

## CONSTRUCTION OF SELECTION INDICES BASED ON YIELD RELATED TRAITS FOR ASHGOURD [*BENINCASA HISPIDA* (COGN.)] GENOTYPES

LOVELY B. & VIJAYARAGHAVA KUMAR

Research Scholar, Kerala Agricultural University, Thrissur, Kerala, India

### ABSTRACT

A research program was carried out, at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani with the objective of assessing the genetic variability, present in a population of twenty-five ash gourd genotypes. Analysis of variance revealed significant differences, for almost all the characters studied. Yield per plant showed strong positive genotype correlation, with mean fruit weight, fruit length, fruit girth, flesh thickness and seeds per fruit. The discriminant function technique was adopted, for the selection of construction index for yield using characters, which showed a relatively stronger association with yield. The genotypes BH 2 and BH 3, ranked the first with high index values.

**KEYWORDS:** Discriminant Function Analysis, Ash Gourd, Correlation

### INTRODUCTION

Vegetables play a vital role in the health and nutrition of people, throughout the world. They are valuable sources of vitamin, minerals, carbohydrates and proteins. Several cucurbitaceous crops constitute a principal group of cross fertilized vegetables. Ash gourd is an important vegetable, grown in many parts of the world and is believed to have originated in southeastern Asia. No wild species are reported in this crop, and it is the only member of the genus *Benincasa*. Being a cross fertilized crop, there exists considerable scope for improvement in this crop. Most of the economically important traits like yield are an extremely complex character, and is the result of many growth functions of the plant. An estimation of the interrelationship of yields with other traits is of immense help, in any crop improvement program. The economic worth of a plant depends upon several characters. So, while selecting a desirable plant from a segregating population, the plant breeder has to give due consideration to characters of economic importance. Selection index is one such method of selecting plants for crop improvement, based on several characters of importance. The present investigation was carried out, with the objective to study relationship between yield and yield component characters, and to construct selection indices for improvement of yield in ash gourd.

### METHODS

The experiment was carried out at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani ( $8^{\circ} 5' N$  latitude and  $77^{\circ} 1' E$  longitude at an altitude of 29 m above mean sea level), with 25 ash gourd genotypes (Table 1). Soil type is a red loam, belonging to Vellayani series, texturally classified as sandy clay loam. The trial was laid out in a randomized block design, with three replications. In each replication, four plants per genotype were taken and a single plant was maintained in each pit. Normal cultural methods, as per the Package of Practices Recommendations of the Kerala Agricultural University were adopted. Four plants per genotype were selected, for recording the following biometric

observations: days to first male flower, node to first male flower, days to first female flower, node to first female flower, vine length (m), branches per plant, fruits per plant, mean fruit weight (kg), fruit yield per plant (kg), fruit length (cm), fruit girth (cm), flesh thickness (cm), dry matter content (%), seeds per fruit and 100 seed weight (g).

**Table 1: Particulars of Genotypes of Ash Gourd Used For The Study**

Accession /variety	Source
Palakkad	BH1, BH11, BH23
Wayanad	BH2, BH7
Idukki	BH3, BH15, BH17, BH18, BH19
Bangalore	BH4, BH9
Tamilnadu	BH5
Kozhicode	BH6
Thrissur	BH8, BH10
Kottayam	BH12, BH22, BH24, BH25
Thiruvananthapuram	BH13, BH16, BH21
Alleppey	BH14
Kerala Agricultural University	BH20

Data from mean of individual genotypes were subjected, to methods of analysis of variance and statistical analysis was performed, to estimate the correlation coefficients between the characters, as follows:

$$\text{Genotypic correlation } (r_{gij}) = \frac{\sigma_{gij}}{\sigma_{g_i} \sigma_{g_j}}$$

$$\text{Phenotypic correlation } (r_{p_{ij}}) = \frac{\sigma_{p_{ij}}}{\sigma_{p_i} \sigma_{p_j}}$$

$$\text{Environmental correlation } (r_{e_{ij}}) = \frac{\sigma_{e_{ij}}}{\sigma_{e_i} \sigma_{e_j}}$$

