



GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND CORRELATION STUDIES AMONG QUANTITATIVE TRAITS IN OKRA [*Abelmoschus esculentus* (L.) Moench]

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ABSTRACT

Analysis of the genetic variability, heritability, genetic advance and correlation among 15 quantitative traits in 12 okra genotypes sown in randomized block design (RBD) including novel genic male sterility lines was done at ICAR-IIHR, Bangalore. The ANOVA showed highly significant differences among the genotypes for all the traits except for number of branches per plant and number of ridges per fruit indicating the presence of sufficient variability in the experimental materials. Lowest difference between PCV and GCV were recorded for PH followed by NF/P, DFH, FSG, FG and NR/F is the indication of prevalence of genotypic effect rather than environmental effect on their expression. Hence, such traits respond well to selection. High heritability coupled with high genetic advance as per cent mean for NF/P, TY/P, PH, INL, NFF and AFW indicating the prevalence of additive gene action in their inheritance denoting the selection based on these traits to be quite effective. In association study, the traits, PH, INL, NB/P, AFW, NF/P and MY/P being positively correlated with TY/P could be used as traits of interest for indirect selection to improve TY/P in further breeding programme.

KEY WORDS *Abelmoschus esculentus*, genic male sterility, genetic variability, heritability, genetic advance and correlation.

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] is one of the delicious tender fruit vegetable. It is grown extensively in tropics, sub-tropics and warmer seasons of the temperate areas in the world. Okra immature fruits can be used in salads, soups and stews, fresh or dried, fried or boiled (Ndunguru & Rajabu, 2004). High level of dietary fiber, low caloric value and rich source of minerals, like Ca, P, K and Mg has made okra an important component of diet. Fruit is a rich source of iodine which is helpful in curing goitre and leaves are used as remedy for dysentery. Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander. The mucilage of okra binds cholesterol and bile acid carrying toxins dumped into it by the liver (Maramag *et al.*, 2013). Therefore, okra is capsule with potential health benefits. Although 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 (Anon, 2015), its productivity potential is low. To improve productivity, high yielding varieties need to be developed. Yield is a quantitative trait and is the result of actions and integrated function of a number of component traits. Its genetic improvement depends on the degree of variability for the desired traits in parental material and association between yield and its contributing traits. Therefore, knowledge of genetic parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful biometrical tools for understanding the extent of genetic variability in base population which is prerequisite. Conversely, heritable variation cannot be

estimated with the help of GCV alone because yield and its attributes are highly environmentally influenced. According to Burton (1952) GCV along with estimates broad sense heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) would give an idea about the nature of gene action governing a particular character which intern helps in effective genotype based selection making. These studies will be still more constructive along with the correlation analysis which helps in estimation of inter-relationship among the yield contributing components and choosing component characters that are positively correlated with yield (Bhatt, 1973; Diz *et al.*, 1994; Mihretu *et al.*, 2014). With special reference to novel genic male sterility lines of okra developed at Indian Institute of Horticultural Research (IIHR), Bangalore, have made okra hybrid seed production still more easy, economical and commercially feasible (Pitchaimuthu *et al.*, 2012). However, in these lines information pertaining to genetic variability and correlations is very limited. Therefore, the present study was undertaken to analyze the genetic variability, heritability, genetic advance and correlation among quantitative traits in okra genotypes including novel genic male sterility lines.

MATERIALS & METHODS

Experimental material consisted of seven elite okra genotypes (IIHR IIHR-285, IIHR-291, IIHR-294, IIHR-296, IIHR-299, GMS-1 and GMS-4) developed at IIHR and five popular varieties (VRO-6, Parbhani Kranti, Arka Anamika, JNDO-5 and Varsha Uphar). GMS-1 and GMS-

