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# Genetic variability analysis of coloured grape varieties for berry traits

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**Abstract**
Genetic variability present among the genotypes help the breeder to decide the parents for different crossing programmes; besides diversity amongst the parent increases the chances for the exploitation of heterosis. The present investigation was planned to analyse the genetic diversity among twenty six coloured and seeded grape cultivars for five important fruit traits *viz*., berry diameter (mm), berry length (mm), single berry weight (g), average bunch weight and bunch length (mm) using principal component analysis and cluster analysis. For the traits under study, the principal component one (PC1) with Eigen values 3.63 has contributed to 72.61% of variability; whereas principal component two (PC2) has contributed 22.88% variability and the cumulative variability among the 26 grape genotypes depicted by PC1 and PC2 was 95.49%. The twenty six grape genotypes were grouped into three clusters. Among all the clusters, cluster-I has highest number of grape genotypes (15) followed by cluster-III (06) and cluster-II (05) respectively. The high intra and inter cluster distances indicates the presence of substantial amount of genetic diversity in the genetic material.

**Keywords:** Grape, genetic variability. berry traits, clustering and principal component analysis

## 1. Introduction
Grape (*Vitis vinifera* L.) is a high value fruit crop which is being practiced in almost all climatic conditions in India; from tropical to temperate and spread over different states of the country. Grape cultivation on a commercial basis is about seven decades old and now considered as most remunerative amongst all fruit cultivation in the country. India is amongst the major table producer in world and fetching handsome foreign exchange through its export. The narrow genetic base of grape Genepool available in India is major concern restricting the genetic improvement ingenuities. Diversity forms the base for selection. Deciphering the genetic diversity present among available grape gene pool provides the breeder an understanding for planning future breeding programs and to decide the parentage for different breeding endeavours. The chances of exploiting hybrid vigour increases with involvement of genetically diverse parent in crop improvement program. The present investigation was planned in view of getting an insight about the diversity present for important fruit trait which in turn may help in selection of parents.

## 2. Materials and Methods
The present investigation was conducted at ICAR-National Research Centre for Grapes, Pune during 2021-22 to analyse the genetic diversity present among twenty six coloured and seeded grape cultivars for five important fruit traits *viz*., berry diameter (mm), berry length (mm), single berry weight (g), average bunch weight and bunch length (mm) using principal component analysis and cluster analysis. These twenty six coloured and seeded grape genotypes (Table.1) were maintained under uniform horticultural and inter-cultivation practices wherein double pruning and single cropping practice was followed. For recording the observations on different traits; five vines of each genotypes were used; total five bunches per vine were harvested and ten berries from each bunches from top, middle and lower portion were sampled at the time of maturity.

**Table 1:** Coloured and seeded grape genotypes used in present investigation

| No. | Genotype | No. | Genotype |
|---|---|---|---|
| 1 | Amber Queen | 14 | Christmas Rose |
| 2 | Black Champa | 15 | Concord |
| 3 | Ruby Red | 16 | Gulabi |
| 4 | Ribier | 17 | Hussain Black Kabuli |
| 5 | Black Hamburg | 18 | Khalili |
| 6 | Gulabi | 19 | Manjari Medika |
| 7 | Madhu Angoor | 20 | Muscat Hamburg |
| 8 | Benzuhio | 21 | Pusa Navrang |
| 9 | Pusa Navrang | 22 | Red Globe |
| 10 | Olympia | 23 | Red Prince |
| 11 | Carolina Black Rose | 24 | Ribier |
| 12 | Rizamat | 25 | Rizamat |
| 13 | Concord | 26 | Ruby Red |

