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Genetic diversity of ash gourd (*Benincasa hispida* (Thunb) Cogn.) genotypes

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Abstract

A study on genetic divergences was carried out on 45 diverse ash gourd genotypes. Based on D² analysis, the genotypes were grouped into four different clusters, where the cluster I possessed higher number of genotypes (37) followed by the cluster II (3), and III, IV, V, VI, VII had only one genotype. The genotypes collected from different location were grouped into different clusters. The maximum inter-cluster distance was observed between the cluster III and cluster VII. In case of intra-cluster distance, the maximum distance was observed in the cluster II. Among the twenty two traits studied, maximum contribution was made by fruit circumference followed by number of fruits per vine, fruit yield per vine, average fruit weight. Considering cluster mean, the genotypes of cluster VI and cluster VII could be selected for yield and yield attributing characters. The wider genetic diversity was observed in cluster V, VI, VII which indicate the potentiality of this diverse genotype collection for providing basic material for future breeding programmes.

Keywords: Ash gourd, cluster, divergence, genotypes and yield

Introduction

Ash gourd [*Benincasa hispida* (Thunb) Cogn.] is a cucurbitaceous vegetable crop grown under wide agroclimatic conditions both for mature and immature fruits. It is preferred among the growers and consumers because of long shelf life under ambient conditions. Ash gourd is also known by a variety of names such as winter gourd, winter melon, white gourd, Chinese preserving melon, pith gourd, wax gourd, Chinese wax gourd, tallow gourd and Chinese water melon (Tindall, 1986; Pandey *et al.*, 2015) ^[14, 7]. Indo-China region is the centre of diversity for ash gourd (Rubatzky and Yamaguchi, 1997; Pandey *et al.*, 2015) ^[12, 7]. Indo-China region being a centre of diversity is endowed with great variability in terms of morphological characters especially, growth habit and maturity including shape, size and flesh thickness of fruits (Rubatzky and Yamaguchi, 1997) ^[12].

Ash gourd is an important vegetable mainly valued for its long storage life and good scope for value addition. The fruits are consumed as baked, fried, boiled, pickled or candied/preserved (Robinson and Decker Walters, 1997) ^[11]. World famous confectionery known as Petha is prepared using ripe flesh in sugar syrup. Ash gourd is valued for its medicinal attributes especially in Ayurveda for the cure of peptic ulcer and the fruit juice is used for treating a range of ailments including insanity and epilepsy. It can also prevent kidney damage (Pandey, 2008) ^[7]. Its fruits contain a relatively high level of K and low Na and from the index of nutritional quality value, it has been adjudged as a quality vegetable (Pandey, 2008) ^[7].

In India, although a wide range of variability is available for different component characters in ash gourd (Mandal *et al.*, 2002) ^[6], but no comprehensive systematic research has been done in this crop. The yield potentiality of this crop needs to be improved through an effective systematic and breeding programme. Studies on the variations of yield and yield contributing characters are of great importance before planning a breeding program.

Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetically diverse lines for desirable traits and to reveal genetic distinctness among genotypes (Ali *et al.*, 2008). Assessment of genetic diversity in germplasm collections imposes the categorization of accessions and useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Looking to the above in the present study, we classify the genotypic set based on multivariate analysis for generating more heterotic cross combinations and finally superior useful hybrids.

Materials and Methods

The study was carried out during January 2018 to June 2018 at Vegetable Research Station, Tamil Nadu Agricultural University, Palur. The experiment comprised of forty five genotypes

of ash gourd [*Benincasa hispida* (Thunb) Cogn.] collected from different region of Tamilnadu are presented in Table 1. The experiment was laid out in a randomized block design with three replications at 2×1.5 m row to row and plant to plant spacing. Recommended agronomic practices were followed to raise a good crop. Observations were recorded from five randomly selected plants from each genotype on 22 different characters viz., vine length at harvest, number of branches, internodal length, days to first male flowering, days to first female flowering, node to first male flower, node to first female flower, number of male flowers, number of female flowers, sex ratio, days to first harvest, number of fruits per vine, average fruit weight, fruit length, fruit circumference, number of seeds per fruit, fruit yield per vine, 100 seeds weight, fruit yield per vine, total soluble solids, moisture content (%) and estimated fruit yield t/ha. The analysis of variance and covariance were done for selected characters for divergence studies. Genetic diversity was worked out following Mahalanobis (1936) genetic distance (D^2) extended by Rao (1952) [10] to clustering in Tocher's method.

