Short communication

Genetic variability and association of yield with its component traits in Okra

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ABSTRACT

Forty four accessions from 6 different wild *Abelmoschus species* and 4 check cultivars from cultivated species were evaluated during *Kharif* 2015 to assess the genetic variability and character association. Estimates of genotypic coefficients of variability (GCV) and phenotypic coefficients of variability (PCV) ranged from 6.15-59.14 and 13.98-62.13, respectively. Heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) ranged from 19-98%, 0.40-84.20, 5.58- 98%, respectively. Further classification revealed high GCV (>20.00%), heritability (>60.00%) and GAM (>20.00%) for most of the yield components and PDI of BYVMV, except for first flowering node and stem diameter. Path co-efficient analysis revealed high positive direct effect of fruit weight (0.85), number of fruits per plant (0.532), stem diameter (0.088), plant height (0.069) and fruit diameter (0.046) on fruit yield per plant. Therefore, direct selection based on these combinations of traits will help in harnessing their positive direct effects on yield per plant in okra improvement programmes.

Key words: *Abelmoschus* species, heritability, genetic advance, correlation, path coefficient.

Okra [*Abelmoschus esculentus* (L.) Moench] is one of the delicious fruit vegetables having food, non-food and medicinal uses. High level of dietary fibre, flavonoids, rich source of minerals, like Ca, Fe, Mg, Cu and Mn has made okra an important component of Indian diet (Kumar *et al.*, 8). India is the largest producer of okra with 6.35 million tonnes production (72.9% of total world production) from 0.53-million-hectare area (Anonymous, 1). Although India is the largest producer of okra, its productivity potential is low due to an array of biotic stresses adversely affecting the yield and quality of the product. The important biotic bottlenecks include Bhendi Yellow Vein Mosaic Virus (BYVMV) and insect pests, like whitefly (*Bemisia tabaci* Gen.) and jassids [*Amarasca biguttula biguttula* (Shir.)]. Considering its nutritional, food and socioeconomic importance, genetic improvement of okra has drawn utmost attention.

Knowledge of genetic parameters, like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2), genetic advance (GA) and character association are pre-requisite for okra improvement programme (Nwangburuka *et al.*, 10). Several researchers have emphasized on wild relatives of okra as an important source of useful genes for breeding programmes and resistance to BYVMV, Jassids and other biotic and abiotic stresses (Dhankar *et al.*, 5). Therefore, considering the importance of wild germplasm and their genetic analysis for future use, the present study

was undertaken to analyze the genetic variability and association among yield and biotic stresses in okra germplasm consisted of 44 accessions of 6 okra wild species belonging to *Abelmoschus caillei* (3), *A. manihot* (17), *A. moschatus* (16), *A. tuberculatus* (3), *A. ficulneus* (2) and *A. angulosus* (3) alongwith 4 check cultivars of cultivated specie viz., Pusa Sawani, Pusa A-4, DOV-66 and DOV-92. The experiment was laid out in Completely Randomized Block Design (RCBD) with 2 replications.

The accessions were screened under natural epiphytotic condition for BYVMV following the infector row method (Nene *et al.*, 9). The response of the virus was assessed based on per cent disease incidence [PDI = (Number of diseased plants/Total number of plants) × 100] in each accession at 15 days interval and later averaged to get mean PDI. The mean replicated data on various other biometric traits and mean PDI were subjected to analysis of variance as per the standard statistical procedure. Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (3). Expected genetic gain or advance under selection and correlation coefficient were computed by using the formula of Johnson *et al.* (7). Path coefficient analysis was carried out as per Dewey and Lu (6).

Experimental results revealed broader ranges of mean values indicating presence of enough variation in the experimental material used (Table 1). Estimates of GCV and PCV ranged from 6.15% (first flowering node) to 59.14 % (fruit length) and 13.98% (first flowering node) to 62.13% (fruit length), respectively. GCV estimates were highest for fruit length (59.14%)

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followed by fruit weight (50.20%), and PDI of BYVMV incidence (46.83%). Similarly, PCV was highest for fruit length (62.13%) followed by fruit weight (52.59%) and PDI of BYVMV incidence (47.27%). The trait first flowering node, however recorded the lowest GCV (6.15%) and PCV (13.98%). In general, PCV were slightly higher than the corresponding GCV. However, the difference between PCV and GCV being negligible for majority of the characters, namely days to first flowering, number of nodes on main stem, plant height, fruit length, fruit weight, PDI of BYVMV and yield /plant suggesting thereby genetic governance of these characters. The selection on phenotypic basis would, therefore, hold good. Further, the PCV and GCV values were classified as low (<10 %), moderate (10- 20%) and high (>20%) as suggested by Sivasubramanian and Menon (13). GCV and PCV were high for all the characters, except moderate PCV (13.98%) and low GCV (6.15%) for first flowering node and moderate GCV (18.19%) for fruit diameter. GCV and PCV estimates corroborated with the studies of Reddy *et al.* (11) and Nwangburuka *et al.* (10). The low differences between PCV and GCV estimates for BYVMV incidence indicated genetic predominance than environment in governing the trait emphasizing scope and importance of germplasm used here in selection of BYVMV resistant accessions for future use in breeding programmes.

