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Genetic Variability and Multivariate Analysis in Okra [*Abelmoschus esculentus* (L.) Moench]

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ABSTRACT. *Genetic variability was evaluated for 17 characters in 41 genotypes collected from various sources. Number of branches per plant, disease incidence (Cercospora leafspot, Powdery mildew, YVMV), ascorbic acid content, yield per plant and fruit weight recorded high genotypic co-efficient of variation and phenotypic co-efficient of variation as compared to other characters. High heritability was observed for number of branches per plant, yield per plant, and high genetic advance was recorded for yield per plant, plant height, germination percentage. Highest genetic advance as percentage of mean was recorded for number of branches per plant indicating that the trait is more reliable for improvement through selection. Correlation studies revealed that fruit yield per plant have significant and positive correlation with germination percentage, number of branches per plant, number of ridges per fruit, fruit length, fruit weight and ascorbic acid content. Significant negative correlation of fruit yield per plant was recorded with plant height, number of days taken for first pod setting, fruit volume, shape index, longevity of tenderness. Path analysis revealed high positive direct effect for fruit weight followed by fruit length, germination percentage, number of ridges, plant height, number of branches per plant, number of nodes per plant, fruit volume, ascorbic acid content. A maximum positive indirect effect was recorded between fruit weight (via) number of ridges whereas a maximum negative direct effect was recorded in fruit weight (via) fruit length. Cluster analysis revealed a considerable variation among the genotypes. Forty one genotypes were grouped into 8 clusters. Among all the clusters, cluster IV had a maximum number (8) of genotypes.* D^2 *values ranged from 205.03 to 32666.9. The cluster means revealed that plant height, yield per plant and germination percentage contributed towards divergence.*

INTRODUCTION

Bhendi or okra [*Abelmoschus esculentus* (L.) Moench] of the family Malvaceae is an often cross pollinated crop and predominantly an important vegetable of the tropics and has found its place in India since time immemorial. Almost all parts of Bhendi plant were economical. Fresh Bhendi fruits are used as vegetables while the roots and stems are used for clearing the cane juice from which ‘gur’ or brown sugar is prepared (Chauhan, 1972). Seeds are used for oil extraction. Present cultivars of Bhendi are capable of showing high variability in several characters including yield. But the yields of present cultivars per unit area of land and per unit of time are very low because of their very low yield potential (Balakrishnan and Balakrishnan, 1988).

The success of any crop improvement program largely depends on nature, magnitude of genetic variability, heritability, genetic advance, character association, direct and indirect effects on yield and yield attributes. Inter character relationship is used for indirect selection of characters that are less heritable and not easily measured. Correlation studies are useful in most of the breeding programs. If a number of independent characters is affecting a dependent character in an increasing way, there would be some amount of inter-dependence. In such a situation, correlation becomes inefficient. Then the path analysis helps in understanding relationship among characters. Genetic diversity is important for selecting parents to recover transgressive segregates. For genetic diversity, germplasm is the reservoir, which is quite often exploited to develop new improved varieties. Emphasis on genetic diversity of parents is important in heterosis breeding program. In countries like India, Pakistan, Nepal, Sri Lanka, Iran and Turkey where Bhendi cultivation is old, the varietal groups showed no distinguishing characteristics (Martin et al., 1981). Therefore, D^2 statistics is a suitable statistical procedure in quantifying the degree of divergence between different genotypes and thus helps in selection of diverse and vigorous parents.

MATERIALS AND METHODS

In pursuance of the envisaged objectives, the present study was carried out with forty one diverse genotypes collected from different agro climatic regions of India and other parts of south-east Asia. Seeds of the selected genotypes were planted in a randomized block design with three replications at a spacing of 60 cm between rows and 45 cm between plants. Data were collected by taking 5 competitive plants in each variety on 17 characters. Analysis of variance was done as suggested by Cochran and Cox (1950), coefficients of variation were determined according to Burton and Devane (1953), genetic advance and heritability were estimated as described by Allard (1960) and correlation coefficients were worked out by using formula suggested by Falconer (1981). The path analysis was done as given by Wright (1921) and elaborated by Dewey and Lu (1959) to calculate the direct and indirect contribution of various traits to yield. Cluster analysis was carried out using the formula given by Mahalanobis's (1936) D^2 statistics.