Results and Discussion

Analysis of variance showed significant difference for all the twenty two characters studied among the genotypes. Based on D^2 value 45 genotypes were grouped into seven clusters (Table 2). Maximum number of genotypes (37 genotypes) was grouped in Cluster I. Cluster II consists of 3 genotypes followed by cluster III, IV, V, VI, VII had only one genotype. Cluster The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non-correspondance of geographic origin with genetic diversity were also reported by Khatun *et al.* (2010) [4]; they are agreement with Rashid (2000) in pumpkin, Banik (2003) and Rahman (2004) in snake gourd.

In crop improvement, genetic diversity has been considered as an important factor, which is an essential pre-requisite for any breeding programme as to obtaining high yielding progenies. Quantitative measurement of genetic divergence among individuals have enabled the plant breeders to understand the racial affinities and evolutionary pattern in various crop species or cultivated plants as well as, in decision making for selection of desirable parents in hybridization programme.

Intra and inter cluster distance

The intra and inter cluster distance are presented in (Table 3). Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes.

Average intra and inter cluster D^2 values among 45 genotypes was studied. The values showed (Table 3) that the cluster II had the maximum intra D^2 value (17.10) followed by cluster I (15.30). This is indicative of the fact that the genotypes included in these clusters are very diverse. The inter cluster

D^2 value was found to be maximum between cluster III and cluster VII (42.82) followed by cluster V and cluster VII (40.32) The genotypes belonging to cluster III and cluster VII and cluster V and cluster VII showed that maximum inter cluster distance are expected to obtain high heterosis in hybridization and to show wide variability in genetic make-up. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generation. These results are confirmed with the findings of Krishnamoorthy (2019) [5] in pumpkin and Deepa Devi (2013) [3] in snake gourd.

Cluster mean

The data on the mean for all the twelve characters with respect to ten clusters are summarized in the (Table 4). It is obvious that different clusters exhibited distinct mean values for almost all the twenty two characters studied. Cluster III possessed the highest mean values for number of male flower (33.95), fruit length (44.64) fruit circumference (84.09). Cluster IV exhibited the highest mean values for vine length (7.80), lowest mean value for days to first female flower (60.06), days to first harvest (128.03) fruit yield per vine (11.97) and estimated yield t/ha (33.09). Cluster V showed the highest mean values for average fruit weight (7.70), flesh thickness (5.4), number of seeds per fruit (649.45), 100 seeds weight (5.17). Cluster VI exhibited the lowest mean values for days to first male flower (56.16), node first female flower (24.98), fruit weight (1.50) and highest mean value for number of fruits per vine (6.93). Cluster XII exhibited the highest mean values for number of primary branches (7.23), number of female flower (11.29), sex ratio (2.22), lowest mean value for internodal length (6.00), node first male flower (19.77). Similar results were observed by Chaudhari (2017) [2] in pumpkin and Kalyani Pradhan (2018) in ash gourd.

