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**Meenakshi Ramgiry**Department of Horticulture,  
JNKVV, Jabalpur, Madhya  
Pradesh, India**AK Barholia**Department of Horticulture,  
JNKVV, Jabalpur, Madhya  
Pradesh, India

## Studies on selection indices techniques for enhancement of fruit yield in okra

**Meenakshi Ramgiry and AK Barholia**

### Abstract

The experiment was consisting the sixty different genotypes of okra and check varieties from diverse origin. Discriminant function analysis carried out for six traits namely days to first flowering, number of fruits per plant, fruit length, fruit diameter, fresh fruit weight and fruit yield per plant. The discriminant functions consisting six indices of single character, five indices of two characters, ten indices of three characters, nine indices of four, five index of five characters and one index for six characters respectively. Selection efficiency of the function was found enhancing by increasing the number of characters in the selection index. The index involving all the six characters recorded the maximum genetic gain and selection efficiency. Similarly using the three characters *viz.* fruit diameter, fresh fruit weight and fruit yield per plant ( $X_4 + X_5 + X_6$ ) were resulted more suitable for selecting the parents for hybridization.

**Keywords:** Okra, selection Indies, expected genetic advance

### Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) having chromosome number  $2n = 130$  is an important vegetable crop grown throughout the India for its tender green fruits. It is native to Tropical Africa and commonly known as Bhindi or lady's finger in India. Okra is an allopolyploidy and belongs to the family Malvaceae. It is an often cross-pollinated possess crossing ranging from 5 to 20 percent.

The progenitor of cultivated okra is *Abelmoschus tuberculatus* ( $2n=58$ ). Okra has five related species which are *Abelmoschus tuberculatus* ( $2n=58$ ), *Abelmoschus tetraphyllus* ( $2n=138$ ), *Abelmoschus moschatus* ( $2n=72$ ), *Abelmoschus manihot* ( $2n=68$ ), *Abelmoschus ficulneus* ( $2n=72$ ). The species *Abelmoschus manihotis* occasionally used as a leafy vegetable.

Discriminant function analysis firstly describe by Fisher (1936) <sup>[1]</sup> and first applied by Smith (1936) gives information on proportionate weightage that should be given to a particular yield component. The discriminant function and selection index determines the genetic merits of particular genotype based on linear combination of various characters (Dabholkar, 1999) <sup>[3]</sup>. Thus it helps in discriminating the desirable genotypes from the same or different source of population, which can fulfil the demand of various breeding programmes for development of suitable okra variety for commercial cultivation. To find out a suitable selection indices for the enhancement of fruit yield in okra, the present investigation was conducted on advanced breeding lines derived from different origin.

### Materials and Methods

Sixty genotypes of okra collected from different origin evaluated in Randomized Complete Block Design with three replications at Nursery area, Department of Horticulture, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, (M.P.) during kharif 2015 and 2016. Each genotype was accommodated in a single row of 3 m length. The row to row spacing of 60 cm and plant to plant spacing of 30 cm was adopted. The recommended packages of practices were followed and six traits were recorded on five randomly selected plants of each genotype and replication. Traits namely, Days to 50% flowering=  $X_1$ , Number of fruits per plant=  $X_2$ , Fruit length=  $X_3$ , Fruit diameter=  $X_4$ , Fresh fruit weight=  $X_5$ , Fruit yield per plant=  $X_6$  were recorded.

### Method

Discriminant function analysis described by Dabholkar (1999) <sup>[3]</sup> was used to construct the selection indices. In the present study only those characters which exhibited significant correlation and direct effect with the fruit yield were selected.

**Corresponding Author:****Meenakshi Ramgiry**Department of Horticulture,  
JNKVV, Jabalpur, Madhya  
Pradesh, India

## Results and Discussions

Selection indices in the present study, it has given an interesting result, that the selection of the genotypes for yield and other traits. The discriminant functions consisting six

indices of single character, five indices of two characters, ten indices of three characters, nine indices of four, five index of five characters and one index for six characters were (Tables: 1).