RESULTS

Analysis of variance showed highly significant values for germination percentage, plant height, number of branches per plant, number of pods per plant, number of days for the first pod setting, number of ridges per fruit, fruit length, number of fruits per plant, fruit weight, fruit volume, number of seeds per pot, weight of 100 seeds, longevity, ascorbic acid content, yield, shape index, number of YVMV infected plants, number of powdery mildew infected plants and number of cercospora infected plants. However, longevity of tenderness, number of branches per plant and number of ridges per fruit were not significant. Studies on variability revealed that phenotypic co-efficient of variation (PCV) values were higher than genotypic co-efficient of variation (GCV) values ranged from 3.37 (number of days taken for the first pod setting) to 56.14 (cercospora leaf spot incidence). PCV and GCV were found to be higher in cercospora leaf spot incidence, number of branches per plant, fruit volume and ascorbic acid content indicating the presence of high level of genetic variability for the characters studied. Low GCV was observed for two traits, i.e. days taken for first pod setting and number of ridges. The proportion of variation, which is heritable was not sufficient to determine the GCV alone. This could be done with the help of heritability estimates and genetic advance expressed as percentage of mean. Heritability for all the characters was high. Maximum genetic gain as a percentage of mean was observed for number of branches per plant (Table 1).

TABLE 1

When the environmental, genotypic and phenotypic correlation coefficients among different characters were considered the fruit yield per plant exhibited a significant and positive correlation with germination percentage, number of ridges, fruit length, fruit weight and ascorbic acid content. The genotypic and phenotypic correlations of fruit yield per plant with plant height, number of days taken for first pod setting were significant and negetive. The environmental correlations were positive only between yield per plant and number of pods per plant, and pod yield per plant and edible pod.

Path analysis separates the correlation coefficient into direct and indirect effects and helps in establishing relative importance of factors in determining the yield per plant. The magnitude of direct effects contributed by independent variables to yield per plant revealed the highest positive genotypic and phenotypic effects for fruit weight (0.758 and 0.730, respectively) followed by fruit length (0.41 and 0.286, respectively), germination percentage (0.286 and 0.17, respectively), number of ridges(0.227 and 0.147, respectively). Plant height, number of branches per plant, number of nodes per plant, fruit volume, ascorbic acid content, YVMV incidence, cercospora incidence showed positive direct effect. Maximum negative direct effect was recorded in fruit length (-0.193) followed by number of days taken for first pod setting, shape index, longevity of tenderness and powdery mildew incidence. However, the maximum positive indirect effect was observed between fruit weight via number of ridges (0.351).

Genetic divergence in 41 varieties from different sources were grouped into 8 clusters. Adequate diversity between the genotypes was observed with D^2 values ranging from 205.03 to 32666.90. The maximum D^2 value (326666.90) was observed between V-315 and *Pusa Sawani* and the lowest value (205.03) between 151-10-1,2 Red and 151-10-1,2,3 Red. The cluster pattern explained that geographic diversity did not seem to have a direct association with genetic diversity. Out of 8 clusters, cluster IV had the highest number (8) of genotypes whereas cluster VII had the least number (1) (Tables 2a, 2b, 3a and 3b).

Inter and intra cluster distances (Table 4) revealed the maximum inter-cluster distance between VII and VIII (3.79) and the minimum between II and VIII (0.01). Based on generalized distance, the mutual relationship among various clusters was diagrammatically presented in Fig. 1. It is suggested that the varieties from highly diverse groups and those show high yield potential coupled with quality attributes might be helpful in breeding program. In addition to yield, incorporation of quality oriented characters are equally important. The inter-cluster divergence and the character means of the varieties and cluster means are presented in Tables 5a and 5b. The cluster means estimated for 17 characters in Bhendi revealed that among 8 clusters studied, cluster VI showed high mean values for germination percentage, number of branches per plant, number of ridges per fruit, fruit length, fruit weight and yield per plant indicating that cluster VI is superior to other clusters.