Selection index, refers to a linear combination of characters associated with yield. The various genotypes were discriminated, based on 15 characters using the selection index, developed by Smith (1947) using the discriminant function of Fisher (1936). The selection index is described by the function  $I = b_1x_1 + b_2x_2 + \dots + b_kx_k$ . The function  $H = a_1G_1 + a_2G_2 + \dots + a_kG_k$  describes the merit of a plant, where  $x_1, x_2, \dots, x_k$  is the phenotypic values and  $G_1, G_2, \dots, G_k$  is the genotypic values of the plant, with respect to the characters  $X_1, X_2, \dots, X_k$ .  $H$  denotes the genetic worth of the plant. The economic weight assigned to each character is assumed, to be equal to unity i.e.,  $a_1, a_2, \dots, a_k = 1$ . The regression coefficients  $b_1, b_2, \dots, b_k$  is estimated in a such a way that, the correlation between  $H$  and  $I$  is maximized. The procedure will reduce to an equation of the form  $b = P^{-1}Ga$ , where  $P$  is the phenotypic and  $G$  is the genotypic variance covariance matrix, respectively, from which the  $b$  values were solved out.

## RESULTS AND DISCUSSIONS

The analysis of variance, with respect to the various characters revealed a wide range of variation, for all the characters, which suggests ample scope of improvement (Afroze et al., 2007). The phenotypic and genotypic correlations, among various characters were estimated and results are given in the table 2. The study indicated that, the node to first male flower was positively and significantly correlated with node to female flowers, suggesting the earliness of the crop (Latif et al., 2008). Similarly, the number of days of opening of male and female flowers were also correlated, among themselves. The character number of days to first male flower and female flower, exhibited a negative correlation with fruit yield per plant, which implied that, early opening of the male flowers favored cross- pollination (Kanimozhi et al., 2016).

Table 2: Estimates of Genotypic Correlation Coefficients of Various Yield Related Traits in Ash Gourd

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15
X1	1.000														
X2	0.460**	1.000													
X3	0.349**	-0.027	1.000												
X4	0.367**	-0.041	-0.800**	1.000											
X5	0.104	-0.167	0.199	-0.335**	1.000										
X6	0.525**	-0.030	0.011	0.523**	-0.384**	1.000									
X7	0.433**	0.271	0.196	0.347**	-0.319**	0.354**	1.000								
X8	-0.342**	-0.297**	-0.235	-0.354**	0.390**	-0.224	-0.769**	1.000							
X9	-0.033	-0.316**	0.051	0.044	0.272	0.046	-0.349**	0.845**	1.000						
X10	-0.155	-0.248	-0.172	-0.331**	0.155	0.426**	-0.666**	0.761**	0.625**	1.000					
X11	-0.199	-0.391**	-0.191	-0.350**	0.304**	-0.118	-0.685**	0.849**	0.687**	0.609**	1.000				
X12	-0.260	-0.481**	-0.177	-0.285**	0.151	0.045	-0.655**	0.749**	0.673**	0.840**	0.780**	1.000			
X13	0.188	0.641**	-0.060	-0.050	-0.206	0.247	0.518**	-0.647**	-0.682**	-0.390**	-0.702**	-0.709**	1.000		
X14	-0.309**	-0.321**	-0.251	-0.259	0.219	-0.057	-0.658**	0.679**	0.405**	0.439**	0.685**	0.431**	-0.381**	1.000	
X15	-0.230	-0.176	-0.333**	-0.356**	0.370**	-0.491**	-0.627**	0.559**	0.277	0.328**	0.620**	0.448**	-0.480**	0.341**	1.000

X1- days to first male flower opening, X2- days to first female flower opening, X3- node to first male flower, X4- node to first female flower, X5- vine length, X6- branches per plant, X7- fruits per plant, X8- mean fruit weight, X9- fruit yield per plant, X10- fruit length, X11- fruit girth, X12- flesh thickness, X13- dry matter content, X14- seeds per fruit, X15- 100-seed weight

Fruits per plant had high negative correlation with mean fruit weight, fruit length, fruit girth, flesh thickness, seeds per fruit and 100-seed weight. A positive association was seen with dry matter content. Haqueet al. (2014), also reported negative correlation for number of fruits per plant, with days to female flowering, node number at first male flower and fruit diameter in snake gourd. A positive correlation was recorded by Rani and Reddy (2017) for fruit length, number of seeds per fruit, number of primary branches and yield per plant in bottlegourd.

