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DIVERSITY ANALYSIS IN SCENTED AND NON-SCENTED ASH GOURD [*BENINCASA HISPIDA*. (THUNB.) COGN.] GENOTYPES

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Abstract

An experiment was carried out to assess genetic diversity by Mahalanobis D^2 analysis for yield and its seventeen contributing characters in forty ash gourd genotypes at at Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore (Tamil Nadu), India during 2013-2014. In Mahalanobis D^2 analysis, the accessions were grouped into sixteen clusters. Among the sixteen clusters, the cluster I was the largest with eight accessions followed by cluster XIV (4), cluster XII (3), clusters II to XI (2). The maximum intra cluster distance was shown by cluster XIV (33.84). The maximum inter cluster distance was observed between clusters VII and XII (68.64). The highest cluster mean values were recorded by cluster XVI, followed by cluster XII and cluster VIII for yield and quality characters. Relative contribution of characters ranged from 0.00 to 46 per cent towards total genetic diversity. Yield per vine contributed the highest (46.79%) towards total divergence, followed by number of seeds per fruit, crude fibre content, total soluble solids, protein content, days to first female flower opening and carbohydrate content.

Key words : Mahalanobis D^2 analysis, genetic diversity, clustering pattern, ash gourd.

Introduction

Ash gourd [*Benincasa hispida* (Thunb.) Cogn.] (syn. *Benincasa cerifera*) is an important sub-tropical and tropical cucurbitaceous vegetable. The fruit is a large fleshy pepo. It consists of a thin skin of epidermis, fleshy and juicy mesocarp and swollen, thick placenta. The fruit is tricarpellary syncarpous with peripheral placentation.

The fruit is fuzzy when immature. By maturity, the fruit loses its hairs and develops a waxy coating, giving rise to the name 'wax gourd' and providing a long shelf life.

Indo-China is the centre of diversity of ash gourd (Rubatazky and Yamaguchi, 1999). Its primary basic chromosome number is x = 6. It is perhaps the most important polymorphic crop (chromosome number; 2n = 24) with respect to fruit and other plant characteristics like leaves and growth habits although, it belongs to monotypicus genus '*Benincasa*'. It is widely cultivated in China, Japan, Bangladesh and India. In India, it is mostly grown in Kerala, Tamil Nadu, Andhra Pradesh, Karnataka, Uttar Pradesh, Rajasthan, Haryana, Bihar and West Bengal. However, in India, it is estimated that ash gourd occupies an area of about 2,497 hectares with production of 15,326 t and productivity of 6.13 t/ha (Anonymous, 2006) in India. While, in Tamil Nadu ash gourd is grown in an area over 575 ha with production of 10350 t and productivity of 18 t/ha (tamilnadustat.com, 2005-06).

Ash gourd is extensively grown in India for its nutritional, medicinal as well as curative properties. The fruits are consumed in various ways, as fresh vegetables, candied, dried, pickled and also used in ayurvedic medicine preparation. Fruit of this plant are traditionally used to treat a renal diseases, urinary infection and biliousness (Nayar and More, 1998). The methanolic extract of the fruit is reported to possess anti-ulcer (Grover *et al*., 2001), anti-inflammatory (Chandrababu *et al*., 2002), antihistaminic and antidepressant activities (Anilkumar *et al*., 2002). Fruits of *Benincasa hispida* are traditionally

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used for treatment of week nervousness and debility (Nadhiya *et al*., 2014). It has also great demand in processing industries for preparation of a popular sweet called 'petha'.

Ash gourd is rich in nutrients like carbohydrates (3 g), dietary fibre (2.9 g), fat (0.2 g), protein (0.4 g) and high sodium (111 mg) per 100 gram edible portion with an energy value of 54 kJ. It is also fairly rich in vitamin B complex and C, calcium, iron, magnesium, manganese and phosphorous (USDA Nutrititional database, 2014). Eventhough ash gourd is much priced for its medicinal properties; comparatively little attention had been paid for the improvement of this crop. One disadvantage of this crop is its trailing habit and big sized fruit, which makes the plant rather difficult to handle. Besides, due to this growth habit, the plant occupies considerably larger area thus makes it less profitable than many other cucurbitaceous vegetables. Naturally, therefore, any improvement of this crop should aim at producing more compact plant with small or medium sized fruits.

