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Genetic analysis in okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract

The present investigation was undertaken to obtain information on genetic variability, heritability, genetic advance, correlation and path analysis with respect to various quantitative traits. The experimental material consisted of ten diverse genotypes of okra and forty five F1 crosses generated through 10 x 10 diallel mating design. Analysis of variance revealed significant differences among genotypes for all the traits studied. The maximum range and the highest phenotypic and genotypic coefficients of variability was observed for fruit yield per plot. In general the phenotypic coefficients of variation were slight higher than genotypic coefficients of variation, which indicates the minor role of environment in the expression of traits under observation. The estimates of heritability in broad sense were high for all the characters. The present investigation indicates a great scope in the improvement of these traits as these characters in general possessed high estimates of heritability coupled with high genetic advancement except for days to first flower, days to first fruit set and days to first fruit harvest, number (high heritability but moderate genetic gain) indicating the preponderance of additive gene action for control of these traits. Number of fruits plant$^{-1,}$ number of nodes plant^{-1}, average fruit weight and average fruit length showed positive correlation both at genotypic and phenotypic levels, hence proved their genetic worth for selection and improvement of okra.

Keywords: Genetic variability, heritability, genetic advance, correlation and okra

Introduction

Okra (*Abelmoschus esculentus* L. (Moench), commonly known as lady's finger is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. It is one of the most widely known and utilized species of the family Malvaceae (Naveed *et al*., 2009) [7] It is quite popular in India because of its easy cultivation, dependable yield and adaptability to varying moisture conditions. India ranks first in the world with okra cultivation over an area of 501 thousand hectares with an annual production of 5972 thousand metric tonnes (Anonymous, 2017) [1]. Okra is a powerhouse of valuable nutrients and highly nutritious vegetable. Besides having medicinal importance, it is rich in several carbohydrates, minerals and vitamins, which play a vital role in human diet and health.

Looking to the potentials of okra its improvement is inevitable. So, before taking up any breeding programme, a thorough knowledge is required regarding the nature and magnitude of genetic variability, heritability and genetic advance over mean. The key for any success of any breeding program lies in the availability of genetic variability for desired traits.

Yield is a complex character and is a function of large number of characters, their interaction and is also influenced to a great extent by environment. Therefore a crop breeding programme, aimed at increasing the plant productivity requires consideration not only of yield but also of its components that have a direct or indirect bearing on yield. The necessity of coefficient of correlation is to describe the degree of association between independent and dependent variables. Path Coefficient analysis measures the direct influence of one variable upon another and permits the separation of correlation coefficient into components of direct and indirect effects.

Material and Methods

The present investigation was conducted during *Kharif* 2019 at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar.

The basic materials consisted of ten diverse genotypes of okra (*Abelmoschus esculentus* L. Moench) collected from different agro-climatic regions of India. Forty five F$_1$ crosses generated through 10 x 10 diallel mating design during the year 2018 were evaluated in a Randomized Block Design with three replications during year 2019. The row to row and plant to plant spacing was maintained at 60 x 30 cm. The observations were recorded on five randomly selected plants in each replication. The observations were recorded on the characters*viz.* Days to first flower, Days tofirstfruit set, Days to first fruit harvest, Plant height (cm), Number of nodes plant^{-1}, Internodal length (cm), Number of fruits plant^{-1}, Average fruit length (cm), Average fruit girth (cm), Average fruit weight (g), Fruit yield plant^{-1} (kg), Fruit yield plot^{-1} (kg), Number of seeds fruit^{-1}, Average seed weight fruit^{-1} (g). The data were subjected to standard statistical analysis.

Results and discussion

Analysis of variance revealed significant variation among all the genotypes for all the fourteen characters under study. Mean sum of squares due to genotypes for all the characters were found highly significant indicating presence of variability among the genotypes selected for study. Similar results have been reported by Yadav (2010) [15] and Singh *et al.* (2006) [13].

In general the phenotypic and genotypic coefficients of variation (Table) were almost similar with slight higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation.

It is evident from the data presented in table thatfruit yield plot^{-1} (29.16% and 29.11%) and number of fruits plant^{-1} (23.48% and 22.46%) recorded high phenotypic and genotypic coefficients of variation, indicating that genotypes had broad genetic base for these characters. Similar results have been reported by Yadav (2010) [15]. Days to first flower (3.93% and 3.54%), days to first fruit set (3.74% and 3.30%) and days to first fruit harvest (3.40% and 3.03%), showed low phenotypic and genotypic coefficients of variation indicating these characters were less amenable for improvement through selection. This was in agreement with the results reported by Singh *et al.* (2006) [13] and Hazra and Basu (2000) [4].

