The Pharma Innovation

Genetic divergence in guava (*Psidium guajava* L.) genotypes

Sri Pavani U, Dr. Tanuja Priya B, Dr. Madhumathi C and Dr. Reddi Sekhar M

Sri Pavani U
Department of Fruit Scence
College of Horticulture,
Dr. Y.S. R. Horticultural
University, Anantharajupeta,
Andhra Pradesh, India

Dr. Tanuja Priya B
Senior Scientist (Hort.)
AICRP on Spices, Horticultural
Research Station, Lam, Guntur,
Andhra Pradesh, India

Dr. Madhumathi C
Principal Scientist (Hort) &
Head. Horticulture.
CRS, Petlur, Andhra Pradesh,
India

Dr. Reddi Sekhar M
Professor, Department of
Genetics and Plant Breeding,
Acharya. N. G. Ranga,
Agicultural University, Sri
Venkateswara Agricultural
College, Tirupati, Andhra
Pradesh, India

Abstract
Sixteen guava genotypes were studied for genetic divergence (using Ward's minimum variance method) on the basis of yield and yield related characters. The genetic variation among genotypes was high enough to divide them into five clusters. Majority of genotypes were grouped in cluster IV. The cluster I showed the maximum intra cluster distance (53864.83) followed by cluster V (46774.31) while, the maximum inter cluster D^2 values were recorded between clusters IV and V (168563.80). The genotypes belonging to cluster IV (Allahabad Safeda, Nagpur Seedless, Parkers Dessert, Kohir Safeda, Lalit, Lucknow-49 x Nagpur Seedless) and cluster V (Lucknow-49, VNR-Bihi selection line (ARP)) are genetically more divergent, which indicates that the genotypes in these two clusters are highly heterozygous and are useful in hybridization programme to exploit effective hybrid vigour in future breeding plan.

Keywords: D^2 statistics, genetic divergence, cluster analysis, guava

Introduction
Guava (*Psidium guajava* L.), the apple of tropics has gained its momentum globally on account of its nutritive value, adaptability, moderate price and consumer acceptance (Iqbal *et al.,* 2009) [1]. It originated in Tropical America, stretching from Mexico to Peru, became a commercially significant crop in several countries (Menzel and Paxton, 1986) [6] and belongs to the Myrtaceae family. An accurate knowledge of genetic diversity available and the origin of cultivars would assist in the selection of parents in a hybridization programme. A careful study of germplasm would also help to eliminate duplicates in the germplasm collection, thus saving land, space and time. Deriving information on inheritance is difficult due to the high heterozygosity and highly cross-pollinated nature of the crop, besides a difficulty in crossing. However, it is extremely useful to generate information on genetic distance between varieties so that, based on the pedigree, as regards their parentage. 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 crops. Therefore,to analyze the genetic divergence to identify the superior genotypes.

Materials and Methods
The study was executed with sixteen genotypes *viz*., Allahabad Safeda, Allahabad Safeda selection (ARP), Allahabad Safeda selection-1 (SR), Parkers Dessert, Red Fleshed, Nagpur Seedless, Lalit, Chinese guava, Lucknow- 49, VNR- Bihi selection line (ARP), Allahabad Safeda selection-2 (SR), Safed Jam (Hybrid), Kohir Safeda (Hybrid), Red Fleshed x Saharanpur Seedless (Hybrid), Lucknow- 49 x Nagpur Seedless (Hybrid) and L- 46 under Randomized Block Design (RBD) at HRS, Anantharajupeta. Three replications were maintained and three plants per replication were used for collecting data. The genotypes were assessed quantitatively for yield and yield related characters. Wards minimum variance method was used for analysis. On the basis of D^2 values of all the 25 characteristics, sixteen genotypes were grouped into five clusters based on Wards minimum variance method and the crosses were made between the selected genotypes grouped in different clusters.

Results and Discussion
Genetic diversity is one of the important pre-requisite for any crop improvement programme. Divergence analysis generates valuable information on the nature and degree of genetic diversity, which helps in selecting desirable lines from germplasm for successful breeding

Corresponding Author:
Sri Pavani U
Department of Fruit Scence
College of Horticulture,
Dr. Y.S. R. Horticultural
University, Anantharajupeta,
Andhra Pradesh, India

programme. Involvement of genetically diverse parents is essential to generate new variability and to look for desirable recombinants with respect to enhanced yield, quality and resistance to biotic stresses. The multivariate analysis using Mahalanobis D^2 statistics is a valuable tool for obtaining quantitative estimates of divergence between biological populations.