4 were genic male sterility lines. Total twelve genotypes were raised in randomized block design (RBD) with three replications at spacing of 20 x 30cm in paired row at IIHR Bangalore. Recommended agronomic practices and need based plant protection measures were taken. Data were recorded on five random plant basis for the fifteen characters namely days to first flowering (DFF), days to first harvest (DFH), node at first flower appeared (NFF), plant height (PH) (cm), internodal length (INL) (cm), number of branches per plant (NB/P), final stem girth (FSG) (cm), average fruit weight (AFW) (g), number of fruits per plant (NF/P), total yield per plant (TY/P) (g), marketable yield per plant (MY/P) (g), marketable yield/ha (MY/ha) (t), fruit length (FL) (cm), fruit girth (FG) (cm) and number of ridges per fruit (NR/F). The data recorded were used to analyze genetic parameters like genetic variability, heritability, genetic advance and correlation using Indostat software package.

RESULTS & DISCUSSION

Analysis of variance and genetic variability

The ANOVA showed highly significant differences among the genotypes for all the traits except for number of branches per plant and number of ridges per fruit indicating the presence of sufficient variability in the experimental materials (Table 1). The estimates of mean, genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for 15 quantitative traits in okra genotypes are presented in table 2. Phenotypic variance (PV) agreed closely with genotypic variance (GV) for all the characters but significant magnitude of PV for days to first flowering (DFF), total yield per plant (TY/P) and marketable yield per plant (MY/P) is the indication of prevalence influence of environment on earliness and yield. The values of PCV were higher than GCV for all the characters which was well supported by findings of Sharma and Prasad (2015) and Senapati *et al.* (2011). High difference between PCV and GCV along with PV estimates were obtained for MY/P followed by MY/ha, TY/P, DFF, NFF, NB/P, INL, FL, NFF and AFW is the sign of occurrence considerable environmental influence on their expression. These findings corroborated with studies of Naidu (2007) for TY/P and AFW; Nwangburuka *et al.* (2012) for FL and NB/P; Nagre *et al.* (2011) for INL; Das *et al.* (2012) for NFF, DFF. Lowest difference between PCV and GCV were recorded for PH followed by NF/P, DFH, FSG, FG and NR/F is the indication of prevalence of genotypic effect rather than environmental effect on their expression. Such traits respond well to selection. Hence, it is suggestible that above traits can be improved through simple selection. Similar results were obtained by Kumar *et al.* (2011) for PH and NF/P; Santhakumar and Salimath (2010) for FSG; Sharma and Prasad (2015) for FG and DFH; Das *et al.* (2012) for NR/F. While in contrary Hazra and Basu (2000) reported moderate GCV for PH and NF/P.

Heritability and genetic advance

The heritability provides information on the magnitude of the inheritance of characters from parent to off spring, while genetic advance (also denoted by response to selection) is helpful in finding the actual gain expected under selection (Larik *et al.*, 2000; Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2014). Estimates

of heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) are presented in table 2. In present investigation high heritability coupled with high GAM was observed for NF/P, TY/P, PH, INL, NFF and AFW. These results corroborated with the observations of Das *et al.* (2012), Yadav *et al.* (2016), Ahamed *et al.* (2015), Singh *et al.* (2006) for above mentioned traits. High heritability coupled with low GAM was observed for DFH, FSG, FL and FG. High heritability and low GAM for these were also found from studies of Dhankar and Dhankar (2002) and Reddy and Sridevi (2014). According to Percy and Turcotte (1991), when heritability is mainly due to non-additive genetic 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. Therefore, high heritability and high genetic advance for NF/P, TY/P, PH, INL, NFF and AFW indicated prevalence of additive genetic effects and good response to selection. Hence, it is advisable for straight phenotype based selection to improve these characters. High heritability coupled with low GAM was observed for DFH, FSG, FL and FG is the sign of prevalence of non-additive gene action and favourable influence of environment as a result limited scope for improvement through selection procedures.

