

# Genetic Divergence of Cape Gooseberry (*Physalis peruviana* L.) Genotypes in India

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## Abstract

Genetic divergence of 12 Cape gooseberry Indian genotypes for morphological parameters was estimated using Mahalanobis D<sup>2</sup>-analysis. The genotypes were grouped into four clusters, the cluster-II was the largest with 5 genotypes followed by cluster I and cluster IV with 3 genotypes, and cluster III with 1 genotype. Clustering pattern indicated no association between geographical distribution of genotypes and genetic divergence. The inter-cluster distances were higher than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster value was maximum in cluster I and II and minimum cluster III and IV. The inter-cluster D<sup>2</sup>-values indicated maximum distance between cluster I and IV followed by between I and III, and between I and II, showing wide diversity between the groups. Fruit diameters, duration of fruit set to maturity, number of flower per branch, fruit weight and inter-nodal length showed maximum contribution towards total divergence among the genotypes. Thus, the genetically diverged genotypes identified in this study, could be used as parents in hybridization programme for getting desirable segregants.

## Highlights

- Genetic divergence of Cape gooseberry was estimated by Mahalanobis D<sup>2</sup>-analysis.
- Genotype selection done by divergence method.
- Diversity positively correlates with heterosis.

**Keywords:** Cape gooseberry, genetic divergence, *physalis peruviana*, cluster, D<sup>2</sup> analysis

Cape gooseberry (*Physalis peruviana* L.) is a minor fruit of family Solanaceae and indigenous to South America. It is also found in Asian and African countries, with common name such as "Poha" in Hawaii, Golden Berry in South Africa, and Rasbhari, Makoi or Teparu in India. The plants are green, herbaceous and composed of 8 to 12 nodes in each plant. Flowers are unique, pedunculate and hermaphrodite which are derived from the axillary

bud with five yellow petals. Calyx is green in colour which consist five sepals around 5 cm long, covering completely the fruit during throughout its development. It can grow around 1.0 to 1.5 meters height. However, with training it can exceed up to 2.0 meters height (Fischer 2000). When the fruit is ripened, calyx shows a brown colour which is an indicator for determining the point of harvest (Avila *et al.* 2006).



The fruits of Cape gooseberry are very attractive in colour at maturity and if properly packed it can easily be sent to distant market. The fruit type is berry like a small globe having colour from green to yellowish with the diameter around 12.5 to 25.0 millimeters and a weight ranges from 4 to 10 g, containing around 100 to 300 seeds. The fruit is small round, bright orange and sweet when ripe, making it ideal for preparing natura, pies and jams. Pulp of *Physalis* fruits show high level Moisture (78.9 g/100 g), Protein (0.05–0.3 g /100 g), Lipid (0.15–0.2 g/100 g), Carbohydrate (19.6 g/100 g), Fiber (4.9 g/100 g), Ash (1.0 g/100 g), Calcium (8.0 mg/100 g), Phosphorus (55.3 mg/100 g), Iron (1.2 mg/100 g), Carotene (1.6 mg/100 g), Thiamine (0.1 mg/100 g), Riboflavin (0.03 mg/100 g), Niacin (1.70 mg/100 g) and Ascorbic acid (43.0 mg/100 g) (Ramadan and Morsel 2004). A number of species in the genus are of horticultural and economic importance due to their high nutritional value and high vitamins content, minerals and antioxidants as well as its anti-inflammatory, anti-cancer and other medicinal properties (Martinz *et al.* 2010; Y en *et al.* 2010; Wu *et al.* 2009; Franco *et al.* 2007; Ramdan and Moresel 2003).

In crop improvement programme the choice of superior parents are desired for hybridization, besides the knowledge of combining ability and magnitude of gene action involved in the expression of important traits were it was important at the beginning of our breeding program to discriminate among available genotypes to establish the level of genetic diversity and thereby, identify the most suitable materials for crossing. D<sup>2</sup> statistics (Mahalanobis 1936) based divergence study which includes multivariate analysis of quantitative traits is one of the such a powerful tool for measuring divergence among a set of population using the concept of statistical distance utilizing multivariate measurements. In the present work, twelve poorly characterized genotypes of Cape gooseberry were used to study the genetic divergence, and to identify the suitable parents for hybridization.

## Materials and methods

The field experiment was conducted at the experimental field of Horticulture Garden, Bihar Agricultural College, Sabour, Bhagalpur (87° 2' 42" E, 25° 15' 40" N) at an altitude of 46 m above mean sea level in the heart of vast Indo-Gangatic plains of

north India. The climate of this place is sub-tropical of slightly semi-arid in nature and characterized by dry summer, moderate rainfall and cold winter. Weather condition from January-February are usually the coldest months (mean temperature falls as low as 10.4°C), whereas April-May are generally the hottest months (the maximum average temperature of 37°C).

