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Research Article

Genetics of fruit yield and its component characters in okra (*Abelmoschus esculentus* (L.) *Moench*)

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Abstract

A full diallel cross involving seven okra genotypes was used to study the inheritance of fruit yield and its component characters in okra. Data from the F_1 generation and parents were analyzed using Hayman (1954) method of diallel analysis. The estimates of D were significant for all the traits studied. The values of H_1 and $H_{2,}$ as well as $H_2/4H_{1,}$ indicated that there were unequal frequencies of the alleles at all the loci. An excess of dominant alleles was involved in five out of the eleven traits of interest. The mean degree of dominance was more than unity for all the traits studied, including fruit yield per plant. The narrow sense heritability estimates were higher for four out of the 11 traits studied. In the presence of overdominance for yield, the best recurrent scheme to develop hybrids will be reciprocal recurrent selection.

Keywords

Genetic studies, yield, okra

INTRODUCTION

Working knowledge of the gene action controlling the traits related to fruit is desirable, before undertaking any major endeavor in okra improvement. Such information is necessary to plan an effective breeding programme. The present paper reports the gene effects controlling fruit yield and its component characters in okra.

MATERIALS AND METHODS

Seven diverse okra genotypes viz., Arka Anamika, Varsha Upahar, Thunder, Dhanya, Pusa-7, Basanthi and S-51, were mated in a 7 x 7 complete diallel cross, resulting in 42 hybrids. These hybrids along with their parents were grown in a Randomized Block Design, from July to October, 2017. Each experimental plot consisted of a single row of 3m length. The inter and intra-row spacings were maintained at 45 and 30cm respectively. The data were recorded on five randomly selected plants per entry per replication. The characters studied are listed in Table, 1. The genetic parameters are estimated as per Hayman's analysis of diallel crosses (Hayman, 1954).

RESULTS AND DISCUSSION

Hayman (1954) derived the expectations for the statistics calculated from the diallel and also the expected values of the components of variations (D, H_1, H_2, F, h^2 and E) using the least square technique. The additional statistics needed for the genetic interpretation and the overall information derived from the genetic parameters are detailed in **Table 1.** The estimates $\hat{D}$ were highly significant for most of the traits studied except the traits namely, average fruit weight, number of fruits per plant and fruit yield per plant. This indicated that the component of variation due to additive genetic effects was important for most of the traits except average fruit weight, the number of fruits per plant and fruit yield per plant. The estimate $\hat{D}$ was non-significant, indicating the importance of non-additive genetic effects in the inheritance of average fruit weight, the number of fruits per plant and fruit yield per plant. The estimates H_1 were significant for almost all the traits studied except the trait fruit yield per plant. It indicated that the component of variation due to the dominance effect of the genes was also important for almost all the traits studied (Deepak Arora *et al.,* 2008, Vachhani and Shekhat, 2008, Mrinmoy *et al.,* 2013, Ayesha and Revanappa, *et al*. (2017).

The estimates $\hat{H}_1$ and $\hat{H}_2$ were highly significant and positive for almost all the traits studied in **Table 1**. It indicated that there were unequal frequencies of alleles *i.e.,* u ≠ v at all loci. In this context 'u' ($5x10^{-7}$) refers to the frequency of alleles which increase the mean expression of the characters and are situated at loci, which exhibit dominance. On the other hand, 'v' ($2x10^{-4}$) corresponds to the frequency of dominant alleles at loci that decrease the expression of traits.

Further proof for the unequal distribution of alleles over loci is obtained by the ratio of $H_2/4H_1$, which is the estimate of $\overline{uv}$. In the present study, the $\overline{uv}$ estimates were in the range of 0.16 to 0.22, which is less then the maximum value of 0.25. The maximum value of 0.25 arises, when u = v = 0.5. If u = v, then $H_1 = H_2$, *i.e.,* the increaser (positive dominant) and decrease (negative dominant) alleles at the loci are in equal proportion in the parents. But, in the present inquiry, the estimates were low (*i.e.* in the range of 0.16 to 0.22). This indicated that the positive and negative alleles at the loci exhibiting dominance were not in equal proportions of the parents of interest. However, these estimates did not permit a determination as to which type of allele occurred more frequently. The unequal distribution of positive and negative alleles indicated the operation of non-allelic interaction *i.e.* epistasis. The estimates of were positive for all the eleven traits studied where dominant alleles are more frequent in the parents than recessive alleles, irrespective of whether or not the dominant alleles have increasing or decreasing the effects (Mather and Jinks, 1971).