The genetic variation can be either estimated using Univariate analysis or by multivariate analysis. Conventionally Univariate analysis has been the most accepted biometrical method to work out genetic variations. In recent years, multivariate analysis has gained popularity and Principal Component Analysis (PCA), cluster analysis and Principal Coordinate Analysis (PCoA) have been employed to workout similarities and differences between different genotypes regarding multiple traits under examination [10]. The Principal Component Analysis (PCA) help to identify small number of uncorrelated variables (principal components) from correlated variables which explains the variation present in large data set. Recently various researchers had employed PCA analysis to assess the variability for different traits in many crops like fruit traits in mango [3, 4]; in banana for fruit pulp mineral profile [8]; Phenotypic divergence of grapes [5]; Chemometric Analysis of Grapes [9]; physical and chemical indexes of wine grape used for grape grading [7] etc. Whereas clustering help to partition large datasets into different small sub-groups or clusters based on the similarity measure. This approach is mainly used to find similarities between data points. Over the years various clustering techniques are developed and used. The '*k*-means' clustering algorithm is one of the widely used data clustering methods where the datasets having "*n*" data points are partitioned into "*k*" groups or clusters. The *k*-means grouping algorithm was initially proposed by MacQueen in 1967 [6] and later enhanced by Hartigan and Wong in 1979 [2]. In present study grape genotypes were grouped into different clusters using *k*-mean algorithm based on similarities and differences. The Principal Component Analysis (PCA) and '*k*-means' clustering were carried out using Paleontological Statistics Software Package for Education and Data Analysis [1].

## 3. Results and Discussion

The success of any crop improvement programme depends upon variability present at the genetic level. The statistical examination shown that sufficient variability was present among the cultivars for different fruit traits under study.

### 3.1 Principal Component Analysis

The Principal Component Analysis produced five principal components. A scree plot was drawn from the Eigen values associated with a component in descending order. These components were arranged in scree plot in order of their variability manifestation from largest to smallest (Fig 1). The principal components i.e. PC1 and PC2 has Eigen values more than one and hence as per rule these two components were considered as important ones in view of exploring the variability present among the genotypes.

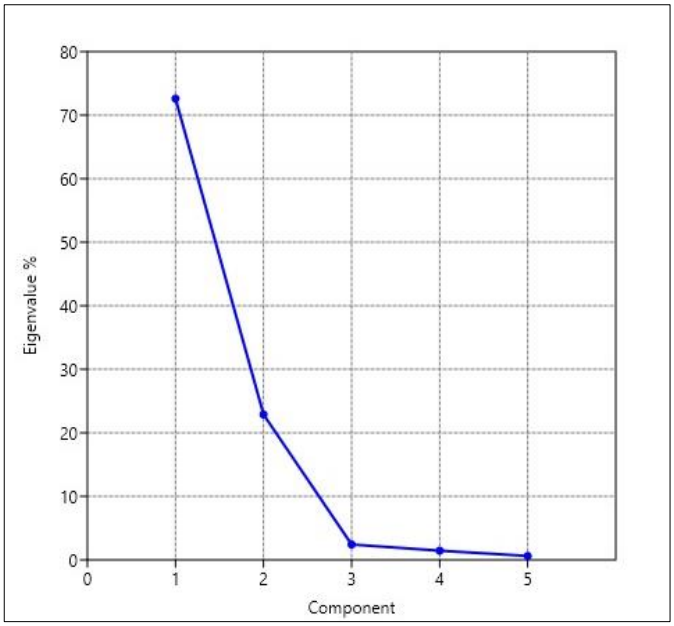


**Fig 1:** Scree plot presenting the Eigen values of different Principal Components

The details of principal components produced, their respective Eigen values, per cent variability portrayed by each component and cumulative per cent of the variability are furnished in Table 2. A total of five principal components were observed signifying the variance of 72.61%, 22.88%, 2.43%, 1.45% and 0.63% respectively. The PC1 with Eigen value 3.63 has deciphered 72.61% variability followed by PC2 with Eigen value 1.14 has interpreted 22.88% variability. The principal components PC1 and PC2 covered the 95.49% variability present for the traits under study and were significant enough to highlight the variability present amongst the genotypes.