Estimates of heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) are presented in Table 1.

Heritability, GA and GAM values ranged from 19-98%, 0.40-84.20% and 5.58- 98%, respectively. The heritability values were classified as low (<30%), moderate (30- 60 %) and high (>60%), while that of GAM as low (<10%), moderate (10-20%) and high (>20%) as suggested by Johnson *et al.* (7). Estimates of heritability were high for days to first flowering (92%), internodal length (76%), number of nodes on main stem (82%), plant height (87%), number of branches per plant (87%), fruit length (91%), number of fruits per plant (75%), fruit weight (91%), PDI of BYVMV incidence (98%) and green fruit yield/plant (96%). Heritability estimates were moderate for stem diameter (45%) and fruit diameter (55%), while low only for first flowering node (19%). The estimates of GAM were also high for days to first flowering (45.41%), internodal length (60.49%), number of nodes on main stem (41.02%), plant height (55.96%), stem diameter (30.01%), number of branches per plant (79.99%), fruit length (115.96%), fruit diameter (27.79%), number of fruits per plant (36.78%), fruit weight (98.70%), PDI of BYVMV incidence (95.56%) and green fruit yield/plant (91.94%). Low GAM (<10.00 %) was recorded only for first flowering node (19%).

During the selection for the improvement of any character, knowledge of both broad sense heritability and GAM are necessary, because broad sense heritability is based on total genetic variance, which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. When heritability is mainly due to non-additive genetic

Table 1. Estimates of genetic parameters for yield and its component traits in wild okra germplasm.

Sl. No.	Character	Mean	GV	PV	GCV (%)	PCV (%)	h^2 (Broad Sense)	Genetic Advancement 5%	Genetic Advance as % of Mean (5%)
1	First flowering node	5.8-9.5	0.19	1.02	6.15	13.98	0.19	0.4	5.58
2	Days to first flowering	43.6-86.3	190.69	207.72	23.01	24.01	0.92	27.26	45.41
3	Internal nodal length	2.26-11.13	4.54	5.94	33.6	38.44	0.76	3.84	60.49
4	No. of nodes on main stem	12.64-31.54	23.44	28.46	21.94	24.18	0.82	9.05	41.02
5	Plant height (cm)	51.56-160.73	756.14	872.12	29.17	31.33	0.87	52.75	55.96
6	Stem diameter (cm)	0.39-2.27	0.09	0.21	21.64	32.15	0.45	0.43	30.01
7	No. of branches per plant	2.7-13.4	10.20	11.71	41.61	44.58	0.87	6.14	79.99
8	Fruit length (cm)	1.57-14.09	11.99	13.24	59.14	62.13	0.91	6.79	115.96
9	Fruit diameter (cm)	1.03-2.95	0.12	0.21	18.19	24.52	0.55	0.53	27.79
10	No. of fruits per plant	10.15-28.50	15.94	21.39	20.68	23.96	0.75	7.1	36.78
11	Fruit weight (g)	2.32-14.45	10.60	11.64	50.2	52.59	0.91	6.4	98.7
12	PDI of BYVMV	7.73-71.34	218.12	222.25	46.83	47.27	0.98	30.14	95.56
13	Fruit yield/ plant	46.26-245.13	2808.07	2923.87	45.54	46.47	0.96	106.98	91.94

effects (dominance and epistasis), genetic advance will be low, while in cases where heritability is chiefly due to additive gene effects, a high genetic advance may be expected. In the present investigation, except for first flowering node, high GAM coupled with high heritability observed for all the characters including PDI of BYVMV indicated prevalence of additive genetic effects (fixable) involved in their expression and such additive gene effects are predicted to show good response to phenotype-based selection in crop improvement programme. Hence, it is advisable for straight phenotype-based selection to improve these characters. High heritability along with high GAM estimates are also obtained by Das *et al*. (4) and Reddy *et al*. (11) in okra. Low heritability coupled with low GAM observed for first flowering node is the sign of prevalence of non-additive gene action and influence of environment showing, thereby, limited scope for improvement of first flowering node through selection.