Contribution of individual character towards total divergent

The contribution of each trait to total divergence is presented in (Table 5). Among the traits studied average fruit circumference contributed maximum divergence of 22.73% followed by number of fruits per vine (13.54%), fruit yield per vine (8.89%), average fruit weight (8.79%), fruit length (7.58%), intermodal length (7.27%) 100 seeds weight (7.17%), sex ratio (5.66%), flesh thickness (4.75%), vine length (3.33%), number of seeds fruit (3.03%), number of primary branches and number of male flower (2.12%), estimated yield t/ha (1.31%), total soluble solids (0.61%), number of female flower and moisture content (0.04%) and days to first harvest (0.03%). The importance of fruit yield per vine in genetic divergence of was already reported by Khatun *et al.* (2010) [4] in chow chow, B.C. Kundu (2012) [1] in bitter gourd and Sultana (2015) [13] in pumpkin.

Table 1: Geographical origin of 45 ash gourd genotypes

Accession No	Accession Name	Source
Bh1	CO.1	TNAU, Coimbatore
Bh2	AG-TCR-2 IC-596984	NBPGR, New Delhi
Bh3	Palur local	Vegetable Research Station, Palur
Bh4	Palur local	Vegetable Research Station, Palur
Bh5	Palur local	Vegetable Research Station, Palur
Bh6	Palur local	Vegetable Research Station, Palur
Bh7	Palur local	Vegetable Research Station, Palur
Bh8	Palur local	Vegetable Research Station, Palur

Bh9	Palur local	Vegetable Research Station, Palur
Bh10	Palur local	Vegetable Research Station, Palur
Bh11	Palur local	Vegetable Research Station, Palur
Bh12	Palur local	Vegetable Research Station, Palur
Bh13	Palur local	Vegetable Research Station, Palur
Bh14	Palur local	Vegetable Research Station, Palur
Bh15	Palur local	Vegetable Research Station, Palur
Bh16	Palur local	Vegetable Research Station, Palur
Bh17	Palur local	Vegetable Research Station, Palur
Bh18	Palur local	Vegetable Research Station, Palur
Bh19	Palur local	Vegetable Research Station, Palur
Bh20	Palur local	Vegetable Research Station, Palur
Bh21	Palur local	Vegetable Research Station, Palur
Bh22	Palur local	Vegetable Research Station, Palur
Bh23	Villupuram local	Vegetable Research Station, Palur
Bh24	AG-TCR-IC 596986	NBPGR, New Delhi
Bh25	Kanchipuram local	Kanchipuram district
Bh26	Vanthavasi local	Vandhavasi, Tiruvanmalai district
Bh27	AG-TCR-21 IC 613445	NBPGR, New Delhi
Bh28	AG-TCR-18 IC 613454	NBPGR, New Delhi
Bh29	Palur local	Vegetable Research Station, Palur
Bh30	Dharmapuri local	Dharmapuri
Bh31	Tiruvanmalai local	Cheyyar, Tiruvanmalai district
Bh32	Vellore local	Gudiyatham ,Vellore district
Bh33	AG-TCR-15 IC 596997	NBPGR, New Delhi
Bh34	Palur local	Vegetable Research Station,Palur
Bh35	Tindivanam local	Tindivanam, Villupram district
Bh36	Salem local	Attur, Salem district
Bh37	AG-TCR- IC 596985	NBPGR, New Delhi
Bh38	AG-TCR-13 IC 596995	NBPGR, New Delhi
Bh39	AG-TCR-23 IC 613456	NBPGR, New Delhi
Bh40	Villupuram local	Olakkur, Villupuram district
Bh41	AG-TCR-16 IC 613454	NBPGR, New Delhi
Bh42	AG-TCR-19 IC 613444	NBPGR, New Delhi
Bh43	AG-TCR-26 IC 613457	NBPGR, New Delhi
Bh44	Palur local	Vegetable Research Station,Palur
Bh45	AG-TCR-33 IC 613454	NBPGR, New Delhi

