Int. J. Agricult. Stat. Sci. Vol. 13, No. 2, pp. 513-518, 2017 *ISSN : 0973-1903*

ORIGINAL ARTICLE

GENETIC DIVERSITY OF SNAPMELON (*CUCUMIS MELO* L. VAR *MOMORDICA*) BASED ON MORPHO-CHEMICAL TRAITS FROM NEH REGION OF INDIA

V. R. Muddarsu, Rakesh K. Dubey*, Vikas Singh, Garima Upadhyay, A. K. Pandey and Sudhakar Pandey[1]

College of Horticulture and Forestry, Central Agricultural University, Pasighat - 791 102, India.
[1]ICAR-Indian Institute of Vegetable Research, Varanasi - 221 305, India.
E-mail : .rksdubey@gmail.com

Abstract : Study on genetic diversity was conducted with 20 snapmelon (*Cucumis melo* L.var. momordica) genotypes of Indian origin. Sixteen quantitative characters were taken into consideration. Cluster analysis was used for grouping of 20 snapmelon genotypes under the study and grouped into five clusters. Cluster I had maximum (9) and cluster IV and V had the minimum number (1) of genotypes. Highest (9321.228) inter cluster distance was observed between cluster IV and V and lowest (404.349) between cluster I and IV. Cluster III (D^2 = 538.09) have exhibited highest intra cluster distance and lowest was observed in cluster II (D^2 = 23.605). Characters *viz*. ascorbic acid and titrable acidity contributed maximum towards divergence. Genetic divergence among 20 genotypes revealed that the genotype CHFSM5 from cluster V was more divergent for improving number of fruit per plant, TSS and ascorbic acid content. Genotypes CHFSM4 and CHFSM11 from cluster II are found to be promising lines for improving vine length, primary branches per plant, fruit diameter, fruit weight and flesh thickness. These genotypes may be taken into consideration as parents for an efficient hybridization programme of snapmelon.

Key words : *Cucumis melo* L. var. *momordica*, Parent selection, Genetic divergence, Yield.

1. Introduction

Snapmelon (*Cucumis melo* L. var. *momordica*) belongs to family Cucurbitaceae, is a native of India and is used as vegetable in a variety of ways. Ripe fruits of snapmelon have a specific characteristic of splitting (cracking), therefore in India, it is locally known as 'phut' (meaning 'to split'). Immature fruits of snapmelon are generally used as salad and cooking purpose, while ripe fruits are consumed as dessert. India being a centre of diversity is endowed with great variability in terms of morphological characters, especially, fruit size and shape, fruit cracking, peeling patterns, flesh colour skin texture and colour of fruit skin [Pandey *et al*. (2011)]. Indian snapmelon accessions have been reported to be a good source for disease and insect pest resistance and many of them are used as reference accessions worldwide [Cohen *et al*. (2003)]. Despite its economic importance and some of the extensive studies for identifying resistance sources, limited attention has been paid to genetic characterization and diversity studies of Indian snapmelon accessions. Snapmelon is grown in almost all the parts of NEH region of India and most of them are local cultivars or landraces. Landraces are variable plant populations adapted to local agro climatic conditions, which are locally named, selected and maintained by the traditional farmers to meet their social, economic, cultural and ecological needs. The snapmelon landraces of North eastern region are heterogeneous and serve as a reservoir of genetic variability for breeder. Genetic divergence existing in the population helps in the selection of suitable parents for utilization in any crop breeding programme leading to reduction in the number of crosses [Guerra *et al*. (1999)]. Selection of parents depends on specific objective of the research programme and their performance. Various statistical analyses are available to select suitable parents. The information on the nature and

***Author for correspondence** **Received** April 27, 2017 **Revised** June 20, 2017 **Accepted** July 06, 2017

degree of genetic divergence is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding [Khodadabi *et al.* (2011), Yatung *et al*. (2014)]. In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary [Yatung *et al*. (2014)]. The standardization of variables is also essential towards determining the genetic distance so that all variables are of similar importance in determining the distance. Various methods have been used in studying of genetic diversity through cluster analysis of which Tocher's methods is the most popular approach. The cluster analysis is an appropriate method for determining family relationships [Mellingers (1972)]. Euclidean distance can theoretically estimate the genetic distance between parents to maximize the transgressive segregation [Hoque and Rahman (2006)]. The higher genetic distance between parents, the higher heterosis in progeny can be observed [Lahbib *et al*. (2012)]. In the present study, 20 snapmelon genotypes from different regions of NEH and other parts of India were collected and cultivated with standard package of practices at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India and analyzed for their genetic diversity based on morpho-chemical traits. The main objective of this study is to capture the potential genetic diversity between snapmelon genotypes grown in India by using cluster analysis and selection of suitable genotypes for future snapmelon hybridization programme.