**Table: 1:** Selection indices for fruit yield per plant and their relative efficiency in okra.

	Characters combination in selection index	Discriminant function	Z value on character mean	Expected genetic advance	Relative efficiency %
1.	DF (X1)	$Z = -0.5917X_1$	-33.4214	5.3410	59.65
2.	NFPP (X2)	$Z = -0.8768 X_2$	-8.7599	4.0020	44.70
3.	FL (X3)	$Z = 2.3356 X_3$	31.1815	6.5183	72.80
4.	FD (X4)	$Z = 19.5362 X_4$	34.3837	9.6921	108.24
5.	FFW (X5)	$Z = 1.0575 X_5$	16.7727	3.9583	44.21
6.	FYPP (X6)	$Z = -0.1086 X_6$	-16.9216	8.9540	100.00
7.	X1 + X6	$Z = -0.8266 X_1 + -0.1270 X_6$	-66.4656	11.5568	129.07
8.	X2 + X6	$Z = 2.6267 X_2 + -0.2310 X_6$	-9.7198	11.0636	123.56
9.	X3 + X6	$Z = 3.1531 X_3 + -0.1312 X_6$	21.6634	12.4161	138.66
10.	X4 + X6	$Z = 26.1855 X_4 + -0.1506 X_6$	22.6378	15.3952	171.94
11.	X5 + X6	$Z = 1.8971 X_5 + -0.1333 X_6$	9.3470	11.2459	125.60
12.	X1 + X2 + X6	$Z = -0.6954 X_1 + 2.0619 X_2 + -0.2201 X_6$	-52.9496	12.5791	140.49
13.	X1 + X3 + X6	$Z = -0.7662 X_1 + 2.9905 X_3 + -0.1471 X_6$	-26.2475	14.1360	157.87
14.	X1 + X4 + X6	$Z = -0.5526 X_1 + 24.0338 X_4 + -0.1594 X_6$	-12.0783	16.1188	180.02
15.	X1 + X5 + X6	$Z = -0.9936 X_1 + 2.3297 X_5 + -0.1610 X_6$	-44.2160	14.1843	158.41
16.	X2 + X3 + X6	$Z = 2.4501 X_2 + 3.0359 X_3 + -0.2444 X_6$	26.9471	13.8130	154.27
17.	X2 + X4 + X6	$Z = 1.1741 X_2 + 24.3082 X_4 + -0.2023 X_6$	23.0206	7.5927	84.80
18.	X2 + X5 + X6	$Z = 4.7869 X_2 + 3.3611 X_5 + -0.3752 X_6$	0.6939	15.4645	172.71
19.	X3 + X4 + X6	$Z = 2.374 X_3 + 23.640 X_4 + -0.1635 X_6$	47.8425	16.6574	186.03
20.	X3 + X5 + X6	$Z = 2.7772 X_3 + 1.4925 X_5 + -0.1479 X_6$	37.7297	13.4819	150.57
21.	X4 + X5 + X6	$Z = 27.5858 X_4 + 2.2082 X_5 + -0.1815 X_6$	55.3289	17.2999	193.21
22.	X1 + X2 + X3 + X6	$Z = -0.6445 X_1 + 1.9332 X_2 + 2.9239 X_3 + -0.2339 X_6$	-14.4714	14.8823	166.21
23.	X1 + X2 + X4 + X6	$Z = 0.5486 X_1 + 1.2548 X_2 + 1.2485 X_3 + 0.2486 X_6$	-18.4784	10.4523	158.21
24.	X1 + X2 + X5 + X6	$Z = -0.8107 X_1 + 4.2498 X_2 + 3.5497 X_5 + -0.3706 X_6$	-6.0902	16.9550	189.36
25.	X1 + X3 + X4 + X6	$Z = -0.5332 X_1 + 2.3276 X_3 + 21.6136 X_4 + -0.1718 X_6$	12.2568	17.2823	193.01
26.	X1 + X3 + X5 + X6	$Z = -0.9154 X_1 + 2.4714 X_3 + 1.9356 X_5 + -0.1718 X_6$	-14.1510	15.6370	174.64
27.	X2 + X3 + X4 + X6	$Z = 1.1896 X_2 + 2.3800 X_3 + 21.7313 X_4 + -0.2159 X_6$	48.2943	16.8909	188.64
28.	X2 + X3 + X5 + X6	$Z = 4.3692 X_2 + 2.2110 X_3 + 2.9112 X_5 + -0.36571 X_6$	62.4240	16.5329	184.64
29.	X2 + X4 + X5 + X6	$Z = 3.2881 X_2 + 22.9324 X_4 + 3.1613 X_5 + -0.33955 X_6$	70.5113	18.6422	208.20
30.	X3 + X4 + X5 + X6	$Z = 1.8319 X_3 + 25.4368 X_4 + 1.9170 X_5 + -0.1874 X_6$	70.4689	17.9525	200.50
31.	X1 + X2 + X3 + X4 + X6	$Z = -0.4916 X_1 + 0.8744 X_2 + 2.3356 X_3 + 20.368 X_4 + -0.2096 X_6$	15.3656	17.4006	194.33
32.	X1 + X2 + X3 + X5 + X6	$Z = -0.7619 X_1 + 3.9011 X_2 + 2.0171 X_3 + 3.1279 X_5 + -0.36226 X_6$	16.1070	17.7694	198.45
33.	X1 + X2 + X4 + X5 + X6	$Z = -0.6348 X_1 + 2.9912 X_2 + 21.0394 X_4 + 3.3255 X_5 + -0.3389 X_6$	31.0624	19.4017	216.68
34.	X1 + X3 + X4 + X5 + X6	$Z = -0.6876 X_1 + 1.6891 X_3 + 23.0989 X_4 + 2.2109 X_5 + -0.2017 X_6$	28.0431	18.8817	210.87
35.	X2 + X3 + X4 + X5 + X6	$Z = 3.0923 X_2 + 1.5830 X_3 + 21.3526 X_4 + 2.8530 X_5 + -0.3352 X_6$	82.6894	19.0930	213.23
36.	X1 + X2 + X3 + X4 + X5 + X6	$Z = -0.6108 X_1 + 2.8196 X_2 + 1.4780 X_3 + 19.6360 X_4 + 3.0314 X_5 + -0.3349 X_6$	43.8966	19.7791	220.90