TABLE 2A

TABLE 2B

TABLE 3A

TABLE 3B

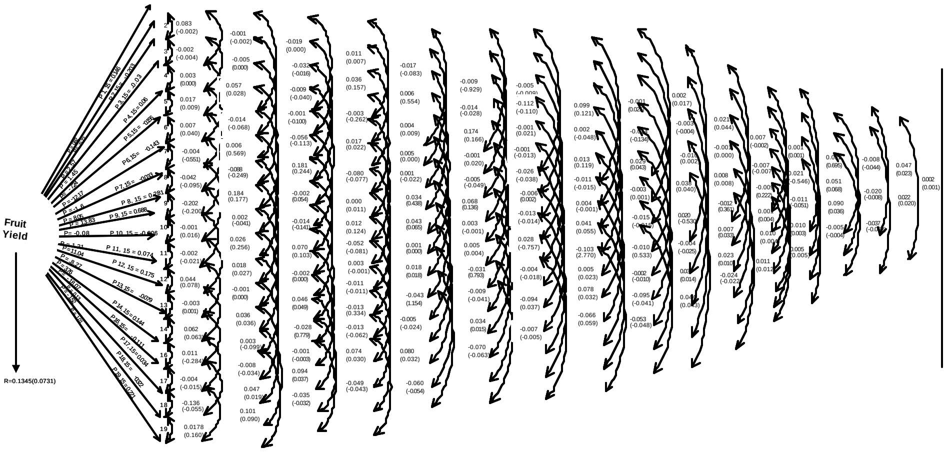
TABLE 4

DISCUSSION

The treatment mean squares were significant for all the characters suggesting the presence of a considerable variation. The character, fruit yield per plant exhibited a wide range of variation which is in conformity with the findings of Gandhi *et al.* (2001).

When the estimates of GCV and PCV were considered, number of branches per plant, fruit yield, fruit weight, fruit volume, ascorbic acid content exhibited magnitudinally higher values than the other traits. Reddy et al. (1985) and Vijay and Manohar (1990) also reported the similar results. High magnitude of genetic variance suggested the presence of high genetic variability. These results are in agreement with the results of Panda and Singh (1997).

Fig. 1. Path Diagram showing cause effect relationship in okra



R = Residual Effect
P = Correlation Coefficient (r)

TABLE 5 A

TABLE 5B

Heritability estimates are said to be satisfactory tools for selection based on phenotypic performance. In the present study heritability estimates were very high for all the characters. High estimates of heritability for the traits suggested that the selection based on phenotypic performance would be more effective. Although estimates of heritability are useful, reliable conclusion can be made when heritability is used in conjunction with genetic advance. In the present study high heritability and high genetic advance were recorded for yield per plant, number of branches per plant, plant height, fruit weight, fruit volume, cercospora leaf spot incidence. These results are in accordance with the findings of Yadav (1986).

Although phenotypic correlation incorporates genotypic, environmental and their interactions, it was observed that in most cases genotypic correlations were higher than their corresponding phenotypic correlations. All the 17 characters were genotypically and phenotypically correlated with pod yield indicating that pod yield may be improved through selections. If characters are correlated phenotypically but not genotypically, it will not produce repeatable estimates of inter character associations and any selection based on that is likely to be unreliable. The significant genotypic correlation between pod yield and number of branches per plant may be related to greater photosynthetic capacity provided by more leaves. More branches promise more fruit bearing nodes.