It is known that diversity in any crop at field level does not reflect its genetic wealth, as phenotype is a result of interaction between genotype and environment. A significant increase in its productivity can be brought about by assessing the available genetic variability, heritability and heterosis. Ash gourd, being a monoecious and cross-pollinated crop, provides an ample scope for exploitation of hybrid vigour. The commercial exploitation of hybrids is easy in ash gourd due to its high seed content and easy seed extraction procedures.

Assessment of genetic diversity for identification of promising genotypes by exploiting variability within the species through a proper breeding strategy is a pre-requisite for hybridization programme of any crop improvement. Mahalanobis D^2 anlysis helps in assessing the diversity among the genotypes and to select the divergent parents for future breeding programmes.

Therefore, an attempt was made to estimate magnitude of genetic divergence available among the forty ash gourd genotypes through D^2 analysis.

Materials and Methods

The field experiment of the present study on "Diversity analysis in scented and non-scented ash gourd [*Benincasa hispida*. (Thunb.) Cogn.] genotypes" was carried out at the College Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore (Tamil Nadu), India during 2013-2014.

Forty genotypes collected from different sources are used as biological materials for this study are furnished in table 1.

All the forty accessions were raised for two seasons during July, 2013 and January, 2014 at the College Orchard, T.N.A.U. in randomized block design (RBD) with three replications. Pits of 60 cm diameter and 30 cm depth were taken at a spacing of 1.5 × 1.0 m^2. The forty genotypes (40 treatments) in each replication consist of ten pits and three seeds were sown in each pit. The cultural and management practices were adopted according to the package of practices recommended by Tamil Nadu Agricultural University and standard methods followed for pollination. Eighteen biometrical traits of ash gourd were recorded on five randomly selected plants in each of the accession per replication. The mean values were utilized for statistical analysis.

Results

The observations recorded in forty ash gourd accessions on eighteen characters *viz*., days to first female flower opening, node at first female flower appearance, sex ratio, vine length, internodal length, number of primary branches, number of fruits per vine, average fruit weight, flesh thickness, polar diameter, equatorial diameter, number of seeds per fruit, hundred-seed weight, yield per vine, carbohydrate content, crude fibre content, protein content and total soluble solids for two seasons were analysed statistically for different genetic parameters.

Genetic divergence using Mahalanobis D^2 analysis

Clustering pattern of 40 ash gourd collections

Pooled values of both *kharif* and summer seasons for the 40 accessions and eighteen different characters were used for diversity analysis. The genetic divergence in the genotypes was estimated by subjecting them to distance analysis, using Mahalanobis D^2 statistics. By using the cluster technique as suggested by Tocher (Rao, 1952), all the 40 ash gourd collections were grouped into sixteen clusters. The distribution of ash gourd accessions for eighteen characters into XVI different clusters is presented in table 2.

Among the sixteen, cluster I had eight genotypes (Bh 1, Bh 2, Bh 3, Bh 4, Bh 5, Bh 6, Bh12 and Bh 24) and was the largest. Cluster XIV had four genotypes (Bh 9, Bh 10, Bh 16 and Bh 17), cluster XII had three genotypes (Bh 7, Bh 22 and Bh 30) and all other clusters had two genotypes each, except Cluster XVI, which is monogenotypic cluster (Bh 19).

Average inter and intra cluster distance

The inter and intra cluster distances (D and D^2 values) for the different clusters are furnished in table 3. Among

Table 1 : List of accessions collected and their source.

