



GRAPHICAL ANALYSIS OF FRUIT YIELD AND ITS COMPONENT CHARACTERS IN SNAKE GOURD (*TRICHOSANTHES ANGUINAL* L.)

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Abstract

A full diallel cross of 6×6 snake gourd pure lines were analyzed, adopting graphical approach. The regression line of V_r , W_r graph intersected the W_r axis well above the origin for the traits fruit length, fruit girth, flesh thickness, single fruit weight and number of seeds per fruit. This indicated the presence of partial dominance in the inheritance of these traits. For the traits viz., number of fruits and fruit yield per plant, the regression line of V_r , W_r graph intersected the W_r axis below the origin. This indicated the existence of over dominance in the inheritance of these traits. The relative value V_r and W_r showed that the high yielding genotypes viz., P_4 - Michaelpalayam local (Dindigul district, Tamil Nadu) and P_1 - Hesaraghatta local (Bangalore, Karnataka) had most dominant genes for fruit yield per plant. The other high yielding genotypes P_2 - Ottanchathiram local (Dindigul district, Tamil Nadu) had most recessive genes for fruit yield per plant. The proximity of the points in V_r , W_r graph revealed sufficient amount of genetic diversity among the parents used in the study.

Key words : Fruit yield, component characters, *Trichosanthes anguina* L.

Introduction

Knowledge of gene actions for various fruit yield and its component characters is a pre-requisite for launching a successful breeding programme in snake gourd. The present article reports information on gene actions for various fruit yield and its component characters in some snake gourd genotypes, employing the graphical approach for diallel analysis (Hayman, 1).

Materials and Methods

The experimental materials comprised of seven genetically diverse genotypes namely, P_1 -Hesaraghatta 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-1 were evaluated in Randomized Block Design with three replications at Department of Horticulture,

Faculty of Agriculture, Annamalai University, Tamilnadu at 2×2 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 F_1 from each replication for nine various characters table 1. Gene actions for various traits were estimated by adopting graphical approach of diallel analysis (Hayman,1).

Results and Discussion

Estimates of the uniformity test t^2 values for V_r , W_r regression were non-significant for all the traits studied table 1. It indicated that the assumptions made by Hayman (1954) were valid for all the traits studied.

Deviation of regression coefficient b for V_r , W_r

Deviation of b from zero was significant for the seven traits namely, number of fruits per plant, fruit length, fruit girth, flesh thickness, single fruit weight, fruit yield per plant and number of seeds per fruit. The deviations of regression coefficients from unity were non-significant for all the eleven traits studied table 3. It indicated that

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Table 1: T^2 value for V_r, W_r regression.

S. No.	Characters	t^2 value
1.	Days to first male flower opening	1.16
2.	Days to first female flower opening	0.87
3.	Number of fruits per plant	0.0002
4.	Fruit length	0.68
5.	Fruit girth	3.60
6.	Flesh thickness	0.87
7.	Single Fruit weight	0.45
8.	Fruit yield per plant	1.06
9.	Number of seeds per plant	0.88
10.	Vitamin C content	0.07
11.	Acidity content	0.35

* - Significant at 5 per cent level.

Table 2: Estimates of Y intercept (a) and Slope (b) of best fitting regression line for ten characters.

S. No.	Characters	$V_r W_r$	
		a	b
1.	Days to first male flower opening	17.73	0.46 ± 0.30
2.	Days to first female flower opening	15.03	0.34 ± 0.29
3.	Number of fruits per plant	-6.46	0.96 ± 0.14
4.	Fruit length	444.22	0.78 ± 0.17
5.	Fruit girth	1.85	0.78 ± 0.01
6.	Flesh thickness	0.003	1.10 ± 0.20
7.	Single Fruit weight	3396.66	1.05 ± 0.22
8.	Fruit yield per plant	-1.41	0.37 ± 0.27
9.	Number of seeds per plant	90.62	0.89 ± 9.12
10.	Vitamin C content	-0.14	0.32 ± 0.41
11.	Acidity content	0.0003	0.12 ± 0.67

Table 3: Significant of deviation of 'b' for W_r/V_r for eleven characters.

