

GRAPHICAL (V_r - W_r) APPROACH AND GENETIC COMPONENT ANALYSIS FOR DIALLEL ANALYSIS FOR FRUIT YIELD, YIELD ATTRIBUTES AND OTHER TRAITS IN SNAKE GOURD

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Abstract

A V_r - W_r graphical approach and genetic component analysis study for diallel analysis was carried out on snake gourd for fruit yield, yield attributes along with fruit quality traits at the farm of the Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Bangladesh during March to June 2019. Griffing half-diallel fashion involving seven parents *viz.*, P₁ (TC 01), P₂ (TC 05), P₃ (TC 24), P₄ (TC 33), P₅ (TC 02), P₆ (TC 46) and P₇ (TC 53) were effected to evolve 21 hybrids in snake gourd. The V_r - W_r graphical analysis demonstrated that over dominant gene action mainly responsible for early flowering and higher yield, partial dominant gene action accounted for number of fruits/ plant and complete dominance gene action responsible for fruit flesh thickness and number of seeds/ fruit. Estimates of genetic components such as D, H₁ and H₂ on traits revealed that the predominance of additive components over dominance components was found for fruit length, while for other remaining characters the predominance of dominance effect over additive effects in their expression.. The value $(H_1/D)^{1/2}$ indicated that a partial dominance was observed for fruit length and number of fruits/ plant but over-dominance was observed in the heritance of other characters in the parents. The unequal distribution of positive and negative alleles were found for all the characters. Narrow sense heritability was moderately high in days to 1st male flowering but high in days to 1st female flowering and fruit length, while it was low for other characters, indicating major part of additive gene action was responsible for the 1st three characters. The selection potential for days to 1st male flower open, days to 1st female flower open and fruit length would be high but it would not be high for other traits; therefore, recurrent selection for these three characters in early generation and hybridization and selection-based breeding methods in advanced generations may be effective for improvement of these traits in snake gourd.

Keywords: Snake gourd, Genetic analysis, Diallel graphical analysis, Additive and non-additive gene, Over dominance.

Introduction

Snake gourd [*Trichosanthes cucumerina* var. *anguina* (L.) Haines] is a rapid-growing vine, cultivated for its edible fruits. It is a diploid ($2n = 2x = 22$) annual climber of the genus *Trichosanthes* in the family 'Cucurbitaceae' (Devi, 2017). Snake gourd originated in India or the Indo-Malayan region in tropical Asia

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(Adebooye, 2008 ; Roy *et al.*, 1991) and is widely distributed in Asian countries (Arawwawala *et al.*, 2009; Liyanage *et al.*, 2016; Ojiako *et al.*, 2008). Its green, tender stems, leaves and fruits are consumed as edible vegetables (Devi, 2017; Liyanage *et al.*, 2016), which have high nutritional value, because they are rich in vitamins, essential minerals, dietary fiber and other nutrients, and are a wholesome, healthy addition to diets (Ojiako *et al.*, 2008; Rana and Pandit, 2011). The fruits of snake gourd are frequently consumed when immature.

Being a monoecious and cross-pollinated crop, a wide range of genetic variability exists in the snake gourd population. Thus, by understanding the genetic structure, the heritability and genetic influence of different traits can improve yield (Hallauer *et al.*, 2010). Therefore, breeding programs to produce a new cultivar need more information about the genetic components as well as the type of gene action of traits in order to increase yield and produce tolerant cultivars (Shajari *et al.*, 2021). Horticultural and yield traits of snake gourd are highly environmentally sensitive and regulated by multiple genes, making them quantitatively complex traits with low inheritance. The genetic improvement of snake gourd for fruit yield and yield attributes is imperative in national economy. Diallel analysis is useful breeding tool to predict additive and dominant effects of a population which can then be used to predict the genetic variability and heritability. The combining ability analysis can be conducted using the Griffing Method (Griffing, 1956), whereas, to study the action of genes, genetic components and heritability can use the Hayman Method (Hayman, 1954). In the plant breeding of high yielding varieties of plants, the plant breeder is challenged with the problem of the selection of parents. The knowledge of the genetic architecture of yield will help to sort out the better crosses much efficiently. The present investigation was therefore, carried out to study of genetics and inheritance pattern of fruit yield and yield attributes as well as fruit quality traits by diallel mating design followed by graphical analysis.