S. no.	Accession no.	Accession name	Source	Scented/non scented type
1.	Bh 1	BH 1	TNAU, Coimbatore	Non- scented
2.	Bh 2	BH 2	TNAU, Coimbatore	Non- scented
3.	Bh 3	BH 3	TNAU, Coimbatore	Non- scented
4.	Bh 4	Chalkumar	TNAU, Coimbatore	Non- scented
5.	Bh 5	Chityal Local	Chityal, Andhra Pradesh	Non- scented
6.	Bh 6	CO 2	TNAU, Coimbatore	Non- scented
7.	Bh 7	Coimbatore Local	TNAU, Coimbatore	Non- scented
8.	Bh 8	DAG 6	IARI, New Delhi	Non- scented
9.	Bh 9	Debpurna	BCKV, West Bengal	Non- scented
10.	Bh 10	Haveri Local	Haveri, Karnataka	Non- scented
11.	Bh 11	HYBH25	TNAU, Coimbatore	Non- scented
12.	Bh 12	IC 339164	NBPGR, New Delhi	Non- scented
13.	Bh 13	IC 339178	NBPGR, New Delhi	Non- scented
14.	Bh 14	IC 339180	NBPGR, New Delhi	Non- scented
15.	Bh 15	IC 339195	NBPGR, New Delhi	Non- scented
16.	Bh 16	Indu	KAU, Thrissur, Kerala	Non- scented
17.	Bh 17	Indu-K	KAU, Thrissur, Kerala	Non- scented
18.	Bh 18	IVAG 10	IIVR, Varanasi	Non- scented
19.	Bh 19	IVAG 3	IIVR, Varanasi	Non- scented
20.	Bh 20	IVAG 90	IIVR, Varanasi	Non- scented
21.	Bh 21	KAG 1	KAU, Kerala	Non- scented
22.	Bh 22	KAG 15	KAU, Kerala	Non- scented
23.	Bh 23	KAG 3	KAU, Kerala	Non- scented
24.	Bh 24	Kashi Surabhi	IIVR, Varanasi	Non- scented
25.	Bh 25	Kashi Ujwal	IIVR, Varanasi	Non- scented
26.	Bh 26	Kashi Dhawal	IIVR, Varanasi	Non- scented
27.	Bh 27	KAU local	KAU, Thrissur, Kerala	Non- scented
28.	Bh 28	Large fruited	KAU, Thrissur, Kerala	Non- scented
29.	Bh 29	PAG 3	TNAU, Coimbatore	Non- scented
30.	Bh 30	PAG 72	TNAU, Coimbatore	Non- scented
31.	Bh 31	Pusa Ujwal	NBPGR, New Delhi	Non- scented
32.	Bh 32	RCAG 15	ICAR Research complex for NEH region, Arunachal Pradesh	Non- scented
33.	Bh 33	RCAG 28	ICAR Research complex for NEH region, Arunachal Pradesh	Non- scented
34.	Bh 34	Shadnagar Local	Shadnagar, Andhra Pradesh	Non- scented
35.	Bh 35	Vaidyakumbalam	KAU, Thrissur, Kerala	Non- scented
36.	Bh 36	Varanasi Local	IIVR, Varanasi	Non- scented
37.	Bh 37	IC 596991	NBPGR, New Delhi	Scented
38.	Bh 38	IC 596992	NBPGR, New Delhi	Scented
39.	Bh 39	IC 596993	NBPGR, New Delhi	Scented
40.	Bh 40	IC 596994	NBPGR, New Delhi	Scented

Table 2 : Cluster members of D square analysis of ash gourd.

Cluster no.	Number of genotypes	Accession no.	Accession name
I	8	Bh 1, Bh 2, Bh 3, Bh 4, Bh 5, Bh 6, Bh 12, Bh 24	BH 1, BH 2, BH 3, Chalkumar, Chityal Local, CO 2, Kashi Surabhi
II	2	Bh 20, Bh 33	IVAG 90, RCAG 28
III	2	Bh 11, Bh 26	HYBH 25, Kashi Dhawal
IV	2	Bh 27, Bh 36	KAU local, Varanasi Local
V	2	Bh 23, Bh 25	KAG 3, Kashi Ujwal
VI	2	Bh 14, Bh 15	IC 339180, IC 339195
VII	2	Bh 37, Bh 40	IC 596991, IC 596994
VIII	2	Bh 29, Bh 32	PAG 3, RCAG 15
IX	2	Bh 38, Bh 39	IC 596992, IC 596993
X	2	Bh 18, Bh 28	IVAG 10, Large fruited
XI	2	Bh 8, Bh 13	DAG 6, IC 339178
XII	3	Bh 7, Bh22, Bh 30	Coimbatore Local
XIII	2	Bh 21,Bh 31	KAG 1, Pusa Ujwal
XIV	4	Bh 9, Bh 10, Bh 16, Bh 17	Debpurna, Haveri Local, Indu, Indu K
XV	2	Bh 34, Bh 35	Shadnagar Local, Vaidyakumbalam
XVI	1	Bh 19	IVAG 3

