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ISSN: 0976-3376

ASIAN JOURNAL OF SCIENCE AND TECHNOLOGY

Asian Journal of Science and Technology
Vol. 4, Issue 10, pp.149-151, October, 2013

RESEARCH ARTICLE

STUDIES ON GENETIC ANALYSIS IN SNAKE GOURD (TRICHOSANTHES ANGUINA L.)

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ARTICLE INFO

Article History:
Received 08th July, 2013
Received in revised form
24th August, 2013
Accepted 28th September, 2013
Published online 30th October, 2013

Key words:
Snake gourd,
Dominance effect, GCA,SCA and
Heritability .

ABSTRACT

An investigation entitled "Heterosis breeding in snake gourd (Trichosanthes anguina L.)" was carried out in the Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamil Nadu, India during 2003-2007. The parents from diversified genotypes and their hybrids in snake gourd were evaluated for fruit yield per plant, yield attributing characters and quality traits with the objective of analyzing gene action. The characters observed were days to first male and female flower opening, number of fruits per plant, fruit length, fruit girth, flesh thickness, single fruit weight, fruit yield per plant, number of seeds per fruit, Vitamin C and acidity content of fruit. Based on the per se performance with specific trait and genetic divergence from different clusters, six genotypes namely P1–Hessaraghatta local (Bangalore, Karnataka), P2–Ottanchathiram local (Dindigul district, Tamil Nadu), P3–IC-212484, NBPGR, Trichur, P4–Michaelpalayam local (Dindigul district, Tamil Nadu), P5–PKM–1 (mutant variety, HC&RI, TNAU, Periyakulam), P6–Vellayani local (Kerala) were selected for crossing in full diallel programme. The analysis of variance indicated that the selected six parents and their 30 hybrids differed among themselves for all the eleven traits studied. Degree of dominance indicated that the traits viz., days to first female flower opening, fruit girth, number of fruits and fruit yield per plant and Vitamin C content of fruit were controlled by over-dominance. The remaining traits were controlled by partial dominance. The positive and negative signs of F and the ratio of H2/4H1 implied that the frequencies of positive and negative alleles in the parents were asymmetrical. All the characters were governed by single group of genes. The narrow sense heritability estimates were high for all the traits except Vitamin C content of fruit. It indicated that all the characters except Vitamin C content have exploitable additive genetic variances. The present study revealed the preponderance of additive gene effects followed by non fixable dominance gene effects in most of the crosses and in almost all the traits studied. As snake gourd is being highly cross pollinated crop, heterosis breeding is an ideal tool to improve fruit yield per plant.

INTRODUCTION

Snake gourd (*Trichosanthes anguina* L.) belongs to the family cucurbitaceae and supposed to be the native of India/Indomalayan region/ the Indian archipelago. It is a quick growing annual climber grown widely in peninsular and eastern India but more in south India. It is a warm season crop with wide adaptation and can be successfully grown in the hills where the temperature is low. The present investigation was carried out to know the gene action for fruit yield and its components in Snake gourd crosses obtained from 6 x 6 diallel mating method.

MATERIALS AND METHODS

The experimental materials comprised of seven genetically diverse genotypes namely, P_1–Hessaraghatta local (Bangalore, Karnataka), P_2–Ottanchathiram local (Dindigul district, Tamil Nadu), P_3–IC-212484, NBPGR, Trichur, P_4–Michaelpalayam local (Dindigul district, Tamil Nadu), P_5–PKM–1 (mutant variety, HC&RI, TNAU, Periyakulam), P_6–Vellayani local (Kerala)as well as 30 F_1's obtained through full diallel fashion during 2004.The 6 parents and 30 hybrids along with a standard check MDU-1were evaluated in Randomized Block Design with three replications at Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamilnadu at 2 x 2 m spacing. All the recommended agronomic practices and need based plant protection measures were followed to raise the good crop of snake gourd. The observations were recorded on five randomly selected competitive plants of each parent and F1 from each replication for nine various characters (Table 1). The heterotic effects were computed as the percentage increase (+) or decrease (-) of F_1 mean values over better parent (heterobeltiosis) and standard check variety MDU-1 (economic heterosis) for all the characters and crosses, following the standard formula. Significance of heterosis was worked out using standard formula suggested by Wynne *et al*., (1970).