Table 2: Clustering Pattern of 45 ash gourd genotypes

Cluster number	Number of genotypes	Name of genotypes
I	37	BH25, BH27, BH-28, BH-41, BH-37, BH-22, BH-40, BH-26, BH-6, BH-11, BH-14, BH-4, BH-8, BH-12, BH-5, BH-7, BH-36, BH-45, BH-18, BH-38, BH-13, BH-33, BH-43, BH-15, BH-35, BH-42, BH-32, BH-44, BH-10, BH-9, BH-17, BH-30, BH-23, BH-20, BH-31, BH-2, BH-34
II	3	BH-19, BH-39, BH-21
III	1	BH-3
IV	1	BH-24
V	1	BH-1
VI	1	BH-16
VII	1	BH-29

Table 3: Inter and intra – cluster D² values of ash gourd genotypes for yield and its related attributes

Cluster	I	II	III	IV	V	VI	VII
I	15.3	18.79	23.62	25.86	24.38	26.05	28.11
II		17.1	30.68	24.2	31.41	24.26	23.3
III			0	30.13	27.11	37.36	42.82
IV				0	40.08	17.4	25.83
V					0	39.73	40.32
VI						0	18.32
VII							0

Table 4: Mean of 22 characters in different clusters of ash gourd genotypes

Characters	Clusters						
	I	II	III	IV	V	VI	VII
Vine length (VL)	5.16	5.32	7.64	7.8	5.27	4.61	4.01
Number of primary branches (NB)	5.65	5.09	4.13	4.9	4.8	4.93	7.23
Intermodal length (IL)	10.34	10.47	15.09	12.44	9.81	6.69	6
Days to first male flower (DFMF)	62.55	64.02	61.03	56.36	64.89	56.16	60.71
Days to first female flower (DFFF)	65.86	66.95	66.35	60.06	66.24	60.37	65.02
Node to first male flower (NFMF)	23.14	21.38	24.94	24.84	21.38	22.75	19.77
Node to first female flower (NFFF)	29.34	31.36	28.93	26.71	31.83	24.98	25.21
Number of male flower (NMF)	29.01	28.38	33.95	29.29	22.41	31.09	26.07
Number of female flower (NFF)	7.69	8.41	7.87	10.86	7.72	10.14	11.29
Sex ratio (SR)	3.78	3.35	4.67	3.43	2.88	3.77	2.22
Days to first harvest (DFH)	133.79	135.69	131.34	128.03	131.53	128.33	131.2
Number of fruits per vine (N.F.P.V)	3.24	4.1	2.8	6.7	1.73	6.93	6.49
Average fruit weight (A.F.W)	2.93	1.59	3.5	1.6	7.7	1.5	1.23
Fruit length (F.L)	34.01	30.06	44.64	25.7	40	21.4	23.09
Fruit circumference (F.C)	58.78	45.74	84.09	44.8	79.15	37.54	37.27
Flesh thickness (F.T)	3.21	3.25	2.5	2.1	5.4	2.6	2.3
Number of seeds fruit (N.S.P.F)	577.9	537.71	486.38	286.38	649.45	257.55	230.19
100 seeds weight (100 SW)	4.82	5.05	3.9	3.78	5.17	3.41	4.01
Fruit yield per vine (F.Y.P.V)	9.45	7.12	10.16	11.97	8.02	11.64	6.93
Total soluble solids (TSS)	2.64	2.75	2.98	2.67	2.5	2.9	4.5
Moisture content (M.C)	95.69	96.49	93.82	96.22	95.48	96.35	96.76
Estimated Yield t/ha (Y/Ha)	26.91	19.66	30.63	33.09	25.4	31.87	27.3

Table 5: Relative contribution to different characters to genetic divergence in ash gourd genotypes