the sixteen different clusters, the maximum intra cluster distance (diagonal values) was shown by cluster XIV (33.84), followed by the cluster XV (27.92) and cluster I (26.91). The lowest intra cluster distance was observed in cluster II (11.29). The maximum inter cluster distance (Off diagonal values) was observed between clusters VII and XII (68.64) followed by the clusters IX and XVI (68.48) and between clusters VII and XVI (68.00). The lowest inter cluster distance (14.53) was observed between cluster III and V.

Mean performance of sixteen clusters for different quantitative characters

The mean values for different clusters were calculated for all the eighteen characters and are furnished in table 4. Wide differences were observed between high and low mean values among the clusters for most of the characters studied. Cluster II recorded the highest mean value for number of primary branches per vine (2.18) and number of seeds per fruit (813.44) and lowest mean value for total soluble solids (1.20). Cluster VI registered lowest values for days to first female flower appearance (59.87), number of primary branches per vine (1.38) and protein content (243.87). Whereas, genotypes of cluster VII recorded maximum days to first female flower appearance (75.33) and total soluble solids (5.52) and the same cluster genotypes recorded lowest mean values for the characters *viz*., node at first female flower appeared (11.39), number of fruits per vine (2.25), average fruit weight (0.54), flesh thickness (2.04), number of seeds per fruit (141.82), and yield per vine (1.12).

Accessions of cluster VIII were observed to have higher mean values for sex ratio (6.11) and crude fibre content (0.53). Cluster IX recorded minimum vine length (114.38), inter nodal length (6.44), fruit equatorial diameter (8.68), hundred - seed weight (6.30) and crude fibre content (0.37) and accessions of the same cluster recorded highest carbohydrate content (5.87). Highest crude fibre content (0.53) was recorded by the genotypes of cluster XI.

Cluster XII recorded maximum vine length (360.34) and fruit equatorial diameter (19.92) and lowest sex ratio (2.80). Cluster XIV showed the highest mean value for fruit polar diameter (22.68) and lowest carbohydrate content (3.46). Cluster XV recorded highest mean value for internodal length (10.93), flesh thickness (5.68) and protein content (373.67).

Accession of cluster XVI registered highest mean values for node at first female flower appeared (22.96), number of fruits per vine (3.66), average fruit weight (5.31), hundred - seed weight (9.68) and yield per vine (16.28). The same cluster showed lowest values for fruit polar diameter (12.10) and carbohydrate content (3.46).

Contribution of various quantitative and qualitative characters towards total genetic divergence

Rank method of D^2 analysis

The percentage contribution of different characters towards genetic divergence is presented in table 5. Ranking character wise D^2 values and adding the ranks for each character for all the entries identified the variables, which contributed towards the divergence except internodal length, number of fruits per vine, average fruit weight and fruit flesh thickness. Yield per vine contributed high (46.79%) towards total divergence. This was followed by number of seeds per fruit (32.95 %), crude fibre content (6.28 %), total soluble solids (5.13%) and protein content (2.05%). Days to first female flower appearance and carbohydrate content (1.67) were contributing equally towards divergence. Internodal length,