S. No.	Characters	$V_r W_r$	
		(b-0)/SE(b)	(b-0)/SE(b)
1.	Days to first male flower opening	1.85	2.16
2.	Days to first female flower opening	1.15	2.28
3.	Number of fruits per plant	7.11**	0.29
4.	Fruit length	4.64**	1.30
5.	Fruit girth	8.41**	2.34
6.	Flesh thickness	5.62**	-0.51
7.	Single Fruit weight	4.87**	-0.23
8.	Fruit yield per plant	2.85*	2.31
9.	Number of seeds per plant	9.78**	1.18
10.	Vitamin C content	0.77	1.65
11.	Acidity content	0.18	1.32

* - Significant at 5 per cent level.

** - Significant at 1 per cent level.

the characters studied had a strong relationship between V_r (variance of each array) and W_r (co-variance between parents and their offspring) of the parental material. This indicated that V_r, W_r graphs

were effective for the genetical studies of the parental materials with respect to the characters of interest other than days to first male and female flower opening, vitamin C and acidity content of fruit. For these traits, the relationship between V_r, W_r were non significant from zero. Hence, the V_r, W_r graphs were not genotype \times environment interactions as suggested by Singh *et al.*, (2001). The regression coefficient of V_r, W_r were non significant from unity for all the traits, indicating that all the traits studied involved additive genes in their inheritance.

Estimates of Y intercept (a) and slope (b) of best fitting regression line

The estimates of y intercept (a) was positive for the traits days to first male and female flower opening, fruit length, single fruit weight and number of seeds per fruit table 2. It indicated that the above mentioned traits involved partial dominance in their inheritance.

The traits namely number of fruits per plant, fruit yield per plant and vitamin c content of fruit showed negative values of Y intercept (a). This indicated that these traits were controlled by over dominance in their inheritance.

However, the characters namely fruit girth, flesh thickness and acidity content of fruit showed the values of Y intercept (a) close to zero. This indicated that these traits were involved by complete dominance in their inheritance. The regression line of V_r, W_r graph intersected the

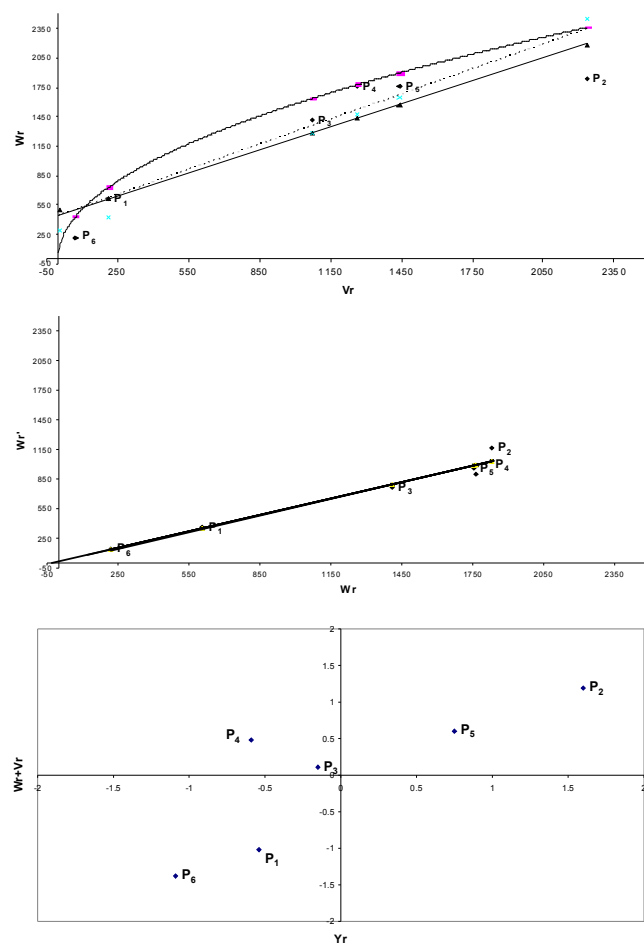
W_r axis above the origin for the traits fruit length and girth, flesh thickness, single fruit weight and number of seeds per fruit. This indicated the presence of partial dominance in the inheritance of these traits. It was supported by the y intercept (a) values.

The regression line of V_r, W_r graph intercepted the W_r axis well below the origin for the traits number of fruits per plant and fruit yield per plant. This indicates the presence of over dominance in the inheritance of these traits. It was also supported by the Y intercept (a) values.