Materials and Methods

The experiment was conducted at the experimental farm of the Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh during March to June 2019. The location of the site is 24.09°N latitude and 90.26°E longitude with an elevation of 8.20 m from sea level under agro-ecological zone (Madhupur Tract) AEZ - 28 (Anon., 1995). The experiment was carried out on 7 parents, namely TC 01 (P₁), Tc 05 (P₂), TC 24 (P₃), TC 33 (P₄), TC 02 (P₅), TC 46 (P₆) and TC 53 (P₇). Among the 55 snake gourd genotypes that were collected from different parts of Bangladesh, these 7 parents were chosen based on their performances from an evaluation trial, genetic diversity and heritability. From August to November 2018, 7 parental lines were grown for crossing all the parents together based on the 7 x 7 half-diallel cross with no reciprocals; it produced 21 hybrids with 7 parental lines. The 7 parental lines and their 21 F₁s were grown in a Randomized Complete Block Design (RCBD) with

three replications during summer season (March to June). Each 63 (21 x 3) F₁s and 21 (7 x 3) parents were grown in 84 unit plots measuring 7.5 x 1.5 m², one row of 7.5 long with a plant to plant distance of 1.5 m and a row to row distance of 1.5 m; thus one unit plot accommodated 5 plants. Fifteen days old healthy seedlings were transplanted in well prepared pits on 20 March 2019. Fertilizers were applied @ 5000-50-24-40-14-1.5-1.0 kg/ha of cow dung-N-P-K-S-Zn-B according to FRG (2012). The sources of N, P, K, S, Zn, and B were Urea, Triple Super Phosphate (TSP), Muriate of Potash (MoP), Gypsum, Zinc Sulphate, Boric Acid (Laboratory Grade). During the final land preparation, the entire amount of cowdung, P, S, Zn, B, and one-third of K, as well as N and the remaining part of K were applied in four equal installments at 7, 21, 35 and 49 days after transplantation of seedlings. Plants were supported with the tops of bamboos for twining. The cultural practices such as irrigation, weeding, thinning and gap filling were done as and when necessary. Observations were recorded on 19 quantitative traits viz., days to male flower open, days to female flower open, node number of first male flower open, node number of first female flower open, main vine length (cm), node number on main vine, number of primary branches/plant, days to 1st harvest, fruit fly infestation (%), number of fruits/plant, fruit yield/plant (kg), fruit yield/ha (ton), individual fruit weight (g), fruit length (cm), fruit diameter (cm), fruit flesh thickness (cm), number of locules/fruit, number of seeds/fruit and 100-seed weight (g).

Statistical analysis

This approach utilizes the graphical (Vr-Wr) analysis as well as genetic component analysis to ascertain the role of additive and non-additive type of gene action in the expression of the traits. Based on parental array variance (Vr) and parent-offspring co-variance (Wr) relationships in diallel cross progenies, a two-way representation or distribution of parental arrays along a regression line of Wr on Vr was first suggested by Jinks and Hayman (1953), and later refined by Hayman (1954). This two-directional depiction is widely known as Vr-Wr graph and the analysis as 'graphical approach'. One of the essential factors for the graph, Wri values were computed for all the arrays with the aid of the formula given by Phundhan and Narayanan (2000); $Wri = (Vri \times V_{OLo})^{1/2}$, where, Vri is the variance of rth array and V_{OLo} is the variance of parents. These values (Wri and Vri) were used in constructing the Vr-Wr graph for all 19 characters. By utilizing the regression values, the Wr-Vr graph was drawn for 19 characters studied and the limiting parabola was constructed. The expected values of Wri are needed for drawing the regression line. These Wri values are obtained by the formula: $Wri = Wr - bVr + bVri$ for drawing regression line, where, Vri is array mean of variances, Wr is array mean of covariances and b is regression coefficient. In general, b>0.5 means absence of epistasis and b<0.5 means presence of epistasis (Sharma, 1988). In addition, the genetic analysis was performed using the diallel analysis of Hayman (1954). It provides information about six components viz. D, H₁, H₂, E, F