High positive correlation was observed, for mean fruit weight with fruit yield per plant, fruit length, vine length, fruit girth, flesh thickness and seeds per fruit. Negatively, with days to male and female flower, node to first male and female flower, fruits per plant, and dry matter content. Vine length was negatively and significantly correlated with node to first female flower, and fruits per plant (Janaranjani and Kanthaswamy, 2015). A significant positive correlation was recorded for vine length, with mean fruit weight, fruit length and 100-seed weight (Ray et al., 2017).

Fruit yield per plant was positively associated with fruit length, fruit girth and flesh thickness (Manikandanetal., 2017), and negatively with days to first female flower (Nagarajuet al., 2016) and fruits per plant (Resmi and Sreelathakumary, 2011).

Fruit length and girth had significant positive association with vine length, fruit weight, fruit yield, seeds per fruit, 100 seed weightand flesh thickness (Dewan et al., 2014). A significant negative correlation was recorded with node to first female flower, fruits per plant, and dry matter content.

Discriminant function technique was adopted, for the construction of selection index for yield, using days to first male flower opening ( $X_1$ ), days to first female flower opening ( $X_2$ ), node to first male flower( $X_3$ ), node to first female flower ( $X_4$ ), vine length ( $X_5$ ), branches per plant ( $X_6$ ), fruits per plant ( $X_7$ ), mean fruit weight ( $X_8$ ), fruit yielded per plant ( $X_9$ ), fruit length ( $X_{10}$ ), fruit girth ( $X_{11}$ ), flesh thickness ( $X_{12}$ ), dry matter content ( $X_{13}$ ), seeds per fruit ( $X_{14}$ ) and 100-seed weight ( $X_{15}$ )

These component characters showed relatively stronger association with yield and could form a valuable selection index, for yield in this crop. The selection index, worked out in the present study is given below.  $I = 3.7134x_1 + 0.5065x_2 + 2.8041x_3 + 0.1843x_4 - 4.14082x_5 - 11.2733 x_6 + 13.6114 x_7 + 22.0967x_8 - 2.4602x_9 + 0.9324x_{10} + 0.4510x_{11} + 7.1841x_{12} + 7.1076x_{13} + 0.9865x_{14} + 0.4901x_{15}$ . The selection index value for each genotype was determined, and they were ranked accordingly (Table3). The genotypes BH2 and BH3 ranked first, with the highest index values. Identification of superior genotypes, based on discriminant function analysis was also done for some workers (Resmi, 2004; Mashiloetal., 2017).

**Table 3. Selection Indices Arranged in Descending Order**

Sl. No.	Accessions	Selection Index Values
1.	BH3	7330.02
2.	BH2	7120.22
3.	BH7	6568.23
4.	BH4	5978.42
5.	BH10	5540.66
6.	BH9	4527.83
7.	BH5	4186.48
8.	BH1	3779.66
9.	BH13	3528.37
10.	BH24	3404.73
11.	BH20	3382.19
12.	BBH25	3308.51
13.	BH17	3284.99
14.	BH14	3230.54
15.	BH23	3158.54
16.	BH12	3136.76
17.	BH22	2930.24
18.	BH15	2644.39
19.	BH11	2466.09
20.	BH19	2412.12
21.	BH6	2327.40
22.	BH8	2067.35
23.	BH16	1744.28
24.	BH21	1553.63
25.	BH18	1528.06

## CONCLUSIONS

Discriminant function technique involves development of selection criteria, on a combination of various yield related characters and helps in indirect selection for genetic improvement in yield. A knowledge on the degree of association, among quantitative characters would help the breeder to pinpoint a character, or characters whose selection would automatically result in an overall progress of such characters, which are positively correlated with yield. In the present study, yield per plant showed strong positive genotypic correlation with mean fruit weight, fruit length, fruit girth, flesh thickness and seeds per fruit. Negative correlation was seen for days to first female flower, fruits per plant and dry matter content. A selection index, based on these considering the genotypic correlation revealed superiority of the genotypes, BH2 and BH3.

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