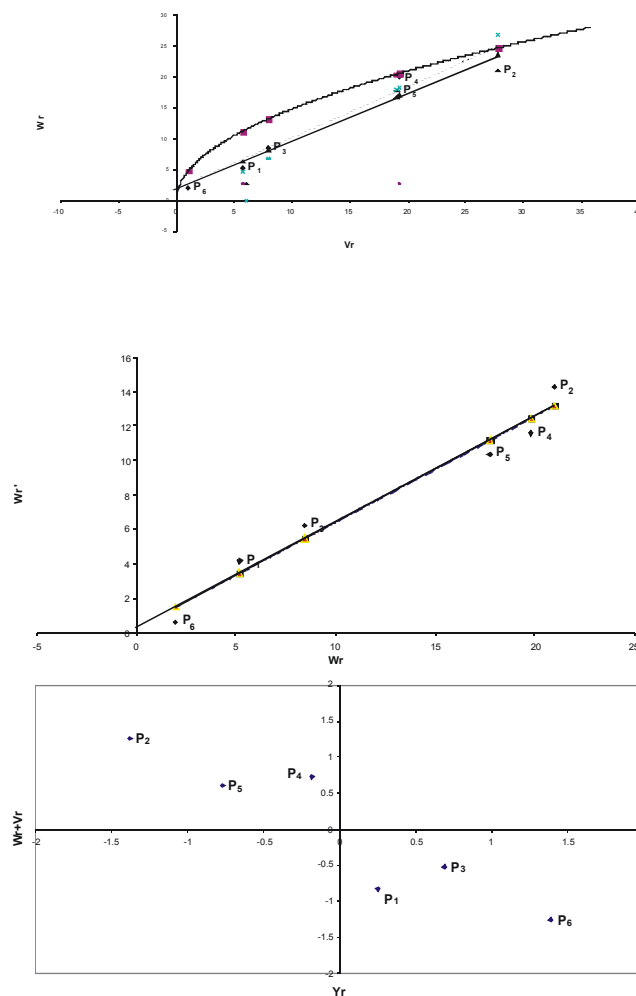
The relative value of V_r and W_r showed that high yielding genotypes *viz.*, P_4 had most dominant genes for fruit yield per plant and number of seeds per fruit, while the P_4 showed most recessive genes for number of fruits, fruit length, fruit girth and single fruit

Table 4: Correlation co-efficient 'r' for Y_r , (W_r+V_r) for eleven characters.

S. No.	Characters	'r'
1.	Days to first male flower opening	0.06
2.	Days to first female flower opening	0.33
3.	Number of fruits per plant	0.76
4.	Fruit length	0.83
5.	Fruit girth	-0.93
6.	Flesh thickness	-0.94
7.	Single Fruit weight	0.66
8.	Fruit yield per plant	-0.53
9.	Number of seeds per plant	0.94
10.	Vitamin C content	-0.61
11.	Acidity content	-0.51

**Fig. 1:** Graphical analysis for fruit length

weight. It has equal frequencies of dominant and recessive genes for flesh thickness. The other high yielding genotype P_1 was endowed with most dominant genes for fruit yield number of fruits, fruit length and fruit girth. It has most recessive genes for number of seeds alone and it had dominant and recessive genes in equal frequencies for the fruit flesh thickness. The third

**Fig. 2:** Graphical analysis for fruit girth

high yielding genotype P_2 was endowed with most recessive genes for fruit yield per plant, fruit length and girth, flesh thickness and number of seeds per fruit, while it had most dominant genes for number of fruits alone. It also had equal frequencies of dominant and recessive genes for single fruit weight.

The hybrids P_4 -Michaelpalayam local (Dindigul district, Tamil Nadu) \times P_2 -Ottanchathiram local (Dindigul district, Tamil Nadu) and its reciprocal, P_4 -Michaelpalayam local (Dindigul district, Tamil Nadu) \times P_5 -PKM-1 (mutant variety, HC&RI, TNAU, Periyakulam), P_2 -Ottanchathiram local (Dindigul district, Tamil Nadu) \times P_4 -Michaelpalayam local (Dindigul district, Tamil Nadu) and its reciprocal and P_1 -Hessaraghatta local (Bangalore, Karnataka), \times P_3 -IC-212484 recorded maximum fruit yield per plant. The pattern of gene distribution for the parents P_4 -Michaelpalayam local (Dindigul district, Tamil Nadu), P_1 -Hessaraghatta local (Bangalore, Karnataka) and P_2 -Ottanchathiram local (Dindigul district, Tamil Nadu) which involved in the above crosses are furnished above. The other parent P_5 -PKM-

