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Research Article

Genetic Divergence Studies in Guava (*Psidium guajava* L.)

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Abstract

Thirty-two guava cultivars were studied for genetic divergence (Ward's minimum variance method) on the basis of growth and yield. Thirty two germplasm were distributed into six clusters. Cluster II was largest having eleven genotypes and was nearest to cluster III (28.200) and farthest to cluster VI (82.786). The maximum inter cluster distance was between cluster IV and cluster VI (222.411). Cluster VI had high mean cluster value for fruit set per cent in rainy and winter seasons and chlorophyll content. Chlorophyll content of leaves which had direct correlation with yield could play an important indication in parental selection. Cluster V and Cluster II had medium mean cluster value for the same characters. For the characters like length and breadth of bearing shoot and number of leaves on bearing shoot, Cluster I accounted for low mean cluster value but in case of fruit set per cent this cluster recorded medium mean cluster value. This cluster may contribute dwarfing characters in hybrids of a breeding program. In the present study, although the cluster distance between cluster IV and cluster VI was highest, keeping in view the lower yield of parent from cluster IV i.e., Barbadose Superior, cross combination between the genotypes of next most divergent clusters viz., Cluster I and Cluster VI can be considered for obtaining segregates of higher merit in future breeding program.

Key Words:
Guava, Genetic Divergence, Shoot Characters, Yield

Introduction

Guava (*Psidium guajava* L.), the champion fruit from family Myrtaceae, is known as poor-man's apple due to low fetching prices and one of the most referred and legendary fruits because of its hardy and prolific bearing nature(Dhaliwal and Singla, 2002). In the world, guava is one of the most important fruit crops. It is believed to be originated in tropical America stretching from Mexico to Peru. India contributes 45% of world production of guava followed by China (10%) and Thailand (6%). In India it is cultivated in an area of 219.7 thousand ha with a total production of 2571 thousand MT of fruit (NHB DATABASE 2010). Guava is successfully grown over a wide range of climatic conditions due to its wider adaptability. The ease in cultivation and precociousness of guava under Jharkhand condition makes it a suitable option for increasing the paddy equivalent yield of existing agriculture production system in this low soil fertility zone. Thus development of guava genotypes with higher yield potential under the eastern plateau condition is one of the important strategies for increasing the profitability of guava orcharding in the region. For crop improvement program aiming at development of model plant ideotype in guava, a proper understanding of interaction between plant growth processes and yield is highly essential. However, some long standing problems such as lack of dwarf and prolific fruit bearing genotypes, lack of soft seeded, colored genotypes require urgent attention of researchers. Estimation of genetic divergence and there from clustering of guava genotypes into homogenous clusters will help in designing hybridization program for harnessing heterosis and hybrid vigor. A study in that direction will provide ample opportunity to the researchers to understand different guava genotypes and their close association with particular characters. As guava bears fruit on current season's growth therefore estimation of genetic divergence on that characters and yield has been taken in the present experiment at ICAR RCER research Center, Ranchi with joint supervision of Visva Bharati.

Material and Methods

The study was conducted at ICAR Research Complex for Eastern Region, Research Centre, Ranchi during 2008-09 and 2009-10. This area is situated at an altitude of 620 m above mean sea level and at 23^0 25' N latitude and 85^0 20' E longitude with average annual rainfall (110-140 cm),high humidity (78.14 %-84.14 %) and low evaporation rate (4.04 mm/day) from June onward up to onset of winter (Sing,1999). The Soil is acidic with a pH range from 5.0-6.5.

The 32 guava genotypes conserved at Field gene bank of the centre were used as the experimental material for this study. The 32 guava genotypes under study was given below (Table1.)

Out of 32 genotypes only the six genotypes produced fruit during summer season. Therefore, the data were standardized to get standardized Euclidean ^{2} Distance. Summer season flowering, fruit set and yield data were excluded from the analysis. The mean data obtained on current season growth characters and rainy and winter and total yield of 2008 and 2009 collected from 32 diverse genotypes of guava were subjected to biometrical analysis and genetic divergence was estimated.

Results and discussion

In plant breeding, genetic diversity plays an important role because hybrids between genotypes of genetically diverse nature, generally, display a greater heterosis than those between closely related plants. This heterosis manifests into superior recombinants in further segregating generations. This has been observed in fescue maize, alfa alfa, cotton and several other crops. Hence, the major task before the plant breeder lies in the selection of suitable parents in order to obtained greater heterotic effects. However, it would be a daunting task to select for the most suitable and genetically diverse parents unless one has been provided with the necessary information with respect to genetic variability and genetic divergence present in the base population.

