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Estimation of genetic variability, correlation and path coefficient in okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

An experiment was conducted comprising 40 genotypes of okra in RCBD with three replications at HRC, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during summer season of 2019. The significant variation and relatively wide range of mean recorded for all characters, indicated the existence of variation among the tested genotypes. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of primary branches and moderate phenotypic coefficient of variation and genotypic coefficient of variation was observed for length of internode, number of nodes per plant, plant height, number of fruits per plant, fruit yield per plant and fruit yield. High GCV along with high heritability and genetic advance as percent of mean was observed for number of primary branches, plant height, number of fruits per plant, fruit yield per plant, number of nodes per plant, fruit yield, length of internode, days to first flower initiation, days to 50% flowering, and days to first fruit set. Fruit yield showed positive and significant correlation with fruit yield per plant, number of fruits per plant, plant height, length of internode, fruit length, number of primary branches and duration of crop at both phenotypic and genotypic correlation coefficient. The path coefficient analysis indicated high positive direct effect for fruit yield per plant, plant height, days to first flower initiation, number of primary branches and days to first fruit picking and high but negative direct effect exhibited by length of internode, number of nodes per plant, number of fruits per plant, fruit length, days to 50% flowering, days to second fruit picking, duration of crop and days to first fruit set on fruit yield.

Keywords: Estimation, genetic variability, correlation, okra

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is popularly known as lady's finger or bhindi belong to the family Malvaceae with chromosome number $2n=130$. It is important spring-summer and rainy season vegetable crop cultivated in tropical and sub-tropical parts of the world. The mature and tender fruits of okra are mostly used as vegetable and culinary preparation as sliced and fried pieces. Its fruits have high nutritive, medicinal and industrial value and export potential. Its fruits are rich in vitamins, calcium, potassium and other mineral matters (Effing *et al.*, 2009) [7]. Dried stems and roots of okra have been reported to be utilized for cleaning sugarcane juice from which molasses is prepared. Crude fibre is present in mature pods and stems which is utilized by the paper industry. It is rich in iodine and other nutrients (Benchasri, 2012) [2].

Materials and Methods

The present study was carried out during summer season 2019 at the Horticulture Research Centre, Department of Horticulture, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, U.P. A group of forty genotypes were evaluated under field condition using randomized block design with three replications. Each genotype was sown in 60 cm spaced. Plant to plant distance maintained 30 cm. observations were recorded on five randomly selected plant from each replication of each plot. Observations were recorded on days to first flower initiation, days to 50% flowering, plant height, number of primary branches, number of nodes per plant, length of internode, fruit length, days to first fruit set, number of fruits per plant, days to first fruit picking, days to second fruit picking, duration of crop, fruit yield per plant and fruit yield (q/ha). Mean values of five Randomly selected plants were used for statistical analysis. The estimates of variability parameters work out according to the method suggested by Lush (1940). Phenotypic and genotypic coefficient of variation were calculated based on the approach cracked by Burton (1952) [4].

Broad sense heritability was estimated (Allard, 1960)^[1] and expressed in percentage. Genetic advance as percent of mean was calculated by the method advocated by Johnson *et al.*, (1955)^[8]. Characters association genotypic and phenotypic correlation coefficient levels and path coefficient analysis for fruit yield was taken as the dependent variable while rest of the traits were considered as independent variable simultaneous equations. which expressed the basic relationship between path coefficient which were solved to estimate the direct and indirect effects with the formula of suggested by Dewey and Lu (1959)^[6].

