RESEARCH ARTICLE

GENETIC DIVERGENCE STUDIES IN ASH GOURD [*BENINCASA HISPIDA* (THUNB.) COGN.]

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Abstract: An experiment was carried out to analyze genetic diversity for yield and its contributing traits in 60 ash gourd genotypes at Research cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), India, during *Kharif* 2015-16. The cluster analysis grouped all 60 ash gourd genotypes into 5 major clusters based on D^2 value. Extreme genetic divergence was estimated among clusters. Maximum number of genotypes were grouped into cluster I included nineteen genotypes, whereas, cluster IV included seventeen genotypes. The cluster V had seventeen genotypes, cluster II included five genotypes and which is followed by cluster III had only two genotypes in each cluster. Average inter cluster distance was found maximum (10.742) between cluster III and cluster II which would be fruitful for developing heterotic cross combination. Cluster III showed highest mean value for number of branches per plant, fruit length, fruit girth, average fruit weight, number of seeds per fruit, number of fruits per plant, total soluble solid, 100 seed weight and fruit yield per plot (kg). The characters like number of seeds per fruit, duration of crop, 100 seed weight contributed maximum to divergence. Hence, ash gourd crop improvement could be tried with the genotypes of divergent clusters for better heterotic effects.

Keywords: Ash gourd, Cluster, divergence, Genotypes, Yield

INTRODUCTION

The Cucurbitaceae is one of the most genetically diverse groups of plants in the plant kingdom. It consists of about 118 genera and 825 species. (Robinson and Decker- walters, 1996).

Ash gourd [*Benincasa hispida* (Thunb.) Cogn.] popularly known as Wax gourd, or White pumpkin is important cucurbitaceous vegetable grown thought India in rainy season. It belongs to the family cucurbitaceae having chromosome number 2n=24. It is indigenous to Asian subtropics, De Candolle (1982) found its wild species in the sea shore of Java and it has been spreaded northwards to Japan and also to Central America and West Indies (Seshadri, 1986).

Among the cucurbits, ash gourd is considered a prized vegetable because of its high nutritional value, long storage life and good transport qualities, besides its medicinal properties. The mature fleshy fruit is either eaten raw or cooked as vegetable marrow or ‘candied’ as sweetmeat popularly known as ‘petha’. It is a good source of carbohydrate, vitamin A, vitamin C and minerals like iron and zinc (Randhawa *et al.*, 1983 and Sureja *et al.*, 2006). An enzyme extracted from ash gourd juice can be used in place of calf rennet for producing cheddar cheese (Gupta and Eskin, 1977). Ash gourd juice has potential to improve the weak nervous system (Arora, 2003).

In India, widest genetic variability is present for its fruit shape, size, days to flowering, wax deposition and other vegetative characters. Chhattisgarh state has good genetic diversity for various characters, especially for fruit characters, days to flowering and days to maturity and no exploration has been taken to trap the diversity. It may be mentioned that until to-date there is lack of released variety of ash gourd with high yield potential and better quality. Further, very limited attempt had been made for genetic improvement of this crop because of its high cross-pollination; hardly any genetically pure strain is available to the growers. Lacks of high yielding, disease and pest tolerant varieties are the main constraints towards its production.

A wide range of genetic diversity among parents is essential feature for any hybridization programme. Hence, plant breeders are interested to estimate the extent of genetic diversity among different genotypes which will help them to achieve the set goal through appropriate breeding strategy. Mahalanobis D^2 analysis provides a means for assessment of genetic diversity among crop plants (Mahalanobis, 1936) and an attempt was made in the present investigation in ash gourd.

MATERIAL AND METHOD

The study was carried out during *Kharif* season (2015-16) at Research cum Instructional farm, IGKV, Raipur (C.G.), India. The experiment comprised of sixty genotypes of ash gourd collected from different region of southern Chhattisgarh. The experiment was laid out in a randomized block design with three replications at 3.0 × 0.75 m row to row and plant to plant spacing. All the recommended cultural practices were adopted to raise a healthy crop. Data were recorded on five randomly selected plants with respect to characters *viz.*, days to 50% flowering, number of branches per plant, node number of first female flower appears, days to first

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female flower appears, node number of first male flower appears, days to first male flower appears, days to fruit set, days to first fruit harvest, fruit length (cm), fruit girth (cm), average fruit weight (g), number of seeds per fruit, number of fruits per plant, total soluble solid (%), 100 seed weight (g), fruit yield per plot (kg), and duration of crop (sowing to last harvest). The data obtained on above 17 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952). The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude.