Sixteen genotypes were grouped in to five clusters based on the wards minimum variance method. Among the five clusters, cluster IV was the largest, comprising of six genotypes (Allahabad Safeda, Parkers Dessert, Nagpur Seedless, Kohir Safeda, Lalit and Lucknow-49 x Nagpur

Seedless) followed by cluster I with three genotypes (Allahabad Safeda selection-2 (SR), Allahabad Safeda selection -1(SR) and L-46), cluster III with three genotypes (Red Fleshed, Red Fleshed x Sahranpur Seedless and Chinese guava), cluster II with two genotypes (Allahabad Safeda selection (ARP), Safed Jam) and cluster V with 2 genotypes (Lucknow-49 and VNR- Bihi Selection line (ARP)), respectively (Table 1 and Fig 1). The pattern of distribution of genotypes into different clusters was at random. The genotypes belonging to same geographic origin were included in different clusters.

Table 1: Cluster composition of 16 guava genotypes

| S. No	Cluster	No. of genotypes included	Genotypes
1.	I	3	Allahabad Safeda selection -2(SR), Allahabad Safeda selection -1(SR), L-46
2.	II	2	Allahabad Safeda selection (ARP), Safed Jam (Hybrid)
3.	III	3	Red Fleshed, Red Fleshed x Sahranpur Seedless, Chinese guava
4.	IV	6	Allahabad Safeda, Parkers Dessert, Nagpur Seedless, Kohir Safeda (Hybrid), Lalit Lucknow-49 x Nagpur Seedless
5.	V	2	Lucknow-49, VNR- Bihi Selection line (ARP)
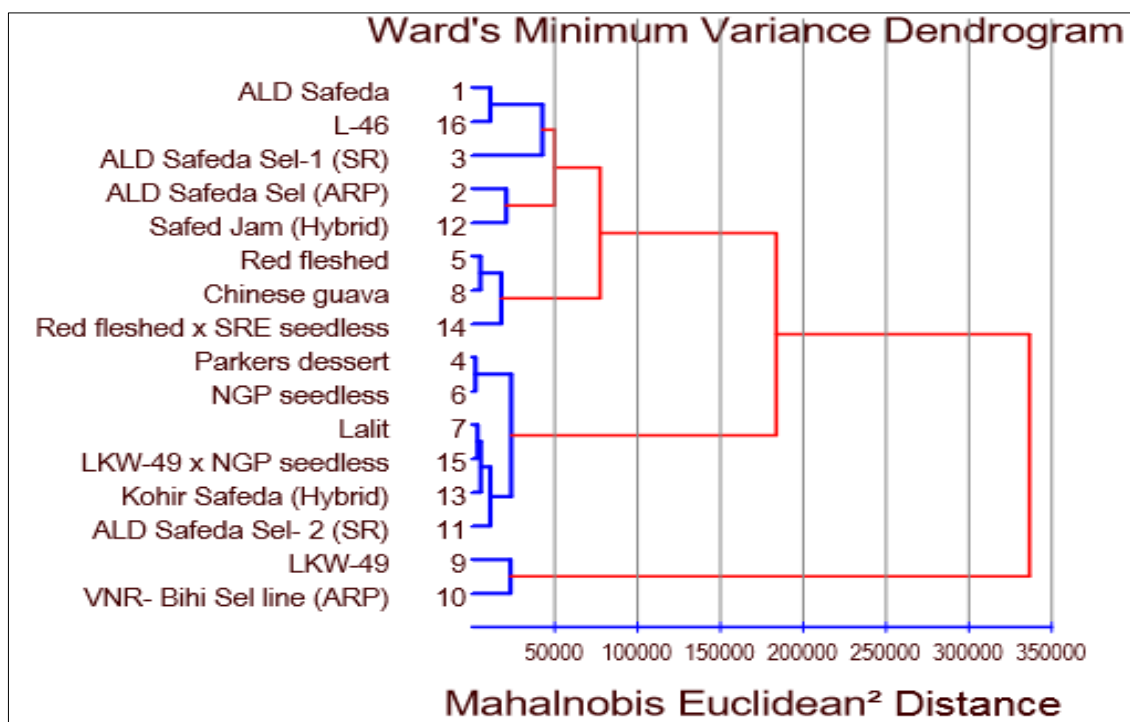
Fig 1: Dendrogram showing cluster pattern (wards minimum variance method) of sixteen guava genotypes