Result and Discussion

The analysis of variance revealed a significant genetic variance among genotypes for all traits under investigation, indicating the existence of sufficient genetic variability among the genotypes (Table-1). The mean performance and phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability in broad sense and genetic advance as percent of mean are presented in (Table-2). Estimates phenotypic coefficient of variance (PCV) were higher than genotypic coefficient of variance (GCV) for all fourteen traits studied, which indicating minor influence of environment. High estimates of PCV for number of primary branches (32.80). The moderate phenotypic coefficient of variation (10-25%) was observed for length of internode (19.88), number of nodes per plant (17.34), plant height (15.21), number of fruits per plant (14.52), fruit yield per plant (12.67), fruit length (12.01), fruit yield (11.04) and days to first flower initiation (10.23). However, low phenotypic coefficient variation (<10%) was observed for days to first fruit set (9.68), days to 50% flowering (9.43), days to first fruit picking (8.70), days to second fruit picking (8.05) and duration of crop (5.66). Selection may be effective based on these traits and their phenotypic expression would be good indication of the genotypic potential. (Thulasiram *et al.*, 2017, Syfullah *et al.*, 2018 and Kumari *et al.*, 2019)^[17, 16, 9]. To success of a breeding plan mainly depends on the extent of additive genetic variance available in the genetic material for related traits. In the present investigation plant height (97.07), number of fruits per plant (92.34), fruit yield per plant (92.08), number of nodes per plant (90.86), number of primary branches (90.70), fruit yield (82.01), length of internode (81.89), days to first flower initiation (81.83), days to 50% flowering (81.12), and days to first fruit set (80.91), exhibited high heritability (>60%). The moderate heritability (<60%) was observed for days to first fruit picking (74.91),

days to second fruit picking (74.45), fruit length (44.42) and duration of crop (42.97). (Sraavanthi *et al.*, 2017, Verma *et al.*, 2018 and Kumari *et al.*, 2019)^[15, 9]. High genetic advance expressed as percentage of mean was high (>20%) for number of primary branches (61.28), length of internode (33.53), number of nodes per plant (32.45), plant height (30.42), number of fruits per plant (27.63) and fruit yield per plant (24.03), while moderate genetic advance (<20 to 10%) was observed for fruit yield (18.66), days to first flower initiation (17.25), days to first fruit set (16.14), days to 50% flowering (15.76), days to first fruit picking (13.43), days to second fruit picking (12.34) and fruit length (10.99), whereas, duration of crop (5.01) showed low genetic advance (<10%) indicates the presence of additive genetic variance for these traits in the genotypes and the selection of these characters may be helpful for enhancement of fruit yield. (Syfullah *et al.*, 2018 and Rambabu *et al.*, 2019)^[16, 13]. Estimation of phenotypic and genotypic correlation coefficient of traits is presented in (Table-3). The result exhibited that genotypic correlation coefficient was higher than the phenotypic correlation coefficients, which indicate the inherent association among various traits independent of environmental influence. Fruit yield showed positive and significant correlation with fruit yield per plant (0.967**), number of fruits per plant (0.908**), plant height (0.734**), length of internode (0.458**), fruit length (0.356**), number of primary branches (0.270**) and duration of crop (0.189*). Negative and non-significant correlation was observed for days to 50% flowering (-0.125), days to first flower initiation (-0.113), days to first fruit set (-0.085), days to first fruit picking (-0.085), days to second fruit picking (-0.072) and number of nodes per plant (-0.013) at phenotypic and genotypic and showed similar trends levels with little variation. (Mohammad *et al.* 2017, Raval *et al.* 2019 and Chavan *et al.* 2019)^[11, 14, 5]. The results obtained at genotypic and phenotypic levels of path coefficient are presented in (Table-4). The high positive direct effect observed for fruit yield per plant (0.973) followed by plant height (0.356), days to first flower initiation (0.154), number of primary branches (0.015) and days to first fruit picking (0.006) on fruit yield. High but negative direct effect exhibited by length of internode (-0.330), number of nodes per plant (-0.280), number of fruits per plant (-0.074), fruit length (-0.053), days to 50% flowering (-0.047), days to second fruit picking (-0.030), duration of crop (-0.030) and days to first fruit set (-0.0006) on fruit yield indicating that simple selection could be effective for these traits. (Pithiya *et al.*, 2017, Chavan *et al.*, 2019 and Binopal *et al.*, 2019)^[12, 5, 3].