Table 3 : Inter and intra cluster D^2 and D (with in parentheses) values of ash gourd.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	724.29 (26.91)	659.91 (25.69)	440.81 (21.00)	683.78 (26.15)	448.04 (21.17)	613.05 (24.76)	2167.29 (46.55)	996.98 (31.58)	1862.19 (43.15)	601.16 (24.52)	1016.64 (31.89)	1546.37 (39.32)	643.69 (25.37)	916.58 (30.28)	1504.20 (38.78)	2613.66 (51.12)
II		127.54 (11.29)	331.17 (18.20)	1184.54 (34.42)	486.87 (22.07)	600.79 (24.51)	3222.93 (56.77)	1507.42 (38.83)	2605.27 (51.04)	1016.33 (31.88)	1695.49 (41.18)	1381.90 (37.17)	884.56 (29.74)	561.71 (23.70)	2458.44 (49.58)	3242.50 (56.94)
III			130.28 (11.41)	558.73 (23.64)	211.08 (14.53)	224.91 (15.00)	1980.37 (44.50)	1023.58 (31.99)	1560.62 (39.51)	502.63 (22.42)	837.42 (28.94)	1614.65 (40.18)	401.05 (20.03)	631.74 (25.13)	1591.46 (39.89)	2967.28 (54.47)
IV				131.79 (11.48)	451.94 (21.26)	551.30 (23.48)	1148.76 (33.89)	517.43 (22.75)	1033.87 (32.15)	211.96 (14.56)	299.35 (17.30)	1613.45 (40.17)	372.61 (19.30)	1365.08 (36.95)	742.81 (27.26)	1751.64 (41.85)
V					150.88 (12.28)	282.62 (16.81)	1656.64 (40.70)	848.36 (29.13)	1299.31 (36.05)	467.00 (21.61)	747.93 (27.35)	1718.78 (41.46)	347.99 (18.650	695.49 (26.37)	1240.86 (35.23)	2720.44 (52.16)
VI						159.02 (12.61)	1759.71 (41.95)	960.14 (30.99)	1434.51 (37.88)	630.56 (25.11)	634.25 (25.18)	2093.63 (45.76)	338.30 (18.39)	827.48 (28.77)	1387.00 (37.24)	3249.96 (57.01)
VII							169.54 (13.01)	1936.94 (44.01)	307.58 (17.54)	1396.17 (37.37)	903.54 (30.06)	4712.06 (68.64)	1381.69 (37.17)	3152.26 (56.15)	1324.40 (36.39)	4624.28 (68.00)
VIII								176.08 (13.27)	1890.93 (43.49)	616.39 (24.83)	746.82 (27.33)	1726.94 (41.56)	563.99 (23.75)	1653.89 (40.67)	682.79 (26.13)	1746.69 (41.79)
IX									204.90 (14.31)	1311.65 (36.22)	1014.11 (31.85)	4370.61 (66.11)	1191.41 (34.52)	2643.13 (51.41)	1677.70 (40.96)	4690.04 (68.48)
X										237.45 (15.41)	458.34 (21.41)	1338.74 (36.59)	467.83 (21.63)	1169.81 (34.20)	807.28 (28.41)	1807.27 (42.51)
XI											262.56 (16.20)	2520.94 (50.21)	488.22 (22.10)	1744.48 (41.77)	619.59 (24.89)	2633.85 (51.32)
XII												643.58 (25.37)	2014.55 (44.88)	1866.10 (43.20)	2700.24 (51.96)	1117.98 (33.44)
XIII													460.84 (21.47)	1067.67 (32.68)	946.16 (30.76)	2659.12 (51.57)
XIV														1144.85 (33.84)	2363.44 (48.62)	3564.81 (59.71)
XV															779.40 (27.92)	2294.88 (47.91)
XVI																0.00 (0.00)

Table 4 : Cluster mean values for 18 characters in ash gourd.

