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Multivariate analysis of seed traits in coloured grapes

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Abstract

Genetic diversity present amongst the available Genepool is a crucial factor which decides the way and direction of any crop improvement program. It helps in exploitation of the important traits through heterosis and also help in obtaining transgressive segregants in segregating generations. The present investigation was planned to analyse the genetic diversity among forty coloured and seeded grape cultivars for seven important seed traits *viz.*, number of seeds per berry, seed weight per berry (mg), seed length (mm), seed width (mm), single seed weight (mg), total berry weight (mg), and seed index using principal component analysis and cluster analysis. The principal component one (PC1) with Eigen values 2.648 has contributed to 37.83% percent of variability; whereas principal component two (PC2) has contributed 28.20% variability and principal component three (PC3) defined 19.69% variability; the cumulative variability among the 40 grape genotypes depicted by PC1, PC2 and PC3 was 85.72%. The K-mean clustering grouped these forty grape genotypes into three clusters.

Keywords: Coloured grapes, variability, seed index, clustering and multivariate analysis

1. Introduction

Grape (*Vitis vinifera* L.) is an important fruit crop of India. Although India had started grape cultivation on commercial scale after late 1960s; now India is major table grape producer as well as grape exporter in world. The improvements in crop husbandry practices done by the Indian grape growers coupled with the scientific inputs provided by various Indian research has made it a premium fruit crop of the country. The genetic variability present among the genotypes help the breeder to decide the parents for different crossing programmes aimed with particular trait improvement. Likewise more the diverse parents more will the chances of exploiting hybrid vigour. Seedlessness is preferred characteristic in table grape which elevate its palatability amongst the consumer. Parthenocarpy and stenospermocarpy are two mechanism responsible for seedless in grape. Seed index number which is the ratio of berry weight to seed weight is another factor which influence the recovery of seedless progeny. H.P Olmo (1942) [5] obtained increased proportion of seedless hybrids when mother parent with high seed index number (berry to seed weight ratio) was crossed with seedless male. He suggested that when seeded female with high seed index and which segregate at desired level of seedlessness when crossed with seedless male, then chances of obtaining seedless hybrids increases. The current investigation was planned to reveal the genetic diversity present among the forty coloured and seeded genotypes pertaining to seed traits so that they can be used in upcoming breeding programmes for induction of seedlessness.

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 among forty coloured and seeded grape cultivars for seven important seed traits *viz.*, number of seeds per berry, seed weight per berry (mg), seed length (mm), seed width (mm), single seed weight (mg), total berry weight (mg), and Seed Index (SI) using principal component analysis and cluster analysis. These forty coloured and seeded grape genotypes were maintained under uniform horticultural and inter-cultivation practices wherein double pruning and single cropping practice was followed (Table 1). Three vines of each genotypes were used of recording observations; 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.

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Table 1: The coloured and seeded grape genotypes used in present investigation

| No. | Genotype | No. | Genotype |
|-----|------------------------|-----|----------------------|
| 1 | Amber Queen | 21 | Izabel |
| 2 | Black Champa | 22 | Amber Sweet |
| 3 | Ruby Red | 23 | Red Globe |
| 4 | Ribier | 24 | Athens |
| 5 | Black Hamburg | 25 | Champion |
| 6 | Gulabi | 26 | Hussain Black Kabuli |
| 7 | Madhu Angoor | 27 | Red Prince |
| 8 | Benzuhio | 28 | Christmas Rose |
| 9 | Pusa Navrang | 29 | Red Muscat |
| 10 | Olympia | 30 | Rose of Peru |
| 11 | Carolina Black Rose | 31 | Alden |
| 12 | Rizamat | 32 | Castiza |
| 13 | Concord | 33 | Black Round |
| 14 | Muscat Hamburg | 34 | Angoor Kalan |
| 15 | James | 35 | Banglore Purple |
| 16 | Black Muscat | 36 | Charas |
| 17 | Manjari Medika | 37 | Alamvick |
| 18 | Convergent Large Black | 38 | Isabella |
| 19 | Khalili | 39 | Catawba |
| 20 | Barbarosa | 40 | Alicante Bouschet |

