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Studies on Genetic Variability, Heritability and Genetic Advance in Genotypes of Okra [*Abelmoschus esculentus* (L.) Moench]

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ABSTRACT

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Genetic variability analysis on 29 genotypes of okra revealed high magnitude of genetic variability and high degree of transmission of majority of the growth, earliness and yield associated traits under study. High magnitude of genotypic coefficient of variation (>20%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicated high degree of genetic variability offering great scope for selection of these characters. High heritability (>60%) coupled with high expected genetic advance (>20%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicated the involvement of additive gene action and more chances of fixing by selection to improve such traits.

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] belongs to the class dicotyledonae, order Malvales, family Malvaceae and genus *Abelmoschus* (Schippers, 2000). It is native to West Africa (Murdock, 1959). The crop was taken to other parts of the world by the Portuguese (Sinnadurai, 1992). It is one of the important vegetables grown for its immature green non-fibrous edible fruits in the tropical and subtropical parts of the world. Okra has a prominent position among fruit vegetables due to its multiple virtues like high nutritive and

medicinal value, ease of cultivation, wide adaptability, year round cultivation, good portability, export potential and bountiful returns (Reddy, 2010).

Being an upright, quick growing and medium duration annual herb, it fits well into multiple cropping systems either as a sole crop or intercrop (Reddy, 2010). It is the main fruit vegetable crop in many parts of the world, predominantly in Asia and Africa. Okra is a drought and heat tolerant crop (Reddy *et al.*, 2013). It is an important cash crop for marginal, small and large farmers, with a

potential to boost food, nutritional and health security, foster rural development and support sustainable land care (Reddy, 2010).

The average productivity of okra has remained very low and almost stagnant over the last few decades. A major constraint to okra productivity is the low genetic potential of the current varieties that have poor plant type, late maturity, early senescence, short fruiting period, long crop duration and susceptibility to a range of biotic and abiotic stresses. To meet the demand of ever growing human population in the country, it is thus imperative to find alternative means for increasing the yield potential of okra in a sustainable manner.

A successful variety in any vegetable crop must meet minimal criteria for numerous traits that are potentially valued in the markets (Reddy *et al.*, 2014). Superiority for multiple 'yield' and 'quality' traits is essential for economic sustainability of a variety (Reddy *et al.*, 2014). The major emphasis in okra breeding is on the development of HYVs coupled with acceptable pod quality and resistance to yellow vein mosaic virus (Reddy *et al.*, 2012a). Inbred lines are important plant genetic resources for the development of open-pollinated varieties and/or single cross hybrids.

Knowledge on the nature and magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in formulating successful breeding programme for evolving superior cultivars. Genetic variability analysis is helpful to know about the nature and extent of variability that can be attributed to different causes, sensitive nature of the crop to environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding in evolving varieties to various environmental conditions. Genetic variability is essential in order to realize response to

selection pressure. The success of a breeding programme for the genetic improvement of quantitative characters depends on the magnitude of genetic variability existing in the germplasm and the extent to which the desirable characters are heritable. The determination of genetic variability and partitioning it into heritable and non-heritable components using the genetic parameters viz., phenotypic and genotypic coefficients of variation (GCV and PCV), heritability and genetic advance is necessary to have an insight into genetic nature of yield and its components on which selection can be effectively carried out. Character like yield is complex in inheritance and is improved through its component traits. High yield can be achieved by selection of those yield contributing characters that have high heritability coupled with high genetic advance.

Germplasm is an indispensable material to vegetable breeders. Germplasm development plays a key role for genetic improvement of any crop. Inbred line development is an important means of new germplasm development. In okra, pod yield is a complex quantitative trait as it is governed by a large number of genes and considerably affected by the environment.

Hence, selection of lines based only on yield is not effective. Efficient selection for yield in crops requires the estimation of genetic parameters for the strategic planning and allocation of limited resources. Determining the components of variability in yield and its components will also enable us to know the extent of environmental influence on yield. Improvement of complex characters such as yield may be accomplished through the component approach of breeding. Investigation of the interrelationships among growth, earliness and yield related attributes will improve the efficiency of a breeding programme with appropriate selection criteria.

