days to 50% silking	58	1.84 %
3	Plant height ( cm)	1337	42.31 %
4	Ear height ( cm)	532	16.84 %
5	Baby corn length (cm)	544	17.22 %
6	Baby corn girth	45	1.42 %
7	Cob weight (g)	48	1.52 %
8	Number of cobs per plant	8	0.25 %
9	Cob yield per plant (g)	11	0.35 %
10	Cob yield (Kg/ha)	252	7.97 %
11	Green fodder yield (q/ha)	153	4.84 %
12	TSS	47	1.49 %
13	Moisture percentage (%)	19	0.60 %

Table 5. Contribution Of Different Characters Towards Genetic Divergence ( $D^2$ ) In 80 Genotypes Of Baby Corn

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