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Analysis of heritability in narrow sense and genetic advance in percent of mean in sponge gourd (*Luffa cylindrica* (L.) Mj. Roem)

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Abstract

The experiment were carried out in two years with aims to determine gene action involving 9 parental lines *viz*., NDSG-1, NDSG-20, NDSG-22, NDSG-24, NDSG-26, NDSG-28, NDSG-30, NDSG-32 and Pusa Chikni of sponge gourd and their 36 F1 hybrids at MES, Vegetable Science, N.D.U.A.&T., Kumarganj, Faizabad (U.P.) during crop seasons of summer (Zaid) 2014 and 2015. The experiments were laid out in RBD with three replications having each experimental unit of single row with spacing of 3 m x 0.5 m. Heritability is a useful measure for considering the ratio of genetic variance to the total variance and is generally represented in percentage. This is an index of transmissibility of characters from the parents to their off springs and is a measure of genetic relationship between parents and progeny, hence changing the characteristics of the population through selection can be predicted only from knowledge of the degree of correspondence between phenotypic and breeding values.

Keywords: Heritability, genetic advance, hybrid vigour

Introduction

In India, a number of major and minor cucurbits are cultivated which share about 5.6 percent of the total vegetable production. They are consumed in various forms i.e., salad (cucumber, gherkins, long melon), sweet (ash gourd, pointed gourd), pickles (gherkins), and deserts (melons). Sponge gourd is an annual and monoeceous cucurbit plant. Genetic variability is the raw materials on which selection acts to evolve superior genotypes or varieties in vegetable breeding programme. The genetic variability for various characters available in the breeding populations or materials is systematically subjected to selection to change the genetic architecture of plant characters and consequently of the plant as a whole to develop improved genotypes having higher economic yield. The variability exploited in breeding programme is derived from the naturally occurring variants and the wild relative of crops as well as artificially developed strains and genetic stocks by human efforts. The reservoir of variability for different characters of a plant species resulting from available natural or artificially synthesized variants or strains constitutes its germplasm. Thus, germplasm may include improved strains, primitive cultivars, wild relatives, obsolete cultures, special genetic stocks, seeds pollen and vegetative parts etc. most of the germplasm collections are in inadequately evaluated or screened for assessment of genetic variability. Heritability is a useful measure for considering the ratio of genetic variance to the total variance and is generally represented in percentage. This is an index of transmissibility of characters from the parents to their off springs and is a measure of genetic relationship between parents and progeny, hence changing the characteristics of the population through selection can be predicted only from knowledge of the degree of correspondence between phenotypic and breeding values.

Materials and Methods

The present investigation entitled "Estimation of Heritability in sponge gourd (*Luffa cylindrica* (L.) Mj. Roem)" was conducted during crop season of summer (Zaid) 2014 and 2015 to evaluate the components of genetic variation in sponge gourd (*Luffa cylindrica* (L.) Mj. Roem) using diallel mating design (excluding reciprocals) at the Main Experiment Station (MES) of the Department of Vegetable Science, N.D. University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) India.

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The selected parental lines viz., NDSG-1 (P1), NDSG-20 (P2), NDSG-22 (P3), NDSG-24 (P4),NDSG-26 (P5), NDSG-28 (P6), NDSG-30 (P7), NDSG-32 (P8) and Pusa Chikni (P9) (national check) were crossed in the all possible combinations, excluding reciprocals, during summer, 2014 to get 36 F_1 seeds for the study on heritability (narrow sense) and genetic advance for 14 fruit yield traits.

Heritability

Following Mather and Jinks (1971) [8], narrow sense heritability was obtained as:

$$h^2(n) = \left[\frac{1/2D + 1/2\ H_1 - 1/2\ H_2 - 1/2\ F}{1/2D + 1/2\ H_1 - 1/4\ H_2 - 1/2\ F + E} x100 \right]$$

On the other hand broad heritability was calculated as:

$$h^2(b) = \left[\frac{1/2D + 1/2\ H_1 - 1/4\ H_2 - 1/2\ F}{1/2D + 1/2\ H_1 - 1/4\ H_2 - 1/2\ F + E} x100 \right]$$

Where, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{E}$ components are explained earlier.

(b) Genetic advance (GA)

The genetic advance was calculated by the formula given by Johnson *et al.* (1955) [9].