2. Materials and Methods

The experimental material for the present study was comprised of 20 genotypes of snapmelon (Table 1) were collected from different parts of the India and grown at the research farm of department of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India (altitude 153 m above mean sea level and 28°04'N and 95022'E). The soil is sandy loam with pH 6.7. The experiment was laid out in RCBD with three replications during April-September, 2012. Snapmelon seeds were sown using 3.0 m × 1.0 m row to row and plant to plant. The standard cultural operations like, fertilizing, weeding, hoeing, irrigation and plant protection measures were adopted whenever needed. The observations were recorded on five plants from each genotype in each replication. Analysis of variance, cluster analysis based on Tocher's method using squared Euclidean distance [Kumar *et al.* (2009)] was performed using the statistical software Indostat and statistical package for agricultural research (SPAR) version 2.0 programme. The genetic divergence was calculated according to Mahalanobis D^2 statistics (1936).

Table 1 : Description of studied snapmelon genotypes.

Genotype	Pedigree/Source
CHFSM 1	A land race of district Faizabad, Uttar Pradesh
CHFSM 2	A land race of Mari village, Arunachal Pradesh
CHFSM 3	A land race of East Siang district, Arunachal Pradesh
CHFSM 4	A land race of East Siang district, Arunachal Pradesh
CHFSM 5	A land race of East Siang district, Arunachal Pradesh
CHFSM 6	A land race of district Jaunpur, Uttar Pradesh
CHFSM 7	A land race of district Jaunpur, Uttar Pradesh
CHFSM 8	A land race of district Jaunpur, Uttar Pradesh
CHFSM 9	A land race of district Jaunpur, Uttar Pradesh
CHFSM 10	A land race of district Jaunpur, Uttar Pradesh
CHFSM 11	A land race of East Siang district, Arunachal Pradesh
CHFSM 12	A selection from local land race of Banglore, Karnataka
CHFSM 13	A selection from local land race of Banglore, Karnataka
CHFSM 14	A selection from local land race of Banglore, Karnataka
CHFSM 15	A land race of East Siang district, Arunachal Pradesh
CHFSM 16	A land race of East Siang district, Arunachal Pradesh
CHFSM 17	A land race of East Siang district, Arunachal Pradesh
CHFSM 18	A land race of East Siang district, Arunachal Pradesh
CHFSM 19	A land race of East Siang district, Arunachal Pradesh
CHFSM 20	A land race of East Siang district, Arunachal Pradesh

3. Results and Discussion

Analysis of variance (Table 2) exhibited significant differences among the genotypes for all the traits under study which indicated considerable amount of genetic

Table 2 : Analysis of variance, mean, coefficient of variation and least significant differences for studied in snapmelon genotypes.

Source of variation	D.F.	Days to 50% germination	Vine length (m)	No. of primary branches /plant	Days to first staminate flower anthesis	Days to first pistillate flower anthesis	Days to first harvest	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (kg)	Flesh thickness (cm)	No. of fruit /plant	No. of seed/ fruit	TSS (%)	Ascorbic acid (mg)	Titrable acidity (%)	Yield/ plant (kg)
Replication	2	0.15	0.032	1.084	1.816	1.0167	6.466	1.552	0.163	0.002	0.0049	1.605	6598.514	0.0029	0.0048	0.0002	0.0471
Genotype	19	7.88**	0.49**	3.59**	105.64**	84.24**	321.08 **	109.95 **	10.65 **	0.3150 **	0.803 **	33.55 **	84335.9 9**	6.68 **	29.13 **	0.0271 **	5.8204 **
Error	38	0.6412	0.1632	1.0903	7.0096	26.3149	68.5018	7.0551	1.1249	0.0105	0.1136	1.1002	2450.914	0.0202	0.0129	0.0001	0.1107
Mean		7.60	4.03	5.48	40.33	50.58	82.42	17.25	9.77	0.82	2.13	5.89	470.65	3.84	8.46	0.32	3.10
CV%		10.54	10.02	19.04	10.23	10.14	10.04	15.39	10.86	12.45	15.82	17.80	10.52	3.71	1.34	2.72	10.72
CD (5%)		1.32	0.67	1.73	6.82	8.48	13.68	4.39	1.75	0.17	0.56	1.73	81.83	0.23	0.19	0.01	0.55