The present investigation was undertaken to study the genotypic and phenotypic coefficients of variation, heritability and genetic advance for growth, earliness and yield attributing traits in okra.

Materials and Methods

The experimental material for the present study comprised of twenty five inbred lines of okra (RNOYR-30 to RNOYR-54) developed at the Vegetable Research Station, Rajendranagar, Hyderabad along with one YVMV resistant check (RNOYR-16) one YVMV susceptible check (RNOYR-19) and two commercial checks (Pusa Sawani and Arka Anamika). The experiment was laid out in a randomized block design with 3 replications during summer, 2014. In each replication each inbred line was raised in a single-row plot of 3.0 m length and 0.6 m width. A row-to-row spacing of 60 cm and a plant-to-plant spacing of 30 cm was adopted. A plant population of 10 plants per row, plot and inbred line was maintained (Table 1). Recommended package of practices were followed and necessary plant protection measures were carried out uniformly to safeguard the crop from major pests and diseases. Biometric data on eighteen quantitative characters were recorded on five competitive and randomly selected plants in each replication for plant height (cm), number of branches per plant, internodal length (cm), first flowering node, first fruiting node, fruit length (cm), fruit width (cm) and fruit weight (g) except days to 50% flowering, first flowering node, days to first fruit harvest, days to last fruit harvest, fruiting period, total number of fruits per plant, number of marketable fruits per plant, total yield per plant (g), marketable yield per plant (g), YVMV infestation (%) and pod borer infestation (%) which were recorded on whole plot basis. The replicated mean values of pod borer infestation on fruits (%) were subjected

to square root transformation and arcsin transformed values for per cent yellow vein mosaic virus infestation (YVMV) to restore the distribution to normality. The mean replicated data on various biometric traits were subjected to analysis of variance as per the standard statistical procedure (Panse and Sukhatme, 1985). Phenotypic and genotypic components of variance were estimated as per the formulae suggested by Lush (1940). Estimates of phenotypic and genotypic coefficients of variation were calculated as per the standard formulae (Burton, 1952). The broad sense heritability was estimated for all the characters as the ratio of genotypic variance to total or phenotypic variance (Lush, 1940). The expected genetic gain or advance under selection for each character was estimated by following the method suggested by Johnson *et al.*, (1955).

Results and Discussion

The analysis of variance revealed highly significant differences for eighteen agro-economic traits among 29 genotypes of okra (Table 2). Highly significant differences for all the characters indicated presence of great amount of variability in all the characters studied. No significant differences were observed within replications, which suggested that the genotypes have enough variability for almost all the traits to carry out further genotypic studies. Generally, the significant differences revealed among the agro-economic traits may be due to environmental influences on the genotypes as well as differences in the genetic potential of the different okra genotypes (inbred lines and checks). This corroborates findings of Ariyo (1993) and Adeniji (2003) who mentioned the role of environmental factors as well as differences in the genetic makeup of different varieties in yield determination of okra. The simple measures of variability like mean and range are presented in (Table 3). The range of mean

values could present a rough estimate about the variation in magnitude of variability present among genotypes. The characters showing high range of variation have more scope for improvement. All the eighteen characters under study exhibited high variability as evident from the ranges of mean values. However, the characters marketable yield per plant, total yield per plant and plant height having wide range of variation in mean values indicated the presence of high variability for these characters and thus offering greater scope for selecting desirable genotypes. These findings are in consonance with the findings of earlier workers (Dhankar and Dhankar, 2002; Singh *et al.*, 2006; Mohapatra *et al.*, 2007; Reddy *et al.*, 2012b) in okra.