Table 1: Analysis of variance for 14 characters in Okra [*Abelmoschus esculentus* (L.) Moench]

Source of variation	DF	Days to first flower initiation	Days to 50% flowering	Plant height (cm)	Number of primary branches	Number of nodes per plant	Length of internode (cm)	Fruit length (cm)
Replication	2	1.25	3.48	0.08	0.03	0.67	0.04	0.24
Treatment	39	54.73**	52.77**	428.93**	1.73**	33.75**	1.81**	2.25**
Error	78	3.77	3.80	4.28	0.06	1.10	0.12	0.66

Source of variation	DF	Days to first fruit set	Number of fruits per plant	Days to first fruit picking	Days to second fruit picking	Duration of crop	Fruit yield per plant (gm)	Fruit yield (q/ha)
Replication	2	0.49	0.29	3.71	0.38	7.78	17.69	3.09
Treatment	39	52.96**	6.29**	49.82**	50.88**	56.28**	502.64**	152.76**
Error	78	3.86	0.17	5.00	5.22	17.25	14.01	10.41

*, ** significant at 5% and 1% level, respectively

Table 2: Estimates of genetic variability parameters for fourteen characters of okra [*Abelmoschus esculentus* (L.) Moench]

Characters	Mean	Mean		PCV (%)	GCV (%)	Heritability (%)	GA	Genetic advance as % mean
		Min	Max					
Days to first flower initiation	44.52	38.80	56.47	10.23	9.26	81.83	7.68	17.25
Days to 50% flowering	47.56	42.50	59.40	9.43	8.50	81.12	7.50	15.76
Plant height (cm)	79.39	62.60	108.60	15.21	14.99	97.07	24.15	30.42
Number of primary branches	2.39	1.67	5.07	32.80	31.24	90.70	1.47	61.28
Number of nodes per plant	19.96	14.62	32.85	17.34	16.53	90.86	6.48	32.45
Length of internode (cm)	4.16	2.11	5.35	19.88	17.99	81.89	1.40	33.53
Fruit length (cm)	9.09	7.70	11.20	12.01	8.00	44.42	1.00	10.99
Days to first fruit set	46.44	40.40	58.43	9.68	8.71	80.91	7.50	16.14
Number of fruits per plant	10.24	8.37	15.40	14.52	13.96	92.34	2.83	27.63
Days to first fruit picking	51.33	44.60	63.03	8.70	7.53	74.91	6.89	13.43
Days to second fruit picking	56.18	48.73	66.90	8.05	6.94	74.45	6.93	12.34
Duration of crop	97.18	85.97	110.70	5.66	3.71	42.97	4.87	5.01
Fruit yield per plant (gm)	104.98	87.00	146.97	12.67	12.16	92.08	25.23	24.03
Fruit yield (q/ha)	68.88	58.83	92.15	11.04	10.00	82.01	12.85	18.66

Table 3: Estimates of correlation coefficient for genotypic and phenotypic levels among 14 characters of okra [*Abelmoschus esculentus* (L.) Moench]