Correlation co-efficient

In the present study correlation analysis revealed the mutual relationship between characters. Genotypic and phenotypic correlation coefficients among yield and yield affecting characters are presented in Table 3. In most of the cases, genotypic correlation coefficients were found to be higher than corresponding phenotypic correlation coefficients. This reflects the character expressions had been appreciably influenced by genetic reasons rather than the environmental effects. The low phenotypic value might be imputed to differential interaction of the genotypes with the environment. Higher magnitude of genotypic correlation coefficients compare to their corresponding phenotypic correlation coefficients were found in earlier studies of Kumar and Yadav (2009) and Niranjan and mishra (2003). Out of 15 characters studied PH, INL, NB/P, AFW, NF/P, MY/P and NR/F showed positive genotypic correlation with TY/P. This indicated that fruit yield can be improved by making selection on the basis of these characters. Positive association of PH, INL, NB/P, AFW, NF/P and MY/P with TY/P also reported by Nagre *et al.* (2011), Mihretu *et al.* (2014), Bendale *et al.* (2003) Hazra and Basu (2000) and Sreenivas *et al.* (2015).

Negative correlation was observed for TY/P with DFF, DFH, NFF, FSG, FL and FG. This indicates that prioritising selection of genotypes showing early flowering at lower number of node and giving optimum marketable sized tender fruit will help in improving fruit yield of okra. Negative correlation coefficients for above characters also reported by Saryam *et al.* (2015), Singh *et al.* (2006), Nagre *et al.* (2011) and Hazra and Basu (2000).

TABLE 1. Analysis of variance (mean sum of squares) for 15 quantitative traits in okra

Source	Df	DF	DFH	NFF	PH	INL	NB/P	FSG	AFW	NE/P	TY/P	MY/P	MY/ha	FL	FG	NR/F
Replications	2.00	8.53	9.53	0.38	0.62	0.50	0.06	0.88	5.72	0.61	307.04	337.73	4.73	3.52	0.04	0.52
Varieties	11.00	16.45	35.20**	0.73**	361.67**	2.46**	0.08	0.04*	13.81*	34.36**	1282.28*	1079.41*	15.07*	6.64*	0.10*	0.26
Error	22.00	14.83	7.86	0.19	10.17	0.58	0.08	0.02	4.37	2.72	504.82	536.26	7.49	2.89	0.03	0.18
S Em ±		2.13	1.55	0.24	1.76	0.42	0.15	0.07	1.16	0.91	12.42	12.80	1.51	0.94	0.10	0.24
CV (%)		9.78	5.93	12.82	3.08	16.31	8.26	6.92	11.04	9.09	15.95	20.53	20.53	11.74	9.16	8.19

*and** indicate significance of values at p=0.05 and p=0.01, respectively.

TABLE 2. Estimates of mean, range, genotypic and phenotypic variances, genotypic and phenotypic coefficient of variations, heritability and genetic advance

Characters	Mean	Range	GV	PV	GCV	PCV	h ² (Broad Sense)	GA	GAM %
DF	39.36	35.67-44.00	0.54	15.37	1.87	9.96	3.50	0.28	0.72
DFH	47.28	42.67-53.33	9.11	16.98	6.39	8.72	53.70	4.56	9.64
NFF	3.44	2.78-4.57	0.18	0.37	12.31	17.77	48.00	0.60	17.56
PH	103.60	89.07-125.83	117.17	127.34	10.45	10.89	92.00	21.39	20.65
INL	4.69	3.13-6.23	0.63	1.21	16.88	23.47	51.70	1.17	25.01
NB/P	3.32	3.07-3.50	0.003	0.078	1.61	8.41	3.70	0.02	0.63
FSG	1.90	1.70-2.16	0.01	0.03	4.88	8.47	33.30	0.11	5.80
AFW	18.95	15.20-21.78	3.15	7.52	9.36	14.47	41.80	2.36	12.47
NE/P	18.16	12.67-23.10	10.55	13.27	17.89	20.06	79.50	5.97	32.85
TY/P	140.87	101.97-170.54	259.15	763.98	11.43	19.62	33.90	19.31	13.71
MY/P	112.82	74.06-133.97	181.05	717.31	11.93	23.74	25.20	13.93	12.34
MY/ha	13.33	8.75-15.83	2.53	10.02	11.92	23.74	25.20	1.65	12.33
FL	14.49	11.79-16.27	1.25	4.14	7.71	14.05	30.10	1.26	8.72
FG	2.03	1.63-2.30	0.02	0.06	7.51	11.84	40.20	0.20	9.80
NR/F	5.20	5.00-5.60	0.03	0.21	3.15	8.78	12.90	0.12	2.32