The intra-cluster distance was found to be maximum in cluster I (53864.83), while the inter-cluster distance was maximum between IV and V (168563.80) (Table 2 and Fig 2). The genotypes belonging to cluster IV (Allahabad Safeda, Nagpur Seedless, Parkers Dessert, Kohir Safeda, Lalit, Lucknow-49 x Nagpur Seedless) and cluster V (Lucknow-49, VNR-Bihi selection line (ARP)) are genetically more divergent, which indicates that the genotypes in these two clusters are highly heterozygous and are useful in hybridization programme to exploit effective hybrid vigour. Thus, these constituent genotypes from diverse clusters could be used for increasing fruit yield through intra varietal hybridization (Mandal and Banerjee 1991) [5].

The magnitude of inter-cluster distance measures the genetic distance between two clusters while the intra-cluster distance measures the extent of genetic diversity between the genotypes of same clusters (Krishna veni *et al*., 2008) [3]. In

general, the inter-cluster distance was relatively higher. The maximum inter cluster D^2 values were recorded between cluster IV and V (168563.80), while the minimum D^2 value was found between cluster I and II (70166.78) (Table 2). Average inter and intra cluster distances revealed that inter cluster distances were much higher than those of intra cluster distances.

Table 2: Average intra and inter cluster D^2 values of guava genotypes

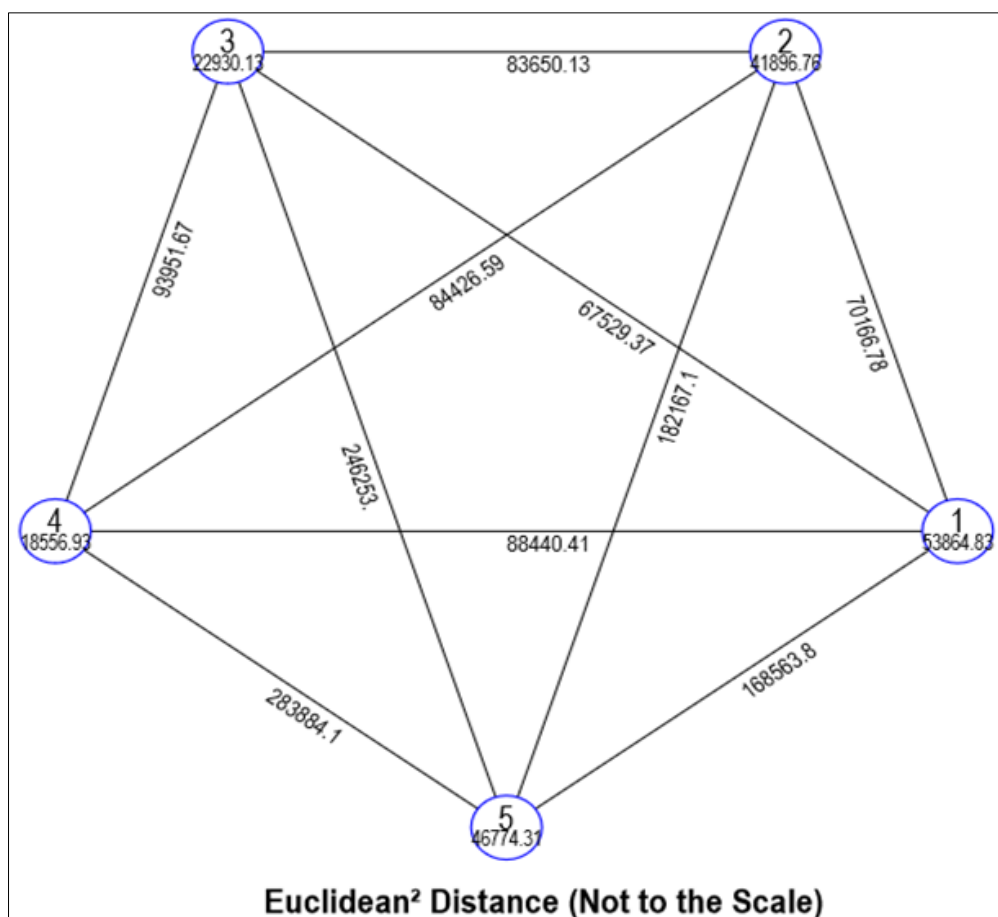| Cluster	I	II	III	IV	V
I	53864.83	70166.78	67529.37	88440.41	168563.800
II		41896.76	83650.13	84426.59	182167.100
III			22930.13	93951.67	246253.000
IV				18556.93	283884.100
V					46774.310