Generally, phenotypic or geographic diversity is considered as measure of genetic diversity. The genetic divergence had little relationship with the geographic distance as absorbed by random pattern of distribution of genotypes into various characters. Likewise, genotypes from different sources were grouped into the same cluster, thus, suggesting that geographical diversity does not necessarily represent genetic diversity. The findings in the present study were supported by Rai *et al.,* (2002); Saran *et al.,* (2006) and Santos *et al.,* (2011). Multivariate analysis by means of Ward's minimum variance algorithm is a potent tool in quantifying the degree of divergence among biological populations. The extensive use of this technique to assess the genetic diversity has long been recognized by several workers in different crop including Meghala *et al.,* (2005) in sapota, Rajan *et al.,* (2007) in guava, Saran *et al.,* (2007) in ber and Panda *et al*., (2009) in blue berry.

The multivariate analysis using Euclidean ^{2} Distance statistic in the population revealed that the genotypes were grouped into six clusters (Table 1). Cluster II comprised of maximum number of genotypes i.e. 11 followed by Cluster III with 9 genotypes, Cluster V with 5 genotypes, Cluster I with 4 genotypes and cluster VI with 2 genotypes. Only cluster IV was monogenotypic.

Further the magnitude of D^2 values suggest that there was considerable diversity in the material used in the present investigation.

Among 19 characters under study only 10 characters were observed to be vital in contributing to the genetic divergence. The maximum genetic divergence was contributed by fruit set in winter (F ratio 81.96, $P \leq 0.0001$) which was highly significant followed by chlorophyll in rainy season shoot (F ratio 56.04, $P \leq 0.0001$), chlorophyll content of winter season crop (F ratio 53.99, $P \leq 0.0001$), chlorophyll content of the summer (F ratio 46.00 $P \leq 0.0001$), number of flowers in bearing shoot in rainy (F ratio 37.09 $P \leq 0.0001$), number of flowers in bearing shoot in winter (F ratio 34.26 $P \leq 0.0001$) and winter season yield(F ratio 31.87 $P \leq 0.0001$). Other traits like rainy season yield (F ratio 24.06 $P \leq 0.0001$), total yield (F ratio 17.86 $P \leq 0.0001$) and number of leaves on bearing shoot in rainy season (F ratio 17.09 $P \leq 0.0001$) contributed meagerly to the total divergence.

The maximum genetic divergence (D^2 value) was observed between Cluster VI and Cluster IV (222.41) followed by Cluster VI and Custer I (140.618) and Cluster V and Cluster IV (125.442). The minimum inter cluster distance was obtained between Cluster II and Cluster I (25.049). Among the clusters Cluster IV showed minimum intra cluster distance (0.000) and Cluster III showed the maximum intra cluster distance 18.166. Hence, Cluster III possessed maximum degree of divergence within itself.

It is evident that Cluster VI had high mean cluster value (Table 3) for fruit set per cent in rainy and winter seasons and chlorophyll content. Chlorophyll content of leaves which had direct correlation with yield could play an important indication for parent selection. Cluster V and Cluster II had medium mean cluster value for the same characters. Cluster III exhibited medium mean cluster value for all the characters. Therefore, superior heterozygotes may not be obtained if parents are selected from this cluster (III). For the characters like length and breadth of bearing shoot and number of leaves on bearing shoot, Cluster I accounted for low mean cluster value but in case of fruit set per cent this cluster showed medium mean cluster value. This cluster may contribute dwarfing characters in hybrids of a breeding program. Having being lower fruit set mean value the genotypes in the Cluster IV should not be taken for hybridization program. Hence, with the objective to create dwarf and high yielding genotypes parent selection from Cluster VI and Cluster I are important.

For an efficient breeding program, selection of genetically divergence and superior genotypes is important. Therefore, making crosses between genotypes which would ensure the exploitation of heterosis and development of transgressive segregants. For estimation of maximum heterotic effects, selection of parents belonging to different clusters would be profitable. In this case, the gene pool of exotic germplasm like Barbadose Superior may be incorporated into indigenous germplasm belonging to different clusters. This may also help in obtaining transgressive segregation. For example, crosses could be effective between the genotypes in Cluster IV (Barbadose Superior) and with genotypes of Cluster VI (Sardar and Allahabad Safeda) or Cluster VI (Sardar and Allahabad Safeda) and Cluster I (Barkhana, Banarasi, Kairala Seedling and Apple Colour) or Cluster IV (Barbadose Superior) and Cluster V (Chittidar A.C., White Fleshed CHG-5, Chittidar, and CHG -1)

As cluster IV (Barbadose Superior) showed lower yield than average the cross combinations, Barbadose Superior x Sardar or Barbadose Superior x Allahabad Safeda are not recommended. However, transgressive segregants of higher merit may be obtained from these above cross combinations but probability would be very less. Therefore, crosses among second next genetically divergence groups Cluster VI (Sardar and Allahabad Safeda) and Cluster I (Barkhana, Banarasi, Kairala Seedling and Apple Colour) may be encouraged. The cross combination from parents of these clusters may be made to get dwarf and high yielding guava hybrid.