### The Expected genetic advance

The expected genetic advance for fruit yield per plant which assumed 100 percent efficiency in selection indices. Among the single character indices, fruit diameter recorded the highest genetic advance 9.69%, followed by fruit yield per plant (8.95%), fruit length (6.51%) and plant height (5.34%), respectively.

The maximum genetic advance (15.39%) was obtained when selection was simultaneously based on discriminant function of two characters, e.g. fruit diameter (X4) + fruit yield per plant (X6) followed by fruit length (X3) + fruit yield per plant (X6) and days to 50% flowering (X1) + fruit yield per plant (X6) 12.41 with 11.55% genetic advance, respectively.

Combination of three characters indices revealed fruit diameter + fresh fruit weight + fruit yield per plant at a time still recorded highest genetic advance of 17.29% followed by those of fruit length + fruit diameter + fruit yield per plant, days to 50% flowering + fruit diameter + fruit yield per plant. Sherpa *et al.* (2014) <sup>[4]</sup> observed the fruit weight, number of

flower clusters per plant and number of fruits per cluster were found most important traits for selection indices.

When four characters, e.g. number of fruits per plant + fruit diameter + fresh fruit weight + fruit yield per plant were taken together, the genetic advance increased to 18.64%, followed by those of fruit length + fruit diameter + fresh fruit weight + fruit yield per plant (17.95%), days to 50% flowering + fruit length + fruit diameter + fruit yield per plant (17.28%) and days to 50% flowering + number of fruits per plant + fresh fruit weight + fruit yield per plant (16.95%).