Fig 2: Allocation of clusters based on intra and inter-cluster distance

Differences in genetic constitution and the presence of unabated influence of environmental factors might be responsible for this type of clustering pattern (Rahaman *et al*., 1997) [8]. In addition, the clustering pattern in the present study indicated that genetic diversity was not necessarily related to geographical distribution. Further, genotypes from different geographical regions were grouped in the same clusters. This might have been due to the free exchange of propagating materials from one place to another. The findings in the present study were supported by Sharma *et al*. (2010) [10], Santos *et al*. (2011) [9], Nasution and Hadiati (2014) [7], Singh *et al*. (2014) [11] and Jana *et al*. (2015) [2]. The higher inter cluster distances compared to intra cluster distances suggests homogeneous and heterogeneous nature of the germplasm lies within and between the clusters, respectively. Hence, hybridization between the genotypes included in these clusters may exert high heterotic effects and consequently may generate desirable segregants.

It is indicated that low to moderate genetic diversity among the guava genotypes might be due to the existence of natural seedling selections from various varieties.

Conclusion

Grouping of accessions into different clusters and the information on inter and intra cluster distances depict the choice of parents for evolving progenies with high heterotic effect (Meena and Bahadur, 2013). Thus, the present study revealed that the genotypes of cluster IV & V may be utilized as best combining parents in hybridization programme for successful recombination to accrue constructive genes in particular variety.

References

1. Iqbal M, Khan MO, Jalal-ud-din KR, Munir M. Effect of foliar application of NAA on fruit drop, yield and physico-chemical characteristics of guava (*Psidium guajava* L.) Red Flesh cultivar. Journal of Agricultural Research. 2009;47:259-69.
2. Jana BR, Munsi PS, Manna DC, Sarkar H, Bikash Das. Genetic divergence studies in guava (*Psidium guajava* L.). Electronic Journal of Plant Breeding. 2015;6(1):161-166.
3. Krishna Veni B, Pramila Rani B, Raman MV. Genetic divergence studies in soyabean (*Glycine max* L.). Soyab. Res. 2008;6:77-80.
4. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Institute of Science, India. 1936;2:49-55.
5. Mandal AB, Banerjee SP. Genetic divergence in Safflower (*Carthamus tinctorius* L.). Phytobreedon. 1991;7:29-36.
6. Menzel CM, Paxton BF. The pattern of growth, flowering and fruiting of guava varieties in subtropical Queensland. Australian Journal of Experimental Agriculture. 1986;26:123-28.
7. Nasution F, Hadiati S. Characterization and clustering of some guava germplasm collections based on leaf and fruit characters. Agrivita Journal of Agricultural Science. 2014;36:91-100.
8. Rahaman M, Hossain M, Das ND. Genetic divergence in Betelvine (*Piper betle* L.). Journal on Plantation Crops. 1997;25:57–61.
9. Santos CAF, Correa, LC, Costal SR. Genetic divergence

among *Psidium* accessions based on biochemical and agronomic variables. Crop Breeding and Applied Biotechnology. 2011;11:149-56.

10. Sharma A, Sehrawat SK, Singhrot RS, Tele A. Morphological and chemical characterization of *Psidium* Species. Notulae Botanicae Horit Agrobotanici Cluj-Napoca. 2010;38(1):28-32.

11. Singh BK, Singh S, Pal AK. Morphological Chemical attributes of guava (*Psidium guajava* L.) cultivars. Indian Horticulture Journal. 2014;4(3/4):2249-6823.