Cluster	VL	INL	NPB	DTFFO	NFFA	SR	NFPV	AFW	FT	PD	ED	NSF	HSW	CHO	CF	PRO	TSS	YPV
I	327.172	10.870	1.57	67.287	18.90	3.252	2.727	2.975	3.427	19.277	17.394	589.638	8.125	4.004	0.520	340.784	2.019	6.846
II	321.855	10.732	2.183	64.987	18.055	3.100	2.663	3.070	3.167	21.408	18.417	813.437	9.147	4.202	0.493	312.66	1.200	6.847
III	314.108	10.052	1.430	62.233	20.123	3.093	2.572	2.827	2.825	19.958	18.933	634.992	8.343	3.878	0.482	262.912	1.833	5.707
IV	273.962	9.302	1.558	63.345	17.862	3.187	2.932	2.642	3.133	14.317	12.433	362.872	8.228	5.082	0.492	300.722	2.825	7.202
V	245.575	9.817	1.567	71.268	18.360	2.923	2.382	2.800	4.758	17.900	15.508	571.84	8.272	3.800	0.438	343.697	2.233	5.612
VI	301.602	10.082	1.383	59.872	13.075	3.033	2.657	1.987	4.625	17.517	16.85	599.848	9.362	4.147	0.433	243.865	2.167	4.753
VII	195.118	7.848	1.845	75.328	11.390	3.085	2.245	0.542	2.042	12.142	9.758	141.820	6.882	4.632	0.425	317.962	5.517	1.122
VIII	320.973	8.965	1.552	66.950	15.997	6.107	2.937	2.887	5.467	17.992	15.333	439.180	8.88	4.393	0.525	335.338	3.008	6.927
IX	114.382	6.440	1.632	72.617	12.650	3.492	2.362	0.605	2.108	13.458	8.675	256.522	6.295	5.867	0.365	318.808	5.400	1.260
X	336.798	9.903	1.548	69.028	18.293	2.887	2.922	3.260	3.158	21.242	15.658	416.988	7.717	4.730	0.485	296.628	3.508	7.573
XI	351.623	10.023	1.510	60.545	18.478	3.028	2.427	1.905	3.483	18.308	13.525	294.315	9.188	5.083	0.530	312.925	2.583	5.135
XII	360.337	10.596	1.842	64.768	18.742	2.777	3.437	4.967	2.861	21.378	19.922	624.929	8.808	4.120	0.493	309.951	1.978	14.028
XIII	283.752	9.610	1.513	64.782	18.298	3.850	3.003	1.897	3.500	17.567	14.333	508.562	9.538	3.515	0.443	279.815	2.517	5.055
XIV	336.506	10.708	1.506	68.924	18.594	2.963	2.469	3.106	4.092	22.679	17.138	757.699	9.052	3.459	0.448	339.546	1.779	6.505
XV	345.737	10.927	1.407	74.140	15.103	3.775	2.858	2.842	5.658	20.450	16.875	221.018	8.882	3.790	0.450	373.667	3.433	6.052
XVI	288.443	10.600	1.703	63.893	22.963	2.813	3.660	5.307	3.183	12.100	13.85	268.39	9.677	3.457	0.387	317.190	2.517	16.280

Whereas,

DTFFA Days to first female flower opening
NFFA Node at first female flower appeared
SR Sex ratio
VL Vine length
INL Inter nodal length
NPB number of primary branches
NFPV Number of fruits per vine
AFW Average fruit per vine
FT Flesh Thickness
PD Polar diameter
ED Equatorial diameter
NSF Number of seeds per fruit
HSW Hundred seed weight
CHO Carbohydrate content
CF crude fiber content
PRO Protein content
TSS Toatal soluble solids
YPV Yield per vine

number of fruits per vine, average fruit weight and fruit flesh thickness had zero per cent contribution and remaining characters showed negligible amount towards total genetic divergence.

Discussion

The exploration of genetic diversity in the available germplasm is a pre-requisite in a breeding programme for effective selection of superior genotypes. A plant breeder has to identify the source of favourable genes to incorporate them into breeding populations and select for a combination of desirable traits that might result in the isolation of productive genotypes and cultivars. A plant breeder therefore, sets hopes of improvement on the extent of genetic variation and degree of improvement possible on the beneficial genetic variability (Kulkarni, 2006).

Several methods have been advocated by several workers to estimate the genetic divergence in crop plants (Murthy and Arunachalam, 1966; Bhatt, 1970; Hussain, 1973). Out of several methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than inferring from indices based on morphological similarities and phylogenetic relationships.

In the process of genetic improvement of any crop, genetic diversity among germplasm plays a major role, since it opens the way to determine the most divergent parents based on the contribution of different qualitative and quantitative traits, for further utilisation in any hybridisation programme (Shukla *et al*., 2009). Extent and magnitude of genetic divergence were determined for the purpose of identifying more diverse parents which are expected to engender maximum variability (Pandey and Singh, 2011). The results obtained on genetic divergence of ash gourd are discussed hereunder.

In the present study, D^2 analysis was

Table 5 : Relative contribution of each character towards genetic divergence.