Path coefficient analysis (Table 2) is an efficient technique to partition the correlation coefficient of each of the trait with yield into direct and indirect effects which helps in explaining relative importance of each of the trait and their reliability in selection. Fruit weight (0.85) exhibited highest positive direct effect on fruit yield/ plant followed by number of fruits/ plant (0.532), internodal length (0.148), stem diameter (0.088), plant height (0.069) and fruit diameter (0.046). These traits also possessed their significant positive correlation with fruit yield per plant (except internodal length) indicating that direct selection based on these traits help in yield improvement. These findings are in line with those of Sharma and Prasad (12). Number of nodes on main stem (-0.574) followed by % BYVMV incidence (-0.268), first flowering node (-0.061), fruit length (-0.062), number of branches/ plant (-0.039) and days to first flowering (-0.031) exhibited negative direct effects on fruit yield per plant. Among these negatively effecting traits, first flowering node and PDI of BYVMV also possessed negative significant correlation with fruit yield/ plant indicating their true relation.

Growth attributes, like number of nodes on main stem, fruit length and days to first flowering showed negative direct effect on fruit yield/ plant, although positively correlated with fruit yield/ plant. In such a situation, the positive significant correlation obtained with fruit yield/ plant may be due to the positive indirect effects. As a result, negative direct effect showing number of fruits/ plant showed significant positive correlation due to positive indirect effects via number of fruits/ plant (0.510), fruit weight (0.221), PDI of BYVMV (0.093), internodal length

Table 2. Genotypic path coefficient among different traits in wild okra genotypes.

Characters	First flowering node	Days to first flowering	Internal nodal length	No. nodes on main stem	Plant height (cm)	Stem diameter (cm)	No. of branches/ plant	Fruit length (cm)	Fruit diameter (cm)	No. of fruits/ plant	Fruit weight (g)	PDI of BYVMV	Correlation with fruit yield/ plant
	1	2	3	4	5	6	7	8	9	10	11	12	13
1	**-0.061**	0.027	-0.145	0.386	-0.074	0.004	0.002	0.031	-0.016	-0.228	-0.348	0.003	-0.419**
2	0.053	**-0.031**	0.120	-0.324	0.056	-0.015	-0.006	-0.007	0.030	0.326	0.033	0.023	0.256*
3	0.060	-0.025	**0.148**	-0.346	0.047	-0.020	-0.011	0.001	0.023	0.332	-0.194	0.016	0.03
4	0.041	-0.018	0.089	**-0.574**	0.047	0.047	-0.012	-0.019	0.002	0.510	0.221	0.093	0.427**
5	0.065	-0.026	0.101	-0.388	**0.069**	0.010	0.005	-0.032	0.021	0.363	0.389	0.030	0.606**
6	-0.003	0.005	-0.033	-0.306	0.008	**0.088**	-0.010	-0.012	-0.009	0.252	0.270	0.072	0.322**
7	0.004	-0.005	0.041	-0.169	-0.009	0.022	**-0.039**	0.042	-0.013	0.136	-0.549	0.077	-0.462**
8	0.031	-0.004	-0.003	-0.177	0.035	0.017	0.026	**-0.062**	0.006	0.162	0.836	-0.014	0.852**
9	0.021	-0.020	0.074	-0.023	0.031	-0.017	0.011	-0.009	**0.046**	0.111	0.109	0.012	0.346**
10	0.026	-0.019	0.092	-0.550	0.047	0.042	-0.010	-0.019	0.010	**0.532**	0.235	0.112	0.498**
11	0.025	-0.001	-0.034	-0.149	0.032	0.028	0.025	-0.061	0.006	0.147	**0.850**	0.011	0.878**
12	0.001	0.003	-0.009	0.200	-0.008	-0.024	0.011	-0.003	-0.002	-0.222	-0.034	**-0.268**	-0.355**

Residual Effect =0.36

(0.089), plant height and stem diameter (0.047). Similarly, positive indirect effects are responsible for positive significant correlation of fruit length and days to first flowering with fruit yield/ plant. Under these circumstances, to make use of these positive indirect effects a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects and simultaneous prioritized selection on positive indirect effects. These findings corroborated with Das *et al*. (4) and Choudhary and Sharma (2). The residual effect was low (0.36), suggesting inclusion of maximum fruit yield influencing characters of okra in the present analysis.

Based on the results obtained from the present study, high genetic variability and heritability estimates obtained for earliness, growth, yield and PDI of BYVMV indicated prevalence of additive genetic effects (fixable) governing their expression. Character association study revealed significant positive association and high positive direct effect of fruit weight (0.85) number of fruits per plant (0.532), stem diameter (0.088), plant height (0.069) and fruit diameter (0.046) on fruit yield per plant. Therefore, direct selection based on these combinations of traits help in harnessing their positive direct effects on yield per plant in okra improvement programmes.

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