The Principal Component Analysis and ‘K-mean’ cluster analysis were used in the study to decipher the genetic variation present among the genotypes for seed traits. The Principal Component Analysis (PCA) help to identify small number of uncorrelated variables (Principal Components) from correlated variable which explains the variation present in large data set [8]. Whereas ‘k-means’ algorithm was used to group these genotypes into different clusters. The clustering help to partition large datasets into different small subgroups or clusters based on the similarity measure. The k-means grouping algorithm was initially proposed by MacQueen in 1967 [4] and later enhanced by Hartigan and Wong in 1979 [2]. Recently various researcher had employed PCA analysis to assess the variability for different traits in grapes for phenotypic divergence of grapes [3], physical and chemical indexes of wine grape used for grape grading [6]; Chemometric Analysis of Grapes [7], etc. The Principal Component Analysis (PCA) and ‘k-means’ was carried out using Paleontological Statistics Software Package for Education and Data Analysis [1]. Seed index (SI) was calculated as ratio of berry weight to seed weight [5]. The genotypes were grouped as per their seed index (SI) into four groups viz., group-A (SI ≥10:1 to 20:1), group-B (SI ≥20:1-30:1), group-C (SI ≥30:1 to 40:1) and group-D (SI ≥40:1).

3. Results and Discussion

The variability present among the coloured and seeded grape cultivars for berry and seed traits was deciphered using Principal Components Analysis and cluster analysis as below;

3.1 Principal components analysis (PCA): The PCA analysis produced seven principal components. The PC1, PC2 and PC3 has Eigen values more than one and hence as per rule these three components were considered as important ones in view of exploring the variability present among the genotypes. A scree plot was drawn from the Eigen values associated with a component in descending order which highlights the variability expresses by each principal component (Fig 1).

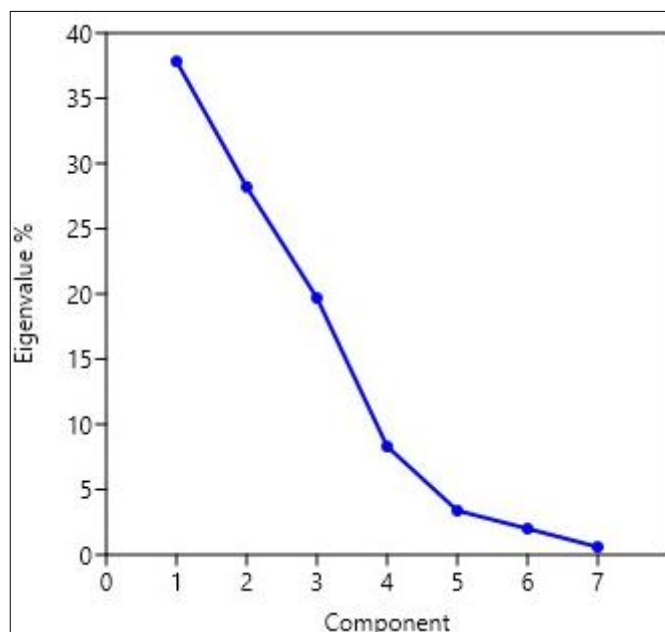


Fig 1: Scree plot showing the Eigen values of different principal components

The principal components, their respective Eigen values, percent variability portrayed by each component and cumulative percent of the variability are furnished in Table 2. Seven principal components were observed and first three PCs were found important which revealed the variance of 37.83%, 28.20%, and 19.69% respectively. Thus collectively these three components (PC1, PC2 and PC3) had covered the 85.72% variability present amongst the genotypes for the traits under study.

Table 2: Contribution of the Principal Components towards variability

| Principal Component | Eigenvalue | Variance (%) | Cumulative variability (%) |
|---------------------|------------|--------------|----------------------------|
| PC1 | 2.648 | 37.83 | 37.83 |
| PC2 | 1.974 | 28.20 | 66.03 |
| PC3 | 1.378 | 19.69 | 85.72 |
| PC4 | 0.581 | 8.30 | 94.02 |
| PC5 | 0.237 | 3.38 | 97.40 |
| PC6 | 0.140 | 2.00 | 99.40 |
| PC7 | 0.042 | 0.60 | 100.00 |

The correlation of different variables with respective principle components showed that all seven seed traits have positive loading on PC1 with highest positive correlation shown by seed length and seed width followed by total berry weight

(Table 3 and Fig 2). Whereas seed weight per berry and number of seeds per berry were the most influencing variable for PC2. The number of seeds per berry, total berry weight and seed index had greater influence on composition of PC3.