Table 1. Estimates of genetic parameters for ten characters in okra

S. No.	Characters	$\hat{D}$	$\hat{F}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{h}^2$	$\hat{E}$
1.	Days to first flowering	2.09±0.52**	1.88±1.24	7.27±1.24**	5.95±1.09**	12.87±0.73**	0.24±0.18
2.	Plant height	499.30±70.89**	508.70±170.07*	1042.47±170.67**	890.11±150.39**	2.88±101.00*	2.39±25.06
3.	Internode distance	0.75±0.16**	0.62±0.39	1.42±0.40**	1.21±0.35**	0.29±0.23	0.05±0.06
4.	Days to fruit maturity	0.41±0.11*	0.73±0.25*	1.08±0.25**	0.75±0.22*	1.42±0.15**	0.10±0.04
5.	Number of immature seeds per fruit	48.81±7.41**	67.56±17.78*	95.48±17.84**	60.40±15.72*	7.67±10.56*	1.96±2.62
6.	Fruit length	3.50±0.67**	6.65±1.60**	12.17±1.61**	8.74±1.42**	3.79±0.95*	0.03±0.24
7.	Fruit girth	0.37±0.16	0.59±0.38	1.40±0.38*	1.02±0.33*	0.01±0.22	0.02±0.06
8.	Number of branches per plant	0.41±0.14*	0.52±0.33	0.89±0.33*	0.65±0.29*	0.01±0.20	0.01±0.05
9.	Number of fruits per plant	4.16±2.98	1.28±7.14	18.42±7.17*	15.98±6.32*	3.34±4.24*	0.50±1.05
10.	Fruit weight	5.30±2.47	10.83±5.94	23.18±5.96*	16.19±5.25*	0.63±3.52	0.44±0.87
11.	Fruit yield per plant	244.97±3136.33	1038.67±7524.01	17603.36±7550.64	15458.20±6653.17	611.01±4468.58*	135.01±1108.86

D = Additive genetic variance of the parents, F = Relative frequencies of dominant and recessive alleles in parents, H_1 = Dominance of genetic variance, H_2 = Adjusted dominance variance according to gene distribution, h^2 = Overall dominance effects, E = Environmental effects

* - Significant at 1 per cent level ** - Significant at 5 per cent level

In fact, the aforementioned trend was supported by the proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}$ $1/211111122222^{111dd}$fdfgffgfg– F]. As per this ratio, all the eleven traits studied had more than unity. Hence, it can be assumed that the parents used for this study, carried more dominant alleles than the recessive alleles for all the traits studied. The estimate $\hat{h}^2$ was positive and significant for most of the traits studied. It indicated the dominance effect expressed as the algebraic sum over all loci in heterozygous phase in all the crosses for almost all the traits. The ratio of $(H_1/D)^{1/2}$ was more than unity for all the eleven traits studied. This revealed that the degree of dominance, averaged over all loci was over dominance for all the traits studied including fruit yield per plant.

The estimates of the number of effective factors (h^2/H_2) were more than one for the traits *viz.,* days to first flowering, and days to fruit maturity. It measures only those factors which show some degree of dominance. Accordingly, the above said characters were controlled by at least one effective block of genes. For the remaining nine traits, the ratio was less than one. This underestimation may be due to the fact that the dominance effects of the genes affecting these traits are not equal in size and direction or if the distribution of genes is correlated (Mather, 1949 and Jinks, 1954). Anyone of these two reasons mentioned maybe the cause for the low value of the ratio of h^2/H_2.

The narrow sense heritability estimates of the present study were low for the traits, plant height, days to fruit maturity, the number of immature seeds per fruit, fruit length, fruit girth, the number of branches per plant and average fruit weight and medium for the traits days to first flowering, internode distance and fruit yield per plant and high for the trait number of fruits per plant. The trait number of fruits per plant alone may be largely controlled by additive genetic variance. So, the other traits except for the number of fruits per plant may be largely controlled by non-additive genetic variance or the number of genes controlling these characters may be more or these traits may largely be influenced by a large number of modifiers or might be largely influenced by the environment. As the estimates of environmental effects were generally low, the observed low heritability for almost all traits might be due to other factors other than the environment. The traits studied are difficult to improve by simple selection. It necessitates for progeny testing. The estimate of environmental effects $(\hat{E})$ was maximum for fruit yield per plant alone. The trait fruit yield per plant as a complex character indicated that this trait is vulnerable to changes in environmental conditions (**Table 2**).

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Table 2. Ratios of genetic parameters for ten characters in okra

S. No.	Parameters Characters	$(H_1/D)^{1/2}$	$H_2/4H_1$	$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	h^2/H_2	Heritability in narrow sense (per cent)
1.	Days to first flowering	1.86	0.20	1.63	2.16	18.45
2.	Plant height	1.44	0.21	2.09	0.01	8.9
3.	Internode distance	1.37	0.21	1.86	0.25	15.35
4.	Days to fruit maturity	1.63	0.17	3.42	1.88	0.35
5.	Number of immature seeds per fruit	1.40	0.16	2.96	0.13	8.99
6.	Fruit length	1.86	0.18	3.08	0.43	1.52
7.	Fruit girth	1.93	0.18	2.39	0.01	8.66
8.	Number of branches per plant	1.47	0.18	2.52	0.01	8.45
9.	Number of fruits per plant	2.10	0.21	1.16	0.21	33.51
10.	Fruit weight	2.09	0.17	2.91	0.03	4.7
11.	Fruit yield per plant	8.48	0.22	1.67	0.04	12.11

1. $(H_1/D)^{1/2}$ - Average degree of dominance,
2. $H_2/4H_1$ – Proportion of alleles with positive and negative effects in parents,
3. $\frac{(4DH_1)^{1/2}+F)}{(4DH_1)^{1/2} - F)}$ - Proportion of dominant and recessive alleles in parents,
4. h^2/H_2 _ Number of genes controlling the character and exhibit dominance

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