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Genetic Analysis in Okra Hybrids

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Abstract

Twelve genotypes of Okra *Abelmoschus esculentus* (L.) Moench hybrids including checks were evaluated in *kharif* seasons from 2007 to 2009. The analysis of variance exhibits a wide spectrum of variability among the characters of the hybrids. The largest variability was recorded in fruit yield (58.163—125.077 q/ha) followed by plant height (138.800—182.267 cm). In general phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) in all quantitative traits due to environmental influence. High heritability estimates were obtained in YVMV disease incidence (98.02%), fruit yield (93.92%), edible maturity (90.98%) and days to 50% flowering (89.02%) indicating that these characters might be heritable and less influenced by environment. High heritability estimates coupled with high genetic advance were obtained for characters such as fruit yield (93.92, 38.89%) and YVMV incidence (98.06, 30.64%). Correlation studies exhibited that the genotypic estimates were higher than the phenotypic ones for the most of the traits, indicated a strong inherited association between the characters. Fruit yield is the most important economic trait showed positive and significant association with number of nodes/plant, number of fruits/plant and fruit length. Path coefficient analysis revealed that the number of fruits/plant (0.242), fruit girth (0.218) and fruit length (0.058) exhibited maximum direct effects on fruit yield as phenotypic level. On the basis of above findings, it was concluded that the number of fruits/plant and fruit length would be considered for improvement of fruit yield of okra hybrid and among the genotypes, JOH 05-9 was found the most promising hybrid followed by HOK 152 and AOH-23.

Key words : Okra hybrid, Genetic variability, Correlation, Path coefficient analysis.

Okra *Abelmoschus esculentus* (L.) Moench is cultivated in most of the tropical and subtropical countries of the world. It is one of the most popular vegetable grown in *kharif* and summer seasons. But its quick growth, short duration and photoinsensitive character enable to raise three crops in a year. Large flower, caducous calyx and monoadelphous nature of stamens in okra make hybridization much easier. In spite of difficulties, at present a good number of hybrids are developed. Keeping this in view, this trial was conducted to study the performance, variability, correlation and path coefficient analysis.

Methods

The experiment was conducted on twelve okra hybrids including five checks namely AOH-23, NOH-100, AROH-465, VROH-7, VROH-8, JOH 05-9, CoBhH-1, Prerna (Ch), Arka Anamika (Ch), HOK-152 (Ch), Pusa Sawani (Ch) and Parbhanikranti (Ch) in *kharif* seasons from 2007 to 2009 at experimental plots of All India Co-ordinated Research Project on Vegetable Crops, Orissa University of Agriculture & Technology, Bhubaneswar. The seeds were sown on 11 July 2007, 8 July 2008 and 25 July 2009 in randomized block design with three replications in each year. Each treatment comprised 45 plants maintained 60 cm row to row and 30 cm plant to plant. Observation on days to flowering, maturity and yellow vein mosaic virus disease was recorded on plot basis and plant height (cm), number of nodes/plant, number of fruits/plant, fruit length (cm) and girth (cm), average fruit weight (g) and fruit yield (q/ha) were recorded on five random plants per plot. Data were statistically analyzed for genotypic and phenotypic coefficients of variation (1), heritability (2) and genetic advance (3). Correlation coefficients were estimated by following standard methods (4) and path coefficient analysis was done (5).

Results and Discussion

Analysis of variance showed significant difference existed in all the characters among the hybrids

Table 1. Genetic parameters of eleven quantative characters in okra hybrids. Values in parentheses are transformed value.

	Characters	General mean	Range	Phenotypic coefficient of variance (PCV)	Genotypic coefficient of variance (GCV)	Heritability in broad sense (%)	Genetic advance (at 5% level)	Ga expressed in % of mean
1	Days to 50% flowering	44.72	43.00—47.33	3.16	3.00	89.92	2.62	5.85
2	Days to edible maturity	47.19	45.00—51.00	3.78	3.60	90.98	3.34	7.089
3	Plant height (cm)	159.47	138.80—182.26	8.85	6.93	61.31	17.82	11.17
4	Height from base to first fruiting	25.84	16.30—33.16	21.17	14.82	49.01	5.52	21.37
5	Number of nodes/plant	20.69	17.00—28.43	14.42	12.27	72.41	4.45	21.51
6	Number of fruits/plant	14.47	11.13—18.66	16.49	13.02	62.37	3.07	21.18
7	Fruit length (cm)	14.74	13.16—17.42	8.51	7.13	70.16	1.81	12.30
8	Fruit girth (cm)	5.10	4.79—5.50	4.94	2.78	31.80	0.17	3.23
9	Average fruit weight (g)	15.47	12.66—17.46	9.54	7.83	67.28	2.05	13.22
10	YVMV incidence	19.11 (26.49)	3.6—71% (10.91—57.47)	64.54	64.01	98.06	30.64	130.57
11	Fruit yield (q/ha)	95.86	58.16—125.07	20.97	20.32	93.92	38.90	40.58

