Variation of Selected Quantitative Traits in F₂ Generation of Okra (*Abelmoschus esculentus* (L) Moench)

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Abstract

Assessment of genetic variability and the heritability of traits concern in the breeding program of Okara are important for the selection. Hence a study was carried out at Grain Legumes & Oil Crops Research & Development Centre (GLORDC), Angunakolapelessa during 2012 Yala season and the objectives were to study the genetic variability of quantitative characters in Okra to quantify broad-sense heritability for yield, and yield associated traits and other agronomic traits. F₂ populations of cross -1 (Acc 00843 X MI 5) and cross-2 (ANK 00007 X Haritha) were evaluated for plant characters such as days to first flowering (DF), plant height (PH), total fruit yield per plant (TY), average fruit weight (AW), total number of fruits per plant (TNF) and fruit characters such as fruit length (FL), fruit width (FW) and number of ridges per fruit (NR). Their parental plants were also planted in GLORDC following single plant randomization method. In these crosses, Acc 00843 and ANK 007 were used as female parents and Haritha and MI 5 were used as male parents. Mean performance of parents and their F₂ in each cross, phenotypic, environmental and genetic variances present in each trait of F₂ populations and comparisons of broad sense heritability in the traits of F₂ populations were evaluated. Significant parental differences were observed for NR in cross 1 that of TNF, TY and FW in cross 2. From the mean performance analysis, important economical traits such as TNF, TY showed significant differences when compared F2 population means with their better parent in cross 1. Also cross 1 expressed relatively higher broad sense heritability values for the traits of TNF and TY. While assuming that there was no environmental variation those traits could be considered for selecting genotypes with further advancement. Therefore Cross 1 can be considered as highly potential cross that can be continued for selecting new recombinant inbred lines based on mean and heritability analysis of the study.

Keywords: Breeding, Okra, Quantitative genetics

Introduction

Okra *Abelmoschus esculentus* L. (Moench), is a potentially self pollinated crop and belongs to the family Malvaceae. It is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. Also it is one of the most popular fruit vegetables grown in wet, intermediate and dry zone of Sri Lanka. The total area under okra cultivation is reported to be 7066 ha producing average yield of 5.3 t ha⁻¹ thus the total annual okra production in Sri Lanka is 37,330 MT with a per capita availability of 2.0 kg (year)⁻¹ (Department of Agriculture, 2010).

The breeding programme of okra at Grain Legumes & Oil Crops Research & Development Centre (GLORDC), Angunakolapelessa is aimed at developing varieties with high yielding, resistant to YVMV, powdery mildew, insect pests such as shoot and fruit borer *etc.* Genetic variability for economic traits is pre-requisite for any successful breeding programme. The presence of genetic variability for economic traits is a key factor for improving the variety with regard to specific traits. At the same time, improvement is possible on the basis of heritable variations meaning transmissibility of the

characters to the progenies. The quantitative characters showing continuous range of variability are controlled by multiple genes or poly genes. The genetic variation present in F_2 population can be studied by genetic analysis of quantitative traits.

Assessment of genetic variability and the heritability of traits concern in the breeding programme is important to decide whether selection should be practiced in early generation or later generation. A high broad sense heritability for traits indicated that selection in the early generations for these characters should be highly effective in developing a breeding strategy and a good genetic base for crop yield improvement.

The study was carried out at GLORDC, Angunakolapelessa during 2012 Yala season and the objectives were to study the genetic variability of quantitative characters in okra and to quantify broad-sense heritability for yield, yield associated traits and other agronomic traits.

Materials and methods

The experimental materials were comprised of F_2 populations of two single crosses and their parents.

   i.   Female parents: Acc 00843 and ANK 0007

   ii. Male parents: Haritha and MI 5

   iii. F2 populations of following crosses,

      Cross 1 - (Accession 00843 X MI 5)

      Cross 2 - (ANK 00007 X Haritha)

The two F_2 populations and parental plants were planted in GLORDC field following single plant randomization method. Each plot of F_2 single cross comprised with 10 male parent plants, 10 female parent plants and 60 F_2 plants assigned randomly. Plot size for F_2 okra populations and parents in each cross was 26 m^2 and the spacing between rows and plants was 90 cm and 60 cm respectively.

F_2 populations of cross -1 (Acc 00843 X MI 5) and cross-2 (ANK 00007 X Haritha) were evaluated for plant characters such as days to first flowering (DF), plant height (PH), total fruit yield per plant (TY), average fruit weight (AW), total number of fruits per plant (TNF) and fruit characters such as fruit length (FL), fruit width (FW) and no of ridges per fruit (NR).

Data analysis

1. Mean performance of parents and their F_2 of two crosses

Mean differences of each quantitative trait of each cross were analyzed and tested for significance. Analysis of variance and mean separation was done in "Duncan's multiple Range Test" according to the Complete Randomized Design (CRD) at the 0.05 significant level using SAS statistical software package 9.1.3. version.

2. Phenotypic, environmental, genetic variances present in each trait of F_2 crosses

Variance of means for each quantitative trait of each cross were computed using SPSS statistical software package.

3. Comparisons of broad sense heritability in the traits of F_2 crosses

Broad-sense heritability on the basis of single plant was estimated as follows,

Phenotypic variance   = V(P) = V(F2)

Environmental variance = V(E) = [V(P1)+ V(P2)]/2

Genetic variance   = V(G) = V(P) – V(E)

Broad sense heritability (H_{BS}) = [V(P) – V(E)] / V(P)

= [(VF2 – (VP1 + VP2)/2] / VF2

Where, H_{BS} is the broad sense heritability for a specific trait at each location;

VP1, VP2, and VF2 are phenotypic variances among parent 1, parent 2 and F2 plants for a specific trait at each location.