Genetic advance = $\sigma_p \times h^2 \times K$

Genetic advance in percent over mean of the character:

$$\text{Genetic advance (\%)} = \frac{\sigma_p \times h^2 \times K}{\overline{X}} \times 100$$

Where,

σ_p = phenotypic standard deviation.

h^2 = heritability coefficient in narrow sense.

k = selection differential at 5% selection intensity (K = 2.06)

$\overline{X}$ = the mean value of the character under study.

Result and Discussion

Heritability in narrow sense and genetic advance in percent of mean

Estimates of heritability in narrow sense (h^2ns) and genetic advance in percent of mean were estimated for all the fourteen traits and result have been presented in Table. In respect to facilitate the description of the estimates of heritability (h^2ns), the observed values of the estimates were classified according to Robinson (1966), as (i) High (> 30%), (ii) Moderate (above 10% to 30%) and low (< 10%). The category wise distributions of different characters are presented below.

The higher values of heritability (h^2ns) estimates (> 75%) were observed only for number of primary branches per vine at last harvest (84.8% and 83.4%), vine length at last harvest (82.8% and 82.6%), node number to first staminate flower anthesis (81.8% and 77.0%) and average fruit weight (78.9% and 80.4%) in both the years. However, moderate heritability were estimated for rest of the characters over both the yeas except fruit diameter and inter nodal length which showed low heritability.

In order to facilitate the interpretation of the estimates of heritability in broad sense (h^2bs) were classified according to Robinson (1966), as (i) high (> 75%), moderate (> 50 to 75%) and low (< 50%). The high estimates of heritability in broad sense (> 75%) were observed for node number to first staminate flower anthesis (97 and 96%), node number to first pistillate flower anthesis (93 and 91%), vine length at last harvest (90 and 91%), marketable fruit yield per plant (89 and 90%) , number of fruits per plant (87 and 87%), average fruit weight (86 and 87%), number of primary branches per vine at last harvest (86 and 86%), fruit length of marketable fruits yield (82 and 79%), number of nodes per vine at last harvest (79 and 78%) and inter nodal length (74 and 77%) in both the years. Whereas, moderate heritability in broad sense (> 50 to 75%) were noticed for fruit diameter (73 and 54%), days to first pistillate flower anthesis (67 and 70%). Whereas, days to first fruit harvest showed low heritability (< 50%).

For easy explanation, genetic advance in percent of mean was classified into three groups such as (i) high (50%) (ii) moderate (> 35% to 50%) and (iii) low (< 35%). The genetic advance in percent of mean ranged from 9.85 and 12.71 percent days to first fruit harvest to 66.75 and 68.25 percent for node number to first staminate flower anthesis in both the years, respectively. High genetic advance in percent of mean were estimated for two traits, these traits were node number to first staminate flower anthesis (66.75 and 68.25 %), vine length at last harvest (53.61 and 55.69%) in both the years, respectively.

The moderate genetic advance (35 to 50%) were observed for three traits *viz.*, number of fruits per plant, average fruit weight and marketable fruit yield per plant, while, rest of traits showed low genetic advance (< 35%) in both the years.

Table 1: Estimates of mean, range, coefficient of variation, heritability and genetic advance in sponge gourd over two years (2014 and 2015)

Characters	Years	Grand mean	Range of mean values		Coefficient of variation			Heritability in narrow sense (%)	Heritability in Broad sense (%)	Genetic advance in percent of mean
			Parents	Crosses	PCV	GCV	ECV			
		1	2	3	4	5	6	7	8	9
Node number to first staminate flower anthesis	Y₁	7.69	4.73 to 15.33	4.77 to 13.43	33.51	32.95	6.08	81.8	97	66.75
	Y₂	7.81	4.17 to 15.53	4.70 to 13.10	34.48	33.80	6.84	77.0	96	68.25
Node number to first pistillate flower anthesis	Y₁	11.51	7.10 to 18.23	7.57 to 18.23	24.79	23.93	6.46	55.7	93	47.60
	Y₂	11.59	7.10 to 20.43	7.03 to 19.23	26.70	25.51	7.89	55.9	91	50.21
Days taken for anthesis of first staminate flower	Y₁	36.23	28.50 to 48.47	27.37 to 49.80	15.68	13.35	8.22	58.9	73	23.42