of okra (Table 1). The widest range was recorded for YVMV incidence (3.6—71.0%) followed by fruit yield (58.16—125.07 q/ha), height from base to first fruiting (16.30—33.16 cm) and number of nodes/plant (17.00—28.43). In general, phenotypic coefficients of variation (PCV) were greater than their corresponding genotypic coefficients of variation (GCV) in all quantitative traits due to environmental influence. High PCV was estimated for YVMV incidence (64.64%), height from base to first fruiting (21.17%)

Table 2. Phenotypic (r_p) and genotypic (r_g) correlation coefficients between all pairs of quantitative traits. *and **indicates significant at 5% and 1% level, respectively.

Characters		Days to edible maturity	Plant height (cm)	Height from base to first fruiting (cm)	Number of nodes/ plant	Number of fruits/ plant
Days to 50% flowering	r_p	0.917**	0.564	0.785**	-0.419	-0.578
	r_g	0.973**	-0.758	0.980**	-0.469	-0.708
Days to edible maturity	r_p		-0.661	0.592**	-0.226	-0.506
	r_g		-0.871	0.948**	-0.276	-0.696
Plant height (cm)	r_p			-0.353	-0.091	0.260
	r_g			-0.576	-0.125	0.512*
Height from base to first fruiting	r_p				-0.448	-0.479
	r_g				-0.789	-0.802
Number of nodes/plant	r_p					0.824**
	r_g					0.772
Number of fruits/plant	r_p					
	r_g					
Fruit length (cm)	r_p					
	r_g					
Fruit girth (cm)	r_p					
	r_g					
Average fruit weight (g)	r_p					
	r_g					
YVMV incidence	r_p					
	r_g					

Table 2. Continued.

Characters		Fruit length (cm)	Fruit girth (cm)	Average fruit weight (g)	YVMV incidence	Fruit yield (q/ha)
Days to 50% flowering	r_p	-0.349	-0.217	-0.567	0.285	-0.420
	r_g	-0.433	-0.407	-0.744	0.312	-0.458
Days to edible maturity	r_p	-0.421	-0.232	-0.529	0.145	-0.342
	r_g	-0.537	-0.556	-0.726	0.161	-0.358
Plant height (cm)	r_p	0.549	0.299	0.585*	0.115	0.047
	r_g	0.715**	0.432	0.785**	0.146	0.092
Height from base to first fruiting	r_p	-0.325	-0.254	-0.487	0.294	-0.364
	r_g	-0.508	-0.650	-0.895	0.376	-0.533
Number of nodes/plant	r_p	0.142	0.334	0.432	-0.670	0.781**
	r_g	0.141	0.548*	0.576*	-0.810	0.957**
Number of fruits/plant	r_p	0.591**	0.265	0.639**	-0.794	0.939**
	r_g	0.874**	0.431	0.901**	-0.908	0.998**
Fruit length (cm)	r_p		0.305	0.746**	-0.526	0.577*
	r_g		0.165	0.731**	-0.666	0.690**
Fruit girth (cm)	r_p			0.648**	0.006	0.155
	r_g			0.829**	-0.006	0.184
Average fruit weight (g)	r_p				-0.520	0.569*
	r_g				-0.653	0.697**
YVMV incidence	r_p					-0.922
	r_g					-0.958

and fruit yield (20.97%) and moderate for number of fruits/plant (16.49%) and number of nodes/plant (14.42%) and low for rest of the traits. More or less similar trend was observed in the estimates of GCV for all the characters. Heritability estimates were high for fruit yield (q/ha), YVMV incidence, days to edible maturity and days to 50% flowering indicating that these characters might be heritable and less influenced by environment. This has been reported earlier in okra (6, 7). The heritability estimates may not be solely and useful index of genetic potentiality of a character. Hence high heritability estimates coupled with high genetic advance for the characters such as YVMV incidence (98.06, 130.57%), fruit yield (93.92, 40.58%) and number of nodes/plant (72.41, 21.51%) indicated that heritability of the traits is mainly due to additive effects, therefore selection may be effective of these traits (8—10).