The significant genotypic and phenotypic correlation of pod weight with pod length and pod width would be a good index for selecting for high yielding lines as plump pods will substantially increase total yield through relatively greater weight. Although there was a significant genotypic correlation between pod weight and number of pods per plant, not much success may be expected in selecting for a large number of pods per plant through edible pod weight since the two characters are not phenotypically correlated. Environmental correlations, which are estimated from the error variance and covariance components, involve mainly the effect of soil heterogeneity, cultural variations and chance error occurring during the conduct of experiments as stated by Sikka and Maini (1962) and Dhall *et al*. (2001). The magnitude of environmental correlation coefficients was less compared to both phenotypic and genotypic correlation coefficients in the present study.

The results of correlation coefficients revealed that the nature of correlations among various characters showed considerable variation, which occurred because of differential response of genotypes. However, significant positive correlations among the characters imply that plant breeder can rely more on these characters for selection of superior genotypes in Bhendi production.

When the interdependence of the component characters was considered, the residual values in a path coefficient analysis (Tables 2a, 2b, 3a and 3b) for 17 characters was only 0.1047. This indicates that 17 yield contributing traits have adequately explained the variation. Path analysis revealed that fruit weight had the maximum direct effect on yield per plant (0.758). This was in accordance with results obtained by Ariyo *et al*. (1987) and Gondane *et al*. (1995).

Study on genetic divergence of 41 genotypes resulted 8 distinct clusters. However, these clusters do not represent their place of origin indicating that the genotypes in a cluster were geographically diverse, while genotypes obtained from the same region were genetically different. This was also observed by Bindhu *et al.* (1994) and Warade *et al*. (1997).

On the basis of high yield, important yield components and fruit quality, four genetically diverse and superior genotypes (V-315, *Arka Anamika*, *Pusa Mukhamali*, VB-19) were selected. It is proposed that these genotypes could be used in a multiple crossing program to recover transgressive segregates with high genetic yield potential.

CONCLUSIONS

Forty one genotypes were grouped into 8 clusters. Among all the clusters, cluster IV had a maximum number (8) of genotypes. D^2 values ranged from 205.03 to 32666.9. The cluster means revealed that plant height, yield per plant and germination percentage contributed towards divergence. Four genetically diverse and superior genotypes (V-315, *Arka Anamika*, *Pusa Mukhamali*, VB-19) were selected based on their remarkable yield traits.

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Table 5. Estimation of direct and indirect effects between yield and yield components