References

Dhaliwal, G.S. and Singla, R. 2002. Studies on the time of anthesis and dehiscence in different genotypesof guava in winter and rainy season crops. *Indian J. of Hort*., **59**: 157-161.

Meghala, R., Ravishankar, K.V., Anand, L. and Rekha, A. 2005. Genetic diversity of Indian sapota (*Manilkhara zapota*) genotypes characterized by RAPD markers. *Plant Genet. Res.*, **142**(1): 43-46.

Mitra, S.K. and Bose, T.K. 1996. Guava. **In**: Fruits: *Tropical and Subtropical*. T.K. Bose. and S.K. Mitra(eds.). Naya Prakash. Culcutta, pp 280-303.

National Horticulture Board. Data Base. 2010. Gourgaon, Haryana, India.

Panda, S.S., Hoogenboom, G. and Paz, J. 2009. Distinguishing blueberry bushes from mixed vegetation land use using high resolution satellite imagery and geospatial techniques. *Computer and Electronics in Agric.*, **67**(**1-2**): 51-58

Pandey, R. and Misra, K.K. 1984. Amrud. ICAR, New Delhi.

Radha, T. and Mathew, L. 2007. Fruit Crops. *Horti. Sci. Series-3*. K.V.Peter (Ed). P 59-72.

Rai, D., Mishra K.K. and Sing, V.P. 2002. Analysis of genetic divergence in bael gerplasm. *Prog.Hort.* **34**(**1**):35-38.

Rajan, S., Yadava, L. P., Kumar, Ram and Saxena, S. K. 2007. Genetic divergence in seed characteristics of guava: A basis for parent selection in hybridization. *Indian J. Hort.*, **64**(3): 290- .

Santos, C. A. F., Correa, L. C. and Da Costa, S. R. 2011. Genetic divergence among *Psidium* accessionsbased on biochemical and agronomical variables. *Crop. Breed . & App. Biotech.*, ***11:*** 149-156.

Saran, P.L., Godara, A.K. and Dalal, R.P. 2007. Biodiversity among Indian jujube (*Ziziphus mauritiana* Lamk.) genotypes for powdery mildew and other traits. *Not .Bot. Hort .Agrobot.* Cluj **35**(**2**): 15-21.

Saran, P.L., Godara, A.K., Yadav, I.S., Sehrawat, S.K. and Lal, G. 2006. Morphology diversity among Indian jujube (*Ziziphus mauritiana* Lamk.) genotypes collected at Hisar. *J.Food. Agric. & Environment.* **4**(**2**): 172-175.

Singh, H.P. 1999. Horticulture development in tribal areas. *Proc.Nat. Seminar on Sustainable Horti. Production in Tribal Regions.* July 25-26. pp 5-18.

Singh, S. and Chowdhary, B. D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi pp: 215-238.

Ward Jr. J. H. 1963. Hierarchical grouping to optimize an objective function. *J. American Stat. Assoc.* **58**: 236-244.