Characters which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. Wide ranges of variability along with high estimates of phenotypic and genotypic coefficients of variation further indicate that these attributes would respond to selection.

Heritability (b.s.) was high for all the characters and ranged from 77 to 99 per cent indicating that the characters are less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of characters and thus selection based on phenotypic expression could be relied upon.

High estimate of heritability along with genetic gain (per cent of mean) is more reliable than heritability alone for predicting the effect of selection (Johnson *et al*., 1955) [6]. The characters viz., fruit yield plant^{-1}, fruit yield plot^{-1}, average fruit length, number of fruits plant^{-1}, internodal length, number of nodes plant^{-1}, average fruit weight, average fruit girth, number of seeds fruit^{-1} and average seed weight fruit^{-1}showed high estimates of heritability coupled with high genetic advance as per cent of mean (GAM), indicating the preponderance of additive gene action for control of these traits. This suggests that real progress in improvement through selection could be made for yield. These results are in conformity with several workers viz. Dhankhar *et al.* (2008) [3] and Prakash (2011) [9].

Fruit yield plot^{-1} is an important character, which decides the commercial viability of the hybrid/variety. Thus the trait deserves the highest priority in any breeding programme. High heritability along with high genetic advance as per cent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection.

Correlation explains the interrelationships between characters and helps in effective identification of potential genotypes. Association analysis of different morphological, reproductive and nutritional characters with fruit yield of okra genotypes and their inter-relationships were investigated through the study of both phenotypic and genotypic correlation co-efficients. Correlation coefficients revealed that the economically important trait i.e. fruit yield plot^{-1}exhibited significant positive association with number of fruits plant^{-1}, number of nodes plant^{-1}, average fruit weight and average fruit lengthboth at genotypic and phenotypic levels. These findings were supported by Osekita and Akinyele (2008) [8] and Das *et al*. (2012) [2].

Internodal length, days to first fruit harvest and days to first fruit set, exhibited significant negative association with fruit yield plot^{-1} (fig-2). Similar results were shown by Sateesh *et al.* (2011) [11], Sogalad *et al.* (2012) [14] and Das *et al*. (2012) [2].

Table 1: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as% of mean) for different growth characters in okra (*Abelmoschus esculentus* L. Moench)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (bs)	Genetic advance (as% of mean)
1.	Days to first flower	60.63	57.13-64.63	5.7	4.63	3.93	3.54	0.81	6.58
2.	Days to first fruit set	62.93	60.13-67.53	5.55	4.32	3.74	3.3	0.77	6.00
3.	Days to first fruit harvest	65.96	62.96-70.3	5.03	4.01	3.40	3.03	0.79	5.58
4.	Plant height (cm)	189.20	131.9-230.6	337.7	334.5	9.71	9.66	0.99	19.82
5.	No. of nodes plant^{-1}	24.93	15.6-35.33	23.26	21.7	19.34	18.68	0.93	37.18
6.	Internodal length(cm)	7.84	4.03-11.13	2.81	2.6	21.40	20.56	0.92	40.71
7.	Number of fruits plant^{-1}	23	13.66-35.33	29.16	26.69	23.48	22.46	0.91	44.26
8.	Average fruit length (cm)	11.98	7.46-21.13	9.7	9.14	26.03	25.22	0.93	50.32
9.	Average fruit girth (cm)	1.49	1.2-1.96	0.04	0.03	14.68	12.96	0.78	23.58
10.	Average fruit weight (g)	10.02	5.26-14.16	3.37	2.96	18.32	17.16	0.88	33.13
11.	Fruit yield plant^{-1}(g)	253.4	140.1-470.1	5461.7	5443.2	29.16	29.11	0.99	59.87
12.	Fruit yield plot^{-1} (kg)	2027.3	1120.8-3761.0	349554.73	348366.79	29.16	29.11	0.99	59.87
13.	Number of seeds fruit^{-1}	58.92	31.46-81.66	129.75	126.89	19.33	19.11	0.98	38.94
14.	Average seed weight fruit	5.00	2.67-6.94	0.93	0.91	19.33	19.11	0.98	38.94