	Y_2	36.38	29.53 to 49.53	28.87 to 46.90	15.83	13.46	8.34	55.9	72	23.57
Days taken for anthesis of first pistillate flower	Y_1	39.99	34.37 to 50.33	32.47 to 48.73	13.38	10.99	7.63	64.0	67	18.60
	Y_2	39.89	34.73 to 48.43	31.83 to 48.50	13.65	11.44	7.45	55.6	70	19.75
Days to first Fruit harvest	Y_1	53.91	47.50 to 62.50	44.13 to 64.20	11.73	7.49	9.03	56.9	41	9.85
	Y_2	54.30	46.63 to 63.53	45.53 to 65.00	10.57	8.07	6.81	54.7	58	12.71
Number of Nodes per vine at last harvest	Y_1	55.41	41.23 to 75.63	40.47 to 71.40	19.09	17.01	8.67	72.2	79	31.21
	Y_2	55.05	39.37 to 72.63	40.40 to 70.60	18.69	16.48	8.81	73.1	78	29.94

		1	2	3	4	5	6	7	8	9
Inter nodal length (cm)	Y_1	7.31	4.00 to 8.90	5.20 to 10.37	16.19	13.93	8.25	31.1	74	24.69
	Y_2	7.35	4.40 to 9.30	4.70 to 10.50	16.93	14.89	8.05	32.7	77	26.99
Vine length (m) at last harvest	Y_1	4.20	2.20 to 6.20	2.20 to 6.10	28.84	27.39	9.01	82.8	90	53.61
	Y_2	4.13	1.80 to 6.40	2.03 to 6.07	29.84	28.40	9.15	82.6	91	55.69
Number of primary branches per vine at last harvest	Y_1	6.02	4.33 to 9.10	4.03 to 8.83	24.18	22.41	9.06	84.8	86	42.81
	Y_2	5.97	4.10 to 8.50	4.03 to 8.83	24.58	22.86	9.04	83.4	86	43.79
Fruit length (cm) of marketable fruits	Y_1	29.30	15.30 to 38.40	20.17 to 42.83	20.50	18.52	8.79	63.5	82	34.47
	Y_2	30.00	13.30 to 37.80	21.33 to 41.93	20.23	18.01	9.22	67.6	79	33.02
Fruit Diameter (cm)	Y_1	2.84	2.17 to 4.10	2.10 to 3.87	17.07	14.56	8.91	48.2	73	25.59
	Y_2	2.91	2.10 to 3.87	2.47 to 3.63	13.31	9.79	9.01	71.9	54	14.85
Number of fruits per plant	Y_1	23.54	12.33 to 33.60	13.30 to 38.37	25.59	23.86	9.24	72.6	87	45.84
	Y_2	23.40	12.30 to 30.50	14.43 to 37.07	24.34	22.65	8.91	74.6	87	43.42
Average fruit weight (g)	Y_1	167.88	96.23 to 220.33	112.93 to 242.70	20.48	18.99	7.66	78.9	86	36.27
	Y_2	161.99	108.93 to 205.87	104.17 to 247.00	21.22	19.79	7.65	80.4	87	38.03
Marketable fruits yield per plant (kg)	Y_1	3.40	1.64 to 3.76	2.29 to 5.01	23.1	21.83	7.81	57.7	89	42.35
	Y_2	3.28	1.62 to 3.64	2.15 to 5.17	24.73	23.49	7.75	60.3	90	45.95

Conclusion

The experimental material consisting of nine parents/inbred lines of sponge gourd viz., NDSG-1 (P 1), NDSG-20 (P 2), NDSG-22 (P 3), NDSG- 24 (P 4), NDSG-26 (P 5), NDSG-28 (P 6), NDSG-30 (P 7), NDSG-32 (P 8) and Pusa Chikni (P 9). These nine parental lines were crossed in all possible combinations, excluding reciprocals to get 36 F 1 hybrids. All the 45 genotypes (nine parental lines and 36 F 1 hybrids) were evaluated in Randomized Block Design (RBD) with three replications in two years (Y1 and Y 2). The ratio of $(\hat{h}^2/\hat{H}_2)$ which estimates the number of gene groups revealed that at least one gene groups were involved in the inheritance for most of the characters except average fruit weight and marketable fruit yield in both the years and fruit length and fnumber of fruits per plant in Y_2.The positive values of correlation coefficient between parental order of dominance (Wr + Vr) and parental measurement (Yr) for most of the characters in both the years suggested preponderance of recessive genes. Genes with positive and negative effects were asymmetrically distributed with maximum proportion of dominant genes in the inheritance of all the traits of the parents studied. Moderate to high heritability along with high genetic advance in percent of mean were observed for most of the important economic traits showing ample scope of improvement.

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