The maximum genetic advance was achieved to 19.40% by taking five characters at a time, i.e. days to 50% flowering + number of fruits per plant + fruit length + fresh fruit weight + fruit yield per plant followed by number of fruits per plant + fruit length + fruit diameter + fresh fruit weight + fruit yield per plant and days to 50% flowering + fruit length + fruit diameter + fresh fruit weight + fruit yield per plant 19.09 and 18.88%. The function that includes all the six characters together gave the highest genetic advance (19.77%).

**The relative efficiency (%)**

The highest relative efficiency for one character was assumed 108.24 percent for fruit diameter in section indices followed by fruit yield per plant (100%), fruit length (72.8%), respectively. Among the two characters indices, fruit diameter + fruit yield per plant (171.94%) recorded highest, followed by fruit length + fruit yield per plant (138.66%). The maximum relative efficiency of 193.21 percent was obtained when selection was simultaneously based on discriminant function with three characters, e.g. fruit diameter + fresh fruit weight + fruit yield per plant (193.24%) followed by fruit length + fruit diameter + fruit yield per plant and days to 50% flowering + fruit diameter + fruit yield per plant (186.03 and 180.02%), respectively Chattopadhyay *et al.* (2011) [5].

Combination of four characters indices i.e. number of fruits per plant + fruit diameter + fresh fruit weight + fruit yield per plant at a time still recorded highest relative efficiency of 208.20 percent followed by those of fruit length + fruit diameter + fresh fruit weight + fruit yield per plant (200.5%), days to 50% flowering + fruit length + fruit diameter + fruit yield per plant (193.01%) and days to 50% flowering + number of fruits per plant + fresh fruit weight + fruit yield per plant (189.36%), respectively.

The maximum relative efficiency was achieved to 216.68 percent by taking five characters at a time, i.e. days to 50% flowering + number of fruits per plant + fruit length+ fruit diameter + fruit yield per plant followed by number of fruits per plant+ fruit length+ fruit diameter + fresh fruit weight + fruit yield per (213.23%) and days to 50% flowering + fruit length + fruit diameter + fresh fruit weight + fruit yield per plant (210.87%).The function that includes all the six characters together gave the highest relative efficiency (220.9%).

It is concluded that selection indices improve with an increase in number of characters in combination. In present experiment five character combinations gave the maximum expected genetic advance (19.77%) and relative efficiency (220.90%) as compare to other combinations, but it is difficult to use more characters at a time. On the other hand selection based on three characters (X4 + X5 + X6) gave more sufficient genetic advance (17.29%) and relative efficiency (193.21%), comparable to those based on four or more characters together which is more desirable and practically possible to use than the index that includes more number of characters as pointed out by (B. A. Monpara and M. D. Chhatrola, 2010) [6]

**References**

1. Fisher RA. Use of multiple measurements in taxonomic problems. *Annals of Eugenics London*. 1936;7:179-188.
2. Smith HF. A discriminant function for plant selection. *Annals of Eugenics*. 1936;7:240-250.
3. Dabholkar AR. *Elements of Biometrical Genetics (Revised and Enlarged Edition)*. Concept Publishing Company, New Delhi; c1999. p. 444-478.
4. Sherpa P, Pandiarana N, Shende VD, Seth T, Mukherjee S, Chattopadhyay A. Estimation of genetic parameters and identification of selection indices in exotic tomato genotypes. *Electronic Journal of Plant Breeding*. 2014;5(3):552-562.
5. Chattopadhyay A, Sharangi AB, Nuka Dai, Dutta S. Diversity of genetic resources and genetic association analyses of green and dry chillies of eastern India. *Chilean Journal of Agricultural Research*. 2011;71(3):350-356.

6. Monpara BA, Chhatrola MD. Selection indices for improvement of fruit yield in okra [*Abelmoschus esculentus* (L.) Moench]. *Advance Research Journal of crop Improvement*. 2010;1(2):62-66.