Results and discussion

Comparison of Mean Performances of parents and their F_2 of quantitative traits of Cross -1 (Acc 0843 X MI 5) and Cross-2 (ANK 007 X Haritha)

Compared with F2 mean performances with better parent, the F2 population mean differed significantly (P< 0.05) with the better parent for TNF, TY and NR in cross 1 while that of PH, FL, DF and NR in cross 2.

When consider the most economical characters such as TNF, TY in cross 1, F2 population shows more potential than its better parent. But cross 2 showed no significant difference in F2 population when compared with the better parent. Hence there's greater potential of obtaining higher yield from cross1 than cross2 in comparison to their better parent.

P1 stands for better parent of the trait concerned. Female parent is the better parent for all the characters concerned in this study based on breeding objectives.

Table 1. Mean performance of parents and their F2 generation in cross 1 and cross 2

		Characters							
		TNF	TY	AW	PH	FL	FW	NR	DF
P1	Mean	3.11	50.67	16.44	45.56	12.91	1.82	6	46
	SE(±)	0.43	6.71	1.16	2.67	0.67	0.06	0	1.54
P2	Mean	1.2	19	16.1	46.2	14.68	1.79	6.8	49.2
	SE(±)	0.15	2.01	0.82	2.44	0.59	0.07	0.15	0.83
F2	Mean	11.52	181.36	15.41	50.48	13.41	1.75	5.06	45.61
	SE(±)	0.66	11.6	0.33	1.42	0.25	0.02	0.03	0.51
P1 vs P2		ns	ns	ns	ns	ns	ns	*	ns
P1 Vs F2		*	*	ns	ns	ns	ns	*	ns
P2 vs F2		*	*	ns	ns	ns	ns	*	ns
P1	Mean	18.14	360.86	20.41	64.86	18.78	1.75	5	38.86
	SE(±)	0.82	13.23	0.45	1.76	0.14	0.02	0	0.54
P2	Mean	7.75	147.38	18.67	53.75	16.46	1.76	5.56	46
	SE(±)	1.58	32.92	1.1	2.43	0.61	0.04	0.18	2.07
F2	Mean	18.81	378.61	19.96	56.68	15.71	1.56	5.13	38.51
	SE(±)	1.02	23.33	0.44	1.78	0.21	0.02	0.03	0.56
P1 vs P2		*	*	ns	ns	ns	*	ns	ns
P1 Vs F2		ns	ns	ns	*	*	ns	*	*
P2 vs F2		*	*	ns	*	*	*	*	*

Row labels for left margin: (Acc 843 X MI 5) applies to the first block; (Acc 843 X MI 5) is the left-side label.

ns : Not Significant   * : Significance at 5% level

The variance estimates for TNF, TY, AW, PH, FL, FW, NR and DF in the segregating generations which was F_2 population were greater than the variance estimates of the non - segregating generations which were P_1 and P_2.

Important economical traits such as TNF, TY showed significant differences when compared F2 population means with their better parent in cross 1.

Table 2: Phenotypic, environmental and genetic variances and broad sense heritability present in each trait of crosses

Trait	Cross –1 (Acc 843 X MI 5)			H BS	Cross –2 (ANK 007 X Haritha)			H BS
	V (P)	V (E)	V(G)		V (P)	V (E)	V(G)	
TNF	24.55	1.82	22.73	92.59	59.48	26.54	32.94	55.39
TY	7533	243.3	7289	96.77	31029	8619	22409	72.22
AW	6.11	9.73	3.62	59.19	10.88	9.88	1	9.17
PH	113.2	62.49	50.67	44.78	180.5	99.75	80.72	44.73
FL	3.43	3.82	0.39	11.35	2.45	1.99	0.46	18.67
FW	0.03	0.04	0.01	21.61	0.01	0.02	0	2.46
NR	0.06	0.1	0.04	81.44	0.06	0.12	0.06	89.58
DF	14.57	14.98	0.4	2.78	17.75	24.38	6.63	37.33

In cross 1, Acc 843 x MI5, there were very high broad sense heritability values recorded for total number of fruits per plant (92.6%), total yield per plant (96.7%) and number of ridges per fruit (81.4). Also moderate value for average fruit weight (59.1%) (Table 2)

In cross 2, ANK 7 x Haritha, there were moderate broad sense heritability values observed for number of ridges per fruit (89.5), total yield per plant (72.2%), total number of fruits per plant (55.3%) and plant height (44.7%) (Table 2)

Only simple inheritance were considered in the present study and assumed there was no interaction effects between genetic and environment. Further it was considered that dominance gene effects were also absent.

Conclusion

More parental variation was observed from cross 2 (ANK 7 x Haritha) for the traits of Total Number of fruits per plant (TNF), total yield per plant (TY) and days to flowering (DF).

Hence there's a greater potential of obtaining higher yield from cross1 than cross2, which will perform better than their better parent.

Also cross 1 (Acc 0843 X MI 5) was expressed relatively higher broad sense heritability values for the traits of TNF, TY and it can be considered as highly potential cross that can be used for a crop breeding programme when assume no environmental variation for the characters under study. The selection in the early generations for these characters would be highly effective in developing a breeding strategy and a good genetic base for okra yield improvement in cross 1.

References

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