For all the characters under study, phenotypic variances were higher than the corresponding genotypic variances (Table 3). The phenotypic variance was highest for marketable yield per plant (13452.215) followed by total yield per plant (3778.070) and yellow vein mosaic virus infestation (2272.332). Similarly, the genotypic variance was also highest for marketable yield per plant (12069.069) followed by yellow vein mosaic virus infestation (2263.342) and total yield per plant (1662.655). The phenotypic variance was lowest for fruit width (0.003) followed by first flowering node (0.057) and internodal length (0.216).

Similarly, the genotypic variance was lowest for fruit width (0.001) followed by first flowering node (0.029) and internodal length (0.085). The genotypic variance was very low for fruit width, first flowering node and internodal length indicating that the major part of the total variation was not heritable. High genotypic variance as observed for marketable yield per plant, yellow vein mosaic virus infestation and total yield per plant indicated greater stability of the genotypes under

different environmental conditions. Therefore, genotypes with such characters are likely to exhibit uniform performance over locations and seasons. Such a high genotypic variance was also reported for total yield per plant and marketable yield per plant in okra (Reddy *et al.*, 2012b).

The estimates of PCV (Table 3) were highest for yellow vein mosaic virus infestation (77.086%) followed by marketable yield per plant (54.767%) and number of marketable fruits per plant (54.627%), while lowest for fruit width (3.084%) followed by days to first fruit harvest (4.566%) and first flowering node (4.951%). The estimates of GCV (Table 3) were highest for yellow vein mosaic virus infestation (76.933%) followed by number of marketable fruits per plant (52.079%) and marketable yield per plant (51.875%), while lowest for fruit width (1.479%) followed by first flowering node (3.510%) and fruit weight (3.963%).

The estimates of PCV (Table 3) were of high magnitude (>20%) for number of branches per plant (26.245%), number of marketable fruits per plant (54.627%), marketable yield per plant (54.767%), pod borer infestation (21.524%) and yellow vein mosaic virus infestation (77.086%), of moderate magnitude (10 to 20%) for plant height (13.794%), number of nodes on main stem (17.579%), fruiting period (11.675%), total number of fruits per plant (14.608%) and total yield per plant (15.455%) and of low magnitude (<10%) for internodal length (8.596%), days to 50% flowering (5.301%), first flowering node (4.951%), days to first fruit harvest (4.566%), days to last fruit harvest (5.764%), fruit length (5.869%), fruit width (3.084%) and fruit weight (5.576%).

The estimates of GCV (Table 3) were of high magnitude (>20%) for number of marketable fruits per plant (52.079%), marketable yield

per plant (51.875%) and yellow vein mosaic virus infestation (76.933%), of moderate magnitude (10 to 20%) for number of branches per plant (16.815%), fruiting period (10.304%), total yield per plant (10.253%) and pod borer infestation (12.610%) and of low magnitude (<10%) for plant height (9.159%), internodal length (5.393%), number of nodes on main stem (8.387%), days to 50% flowering (4.664%), first flowering node (3.510%), days to first fruit harvest (4.054%), days to last fruit harvest (4.975%), fruit length (5.412%), fruit width (1.479%), fruit weight (3.963%) and total number of fruits per plant (9.273%).

The estimates of phenotypic variability cannot differentiate between the effects of genotype and environment. Hence, the study of genetic variability is effective in partitioning out the real genetic differences. The estimates of GCV and PCV are of greater use in determining the variability present in the material.

In general, the magnitude of phenotypic coefficients of variation was higher than the corresponding genotypic coefficients of variation for all the eighteen characters under study, indicating that the apparent variation was not only due to genotype but also due to the favourable influence of environment and selection for these traits sometimes may be misleading.

This environmental effect could be due to heterogeneity in soil fertility status and other unpredictable factors. Similar projections and findings have been made by Singh *et al.*, (2006), Mohapatra *et al.*, (2007) and Reddy *et al.*, (2012b). However, there was a close correspondence between the estimates of phenotypic and genotypic coefficients of variation for majority of the characters under study indicating the fact that the environment influence is very low. In contrast, the high

magnitudinal differences between the estimates of GCV and PCV for number of branches per plant, number of nodes on main stem and pod borer infestation revealed that these traits were influenced by the environmental effects to a large extent and the greater role of environment in the expression of these traits. This also implies that one should not rely on mean phenotypic values for direct selection of these traits.