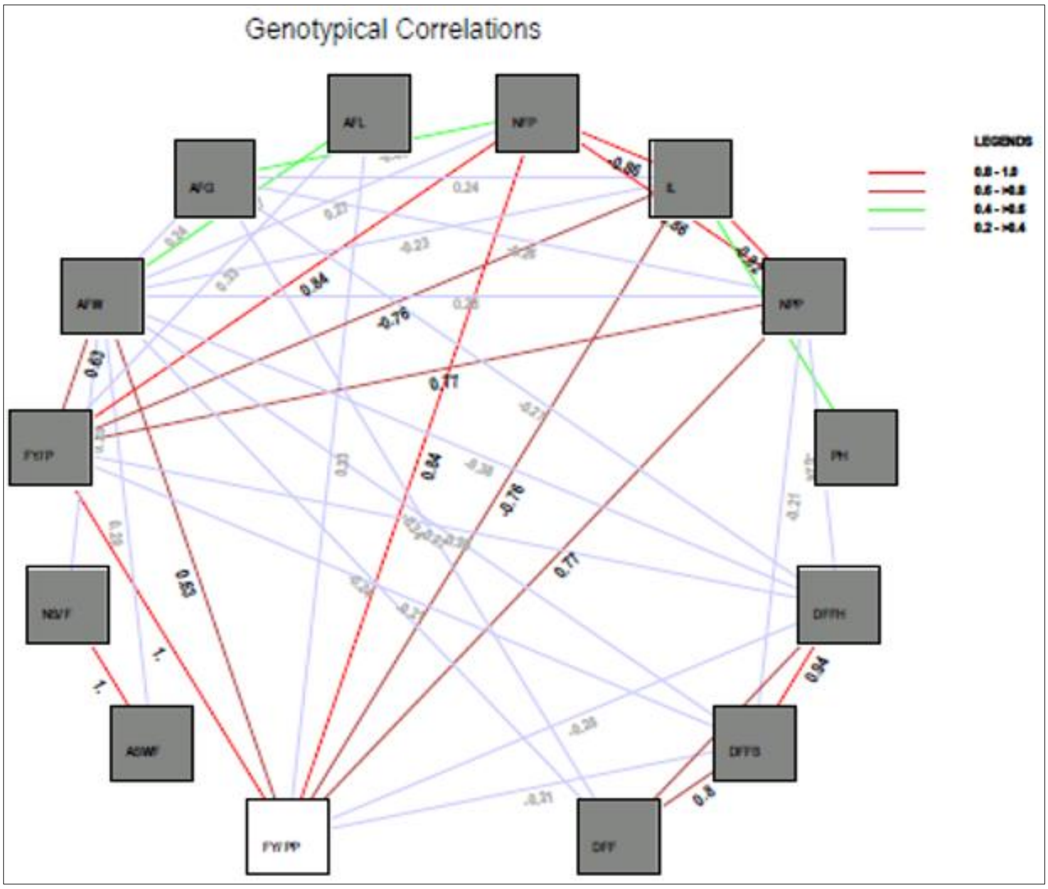

Fig 1.