Characters		Days to first flower initiation	Days to 50% flowering	Plant height (cm)	Number of primary branches	Number of nodes per plant	Length of internode (cm)	Fruit length (cm)	Days to first fruit set	Number of fruits per plant	Days to first fruit picking	Days to second fruit picking	Duration of crop	Fruit yield per plant (gm)	Fruit yield (q/ha)
Days to first flower initiation	G	1.000	0.913**	-0.313**	0.449**	0.429**	-0.503**	-0.032	0.875**	-0.143	0.846**	0.801**	0.652**	-0.155	-0.150
	P	1.000	0.808**	-0.273**	0.403**	0.376**	-0.372**	-0.043	0.873**	-0.111	0.823**	0.775**	0.708**	-0.132	-0.113
Days to 50% flowering	G			-0.293**	0.463**	0.432**	-0.463**	-0.049	0.857**	-0.118	0.875**	0.864**	0.932**	-0.131	-0.117
	P			-0.268**	0.375**	0.347**	-0.390**	-0.014	0.818**	-0.116	0.837**	0.827**	0.375**	-0.131	-0.125
Plant height (cm)	G				0.153	0.038	0.731**	0.489**	-0.305**	0.786**	-0.327**	-0.306**	-0.006	0.769**	0.775**
	P				0.167	0.051	0.666**	0.335**	-0.264**	0.762**	-0.274**	-0.272**	0.008	0.745**	0.734**
Number of primary branches	G					0.012	0.126	0.136	0.467**	0.241**	0.484**	0.431**	0.642**	0.246**	0.266**
	P					0.034	0.150	0.116	0.406**	0.226*	0.383**	0.369**	0.428**	0.242**	0.270**
Number of nodes per plant	G						-0.612**	-0.252**	0.419**	-0.023	0.431**	0.449**	0.079	-0.059	-0.077
	P						-0.529**	-0.144	0.369**	-0.006	0.371**	0.360**	0.063	-0.029	-0.013
Length of internode (cm)	G							0.514**	-0.475**	0.499**	-0.492**	-0.522**	-0.153	0.514**	0.522**
	P							0.349**	-0.389**	0.439**	-0.437**	-0.386**	-0.021	0.466**	0.458**
Fruit length (cm)	G								-0.013	0.494**	-0.100	-0.080	0.274**	0.475**	0.459**
	P								-0.027	0.332**	-0.013	-0.057	0.075	0.343**	0.356**
Days to first fruit set	G									-0.126	0.773**	0.819**	0.847**	-0.140	-0.133
	P									-0.098	0.772**	0.812**	0.504**	-0.100	-0.085
Number of fruits per plant	G										-0.100	-0.089	0.256**	0.964**	0.979**
	P										-0.096	-0.075	0.186*	0.927**	0.908**
Days to first fruit picking	G											0.769**	0.911**	-0.101	-0.097
	P											0.750**	0.468**	-0.114	-0.085
Days to second fruit picking	G												0.980**	-0.113	-0.094
	P												0.398**	-0.069	-0.072
Duration of crop	G													0.279**	0.286**
	P													0.181*	0.189*
Fruit yield per plant (gm)	G														0.978**
	P														0.967**
Fruit yield (q/ha)	G														1.000
	P														1.000

*, ** significant at 5% and 1% level, respectively

Table 4: Path coefficient analysis showing the direct and indirect effects of fourteen characters on fruit yield (q/ha) at genotypic and phenotypic levels of okra [*Abelmoschus esculentus* (L.) Moench]

Characters		Days to first flower initiation	Days to 50% flowering	Plant height (cm)	Number of primary branches	Number of nodes per plant	Length of internode (cm)	Fruit length (cm)	Days to first fruit set	Number of fruits per plant	Days to first fruit picking	Days to second fruit picking	Duration of crop	Fruit yield per plant (gm)	R with Fruit yield (q/ha)
Days to first flower initiation	G	0.154	-0.053	-0.112	0.007	-0.120	0.166	0.002	-0.0007	0.011	0.006	-0.033	-0.020	-0.157	-0.150
	P	-0.008	-0.046	0.006	0.016	0.014	-0.012	-0.001	0.020	-0.009	0.061	-0.032	-0.006	-0.115	-0.113
Days to 50% flowering	G	0.171	-0.047	-0.104	0.007	-0.121	0.153	0.003	-0.0007	0.009	0.006	-0.032	-0.028	-0.132	-0.117
	P	-0.006	-0.058	0.006	0.015	0.013	-0.013	0.001	0.019	-0.010	0.062	-0.035	-0.003	-0.114	-0.125