variability and subjected to further analysis. Dendrogram depicting genetic diversity in snapmelon genotypes based on Tocher's method is shown in Fig. 1. Computation from covariance matrix gave non-hierarchical clustering based on Mahalanobis D^2 values among snapmelon genotypes and grouped them into 5 clusters (Table 3); this clearly showed that the genotypes did not cluster according to geographical distributions. This is similar with the results obtained by Reddy *et al.* (2005) in snapmelon. It explained that cluster I contained highest number of genotypes (9) followed by cluster III having 7 genotypes, cluster II having 2 genotypes, cluster IV and V having 1 genotypes each. CHFSM1, CHFSM3, CHFSM8, CHFSM9, CHFSM10, CHFSM13, CHFSM14, CHFSM16 and CHFSM17 genotypes were classified in first cluster including 45.0% of the total genotypes. The average values of genotypes in this cluster for fruit length, fruit diameter and flesh thickness content is higher than the mean of all genotypes and fruit weight equal to total mean value of all genotypes (Table 4). CHFSM4 and CHFSM11 were classified under second cluster in this cluster all characters showed higher than the mean value of all genotypes except TSS and Titrable acidity, which were showing lesser than total mean value; these results were in agreement with the results of Tomar *et al*. (2008). The genotypes CHFSM2, CHFSM6, CHFSM7, CHFSM12, CHFSM18, CHFSM19 and CHFSM20 were classified under third cluster accounting for 35% of the total genotypes.

Values of fruit length, fruit diameter, fruit weight, flesh thickness, fruit yield per plant and vine length were greater than the total mean. Only one genotype CHFSM 15 belonged to cluster IV accounting for 5% of the total genotypes. In this group mean of fruit length, fruit diameter, flesh thickness and yield per plant was more than the average and for other traits were approximately less than the total average mean (Table 4). CHFSM 5 genotype was classified in cluster V accounting for 5% of the total genotypes. In this cluster number of fruit per plant, TSS and ascorbic acid showed higher value than the total average mean value and other traits were approximately less than the total average mean value (Table 4). According to Mahalanobis's D^2 statistic, the intra and inter cluster distance (D^2) values are presented in (Table 5). The inter cluster D^2 values were found range between 404.349 to 9321.228. Minimum inter cluster distance

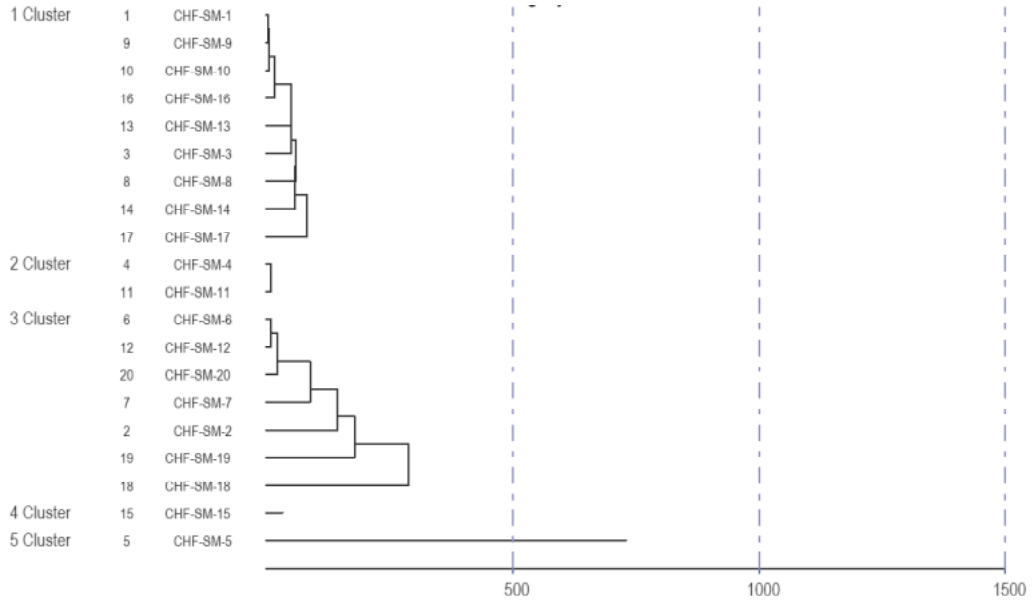

Fig. 1 : Tree diagram of 20 genotypes of snapmelon for 16 studied characters using hierarchical cluster analysis (Tocher's method).