**Table 2:** Contribution of each Principal Component towards variability

| Principal Component | Eigenvalue | Variance (%) | Cumulative variability (%) |
|---|---|---|---|
| PC1 | 3.63 | 72.61 | 72.61 |
| PC2 | 1.14 | 22.88 | 95.49 |
| PC3 | 0.12 | 2.43 | 97.92 |
| PC4 | 0.07 | 1.45 | 99.37 |
| PC5 | 0.03 | 0.63 | 100 |

The correlation of different variables with respective Principle Components showed that all five berry traits i.e. *viz*., berry diameter, berry length, single berry weight (g), average bunch weight and bunch length have positive loading on PC1 (Table 3).

**Table 3:** Correlation of Principal Components with original variables

| Sr. No. | Traits | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|---|
| 1 | Berry diameter (mm) | 0.891 | -0.422 | -0.044 | 0.115 | 0.116 |
| 2 | Berry length (mm) | 0.929 | -0.271 | 0.178 | -0.178 | 0.005 |
| 3 | Single berry weight (mg) | 0.957 | -0.238 | -0.025 | 0.099 | -0.132 |
| 4 | Bunch weight (g) | 0.846 | 0.466 | -0.240 | -0.100 | 0.010 |
| 5 | Bunch length (mm) | 0.586 | 0.787 | 0.172 | 0.089 | 0.018 |

The variables like berry length and single berry weight has maximum impact on defining PC1 whereas for PC2; bunch length and bunch weight were influencing variables (Fig 2).