The plant material consisted of twelve genotypes of Cape gooseberry (*Physalis peruviana* L.) viz., CITH Sel-1, CITH Sel-3, CITH Sel-5, CITH Sel-7, CITH Sel-9, CITH Sel-11, CITH Sel-15, CITH Sel-16, (collection of CITH, Srinagar, Jammu and Kashmir, India), SS/VK/301, SS/VK/401, SS/VK/501 and SS/VK/601 (local genotypes of Bihar). D<sup>2</sup> statistics (Mahalanobis in 1936) was used to measure the group distance based on multiple characters.

## Results and discussion

The grouping of genotypes in distinct clusters is performed to arrange genotypes in order of their relative distances (D<sup>2</sup> values) from each other. After arranging the D<sup>2</sup> values, cluster formation was done using Tocher's method (Rao 1952). The data value of clustering of genotypes is presented in Table 1. Results of D<sup>2</sup> analysis revealed that 12 genotypes were grouped into four clusters as shown in Table 1. the cluster-I consists of genotypes (CITH Sel-7, CITH Sel-9, CITH Sel-16), cluster-II consists of genotypes (CITH Sel-1, CITH Sel-3, CITH Sel-5, CITH Sel-11, CITH Sel-15) and the cluster-III consist of only one genotypes (SS/VK/401), while the cluster-IV consists genotypes (SS/VK/301, SS/VK/501, SS/VK/601)

**Table 1:** Clustering of 12 genotypes on the basis of D<sup>2</sup> analysis

Cluster	Genotypes
I	CITH Sel-7, CITH Sel-9, CITH Sel-16
II	CITH Sel-1, CITH Sel-3, CITH Sel-5, CITH Sel-11, CITH Sel-15
III	SS/VK/401
IV	SS/VK/301, SS/VK/501, SS/VK/601

The average inter and intra cluster distances is shown in Table 2. The highest intra-cluster distance observed for cluster-II (31.76) followed by cluster-I (19.01) respectively. The highest inter-cluster distance observed in between cluster-I and cluster-III (343.71) followed by between cluster-I



and cluster-IV (330.76) and cluster-I and cluster-II (263.73) and cluster-III and cluster-IV (112.43). The lowest value of inter cluster distance was observed between cluster-II and cluster-III (39.29).

**Table 2:** Inter and intra-cluster distances

Cluster	I	II	III	IV
I	19.016	263.735	330.761	343.711
II	263.735	31.764	50.284	39.293
III	330.761	50.284	0.000	112.432
IV	343.711	39.293	112.432	0.000

**Table 3:** Cluster means of four clusters for different characters.

Clusters	Plant Girth (cm.)	Plant Height (cm.)	Inter-nodal length (cm.)	Period of appearance of 50% flowering (days)	Period of bud break to full bloom (days)	flowers/branch	fruits set/branch	Duration of Fruit Set to Maturity (days)	Fruit Weight (g.)	Fruit Diameter (mm)	Fruits/Plant
I	4.237	95.124	9.320	48.208	7.375	13.305	10.654	51.430	15.982	31.084	90.125
II	4.510	117.942	15.612	74.667	7.667	8.055	6.555	59.555	9.258	15.060	47.333
III	4.323	119.220	12.177	76.333	8.333	7.220	6.443	66.113	9.903	15.073	37.667
IV	4.133	115.887	13.510	74.833	6.333	7.000	5.887	56.443	11.523	15.187	34.667
Percent contribution toward total divergence	0.00	0.00	6.06	0.00	0.00	18.18	0.00	18.18	16.67	40.91	0.00

The diversity analysis using  $D^2$  statistics showed that some of the genotypes were very diverse. The clustering on the basis Tocher's method resulted 4 clusters of 12 genotypes namely, the cluster-I consists of genotypes (CITH Sel-7, CITH Sel-9, CITH Sel-16), cluster-II consists of genotypes (CITH Sel-1, CITH Sel-3, CITH Sel-5, CITH Sel-11, CITH Sel-15) and the cluster-III consists genotypes (SS/VK/301, SS/VK/501, SS/VK/601) while the cluster-IV consist of only one genotypes (SS/VK/401). The highest intra-cluster distance observed for cluster-II (31.76) followed by cluster-I (19.01) respectively. Moreover, the genotypes belonging to cluster with the highest inter-cluster distance observed in between cluster-I and cluster-III (343.71) followed by between cluster-I and cluster-IV (330.76) and cluster-I and cluster-II (263.73) and cluster-III and cluster-IV (112.43). It could be desirable for selection of genotypes for hybridization. If more diversity will be their then greater chance of heterosis will be found.

Characters means of Cape gooseberry genotypes falling under different clusters are shown in Table 3. The maximum contribution was shown by fruit diameter (40.91%) followed by number of flower per branch and duration of fruit set to maturity confirming the existence of ample amount of divergence in genotypes with respect to the traits and hence the selection of best genotypes for such traits would be helpful in utilizing the maximum heterosis in future breeding.

## Conclusion

The selection of genotype on the basis of trait contributing most towards divergence could be useful to determine the diverse parent. In this regard the trait like fruit diameter (40.91%) that contributed most in the divergence of genotypes of Cape gooseberry could be a trait of choice while selecting a genotype. Hybrids development can be a good strategy of breeding for this crop. The use of hybrids can improve the yield performance of Cape gooseberry without affecting fruit quality.

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