RESULT AND DISCUSSION

The analysis of variance revealed significant differences among ash gourd genotypes for all characters suggesting considerable genetic variability in the population. Using the estimated D^2 values as squares of generalized distance, all genotypes were grouped into 5 clusters **(**table. 1). Maximum number of genotypes were grouped into cluster I (IAG-1, IAG-2, IAG-4, IAG-17, IAG-20, IAG-21, IAG-23, IAG-29, IAG-30, IAG-31, IAG-42, IAG-43, IAG-48, IAG-50, IAG-51, IAG-52, IAG-53, IAG-57, IAG-58) included nineteen genotypes, whereas, cluster IV (IAG-3, IAG-5, IAG-8, IAG-12, IAG-14, IAG-18, IAG-19, IAG-22, IAG-24, IAG-25, IAG-27, IAG-28, IAG-33, IAG-36, IAG-38, IAG-39, IAG-44) and cluster V (IAG-6, IAG-7, IAG-11, IAG-13, IAG-16, IAG-32, IAG-34, IAG-35, IAG-37, IAG-40, IAG-41, IAG-45, IAG-46, IAG-47, IAG-54, IAG-55, IAG-56) included seventeen genotypes and cluster II (IAG-9, IAG-15, IAG-26 IAG-49, IAG-59) has five genotypes and cluster III (IAG-10, IAG-60) had two genotypes. The pattern of clustering indicated that there was no association between geographic distribution of genotypes and genetic divergence as the same group consisted of genotypes from diverse locations and the genotypes of same source fell into different groups also.

The average inter and intra cluster distances among the five clusters are presented in Table 2. that maximum inter cluster distance was observed between cluster III and cluster II (10.742) followed by cluster III and IV (10.153), cluster III and V (9.274), cluster III and I (8.690), cluster II and V (6.415), cluster I and II (4.943), cluster IV and V (3.834), cluster II and IV (3.690). The minimum inter-cluster distance were recorded in case of cluster I to cluster IV (2.991) followed by cluster I and V (2.523). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those cluster, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The maximum intra cluster distance was observed in cluster II cluster (3.236) followed by cluster V (3.189) indicating maximum diversity within these clusters. Genotypes from distant clusters could be exploited in hybrid development programmes due to their wide genetic distance. These results are in general agreement with the findings of Islam (2004), Singh *et al.* (2007) and Bhardwaj *et al.* (2013).

Table 1. Composition of clusters in ash gourd genotypes.

Cluster	**Number of genotypes**	**Name of genotypes**
I	19	IAG-1, IAG-2, IAG-4, IAG-17, IAG-20, IAG-21, IAG-23, IAG- 29, IAG-30, IAG-31, IAG-42, IAG-43, IAG-48, IAG-50, IAG-51, IAG-52, IAG-53, IAG-57, IAG-58
II	5	IAG-9, IAG-15, IAG-26 IAG-49, IAG-59
III	2	IAG-10, IAG-60
IV	17	IAG-3, IAG-5, IAG-8,IAG-12, IAG-14, IAG-18, IAG-19, IAG-22, IAG-24, IAG-25, IAG-27, IAG-28, IAG-33, IAG-36, IAG-38, IAG-39, IAG-44
V	17	IAG-6, IAG-7, IAG-11, IAG-13, IAG-16, IAG-32, IAG-34, IAG-35, IAG-37, IAG-40, IAG-41, IAG-45, IAG-46, IAG-47, IAG-54, IAG-55, IAG-56

Table 2. Intra (bold) and Inter cluster distance values in ash gourd genotypes.

Cluster Number	**I**	**II**	**III**	**IV**	**V**
I	**3.045**				
II	4.943	**3.236**			
III	8.690	10.742	**2.723**		
IV	2.991	3.690	10.153	**2.901**	
V	2.523	6.415	9.274	3.834	**3.189**

Table 3. Contribution of each character to divergence in ash gourd genotypes.

Characters	**Days to 50% Flowering**	**No. of branches per plant**	**Node number of first female flower**	**Days to first female flower appear**	**Node no. at which 1st male flower**	**Days to first male flower appears**	**Days to fruit set**	**Days to 1st fruit harvest**	**Fruit length (cm)**	**Fruit girth (cm)**	**Average fruit weight (kg)**	**No. of seeds per fruit**	**No of fruits per plant**	**T.S.S (%)**	**100 seed weight (g)**	**Fruit yield /plot (kg)**	**Duration of crop (sowing to last harvest)**	**Total**
Number times appearing first time	0	0	11	51	0	7	10	0	4	85	89	1005	76	0	112	9	311	1770
Percent contribution	0	0	0.62	2.88	0	0.39	0.56	0	0.22	4.80	5.02	56.77	4.29	0	6.32	0.50	17.57	100

Table 4. Mean performance of genotypes in individual cluster for yield and its components in ash gourd genotypes.