Table 3: Correlation of principal components with original variables

| Sr. no. | Variables | Loadings | | | | | | |
|---------|----------------------------|----------|--------|--------|--------|--------|--------|--------|
| | | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 |
| 1 | No of seeds per berry | 0.096 | 0.740 | 0.602 | -0.085 | 0.163 | 0.214 | 0.010 |
| 2 | Seed weight per berry (mg) | 0.593 | 0.742 | 0.155 | 0.126 | -0.057 | -0.217 | 0.090 |
| 3 | Seed length (mm) | 0.816 | -0.157 | 0.065 | -0.478 | -0.266 | 0.073 | 0.010 |
| 4 | Seed width (mm) | 0.807 | -0.155 | -0.384 | -0.223 | 0.354 | -0.051 | -0.011 |
| 5 | Single seed weight (mg) | 0.624 | 0.181 | -0.607 | 0.410 | -0.077 | 0.186 | 0.018 |
| 6 | Total berry weight (mg) | 0.732 | -0.259 | 0.542 | 0.292 | -0.022 | -0.051 | -0.127 |
| 7 | Seed index (ratio) | 0.212 | -0.853 | 0.422 | 0.163 | 0.068 | 0.048 | 0.130 |

Table 4: Observed inter-cluster distances

| Cluster Number | I | II | III |
|----------------|-----------|-----------|-----------|
| I | 0.000 | 2,193.132 | 1,307.590 |
| II | 2,193.132 | 0.000 | 3,500.416 |
| III | 1,307.590 | 3,500.416 | 0.000 |

The forty grape genotypes were grouped into three clusters wherein clusters-I has highest number of grape genotypes (20) followed by cluster-III (12) and cluster-II (08) respectively. The higher inter cluster distances indicated the presence of substantial amount of genetic diversity in the genetic material (Table 5).

Table 5: Cluster and its membership

| Cluster | Member genotypes | No. of entries per cluster |
|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| I | Black Champa, Gulabi, Rizamat, Concord, Muscat Hamburg, Black Muscat, Convergent Large Black, Khalili, Izabel, Amber Sweet, Athens, Champion, Red Prince, Christmas Rose, Red Muscat, Alden, Angoor Kalan, Charas, Alamvick, and Catawba | 20 |
| II | Ribier, Black Hamburg, Madhu Angoor, Benzuhio, Olympia, Carolina Black Rose, Red Globe and Bangalore Purple | 08 |
| III | Amber Queen, Rubi Red, Pusa Navrang, James, Manjari Medika, Barbarosa, Hussain Black Kabuli, Rose of Peru, Castiza, Black Round, Isabella and Alicante Bouschet | 12 |

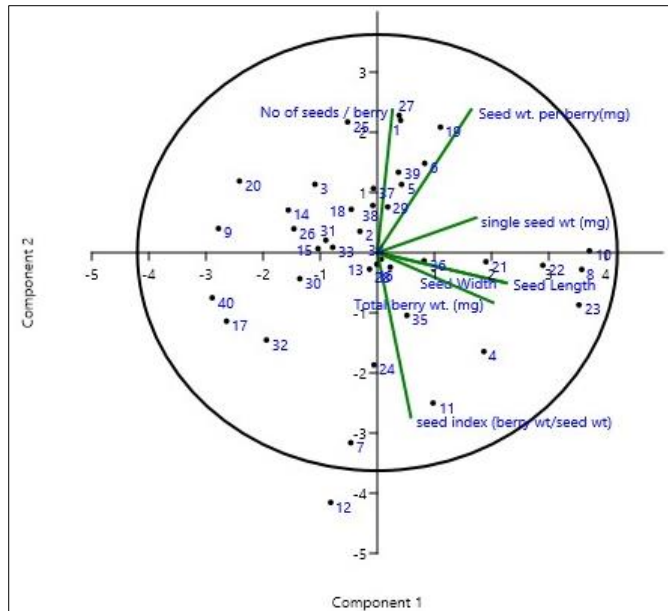


Fig 2: Bi-plot showing the influence of different variables on PC1 and PC2

3.2 K-Mean clustering: The ‘K-mean’ algorithm was employed to group these forty genotypes under study based on the similarities and dissimilarities present among them. Three clusters were formed following an ‘Elbow’ method (Fig 3).