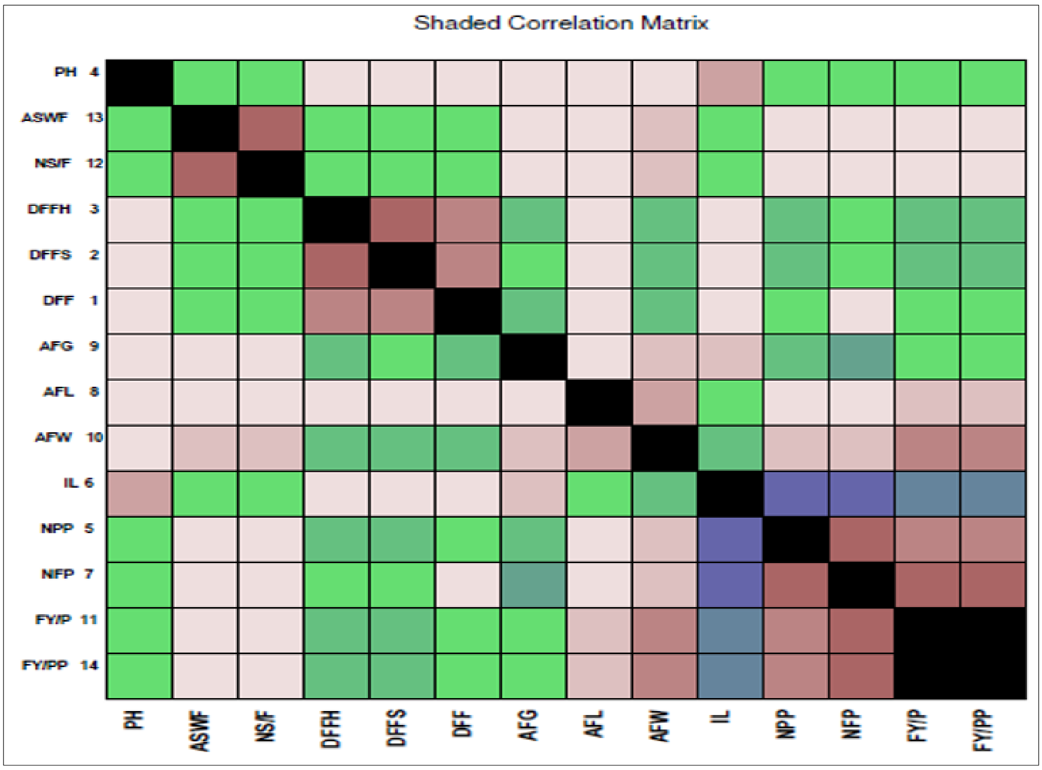

Fig 1.

The path coefficient analysis was computed to find out relative direct and indirect contribution of component traits towards fruit yield plot^{-1} in okra genotypes. The genotypic correlation coefficients were partitioned into direct and indirect effects of component characters on yield and the results are presented in (fig-3).

Path coefficient analysis made it apparent that the highest direct positive effect on fruit yield was recorded by number of fruits plant^{-1} followed by number of nodes plant^{-1}, and average fruit weight. Also the genetic correlation coefficients with fruit yield plant^{-1} of above traits were positive and significant. These findings were supported by Singh *et al.* (2007) [12] and Ramanjinappa *et al.* (2011) [10].

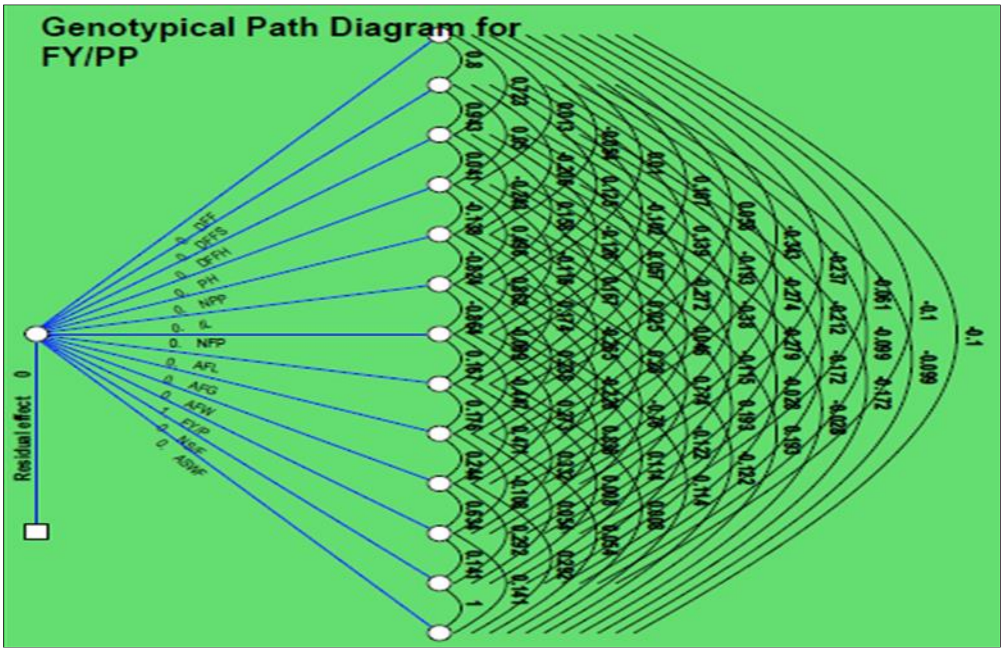

Fig 3.

Conclusion

Analysis of variance revealed highly significant differences among all the genotypes for all the characters studied indicating substantial amount of genetic variability present in the material. The characters viz., fruit yield plant^{-1}, fruit yield plot^{-1}, average fruit length, number of fruits plant^{-1}, internodal length, number of nodes plant^{-1}, average fruit weight, average fruit girth, number of seeds fruit^{-1} and average seed weight fruit^{-1}showed high estimates of heritability coupled with high genetic advance as per cent of mean (GAM), providing good scope for further improvement in advance generation. Number of fruits plant^{-1}, number of nodes plant^{-1}, average fruit weight and average fruit length showed positive correlation both at genotypic and phenotypic levels, hence proved their genetic worth for selection and improvement of okra. Path coefficient analysis made it apparent that the highest direct positive effect on fruit yield was recorded by number of fruits plant^{-1} followed by number of nodes plant^{-1}, and average fruit weight therefore being the most important characters contributing towards fruit yield.

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