Character Cluster		**Days to 50% Flowering**	**No. of branches per plant**	**Node number of first female flower**	**Days to first female flower appears**	**Node no. at which 1st male flower**	**Days to first male flower appears**	**Days to fruit set**	**Days to 1st fruit harvest**	**Fruit length (cm)**	**Fruit girth (cm)**	**Average fruit weight (kg)**	**No.of seeds per fruit**	**No of fruits per plant**	**T.S.S (%)**	**100 seed weight (g)**	**Fruit yield /plot (kg)**	**Duration of crop(sowing to last harvest)**
I	19	91.72	10.54	39.11	75.32	32.10	66.67	80.86	130.01	21.77	52.56	2.92	368.05	8.94	2.31	4.41	23.24	136.25
II	5	106.60	10.00	35.95	77.20	32.84	71.40	94.26	134.69	21.18	52.97	2.72	343.00	8.04	2.24	3.80	18.33	142.97
III	2	87.00	12.27	35.13	70.17	30.34	68.17	77.64	129.98	24.49	59.48	3.29	658.85	13.18	2.53	6.50	41.67	144.23
IV	17	99.22	10.82	38.98	79.82	33.44	65.08	88.28	132.45	21.18	51.60	2.41	330.65	8.37	2.40	4.01	20.81	138.04
V	17	87.12	10.82	40.80	70.00	33.92	64.12	76.37	128.22	22.29	52.08	2.57	419.52	8.74	2.39	4.05	21.84	135.59

Table 5. Desirable genotypes based on cluster mean performance.

No. S.	**Cluster Characters**	**I**	**II**	**III**	**IV**	**V**
1	Days to 50% Flowering	IAG-30	IAG-59	IAG-60	IAG-25	IAG-7
2	No. of branches per plant	IAG-2	IAG-26	IAG-10	IAG-14	IAG-54
3	Node number of first female flower appears	IAG-17	IAG-9	IAG-60	IAG-44	IAG-40
4	Days to first female flower appears	IAG-17	IAG-26	IAG-60	IAG-8	IAG-16
5	Node number of first male flower appears	IAG-17	IAG-49	IAG-60	IAG-27	IAG-16
6	Days to first male flower appears	IAG-21	IAG-15	IAG-60	IAG-12	IAG-13
7	Days to fruit set	IAG-30	IAG-59	IAG-60	IAG-12	IAG-32
8	Days to first fruit harvest	IAG-21&30	IAG-49	IAG-60	IAG-12	IAG-32
9	Fruit length (cm)	IAG-1	IAG-15	IAG-60	IAG-12&38	IAG-11
10	Fruit girth (cm)	IAG-51	IAG-59	IAG-60	IAG-14	IAG-55
11	Average fruit weight (kg)	IAG-50	IAG-9	IAG-10	IAG-36	IAG-34
12	No.of seeds per fruit	IAG-48	IAG-15	IAG-10	IAG-5	IAG-32
13	No. of fruits per plant	IAG-1	IAG-59	IAG-10	IAG-5	IAG-11
14	T.S.S (%)	IAG-52	IAG-26	IAG-10	IAG-39	IAG-7
15	100 seed weight(g)	IAG-48	IAG-59	IAG-10	IAG-36	IAG-46
16	Fruit yield / plot (kg)	IAG-1	IAG-59	IAG-10	IAG-38	IAG-41
17	Duration of crop (sowing to last harvest)	IAG-30	IAG-15	IAG-10	IAG-25	IAG-55

The contribution of each character to divergence is presented in table 3. The result showed that number of seeds per fruit contributes highest (56.77%) to divergence followed by duration of crop (17.57%), 100 seed weight (6.32%), average fruit weight (5.02), fruit girth (4.80), number of fruits per plant (4.29%), days to first female flower appears (2.88%) Whereas, node number of first female flower (0.62%), day to fruit set (0.56%), fruit yield/plot (0.50%), days to first male flower appears date (0.39%), and fruit length (0.22) contribute lowest to divergence. This contribution is an important consideration for the purpose of further selection and choice of parents for hybridization. The results of the present study was close agreement with findings of Islam (2004) who reported that primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most of the total genetic divergence and Mladenovic *et al.* (2012).

The mean performance for different clusters of genotypes for yield and its components are presented in Table 4. Cluster III showed highest mean value for number of branches per plant, fruit length, fruit girth, average fruit weight, number of seeds per fruit, number of fruits per plant total soluble solid, 100 seed weight, and fruit yield per plot and it also showed lowest mean performance for days to 50% flowering, node number of first female flower appears and node number of first male flower appears. Cluster IV showed lowest mean performance for days to first male flower appears. Cluster V expressed lowest mean value for days to first female flower appears, days to fruit set, days to first fruit harvest and duration of crop. The better genotypes can be selected for most of characters on the basis of mean performance in the cluster.

The best genotypes which had chosen for different characters are presented in Table-5. In this study, group constellation showed that cluster V (IAG-10, IAG-60) included genotypes with most of the superior traits hence these genotypes could be directly selected and utilized on the basis of the observations recorded on a diverse group of ash gourd genotypes, it may be concluded that hybridization between genotypes of diverse clusters may help in developing better genotype/varieties for fruit yield in ash gourd for Chhattisgarh plains.

CONCLUSION

The D^2 values recorded for sixty genotypes indicated the presence of appreciable amount of genetic diversity among the genotypes. In this study, group constellation showed that genotype of cluster III i.e. (IAG-10, IAG- 60 were highly divergent from all other genotypes. This indicated that crossing programme with IAG-10, IAG-60, will be planned by using this desirable useful trangressive genotype for fruit yield in ash gourd for Chhattisgarh plains.

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