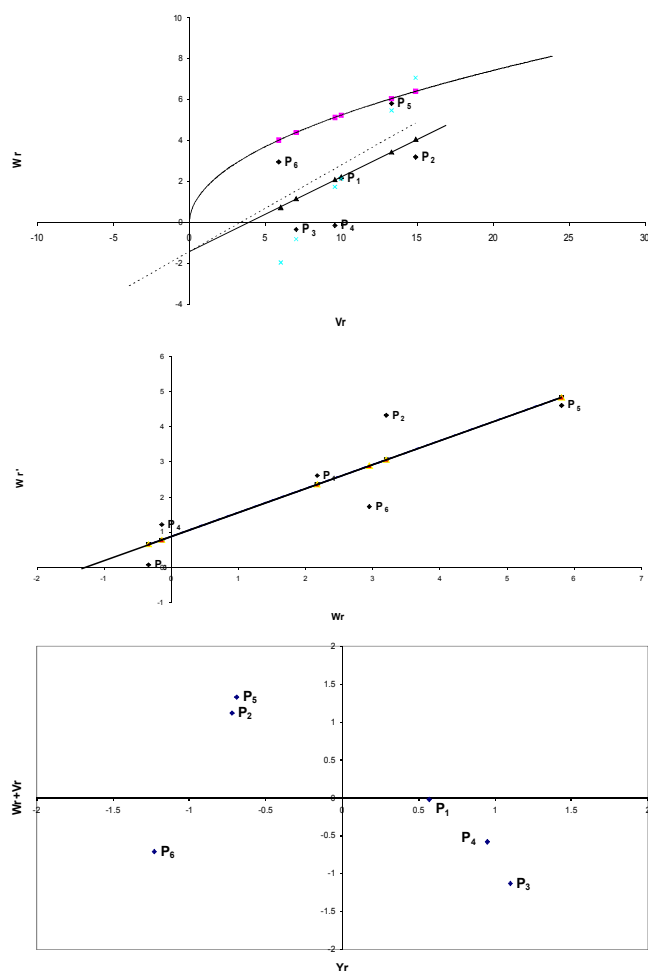


Fig. 3: Graphical analysis for fruit yield per plant

1 (mutant variety, HC&RI, TNAU, Periyakulam) which involved in the above cross was endowed with most recessive genes for fruit yield, number of fruits, fruit length and girth. It had most dominant genes for single fruit weight and number of seeds per fruit. It also had both dominant and recessive genes in equal frequencies for the trait flesh thickness. The another parent P_3 -IC-212484 which involved in the above crosses are endowed with most dominant genes for fruit yield, number of fruits, fruit girth, flesh thickness and number of seeds per fruit while it had most recessive genes for fruit length and single

fruit weight.

This indicated that the distribution of genes in these genotypes were asymmetrical. This asymmetry favors neither high or nor low yield. The F_1 hybrids namely $P_4 \times P_2$ (dominant \times recessive) and its reciprocal (recessive \times dominant), $P_4 \times P_5$ (dominant \times recessive), $P_3 \times P_4$ and its reciprocal (dominant \times dominant) and $P_1 \times P_3$ (dominant \times dominant) could well be utilized for the exploitation of heterotic vigour for fruit yield per plant.

In addition to V_r , W_r graph, the standard deviation graph indicated the direction of effects of dominant or recessive genes in the parents. It almost confirmed the distribution pattern of genes, as inferred from V_r , W_r graph for all the traits.

The correlation coefficients (r) between standardized parental measurements (Y_r) and parental order of dominance ($W_r + V_r$) were non-significant for all the traits studied (Table 4). It suggested that the dominant as well as recessive genes controlled both high and low mean performances.

In V_r , W_r graph, the array points of parents scattered all along the regression line for fruit yield per plant. It was also confirmed by W_r , W_r graph. The same trend was also mostly observed for all other traits in V_r , W_r graph for all the parents. Hence, the parents used in the present study have sufficient amount of genetic diversity. This indicated that the observed heterosis may be partly due to genetic diversity among parents used. Thus, the parents offered a good scope for the inclusion in hybridization programme. Their combinations would offer very good scope for exploiting heterosis for further fruit yield development of snake gourd.

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