Parameter	Germination %	Plant height	No. of branches per plant	No. of pods per plant	No. of days for first pod setting	No. of ridges per fruit	Fruit length	No. of fruits per plant	Fruit weight	Fruit volume
Germination percentage	0.146 (0.555)	0.083 (-0.002)	-0.001 (-0.002)	-0.019 (0.000)	0.011 (0.007)	-0.017 (-0.083)	-0.009 (-0.929)	-0.005 (-0.009)	0.099 (0.121)	-0.001 (0.025)
Plant height	-0.060 (-0.273)	-0.203 (0.004)	-0.002 (-0.004)	-0.005 (0.000)	-0.032 (-0.016)	0.036 (0.157)	0.006 (0.554)	-0.014 (-0.028)	-0.112 (-0.110)	0.002 (-0.048)
No. of branches per plant	-0.003 (-0.014)	0.010 (0.000)	0.030 (0.083)	0.003 (0.000)	0.057 (0.028)	-0.009 (-0.040)	-0.003 (-0.262)	0.004 (0.009)	0.174 (0.166)	-0.001 (0.021)
No. of pods per plant	-0.046 (-0.190)	0.018 (0.000)	0.001 (0.004)	0.060 (-0.001)	0.017 (0.009)	-0.014 (-0.068)	-0.001 (-0.100)	0.017 (0.022)	0.005 (0.000)	-0.001 (0.020)
No. of days for first pod setting	-0.010 (-0.051)	-0.042 (0.001)	-0.011 (-0.030)	-0.007 (0.000)	-0.156 (-0.076)	0.007 (0.040)	0.006 (0.569)	-0.056 (-0.113)	-0.080 (-0.077)	0.001 (-0.022)
No. of ridges per fruit	0.018 (0.099)	0.051 (-0.001)	0.002 (0.007)	0.006 (0.000)	0.008 (0.007)	-0.143 (-0.465)	-0.004 (-0.551)	-0.088 (-0.249)	0.181 (0.244)	0.000 (0.011)
Fruit length	0.039 (0.171)	0.035 (-0.001)	0.003 (0.007)	0.001 (0.000)	0.029 (0.014)	-0.017 (-0.085)	-0.033 (-3.016)	-0.042 (-0.095)	0.184 (0.177)	-0.002 (0.054)
No. of fruits per plant	-0.003 (-0.009)	0.010 (0.000)	0.000 (0.001)	0.004 (0.000)	0.031 (0.016)	0.045 (0.212)	0.005 (0.524)	0.281 (-0.547)	-0.202 (-0.200)	0.002 (-0.041)
Fruit weight	0.021 (0.104)	0.033 (-0.001)	0.008 (0.021)	0.000 (0.000)	0.018 (0.009)	-0.038 (-0.176)	-0.009 (-0.826)	-0.083 (-0.170)	0.688 (0.644)	-0.001 (0.016)
Fruit volume	0.022 (0.096)	0.069 (-0.001)	0.005 (0.012)	0.008 (0.000)	0.024 (0.012)	-0.008 (-0.035)	-0.012 (-1.149)	-0.075 (-0.157)	0.075 (0.074)	-0.006 (0.142)
No. of seeds per pod	0.005 (0.015)	0.039 (-0.001)	0.005 (0.015)	-0.001 (0.000)	0.011 (0.006)	-0.065 (-0.313)	-0.005 (-0.577)	-0.054 (-0.118)	0.245 (0.254)	0.000 (-0.005)
100 seed weight	0.018 (0.093)	0.003 (0.000)	0.005 (0.014)	-0.004 (0.000)	0.023 (0.011)	-0.056 (-0.249)	-0.008 (-0.777)	-0.083 (-0.175)	0.274 (0.263)	-0.001 (0.015)
Longivity (or) tenderness	-0.013 (-0.069)	-0.001 (0.000)	0.004 (0.011)	0.002 (0.000)	0.008 (0.004)	-0.010 (-0.049)	0.001 (0.121)	-0.003 (0.002)	-0.025 (-0.026)	0.000 (0.004)
Ascorbicacid content (mg)	0.001 (0.003)	0.010 (0.000)	0.002 (0.005)	0.016 (0.000)	0.016 (0.008)	-0.040 (-0.178)	0.003 (0.291)	0.009 (0.017)	0.085 (0.082)	0.000 (-0.011)
Shapeindex (l.bratio)	0.029 (0.137)	0.038 (-0.001)	0.002 (0.007)	0.007 (0.000)	0.028 (0.014)	-0.013 (-0.088)	-0.030 (-2.965)	-0.072 (-0.147)	0.189 (0.181)	-0.002 (0.058)
No. of plants infected YVMV (%)	-0.035 (-0.161)	-0.090 (0.002)	-0.010 (-0.028)	0.002 (0.000)	-0.034 (-0.017)	0.015 (0.078)	0.002 (0.206)	0.041 (0.084)	-0.083 (-0.078)	0.002 (-0.039)
No. of plants infected powdery	-0.021 (-0.102)	-0.013 (0.000)	-0.009 (-0.023)	-0.002 (0.000)	0.005 (0.002)	0.010 (0.036)	0.004 (0.338)	0.083 (0.175)	-0.167 (-0.162)	0.002 (-0.042)
No. of plants infected by Cercospora po	0.001 (0.004)	-0.020 (0.000)	-0.005 (-0.014)	-0.001 (0.000)	-0.004 (-0.002)	-0.007 (-0.030)	0.004 (0.343)	0.056 (0.120)	-0.167 (-0.159)	0.002 (-0.043)

Figures in paranthesis are genotypic path values in bhendi;; Residual Effect = 0.1345 (0.0731); Bold letters are the direct effects