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RESULTS AND DISCUSSION

Genetic parameters: The additional genetic statistics needed for the genetic interpretation using Hayman (1954 b) diallel analysis are given below. The components of variation due to additive gene effect D was significant for almost all the traits except fruit yield per plant, while fruit yield per plant showed non-significant D component indicating non-additive genetic variance. The components of variation due to dominance effect of genes (H_1) were significant for all the traits including fruit yield per plant. The results amply indicated the importance of both additive and dominant gene effects in the expression of almost all the traits. The above inference was also supported by the GCA and SCA variances.

Table. 1. ANOVA for yield and yield component characters of snake gourd genotypes

S. No.	Characters	df	MSS	'F' value
1.	Days to first male flower opening	35	139.30	64.66**
2.	Days to first female flower opening	35	134.91	96.29**
3.	Number of fruits per plant	35	82.72	133.27**
4.	Fruit length	35	4898.03	572.26**
5.	Fruit girth	35	58.89	58.92**
6.	Flesh thickness	35	0.08	77.68**
7.	Single Fruit weight	35	94763.91	1296.33**
8.	Fruit yield per plant	35	35.48	542.02**
9.	Number of seeds per fruit	35	717.32	105.47**
10.	Vitamin C content	35	14.71	71.78**
11	Acidity content	35	0.0014	19.81**

** - Significant at 1 per cent level

Table.2. Estimates of genetic parameters for eleven characters of snake gourd

S. No.	Characters	$\hat{D}$	$\hat{F}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{h}^2$	$\hat{E}$
1.	Days to first male flower opening	68.09±10.74 **	6.80±26.24	64.73±27.27 **	62.04±24.36 **	0.75±16.39	0.73±4.06
2.	Days to first female flower opening	61.43±13.05 **	19.23±31.88	87.45±33.13 **	77.16±29.60 **	15.47±19.92	0.47±4.93
3.	Number of fruits per plant	40.07±2.74 **	20.29±6.71 *	69.05±6.97**	55.60± 6.23**	37.31±4.19 **	0.22±1.04
4.	Fruit length	2493.64 ±247.00 **	-66.30±605.50	1634.32±629.19 *	1328.15±562.07 *	186.57 ±378.31	2.79±93.67
5.	Fruit girth	21.54±2.21 **	-6.14±5.42	25.24±5.63 **	21.48±5.03 **	20.64±3.38 *	0.35±0.83
6.	Flesh thickness	0.05±0.004 **	0.01±0.008	0.03±0.009 **	0.03±0.008 **	0.002±0.005	0.0003±0.001
7.	Single fruit weight	48145.00±2919 **	-4700.00±7133.00	30369. ±7412 **	24562±6621 **	495.00±4456	24.00±1103.00
8.	Fruit yield per plant	2.74±2.24	-3.72±5.42	35.64±5.69 **	31.80±5.08 **	24.89±3.42 **	0.02 ±0.85
9.	Number of seeds per fruit	415.29 ± 10.00 **	-46.13±24.44	111.10±25.40 **	108.32±22.68 **	28.09 ±15.27	2.40 ±3.78
10.	Vitamin C content	3.75± 1.91**	2.61±04.67	16.01±4.85 **	14.69±4.33 **	5.60±2.92	0.07±0.72
11.	Acidity content	0.0008±0.0001 **	0.0002 ±0.0003	0.0007±0.0003 *	0.0006±0.0003 *	0.0001±0.0002	0.0001±0.0001

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

Table 3. Ratios of genetic parameters for eleven characters of snake gourd

S. No.	Characters	$(H_1/D)^{½}$	$H_2/4H_1$	$\frac{(4DH_1)^{½} + F}{(4DH_1)^{½} - F}$	h^2/H_2	Heritability in narrow sense (per cent)
1.	Days to first male flower opening	0.98	0.24	1.11	0.01	58.92
2.	Days to first female flower opening	1.19	0.22	1.30	0.20	40.52
3.	Number of fruits per plant	1.31	0.20	1.48	0.70	32.70
4.	Fruit length	0.81	0.20	0.97	0.15	84.36
5.	Fruit girth	1.08	0.21	0.77	0.96	95.17
6.	Flesh thickness	0.79	0.23	1.32	0.10	53.08
7.	Single fruit weight	0.79	0.20	0.88	0.10	95.32
8.	Fruit yield per plant	3.61	0.22	0.68	0.79	54.89
9.	Number of seeds per fruit	0.52	0.24	0.80	0.30	97.00
10	Vitamin C content	2.07	0.23	1.40	0.40	16.46
11	Acidity content	0.93	0.22	1.27	0.21	51.93