TABLE 3. Genotypic (Upper Right) and Phenotypic (Lower Left) correlation coefficients of 15 quantitative traits in Okra

Traits	DEF	DFH	NFF	PH	INL	NB/P	FSG	AFW	NF/P	MY/P	MY/ha	FL	FG	NR/F	TY/P
DEF	1.000	2.236	2.314	-1.283	1.100	1.855	1.914	-1.075	0.734	-2.540	-2.540	-0.398	-0.044	1.951	-2.072
DFH	0.641**	1.000	0.738	-0.398	0.054	1.058	0.261	-0.380	0.419	-1.067	-1.067	0.358	0.284	0.310	-0.763
NFF	0.117	0.221	1.000	-0.092	0.063	-0.597	0.275	-0.239	0.322	-1.560	-1.561	0.408	0.459	0.494	-1.441
PH	-0.258	-0.367*	-0.045	1.000	0.256	-0.432	-0.232	-0.203	-0.096	0.357	0.357	0.108	-0.339	0.259	0.342
INL	-0.049	-0.109	0.045	0.265	1.000	2.344	0.418	-0.262	0.158	0.653	0.654	-0.501	0.404	0.578	0.452
NB/P	0.208	0.199	-0.059	-0.071	0.324	1.000	1.395	-0.483	-0.013	0.726	0.727	-1.630	0.670	-0.315	0.744
FSG	0.048	0.086	0.064	-0.056	0.183	0.064	1.000	0.344	-0.588	-0.051	-0.051	-0.506	-0.643	0.064	-0.114
AFW	-0.077	0.006	-0.213	-0.175	-0.214	0.163	0.215	1.000	-0.851	0.453	0.453	-0.746	-0.489	-0.955	0.390
NF/P	0.185	0.281	0.184	-0.046	0.194	-0.079	-0.294	-0.542	1.000	-0.221	-0.221	0.730	0.806	0.515	0.262
MY/P	-0.291	-0.279	-0.239	0.110	0.068	0.017	0.099	0.107	-0.166	1.000	1.000	-1.143	-0.319	-0.342	0.918
MY/ha	-0.291	-0.279	-0.239	0.110	0.068	0.017	0.099	0.106	-0.166	1.000	1.000	-1.144	-0.320	-0.342	0.918
FL	-0.045	0.169	0.304	0.098	-0.130	0.063	-0.342*	-0.307	0.356*	-0.0188	-0.019	1.000	0.348	0.015	-0.975
FG	0.297	0.316	0.174	-0.183	0.096	0.005	-0.219	-0.093	0.623**	-0.0191	-0.019	0.145	1.000	0.756	-0.253
NR/F	0.185	0.204	0.123	0.040	-0.048	-0.071	-0.199	-0.256	0.220	-0.145	-0.145	-0.131	0.383	1.000	0.022
TY/P	-0.256	-0.203	-0.314	0.128	0.030	0.072	0.052	0.122	0.207	0.968	0.968	-0.027	-0.026	-0.069	

*and** indicate significance of values at p=0.05 and p=0.01, respectively

However, positive genotypic correlation of FL and FG with TY/P as reported earlier by Mihretu *et al.* (2014) and Saryam *et al.* (2015) were found to be in contrast with finding of present study for. These discrepancies may be due to population specificity of results.

CONCLUSION

The traits NFF/P, DFH, FSG, FG and NR/F showed high genetic variability. NF/P, PH, INL, NFF, AFW and TY/P recorded high heritability with high genetic advance as per cent of mean indicating the prevalence of additive gene action in their inheritance denoting the selection based on these traits to be quite effective. In association study, the traits, PH, INL, NB/P, AFW, NF/P and MY/P being positively correlated with TY/P could be used as traits of interest for indirect selection to improve yield in further breeding programme.

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