Table 3 : Clustering pattern of 20 snapmelon genotypes by Tocher's method.

Cluster	Number of genotypes	Genotypes
I	9	CHFSM1,CHFSM 9,CHFSM 10, CHFSM 16, CHFSM 13, CHFSM 3, CHFSM 8 CHFSM 14, CHFSM 17
II	2	CHFSM 4, CHFSM 11
III	7	CHFSM 6, CHFSM 12, CHFSM 20, CHFSM 7, CHFSM 2, CHFSM 19, CHFSM 18
IV	1	CHFSM 15
V	1	CHFSM 5

between cluster I and IV (404.349) indicated that genotypes were genetically close to each other. Maximum inter cluster distance was observed between cluster IV and V (9321.228) and indicated that genotypes are highly divergent. The intra cluster divergence varied from 23.605 to 538.309. Maximum intra cluster distance was achieved in cluster III (538.309), which comprised seven genotypes while minimum divergence was observed in cluster II (23.605). Cluster IV and V showed zero intra cluster distance due to containing only one genotype. On the basis of cluster mean value, it was observed that mean value of days to 50% germination was minimum in cluster IV (6.33) and maximum in a cluster II (8.83), vine length was maximum in cluster II (4.78) and lowest in cluster IV (3.71). Maximum number of primary branches per vine was recorded in cluster II (6.0), whereas minimum was recorded in cluster V (5.0). The cluster IV had the minimum days to appearance of first staminate flower anthesis (34), whereas cluster II had the maximum days to appearance of first staminate flower anthesis (48.33). With regard to days to appearance of first pistillate flower anthesis, cluster IV showed the minimum mean value (40.66) while cluster II showed maximum (56.50). Days to first fruit harvest was minimum in cluster V (71.33) and maximum in cluster II (95.16). The genotypes of cluster III had maximum fruit length (21.10), whereas the genotypes of cluster V had minimum fruit length (4.2). Average fruit weight was maximum (1.37) and minimum (0.04) in cluster II, cluster V, respectively. Similarly, flesh thickness was maximum (3.07) and minimum (0.71) in cluster II, cluster V, respectively. Number of fruit per plant was recorded maximum (16.60) in cluster V and minimum (4.29) in cluster I. Number of seed per fruit was recorded maximum (779.86) in cluster II and minimum (363.66) in cluster IV. TSS was lowest in cluster I (3.25) while, it was highest in cluster V (9.56).

Table 4 : The average of traits for each cluster (above number) and the difference between each cluster with the total mean (below number).

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Cluster I	7.48	3.87	5.11	38.81	49.70	80.29	15.70	9.58	0.73	2.13	4.29	422.02	3.25	6.50	0.35	2.65
	-0.08	-0.176	-0.31	-0.97	0.31	-1.808	0.776	0.304	-0.006	0.11	-3.996	-58.92	-1.43	-3.45	0.06	-0.52
Cluster II	8.83	4.78	6.00	48.33	56.50	95.16	18.14	11.88	1.37	3.07	9.03	779.86	3.32	13.34	0.24	5.57
	1.314	0.734	0.58	8.55	7.11	13.062	3.216	2.604	0.634	1.05	0.744	298.92	-1.36	3.382	-0.05	2.39
Cluster III	7.61	4.10	5.93	41.47	51.76	83.38	21.10	10.07	0.91	2.05	5.51	475.37	3.98	8.98	0.29	3.22
	0.094	0.054	0.51	1.69	2.37	1.282	6.176	0.794	0.174	0.03	-2.776	-5.57	-0.7	-0.97	0.00	0.04
Cluster IV	6.33	3.71	5.06	34.00	40.66	80.33	15.44	10.65	0.63	2.14	6.00	363.66	3.29	4.23	0.29	3.74
	-1.186	-0.036	-0.36	-5.78	-8.73	-1.768	0.516	1.34	-0.106	0.12	-2.286	-117.28	-1.39	-5.72	0.00	0.562
Cluster V	7.33	3.77	5.00	36.33	48.33	71.33	4.24	4.20	0.04	0.71	16.60	363.80	9.56	16.74	0.28	0.71
	-0.186	-0.276	-0.42	-3.45	-1.06	-10.768	-10.684	-5.076	-0.696	-1.31	8.314	-117.14	4.88	6.782	-0.01	-2.46
Mean	7.516	4.046	5.42	39.788	49.39	82.098	14.924	9.276	0.736	2.02	8.286	480.942	4.68	9.958	0.29	3.178

1. Days to 50% germination, **2.** Vine length (m), **3.** Number of primary branch per plant, **4.** Days to first staminate flower anthesis, **5.** Days to first pistillate flower anthesis, **6.** Days to first fruit harvest, **7.** Fruit length (cm), **8.** Fruit diameter(cm), **9.** Fruit weight (kg), **10.** Flesh thickness (cm), **11.** Number of fruit per plant, **12.** Number of seed per fruit, **13.** TSS (%), **14.** Ascorbic acid (mg), **15.** Titrable acidity (%), **16.** Yield / plant (kg).