Table 3. Estimates of direct (diagonal) and indirect effects of eleven characters on yield. P (R) = -0.132, R SQR (PC) = 98.260.

Characters	Days to 50% flowering	Days to edible maturity	Plant height (cm)	Height from base to first fruiting (cm)	Number of nodes/ plant	Number of fruits/ plant
Days to 50% flowering	0.284	-0.317	-0.092	-0.009	-0.064	-0.140
Days to edible maturity	0.260	-0.345	-0.107	-0.007	-0.035	-0.122
Plant height (cm)	-0.160	0.228	0.163	0.004	-0.014	0.063
Height from base to first fruiting	0.223	-0.205	-0.057	-0.011	-0.069	-0.116
Number of nodes/plant	-0.119	0.078	-0.015	0.005	0.153	0.199
Number of fruits/plant	-0.164	0.175	0.042	0.006	0.126	0.242
Fruit length (cm)	-0.099	0.145	0.089	0.004	0.022	0.143
Fruit girth (cm)	-0.062	0.080	0.049	0.003	0.051	0.064
Average fruit weight (g)	-0.161	0.183	0.095	0.006	0.066	0.155
YVMV incidence	0.081	-0.050	0.019	-0.003	-0.103	-0.192

Table 3 Continued.

Characters	Fruit length (cm)	Fruit girth (cm)	Average fruit weight (g)	YVMV incidence	Phenotypic correlation with yield
Days to 50% flowering	-0.020	-0.047	0.228	-0.243	-0.420
Days to edible maturity	-0.024	-0.051	0.213	-0.124	-0.342
Plant height (cm)	0.032	0.065	-0.235	-0.098	0.047
Height from base to first fruiting	0.019	-0.055	0.196	-0.251	-0.364
Number of nodes/plant	0.08	0.073	-0.174	0.572	0.781
Number of fruits/plant	0.034	0.058	-0.257	0.678	0.939
Fruit length (cm)	0.058	0.066	-0.300	0.449	0.577
Fruit girth (cm)	0.018	0.218	-0.260	-0.0065	0.155
Average fruit weight (g)	0.043	0.141	-0.402	0.444	0.569
YVMV incidence	-0.030	0.001	0.209	-0.854	-0.922

The results of correlation coefficients revealed that the genotypic estimates were higher than the phenotypic ones for most of the characters indicating a strong inherited association between the characters. (Table 2). Fruit yield showed positive and significant association with number of nodes/plant, number of fruits/plant, fruit length and average fruit weight, whereas it was negatively correlated with days to 50% flowering, days to edible maturity, height from base to first fruiting and YVMV incidence. Similar results were reported earlier in Okra (11, 12). Path coefficient analysis provides an effective way to find the magnitude of direct and indirect contribution of each trait on the dependent trait. In this study, the response variable i.e. fruit yield and ten predictor variables, plant height, height from base to first fruiting, days to 50% flowering, days to edible maturity, number of nodes/plant, number of fruits/plant, fruit length and girth, average fruit weight and YVMV incidence were studies for path analysis (Table 3).

The data revealed that days to 50% flowering has a strong positive direct effect on fruit yield (0.284). Days to 50% flowering mainly contributed to fruit yield via average fruit weight. The direct effect of days to edible maturity was negative but it has positive indirect through average fruit weight. Plant height contributed positively (0.163) to fruit yield directly and also via edible maturity, number of fruits/plant and fruit girth. Similarly number of fruits/plant, fruit girth, number of nodes/plant and fruit length contributed tremendously to the fruit yield directly as well as indirectly among themselves. These findings were corroborated with results of earlier workers (9, 13, 14).

Out of the ten characters, number of fruits/plant, fruit girth, days to 50% flowering and fruit length had significantly positive direct effect on fruit yield. Besides, genetic analysis revealed that fruit yield, number of fruits/plant and number of nodes/plant had high GCV, heritability and genetic advance. Hence these characters would be considered for improvement of fruit yield. Thus, traits, like number of fruits/plant and fruit length can be used as selection criteria to increase the fruit yield of okra hybrid. On the basis of above characters and YVMV disease infection the genotype JOH-05-9 was found the most promising hybrid followed by HOK-152 and AOH-23.

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