S. No	Characters	Numbers of first rank	Percentage of contribution towards divergence
1	Vine length (VL)	33	3.33
2	Number of primary branches (N.B)	21	2.12
3	Intermodal length (I.L)	72	7.27
4	Days to first male flower (DFMF)	0	0
5	Days to first female flower (DFFF)	0	0
6	Node to first male flower (NFMF)	0	0
7	Node to first female flower (NFFF)	0	0
8	Number of male flower (NMF)	21	2.12
9	Number of female flower (NFF)	4	0.4
10	Sex ratio (SR)	56	5.66
11	Days to first harvest (DFH)	3	0.3
12	Number of fruits per vine (N.F.P.V)	134	13.54
13	Average fruit weight (A.F.W)	87	8.79
14	Fruit length (F.L)	75	7.58
15	Fruit circumference (F.C)	225	22.73
16	Flesh thickness (F.T)	47	4.75
17	Number of seeds fruit (N.S.P.F)	30	3.03
18	100 seeds weight (100 SW)	71	7.17
19	Fruit yield per vine (F.Y.P.V)	88	8.89
20	Total soluble solids (TSS)	6	0.61
21	Moisture content (M.C)	4	0.4
22	Estimated Yield t/ha (Y/Ha)	13	1.31
	Total	990	100

Conclusion

The result indicate that the wider genetic diversity was observed in III and IV, V, VI, VII clusters, suggesting that genotypes of these clusters could be selected for yield and other yield contributing characters. The characters such as yield per hectare, average fruit weight, number of fruits per vine, days to first female flower, node first female flower, number of female flower, flesh thickness and number of seeds per fruit should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence.

References

- Kundu BC, Hossain MM, Khaleque Mian MA, Mian IH. Genetic divergence in bitter gourd (*Momordica charntia* L.). J Asiat. Soc. Bangladesh, Sci. 2012; 38(2):125-134.
- Chaudhari DJ, Acharya RR, Gohil SB, Patel NA. Genetic divergence study in pumpkin (*Cucurbita moschata* Duch. Ex. Poir). Journal of Pharmacognosy and Phytochemistry. 2017; 6(4):744-74.
- Devi DN, Mariappan S. Studies on genetic diversity in Snake Gourd (*Trichosanthes anguina* L.). Afr. J. Agric. Res., 2013; 8(42):5221-5225.
- Khatun M, Rabbani MG, Rahaman EHMS. Estimate of genetic diversity in snake gourd (*Trichosanthes cucumerina*). Bangladesh J Agric. Res. 2010; 35:95-100.
- Krishnamoorthy V, Sampath S. Genetic diversity analysis in pumpkin (*Cucurbita moschata* Duch Ex Poir). International Journal of Chemical Studies. 2019; 7(3):3672-3676.

6. Mandal J, Sirohi PS, Behera TK. Inheritance of fruit characters in ash gourd (*Benincasa hispida* (Thunb.) Cogn.). Veg. Sci. 2002; 29:113-15.
7. Pandey AK, Bhardwaj DR, Dubey Kumar R, Singh, Vikas, Pandey S. Botany, diversity, utilization and improvement of ash gourd (*Benincasa hispida* Thunb. Ex Murray Cogn)-A review. Annals of Hort. 2015; 8:1-15
8. Pandey AK. Underutilized vegetable crops. Satish Serial Publishing House, Delhi, 2008.
9. Pradhan K, Nandi A. Genetic diversity analysis of ash gourd [*Benincasa hispida* (Thunb.) Cogn.] Germplasm by Principal Components. Int. J Curr. Microbiol. App. Sci. 2018; 7(3):2187-2195.
10. Rao CR. Advanced Statistical Methods in Biometrical Research. John Willey and Sons, New York, 1952.
11. Robinson RW, Walters DDS. Cucurbits. CABI Publishing, Cambridge, 1997.
12. Rubatzky VE, Yamaguchi M. World Vegetables. Chapman and Hall, New York. 1997.
13. Sultana MA, Kawochar S, Naznin H, Raihan, Mahmud F. Genetic Divergence In Pumpkin (*Cucurbita Moschata* L.) Genotypes. Bangladesh J Agril. Res. 2015; 40(4):683-692.
14. Tindall HD. Vegetables in the tropics. macmillan education ltd. basingstake, hampshire, UK. 1986, 147.