In the present investigation, the inbred lines were found to possess a high to low phenotypic and genotypic variation as revealed by phenotypic and genotypic coefficients of variation. The characters like number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation having high genotypic coefficients of variation possesses better potential for further gain and improvement through selection. Higher the genotypic coefficient of variation, more are the chances of improvement in those characters.

High magnitude (>20%) of genotypic coefficients of variation were also reported by Reddy *et al.*, (2012b) for number of marketable fruits per plant, Dhall *et al.*, (2003) and Reddy *et al.*, (2012b) for marketable yield per plant and YVMV infestation. Low magnitude (<10%) of genotypic coefficients of variation were also reported by Gandhi *et al.*, (2001), Jaiprakashnarayan *et al.*, (2006), Mehta *et al.*, (2006), Singh *et al.*, (2006), Dakahe *et al.*, (2007) Mohapatra *et al.*, (2007) and Reddy *et al.*, (2012b) for days to 50% flowering, Bendale *et al.*, (2003) for first flowering node, Bendale *et al.*, (2003), Dakahe *et al.*, (2007), Mohapatra *et al.*, (2007) for fruit length, Singh *et al.*, (2006) and Mohapatra *et al.*, (2007) for fruit width. Moderate magnitude (10-20%) of genotypic coefficients of variation was also reported by Dakahe *et al.*, (2007) and Mohapatra *et al.*, (2007) for total yield per plant.

Table.1 List of inbred lines of okra utilized for genetic variability analysis

Genotype	Genotype
RNOYR-30	RNOYR-45
RNOYR-31	RNOYR-46
RNOYR-32	RNOYR-47
RNOYR-33	RNOYR-48
RNOYR-34	RNOYR-49
RNOYR-35	RNOYR-50
RNOYR-36	RNOYR-51
RNOYR-37	RNOYR-52
RNOYR-38	RNOYR-53
RNOYR-39	RNOYR-54
RNOYR-40	RNOYR-16(RC)
RNOYR-41	RNOYR-19 (SC)
RNOYR-42	Arka Anamika(CC)
RNOYR-43	Pusa Sawani (CC)
RNOYR-44	

RC: Resistant check; SC: Susceptible check; CC: Commercial check

Table.2 Analysis of variance for various agro-economic traits of okra

Character	Mean sum of squares		
	Replications (2)	Treatments (28)	Error (56)
Plant height (cm)	408.844	690.506**	205.191
Number of branches per plant	0.368	0.527**	0.171
Internodal length (cm)	0.353	0.386**	0.131
Number of nodes on main stem	0.215	23.147**	12.284
Days to 50% flowering	3.356	16.246**	1.440
First flowering node	0.072	0.115**	0.029
Days to first fruit harvest	2.770	16.032**	1.318
Days to last fruit harvest	22.655	118.221**	12.108
Fruiting period (days)	11.356	146.944**	12.702
Fruit length (cm)	0.189	2.045**	0.114
Fruit width (cm)	0.002	0.004*	0.002
Fruit weight (cm)	1.238	1.915**	0.471
Total number of fruits per plant	0.026	31.098**	10.281
Number of marketable fruits per plant	17.166	196.794**	6.362
Total yield per plant	1679.877	7103.380**	2115.414
Marketable yield per plant (g)	2458.574	37590.353**	1383.146
Pod borer infestation (%)	0.130	0.250**	0.100
Yellow vein mosaic virus infestation (%)	5.090	4555.488**	3.075

*, ** Significant at 5 and 1 percent levels respectively
 Values in parenthesis indicate degrees of freedom