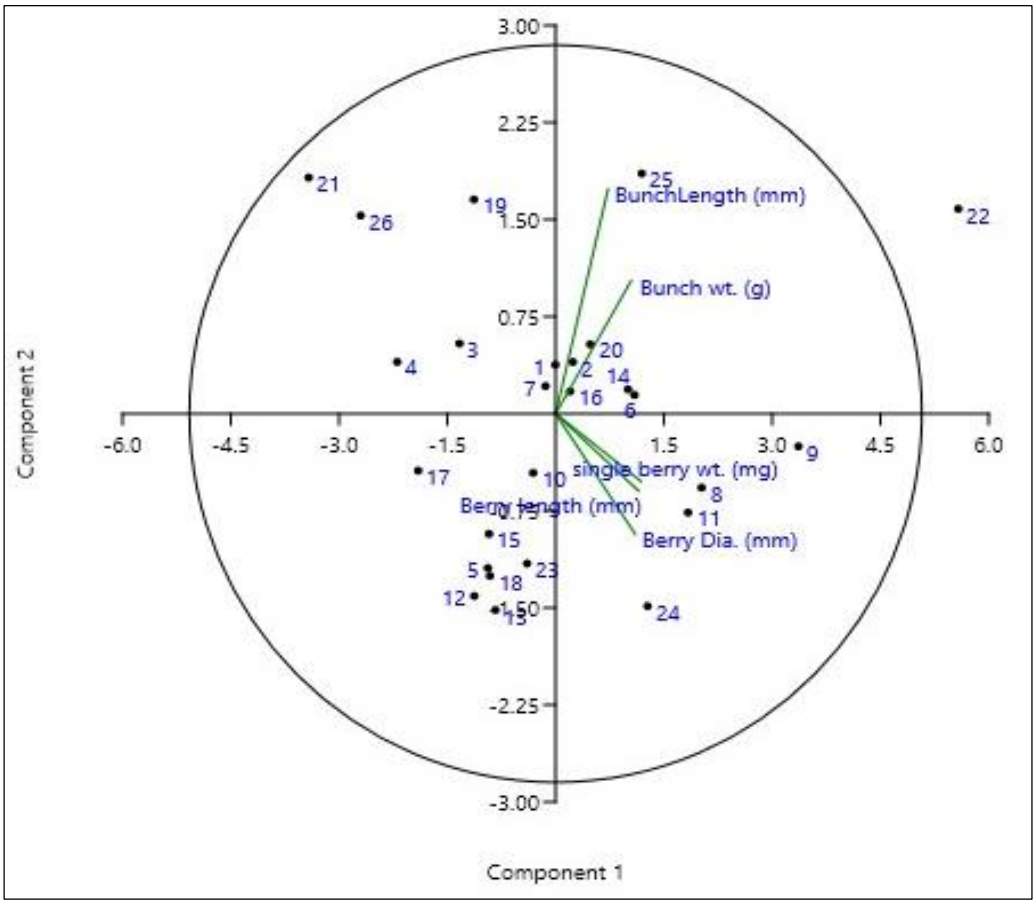


**Fig 2:** Bi-plot showing the influence of different variables on PC1 and PC2

**3.2 K-Mean clustering:** The 'K-mean' algorithm was employed to group the twenty six coloured and seeded grape genotypes under study. Grouping done was based on the similarities and dissimilarities present among the individuals. 'Elbow' method was employed to define the optimal cluster numbers and it helped to put the candidates with similarities in a same cluster. With elbow method three clusters were found optimum. The mutual relationships between the clusters revealed that inter-cluster distance values were greater than intra-cluster values. The high inter cluster distances indicates the presence of substantial amount of genetic diversity in the genetic material (Table 4).

**Table 4:** Inter-cluster distances present amongst the clusters formed

| Cluster No. | I | II | III |
|---|---|---|---|
| I | 0.000 | 2,154.241 | 1,466.131 |
| II | 2,154.241 | 0.000 | 3,618.696 |
| III | 1,466.131 | 3,618.696 | 0.000 |

The twenty six genotypes were grouped into three clusters wherein clusters-I has highest number of grape genotypes (15) followed by cluster-III (06) and cluster-II (05) respectively. Cluster-II had five genotypes *viz*., Banglore Purple, Benzuhio, Carolina Black Rose, Red Globe and Ribier with bold berry size (>18mm) and higher single berry weight (>4g). While cluster-III had all '*tenurier'* genotypes with both skin and flesh having anthocyanin pigmentation in a group except Hussain Black Kabuli and Amber Queen.

**Table 5:** Clusters and its membership

| Cluster No. | Member genotypes | Total Genotypes per cluster |
|---|---|---|
| I | Alamvick, Alden, Amber Sweet, Angoor Kalan, Athens, Black Champa, Catawba, Champion, Christmas Rose, Concord, Gulabi, Khalili, Muscat Hamburg, Red Prince and Rizamat | 15 |
| II | Banglore Purple, Benzuhio, Carolina Black Rose, Red Globe and Ribier | 05 |
| III | Alicante Bouschet, Amber Queen, Hussain Black Kabuli, Manjari Medika, Pusa Navrang and Ruby Red | 06 |

## 4. Conclusion

In the present investigation; the principal component analysis and cluster analysis has showed that significant genetic diversity was present among twenty six coloured and seeded grape cultivars for five important fruit traits *viz*., berry diameter (mm), berry length (mm), single berry weight (mg), bunch weight and bunch length (mm). The principal component one (PC1) has contributed to 72.61% of variability; whereas principal component two (PC2) has contributed 22.88% variability and the cumulative variability among the 26 grape genotypes depicted by PC1 and PC2 was 95.49%. These two components covered maximum variability present for all five fruit traits. The twenty six grape genotypes were grouped into three clusters. The high inter cluster distances indicates the presence of substantial amount of genetic diversity in the genetic material. Cluster-II represented the five genotypes *viz*., Banglore Purple, Benzuhio, Carolina Black Rose, Red Globe and Ribier with bold berry size (>18mm) and higher single berry weight (>4g). The candidates in cluster-II has better fruit traits suitable for table purpose. Whereas cluster-III had all '*tenurier'* genotypes in a group except Hussain Black Kabuli and Amber Queen. The members belonging to different clusters are divergent and if used in breeding programme as parents they may give rise to diverse segregation pattern for aforementioned traits.

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