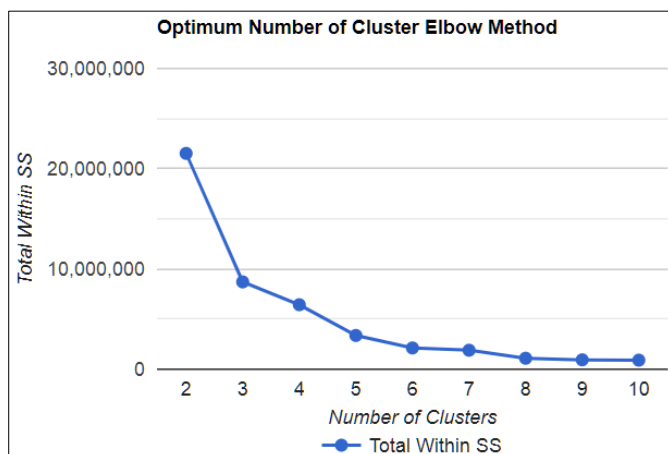


Fig 3: Optimum number of clusters calculated by Elbow method

The clustering help to put the candidates with similarities in a same group. The mutual relationships between the clusters revealed that inter-cluster distance values were greater than intra-cluster values (Table 4).

3.3 Seed index analysis: H.P Olmo (1942) [5] suggested that increased proportion of seedless hybrids can be obtained when mother parent with high seed index (SI) is crossed with seedless male. Seed index (SI) was calculated as ratio of single berry weight to weight of seeds present in a single berry. The forty genotypes were grouped as per their seed index into four groups viz., group-A (SI ≥10:1 to 20:1), group-B (SI ≥20:1 to 30:1), group-C (SI ≥30:1 to 40:1) and group-D (SI ≥40:1). Nine genotypes in group ‘A’, 17 genotypes in group ‘B’, eight genotypes in group ‘C’ and six genotypes in group ‘D’ were placed accordingly. Madhu Angur reported highest SI i.e. 67.74:1 amongst all genotypes. The six genotypes of group ‘D’ viz., Bangalore Purple, Ribier, Red Globe, Carolina Black Rose, Rizamat and Madhu Angoor and Christmas Rose from group ‘C’ i.e. can be suitable female parent for inducing seedlessness especially in table grape improvement program owing to their fruit traits (Table 6). This analysis helped the author of this text to incorporate Madhu Angur, Red Globe, and Christmas Rose in his study for genetic improvement of coloured grapes.

Table 6: Categorization of grape genotypes based on their seed indices

| Group | Seed Index range | Genotype number | Name of genotype | Total genotypes in a group |
|-------|------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| A | ≥10:1 to 20:1 | 1, 3, 9, 20, 39, 38, 19, 25, and 27 | Amber Queen, Rubi Red, Pusa Navrang, Barbarosa, Catawba, Isabella, Khalili, Champion and Red Prince | 09 |
| B | ≥20:1 to 30:1 | 37, 30, 15, 6, 26, 33, 22, 36, 29, 21, 31, 13, 18, 2, 16, 14 and 34 | Alamvick, Rose of Peru, James, Gulabi, Hussain Black Kabuli, Black Round, Amber Sweet, Charas, Red Muscat, Izabel, Alden, Concord, Convergent Large Black, Black Champa, Black Muscat, Muscat Hamburg, and Angoor Kalan | 17 |
| C | ≥30:1 to 40:1 | 17, 28, 10, 40, 8, 32, 5 and 24 | Manjari Medika, Christmas Rose, Olympia, Alicante Bouschet, Benzuhio, Castiza, Black Hamburg, and Athens | 08 |
| D | ≥40:1 | 35, 4, 23, 11, 12 and 7 | Banglore Purple, Ribier, Red Globe, Carolina Black Rose, Rizamat and Madhu Angoor | 06 |

4. Conclusion

The understanding of the genetic diversity present in the Genepool available helps the breeder to plan breeding program. Under present investigation principal component analysis and cluster analysis depicted that substantial diversity was present among the forty coloured and seeded grape genotypes for seven important berry and seed traits *viz.*, number of seeds per berry, seed weight per berry (mg), seed length (mm), seed width (mm), single seed weight (mg), total berry weight (mg), and seed index. First three principal components i.e. PC1, PC2 and PC3 has depicted 85.72% variability collectively. Based on the variability expressed, the forty grape genotypes were grouped into three clusters by K-mean clustering analysis. This study revealed that seven genotypes *viz.*, Bangalore Purple, Ribier, Red Globe, Carolina Back Rose, Rizamat, Madhu Angoor and Christmas Rose with better table quality traits and higher SI (>33:1) can be used as female parents for inducing seedlessness especially in table grape improvement program.

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