Table.3 Estimates of genetic parameters for various agro-economic traits of okra

Character	Range		Mean±S.Em	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance (%)	Genetic advance as percent of mean
	Minimum	Maximum		Pheno- typic	Geno- typic	Pheno- typic	Geno- typic			
Plant height (cm)	112.887	172.067	138.874±8.126	366.963	161.772	13.794	9.159	44.100	17.396	12.527
Number of branches per plant	1.400	3.467	2.049±0.234	0.289	0.119	26.245	16.815	41.100	0.455	22.192
Internodal length (cm)	4.677	6.343	5.403±0.205	0.216	0.085	8.596	5.393	39.400	0.377	6.971
Number of nodes on main stem	15.287	27.437	22.687±1.998	15.905	3.621	17.579	8.387	22.800	1.870	8.244
Days to 50% flowering	44.000	52.667	47.632±0.681	6.375	4.936	5.301	4.664	77.400	4.027	8.454
First flowering node	4.467	5.400	4.835±0.096	0.057	0.029	4.951	3.510	50.200	0.248	5.125
Days to first fruit harvest	51.000	59.667	54.632±0.651	6.223	4.905	4.566	4.054	78.800	4.050	7.414
Days to last fruit harvest	110.000	128.333	119.552±1.974	47.479	35.371	5.764	4.975	74.500	10.575	8.845
Fruiting period (days)	54.000	76.667	64.920±2.022	57.449	44.748	11.675	10.304	77.900	12.162	18.734
Fruit length (cm)	13.200	16.367	14.828±0.191	0.757	0.644	5.869	5.412	85.000	1.524	10.279
Fruit width (cm)	1.613	1.767	1.695±0.026	0.003	0.001	3.084	1.479	23.000	0.025	1.462
Fruit weight (g)	16.433	19.400	17.502±0.390	0.952	0.481	5.576	3.963	50.500	1.015	5.802
Total number of fruits per plant	23.240	35.797	28.408±1.819	17.220	6.939	14.608	9.273	40.300	3.445	12.126
Number of marketable fruits per plant	4.000	28.790	15.298±1.431	69.840	63.477	54.627	52.079	90.900	15.647	102.279
Total yield per plant (g)	314.190	500.543	397.707±26.093	3778.070	1662.655	15.455	10.253	44.000	55.723	14.011
Marketable yield per plant (g)	56.670	399.930	211.778±21.099	13452.215	12069.069	54.767	51.875	89.700	214.360	101.219
Pod borer infestation (%)	10.863	19.493	14.193±1.405	9.333	3.203	21.524	12.610	34.300	2.160	15.218
Yellow vein mosaic virus infestation (%)	0.000	100.000	61.839±1.701	2272.332	2263.342	77.086	76.933	99.600	97.810	158.168

The estimates of heritability (Table 3) were of high magnitude (> 60%) for days to 50% flowering (77.400%), days to first fruit harvest (78.800%), days to last fruit harvest (74.500%), fruiting period (77.900%), fruit length (85.000%), number of marketable fruits per plant (90.900%), marketable yield per plant (89.700%) and yellow vein mosaic virus infestation (99.600%), of moderate magnitude (30-60%) for plant height (44.100%), number of branches per plant (41.100%), internodal length (39.400%), first flowering node (50.200%), fruit weight (50.500%), total number of fruits per plant (40.300%), total yield per plant (44.000%) and pod borer infestation (34.300%) and of low magnitude (<30%) for number of nodes on main stem (22.800%) and fruit width (23.000%).

Heritability in broad sense is the ratio of genotypic variance to total variance in non-segregating population (Hanson *et al.*, 1956). The estimates of heritability were of high magnitude (>60%) for days to 50% flowering, days to first fruit harvest, days to last fruit harvest, fruiting period, fruit length, number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicating that though the characters are least influenced by the environmental effects, the selection for the improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. High magnitude (>60%) of heritability estimates were also reported by Singh *et al.*, (2006) and Mohapatra *et al.*, (2007) for days to 50% flowering, Singh *et al.*, (2006) and Mohapatra *et al.*, (2007) for fruit length, Dhall *et al.*, (2003) and Reddy *et al.*, (2012b) for number of marketable fruits per plant and Dhall *et al.*, (2003) for YVMV infestation. The estimates of heritability were of moderate

magnitude (30-60%) for plant height, number of branches per plant, internodal length, first flowering node, fruit weight, total number of fruits per plant, total yield per plant and pod borer infestation indicating that these characters are moderately influenced by environmental effects and genetic improvement through selection will be moderately difficult due to masking effects of the environment on the genotypic effects.