Plant height (cm)	G	-0.048	0.014	0.356	0.002	-0.011	-0.241	-0.026	0.0002	-0.058	-0.002	0.009	0.001	0.779	0.775**
	P	0.002	0.015	-0.022	0.007	0.002	0.022	0.008	-0.006	0.064	-0.020	0.011	0.001	0.650	0.734**
Number of primary branches	G	0.069	-0.022	0.055	0.015	-0.003	-0.042	-0.007	-0.0003	-0.018	0.003	-0.013	-0.020	0.249	0.266**
	P	-0.003	-0.022	-0.004	0.040	0.001	0.005	0.003	0.009	0.019	0.029	-0.015	-0.003	0.212	0.270**
Number of nodes per plant	G	0.066	-0.020	0.013	0.001	-0.280	0.202	0.013	-0.0003	0.002	0.002	-0.013	-0.002	-0.060	-0.077
	P	-0.003	-0.020	-0.001	0.001	0.037	-0.018	-0.003	0.008	0.001	0.028	-0.015	0.001	-0.026	-0.013
Length of internode(cm)	G	-0.077	0.022	0.260	0.002	0.171	-0.330	-0.027	0.0003	-0.037	-0.003	0.016	0.005	0.521	0.522**
	P	0.003	0.022	-0.015	0.006	-0.019	0.034	0.008	-0.009	0.037	-0.033	0.016	0.001	0.407	0.458**
Fruit length (cm)	G	-0.005	0.002	0.174	0.002	0.070	-0.170	-0.053	0.0001	-0.037	-0.001	0.002	-0.008	0.481	0.459**
	P	0.001	0.001	-0.007	0.005	-0.005	0.012	0.023	-0.001	0.028	-0.001	0.002	-0.001	0.300	0.356**
Days to first fruit set	G	0.165	-0.052	-0.109	0.007	-0.117	0.157	0.001	-0.0006	0.009	0.006	-0.032	-0.026	-0.142	-0.133
	P	-0.007	-0.047	0.006	0.016	0.014	-0.013	-0.001	0.023	-0.008	0.057	-0.034	-0.004	-0.088	-0.085
Number of fruits per plant	G	-0.022	0.006	0.280	0.004	0.006	-0.165	-0.026	0.0001	-0.074	-0.001	0.003	-0.008	0.977	0.979**
	P	0.001	0.007	-0.017	0.009	0.001	0.015	0.008	-0.002	0.084	-0.007	0.003	-0.001	0.810	0.909**
Days to first fruit picking	G	0.167	-0.051	-0.116	0.007	-0.120	0.163	0.005	-0.0007	0.007	0.006	-0.034	-0.028	-0.102	-0.097
	P	-0.007	-0.048	0.006	0.015	0.014	-0.015	0.001	0.018	-0.008	0.074	-0.031	-0.004	-0.099	-0.085
Days to second fruit picking	G	0.169	-0.050	-0.109	0.006	-0.126	0.173	0.004	-0.0007	0.007	0.006	-0.030	-0.030	-0.115	-0.094
	P	-0.006	-0.048	0.006	0.015	0.013	-0.013	-0.001	0.018	-0.006	0.056	-0.042	-0.003	-0.061	-0.072
Duration of crop	G	0.100	-0.044	-0.002	0.010	-0.022	0.050	-0.014	-0.0005	-0.019	0.005	-0.029	-0.030	0.282	0.286**
	P	-0.006	-0.022	0.001	0.017	0.002	-0.001	0.002	0.011	0.016	0.035	-0.017	-0.008	0.158	0.189*
Fruit yield per plant (gm)	G	-0.024	0.006	0.274	0.004	0.017	-0.170	-0.025	0.0001	-0.071	-0.001	0.003	-0.008	0.973	0.978**
	P	0.001	0.008	-0.016	0.010	-0.001	0.016	0.008	-0.002	0.078	-0.008	0.003	-0.001	0.873	0.967**

Resi = 0.0392, *, ** significant at 5% and 1% level, respective

Conclusion

Significant genetic variability present in the genotypes might be used for the further crop improvement to increase the fruit yield for crop substantially. The study of significant positive and negative associations among various characters helps in direct for selection of best performing genotypes for fruit yield. Path coefficient analysis estimates the fruit yield and helps in selecting desirable traits to be used in simple selection to obtained maximum fruit yield. The relationships must be taken into consideration as a change on one during selection might lead to change in other performing traits. This study also helps in selection and improvement of desirable traits to be used or transferred during crossing programme.

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