Table 1. Place and mode of origin of guava genotypes

S.No.	Genotypes	Place of origin	Mode of origin
1.	Kairala Seedling	Basti, U.P., India	Seedling selection
2.	Barkhana	Barkakhana, Jharkhand, India	Farmers' field selection
3.	Florida Fleshed	Florida, USA	Seedling selection
4.	Chittidar A.C.	Allahabad, U.P., India	Farmers' field selection
5.	Mild Fleshed	Eastern U.P., India	Seedling selection
6.	Seed Drop	Eastern U.P., India	Seedling selection
7.	Barbados Superior	Barbados	Seedling selection
8.	Surkhaguddi	Allahabad, U.P., India	Seedling Selection
9.	Chittidar	Eastern UP, India	Seedling selection
10.	Allahabad Collection	Allahabad, U.P., India	Farmers' field selection
11.	Sangam	Allahabad, U.P., India	Seedling selection
12.	Sardar	Lucknow, U.P., India	A selection from open pollinated population of Allahabad Safeda
13.	Allahabad Safeda	Allahabad, U.P., India	Selection made at Puna
14.	Mustafapur	Mustafapur, U.P., India	Seedling selection
15.	Behat Coconut	Saharanpur, U.P., India	Seedling selection
16.	Pear Shaped	Badun, U.P., India	Seedling Selection
17.	Apple Colour	Eastern U.P., India	Seedling Selection
18.	Harijha	Harijha, West Bengal, India	Seedling selection
19.	Banarasi	Banaras, U.P., India	Seedling selection
20.	Superior	Eastern U.P., India	Seedling selection
21.	White Fleshed	Eastern U.P., India	Seedling selection
22.	Guatemala	Guatemala	Seedling selection
23.	CHG-1	CHES, Ranchi, Jharkand, India	Farmers' field selection
24.	CHG-3	CHES, Ranchi, Jharkand, India	Farmers' field selection
25.	CHG-5	CHES, Ranchi, Jharkand, India	Farmers' field selection
26.	CHG-2	CHES, Ranchi, Jharkand, India	Farmers' field selection
27.	Spear Acid	Eastern U.P., India	Seedling selection
28.	Nasik	Nasik , Maharastra, India	Seedling selection.
29.	Eskwala	Ranchi, Jharkhand, India	Farmers' field selection
30.	Sindh	Sindh, Pakistan	Seedling Selection
31.	Patiala	Patiala, Punjab, India	Farmers' field selection
32.	Smooth Green	South India	Seedling Selection

*CHES- Central Horticultural Experiment Station, *CHG- CHES Guava
*A.C.-Allahabad Collection
*(Pandey and Mishra (1984), Mitra and Bose (1996) and Radha and Mathew (2007).

Data were taken on growth and flowering for standard methods. Total chlorophyll was measured by following formula using UV-VIS spectrophotometer Ranganna (1996):Total chlorophyll (mg/lit)= (7.12 x OD at 660nm)+(16.8 x OD at 642.5 nm).

Table 2. Distribution of 32 genotypes in different clusters

Cluster	No. of genotypes	Genotypes
Cluster I	4	Barkhana, Banarasi, Kairala Seedling, Apple Colour
Cluster II	11	Mild Fleshed, Seed Drop, Harijha, Superior, CHG-3,Nasik, Sindh, Pear Shaped, Patiala, Smooth Green, Eskwala
Cluster III	9	Florida Fleshed, Mustafapur, Surkhaguddi, Sangam, Guatemala, Spear Acid, Behat Coconut, Allahabad Collection, CHG-2
Cluster IV	1	Barbadose Superior
Cluster V	5	Chittidar A.C., White Fleshed, CHG-5, Chittidar, CHG-1
Cluster VI	2	Sardar and Allahabad Safeda

Table:3 Intra and Inter cluster average divergence (D^2) values of 6 clusters estimated from 32 genotypes of guava

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**8.609**	25.049	32.155	61.729	63.791	140.618
Cluster II		16.208	28.200	81.151	30.236	82.786
Cluster III			18.166	76.767	32.053	84.435
Cluster IV				0.000	125.442	222.411
Cluster V					12.176	32.014
Cluster VI						7.747

Table 4: Mean values of clusters estimated from 32 genotypes of guava for Current season's growth and yield

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
No. of leaves on bearing shoot(S*)	12.500	13,076	13.648	12.500	13.567	14.000
No. of leaves on bearing shoot(R*)	12.250	12.697	13.741	13.167	14.267	14.667
No. of leaves on bearing shoot(W*)	9.750	9.894	10.426	10.167	10.633	11.333
Length of bearing shoot(S*)	19.858	20.298	21.099	20.033	21.187	21.367
Length of bearing shoot(R*)	23.721	23.479	25.993	24.517	25.337	28.784
Length of bearing shoot(W*)	14.588	14.631	15.385	14.450	15.272	15.542
Breadth of bearing shoot(S*)	1.692	1.851	1.922	1.700	1.903	2.116
Breadth of bearing shoot(R*)	1.564	1.747	1.941	1.725	2.095	2.175
Breadth of bearing shoot(W*)	1.329	1.523	1.689	1.492	1.828	1.842
Chlorophyll content of leaves(S*)	7.490	10.725	8.402	7.583	12.626	16.293
Chlorophyll content of leaves(R*)	8.609	11.602	9.473	8.727	13.732	18.210
Chlorophyll content of leaves(W*)	5.776	8.798	6.645	5.850	10.899	15.201
No. of flower on bearing shoot(R*)	3.000	3.879	3.426	3.167	4.367	5.000
No. of flower on bearing shoot(W*)	2.375	2.758	2.796	0.000	3.500	4.333
Fruit set per cent (R*)	63.192	62.901	61.417	56.663	64.166	74.024
Fruit set per cent (W*)	73.956	67.877	69.288	0.000	72.220	81.667
Yield(R*)	14.587	19.994	17.543	14.634	23.200	26.650
Yield(W*)	8.758	10.252	8.967	0.000	11.870	13.542
**Total Yield (T*)	23.346	31.539	27.476	14.634	36.180	40.191