The estimates of genetic advance as per cent of mean (Table 3) were of high magnitude (>20%) for number of branches per plant (22.192%), number of marketable fruits per plant (102.279%), marketable yield per plant (101.219%) and yellow vein mosaic virus infestation (158.168%), of moderate magnitude (10 to 20%) for plant height (12.527%), fruiting period (18.734%), fruit length (10.279%), total number of fruits per plant (12.126%) and total yield per plant (14.011%) and of low magnitude (<10%) for internodal length (6.971%), number of nodes on main stem (8.244%), days to 50% flowering (8.454%), first flowering node (5.125%), days to first fruit harvest (7.414%), days to last fruit harvest (8.845%), fruit width (1.462%), fruit weight (5.802%) and pod borer infestation (15.218%).

Knowledge of extent of improvement possible through selection is useful in designing breeding programme. Genetic advance under selection is the improvement in the mean genotypic value of the selected families over the base population. The genetic advance shows the improvement that can be made in a particular character by applying certain amount of selection intensity. The genetic advance to be expected depends up on the selection differential, the genotypic coefficient of variation and the square root of the heritability ratio (Johnson *et al.*, 1955). The genotypic coefficient of variation x selection differential estimates the maximum

effectiveness of selection and heritability indicates how closely the goal can be achieved. However, by increasing the diversity of genotypes of okra, the expected genetic advance can still be increased.

The estimates of genetic advance as per cent of mean were of high magnitude (>20.00%) for number of branches per plant, number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicating that these characters are governed by additive genes and selection will be rewarding for improvement of such traits. This suggests that such characters can be improved by direct selection. The estimates of genetic advance as percent of mean were of moderate magnitude (10.00 to 20.00%) for plant height, fruiting period, fruit length, total number of fruits per plant and total yield per plant. Moderate magnitude (10-20%) of genetic advance as per cent of mean was also reported by Gandhi *et al.*, (2001) for plant height, Bendale *et al.*, (2003) and Mohapatra *et al.*, (2007) for fruit length. High magnitude (>20%) of genetic advance as percent of mean was also reported by Singh *et al.*, (2006), Mohapatra *et al.*, (2007) and Jaiprakashnarayan *et al.*, (2006) for number of branches per plant, Dhall *et al.*, (2003) and Reddy *et al.*, (2012b) for number of marketable fruits per plant, Kumar *et al.*, (2010) and Reddy *et al.*, (2012b) for marketable yield per plant and Dhall *et al.*, (2003) and Reddy *et al.*, (2012b) for YVMV infestation.

Estimates of heritability along with genetic advance are more useful in predicting the value of selection than heritability alone (Johnson *et al.*, 1955). High estimates of heritability (>60%) coupled with high genetic advance as percent of mean (>20.00%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation revealed that most

likely the heritability is due to additive gene effects and selection may be effective. Such value of high heritability and high genetic advance may be attributed to the action of additive genes (Panse, 1957). Therefore, such characters having high heritability coupled with high genetic advance would be effective in crop improvement programme through selection methods.

High heritability (>60%) coupled with high expected genetic advance (>20%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicated the involvement of additive gene action and more chances of fixing by selection to improve such traits and a very significant improvement is possible through selection for all these characters through pure line selection, mass selection, progeny selection and hybridization and selection with pedigree breeding.

On the whole, from the genetic variability analysis it is evident that the inbred lines utilized in the present investigation possessed considerable genetic variation. All the genotypes showed considerable variability in the observed agro-economic traits as it is evident from the estimates of coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean. The spectrum of large variability for economically important characters will provide the breeder a good scope for the genetic improvement in okra. High heritability and genetic advance were observed for majority of the characters, which suggested that they are controlled by few genes.

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