Table 5 : Average Inter and intra cluster distance (D^2) for 20 snap melon genotypes.

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**167.320**	2217.485	606.118	404.349	6786.733
Cluster II		**23.605**	1120.246	3775.162	1948.247
Cluster III			**538.309**	1296.945	4547.620
Cluster IV				**0.000**	9321.228
Cluster V					**0.000**

Ascorbic acid content was recorded maximum in cluster V (16.74) and minimum in cluster IV (4.23). Titrable acidity was Maximum in cluster I (0.35) lowest in cluster II (0.24). Fruit yield was highest in cluster II (5.57) and minimum in cluster V (0.71).

4. Conclusion

The twenty genotypes of snapmelon under study were grouped into five clusters irrespective of their origin. Distant parents are able to exert high heterosis. Considering this theme and variability, diversity analysis of the genotypes CHFSM 4 and CHFSM 11 for vine length, primary branches per plant, fruit diameter, fruit weight and flesh thickness and CHFSM 5 for number of fruit per plant, TSS and ascorbic acid content were identified as promising genotypes. From this study, it may be concluded that a wide range of variation for almost all the economically important traits are present in this crop. This implies a great potential for breeding through hybridization programme or direct use as variety for successful snapmelon breeding. Further, one or two promising genotypes from different clusters may be chosen for further genetic studies either by way of diallel or line × tester analysis.

References

Cohen, Y., I. Meron, N. Mor and S. Zurial (2003). A new pathotype of *Pseudoperenospora cubensis* causing downey mildew in cucurbits in Israel. *Phytoparasitica*, **31**, 452–466.

Guerra, E. P., D. Destro, L. A. Miranda and R. Montalván (1999). Parent selection for intercrossing in food type soybean through multivariate genetic divergence. *Acta Science*, **21(3)**, 429-437.

Hoque, M. and L. Rahman (2006). Estimation of Euclidian distance for different morpho physiological characters in some wild and cultivated rice genotypes (*Oryza sativa* L.). *Pak Science*, **1**, 77-79.

Khodadabi, M., M. H. Fotokian and M. Miransari (2011). Genetic diversity of wheat genotypes based on cluster and principal component analyses for breeding

strategies. *Australian Journal of Crop Science*, **5(1)**, 17-24.

Kumar, B., G. Lal, M. Ruchi and A. Upadhyay (2009). Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). *Asian Journal of Agricultural Science*, **1(1)**, 4-6.

Lahbib, K., F. Bnejdi and E. I. Gazzah (2012). Genetic diversity evaluation of pepper in Tunisia based on morphologic characters. *African Journal of Agricultural Research*, **7(23)**, 3413-3417.

Mahalanobis, P.C. (1936). On the generalized distance in Statistics. *Proceedings of National Academy of Sciences India*, **2**, 49-55.

Mellingers, J. S. (1972). Measures of genetic similarity and genetic distance studies in genetics. *V II Univ Tex Publication*, **27(13)**, 145- 153.

Pandey, S., P. K. Singh, S. Singh, A. Jha and R. Raghuwanshi (2011). Inter-trait relationship and variability in segregating population of muskmelon derived from intra-specific cross for total soluble solids and yield. *Indian Journal of Plant Genetic Resources*, **24**, 52–55.

Reddy, A. N. K., A. D. Munshi, T. K. Behera and A. K. Sureja (2005). Correlation and path analysis for yield and biochemical characters in snapmelon. *Sabrao Journal of Breeding and Genetics*, **39(1)**, 65-72.

Tomar, R. S., G. U. Kulakarni, D. K. Kakade, A. D. Patel and R. R. Acharya (2008). Genetic variability correlation and path analysis in muskmelon. *Asian Journal of Horticulture*, **3(1)**, 158-161.

Yatung, T., R. K. Dubey, V. Singh and G. Upadhyay (2014). Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morpho-chemical traits. *Australian Journal of Crop Science*, **8(1)**, 97-102.