The component of h^2 due to dominance effect was significant for the traits viz., number of fruit per plant, fruit girth, fruit yield per plant, number of seeds per fruit and Vitamin C content of fruit. It implied the presence of dominance effect, expressed as the algebraic sum over all loci in heterozygous phase in all the crosses. The expected environmental component of variation E was non-significant for all the eleven traits studied. Mean degree of dominance $(H_1/D)^{1/2}$ was more than unity for the traits viz., days to first female flower opening, number of fruits per plant, fruit girth, fruit yield per plant and Vitamin C content of fruit indicated the presence of over dominance in the inheritance of these traits. Mean degree of dominance $(H_1/D)^{1/2}$ was less than unity for the traits viz., days to first male flower opening, fruit length, flesh thickness, single fruit weight, number of seeds per fruit and acidity content of fruit indicated the presence of incomplete dominance in these traits. The above inference was also confirmed by the regression line of V_rW_r graph. The results are in conformity with the findings of Doijode and Sulladmath (1985) and Sirohi *et al*., (1986) in pumpkin. Whereas V_r, W_r graph showed partial dominance for the trait fruit girth. But the potence ratio of $(H_1/D)^{1/2}$ exhibited over dominance for this trait. It indicated that there was a disturbance in the V_rW_r graph. This difference might be appeared that additive and dominance component might likely to be confounded due to the presence of correlated gene distribution (Jagtap and Kolhe, 1987).

The estimates of H_1 and H_2 were positive and significant for all the traits. It indicated that there were unequal frequencies of alleles i.e., u≠v at all loci. Further proof for the unequal distribution of alleles over loci was obtained by the ratio of $H_2/4H_1$ which was less than 0.25 with ranged from 0.20 to 0.24 and not equal to 0.25. It implied that the proportions (or) frequencies of positive and negative alleles in the parents were unequal or asymmetrical. The unequal distribution of positive and negative alleles indicated the operation of non-allelic interaction i.e. epistasis. However, these estimates did not permit a determination as to which type of allele occurred more frequently. The component of F due to relative frequency of dominant and recessive alleles showed positive sign and the ratio of $(4DH_1)^{1/2}+ F/(4DH_1)^{1/2} – F$ was more than unity for the traits like days to first male and female flower opening, number of fruits per plant, flesh thickness, vitamin C and acidity content of fruit, revealed the presence of more dominant genes in the parents of these traits. The component of F had negative sign and the ratio of $(4DH_1)^{1/2}+ F/(4DH_1)^{1/2} – F$ due to proportion of dominant and recessive genes was less than unity for the remaining traits fruit length, fruit girth, single fruit weight, fruit yield and number of seeds per fruit, implied the presence of more recessive genes in the parents of these traits.

The number of groups of gene (h^2/H_2) indicated that at least one block of genes influenced the inheritance of all the eleven traits studied. The under estimation of (h^2/H_2) (below one) may be due to the fact that the dominance effects of the genes affecting all the traits, are not equal in size and direction or if the distribution of genes are correlated (Mather, 1949). The heritability in narrow sense was higher for almost all the traits except vitamin C content of fruit. However, the trait Vitamin C content exhibited moderate narrow sense heritability. This indicated the preponderance of additive genetic variance in the inheritance of all the traits studied. The above inference was also supported by the ratio of GCA/SCA and the component D and regression coefficient 'b' from unity for V_r, W_r which also inferred the preponderance of additive genetic variance for almost all the traits. This indicated that the individual genotype can be evaluated readily from their phenotypic expression. Similar results were reported by Sharma *et al*., (1983), Maurya *et al*., (1993) and Pal *et al*., (2004) in bottle gourd. Simple selection would be more effective in the sets of materials exhibiting greater additive genetic variability and desirable mean performance. Thus, it merits selection in the next generation. On the other hand, the non-significant D component for the fruit yield per plant alone may be largely controlled by non-additive genetic variance or the number of genes controlling this character may be more, or this trait may largely be influenced by a large number of modifiers or might be largely influenced by environment. As it is known that yield alone is not a character and it is polygenic and complex trait. However, high GCA variance, high heritability and non significant regression coefficient from unity (b=1) were observed for this trait which indicated the importance of additive genetic variance for fruit yield per plant also.

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