*S=Summer, *R=Rainy,*W= Winter, *T=Total
**Total Yield includes summer yield of six genotypes

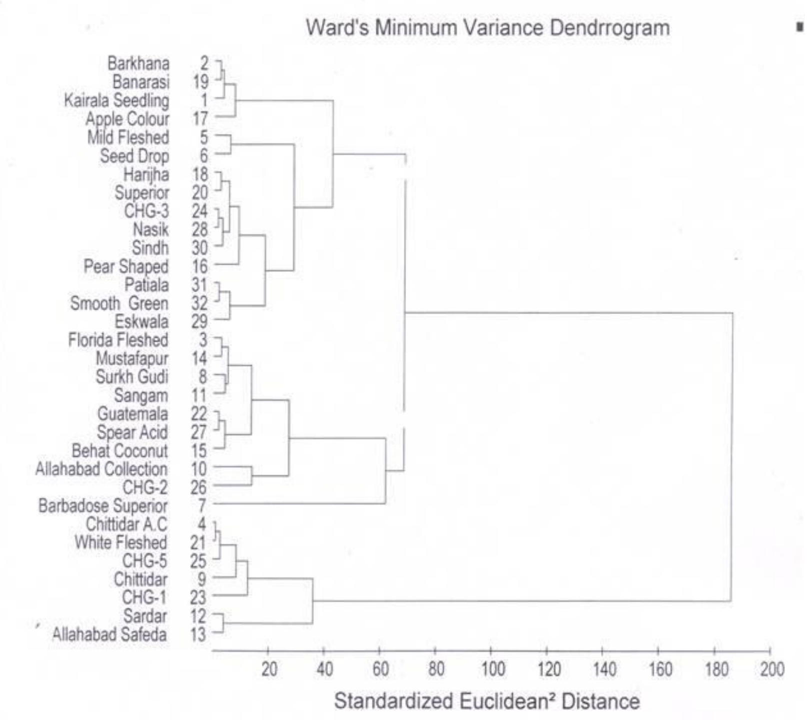

Fig 1. Ward's minimum variance Dendrogram (Standardized Euclidean ^{2} Distance)

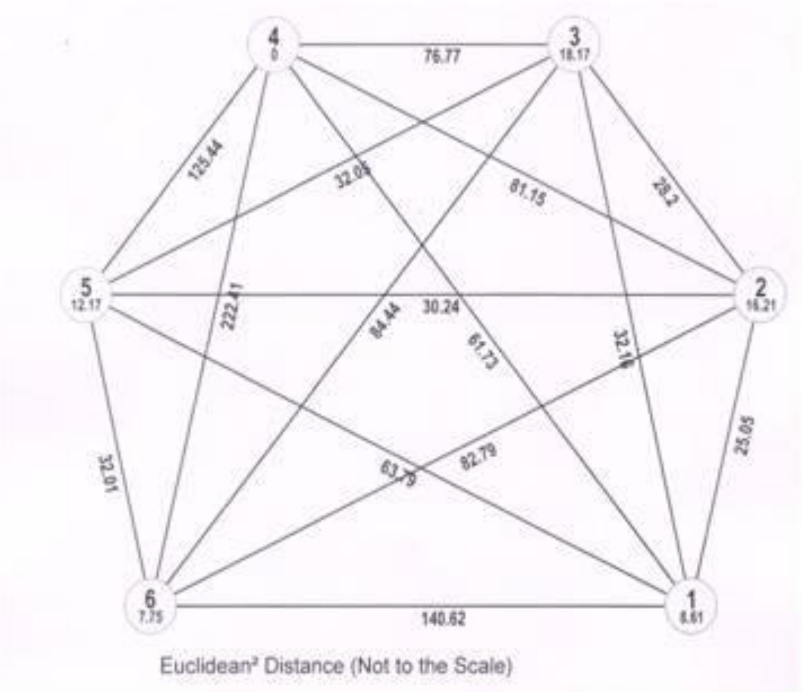

Fig. 2. Configuration of clusters and their mutual relationship through D^2 Analysis