Character	Times ranked first	Contribution (per cent)
Vine length	9	1.15
Internodal length	0	0.00
Number of primary branches	1	0.13
Days to first female flower opening	13	1.67
Node at first female flower appeared	1	0.13
Sex ratio	3	0.38
Average fruit weight	0	0.00
Flesh thickness	0	0.00
Polar diameter	2	0.26
Equatorial diameter	3	0.38
Number of seeds per fruit	257	32.95
Hundred seed weight	8	1.03
Number of fruits per vine	0	0.00
Carbohydrate content	13	1.67
Crude fiber content	49	6.28
Protein content	16	2.05
Total soluble solids	40	5.13
Yield per vine	365	46.79
Total	780	100

carried out using eighteen characters. The presence of high variability among the accessions studied for different characters were further confirmed through the pattern of distribution of 40 ash gourd accessions into sixteen clusters based on genetic divergence D^2 statistics. Among the sixteen, cluster I had eight genotypes (BH 1, Bh 2, BH 3, Chalkumar, CO 2, IC 339164 and Kashi Surabhi) and was the largest. Cluster XIV had four genotypes (Debpurna, Haveri Local, Indu and Indu-K), cluster XII had three genotypes (Coimbatore Local, KAG 15 and PAG 72) and all other clusters had two genotypes each, except Cluster XVI which is a monogenotypic cluster (IVAG 3) indicating wider divergence among the genotypes. These results are in conformity with the findings of Singhal *et al*. (2010) in ash gourd.

The maximum inter cluster distance was observed between clusters VII and XII (68.64), which showed maximum divergence between these two clusters, which may be used for hybridization programme for obtaining a broad spectrum of variability for transgressive segregants for the genetic improvement of ash gourd. The lowest inter cluster distance (14.53) was observed between cluster III and V which indicated that these clusters have maximum common gene combinations. Clustering patterns indicated that accessions (scented ash gourd) falling in cluster VII (IC 596991 and IC 596994) can be used in hybridization programme to generate wide range of transgressive segregants in population for varieties with a better biochemical profile of total soluble solids for imparting scentedness and cluster XII (Coimbatore Local, KAG 15 and PAG 72) can be used in hybridization programme to generate wide range of transgressive segregants in population for varieties/hybrids with higher yield coupled with good quality.

The residual effect from path analysis was 0.120, which indicated the adequacy of the characters chosen for the study and the characters studied contributed about 88 per cent towards yield per vine.

Relative contribution of characters towards genetic divergence may be beneficial for selection in crop improvement. In the present study, yield per vine, followed by number of seeds per fruit, crude fibre content, total soluble solids, protein content, days to first female flower appearance and vine length contributed more than other characters and may be considered in selection programme, which also suggested thereby that diverse accessions can be utilized for improvement of productivity. Further, these characters had positive correlation with yield per vine. Hence, decision based on these yield contributing characters for selection of desirable parents for hybridization as well as recombination breeding may yield fruitful results. Further highly divergent genotypes seem to produce wide variability that helps further selection for genetic improvement (Berwal *et al*., 1993). The contribution of yield per vine, number of seeds per fruit, hundred-seed weight and total soluble solids is in accordance with the findings of Kale *et al*. (2002) and Lakshmi *et al*. (2003) in pumpkin and Reddy *et al*. (2013) in muskmelon.

Based on quantitative data, the potentiality of the ash gourd accessions with respect to yield and its attributing characters and the genetically divergent genotypes identified in the present study have wider applicability in planning the future breeding programmes for increasing quality and productivity of ash gourd.

From the foregoing discussion, it could be concluded that the non scented accessions *viz.*, Coimbatore Local, IC 339164, KAG 15, PAG 72, IVAG 10, Indu, Chalkumar, KAU Local and Shadnagar Local and among the scented genotypes IC 596991, IC 596992, and IC 596994 were identified as the best performing ones for yield and quality attributes based on their *per se* performance. Path coefficient analysis revealed positive direct effect on yield

per vine by vine length, internodal length, number of fruits per vine, average fruit weight, number of seeds per fruit, hundred seed weight, carbohydrate content and total soluble solids. Mahalanobis D^2 analysis grouped the 40 accessions into sixteen clusters using 18 characters. Yield per vine contributed the highest (46.79%) towards total divergence followed by number of seeds per fruit, crude fibre content, total soluble solids, protein content, days to first female flower opening and carbohydrate content.

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