and h^2 , where, D = additive genetic variance, H_1 = dominance variance, $H_2 = H_1 [1-(u-v)^2]$; where, u and v are the proportions of positive and negative genes, respectively, in the parents, E = expected environmental component of variance, F = mean of F_r over the arrays, where, F_r is the covariance of additive and dominance effects in a single array, h^2 = dominance effect, as algebraic sum over all the heterozygous loci phase in all the crosses. Some genetic ratios were determined from the above estimates. The $(H_1/D)^{0.5}$ ratio was used for showing the average degree of dominance of the loci controlling each trait (if the value of this ratio is zero, there is no dominance; if it is greater than 0 (zero) but less than 1, there is partial dominance; if it is equal to 1, there is complete dominance; and if it is greater than 1, it denotes over-dominance; $H_2/4H_1$ is the proportion of genes with positive and negative effects in parents (if this ratio equals 0.25, positive and negative alleles are symmetrically distributed, otherwise the alleles are asymmetrically distributed; h^2/H_2 denotes the number of gene groups/genes, which control the character and exhibit dominance; $K_d/K_r = [(4DH_1)^{0.5} + F]/[(4DH_1)^{0.5} - F]$ denotes the ratio of dominant and recessive genes in the parents (if the ratio is 1, the dominant and recessive genes in the parents are in equal proportion; if it is less than 1, it indicates an excess of recessive genes; but being greater than 1, it indicates excess of dominant genes. In the F_1 generation, narrow sense heritability values were calculated for each trait from the following relationship:

$$h^2n = \frac{1/4D}{\frac{1}{4(D+H_1-F)} + E} \quad (\text{Crumpacker and Allard, 1962})$$

or

$$h^2n = \frac{[(D+H_1)/2] - 0.5H_2 - 0.5F}{[(D+H_1)/2] - 0.25H_2 - 0.5F + E} \quad \text{Zare et al. (2011)}$$

or

$$\text{Heritability (narrow sense), } h^2n = \frac{1}{2}D / (\frac{1}{2}D + \frac{1}{4}H_1 + E).$$

Results and Discussion

Interpretation of V_r - W_r graph

Direction and Order of Dominance

V_r - W_r graphs, the two dimensional depiction made based on the parent offspring covariance (W_r) and parental variance (V_r) are presented in Fig. 1 to 19. Hayman's graphical approach to half diallel analysis is based on monogenic additive model. The regression coefficients (slope b) were positive and greater than 0.50 for days to 1st male flower open (Fig. 1), days to 1st female flower open (Fig. 2), node number of 1st male flower initiation (Fig. 3), main vine length (Fig. 5), node number on main vine (Fig. 7), individual fruit weight (Fig. 10), fruit yield/plant (Fig. 12), fruit yield/ ha (Fig. 13) and fruit length (Fig. 14), fruit diameter (Fig. 15),

indicating absence of epistasis and less than 0.5 for node number of 1st female flower initiation (Fig. 4), fruit fly infestation (Fig. Fig. 9), fruit flesh thickness (Fig. 16), number of locules/fruit (Fig. 17), number of seeds/fruit (Fig. 18), 100-seed weight (Fig. 19) and indicating presence of epistasis. The regression coefficient (slope b) for number of primary branches per plant (Fig. 6) and days to 1st fruit harvest (Fig. 8) were negative indicating presence of non-allelic interaction i.e. epistasis playing role for these two traits.

The Vr - Wr graph (Fig. 1) for days to 1st male open gave a slope $b = 0.86 \pm 0.20$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line for days to 1st male flower open intersected Wr axis below the point of origin, which suggested over dominance gene action for controlling the trait (Fig. 1). The order of dominance of parent for this character was P₂, P₆, P₇, P₁, P₃, P₄ and P₇. The parent P₂, P₆ and P₇ fell close to the origin and hence provided with maximum frequency of dominant alleles, while the parent P₅ occupied a position furthest away from the origin and thus it contained maximum frequency of recessive alleles. The remaining parents P₁, P₃ and P₄ occupied intermediate position and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominance gene action for days to 1st male flower open in snake gourd. Singh *et al.*, 2019 observed over dominant gene action for this trait in pumpkin.

The Vr - Wr graph (Fig. 2) for days to 1st female open gave a slope $b = 0.87 \pm 0.20$ which was greater than 0.5 but less than 1.0 indicating presence of additive-additive nature of genetic system. The regression line intercepted for Wr axis below the origin which suggested over-dominance gene action to regulate days to 1st female flower open (Fig. 2). The order of dominance of parents to this trait was P₆, P₇, P₁, P₂, P₃, P₄ and P₅. The parents P₆, P₇, P₁, P₂ and P₃ occupied the nearest position to the point of origin, hence possessed maximum frequency of dominant gene for earliness. The remaining parent P₄ had equal proportion of dominant-recessive alleles because their points lying middle in the graph, while the parent P₅ occupied a position furthest away from the origin and thus it contained maximum frequency of recessive alleles. The remaining parent P₄ had equal proportion of dominant-recessive alleles because its point lying middle in the graph. Banik (2003) in snake gourd and Dubey and Ram (2007) in bottle gourd found partial dominance gene action for days to 1st female flower open. Singh *et al.*, 2019 observed over dominant gene action for this trait in pumpkin.

The slope of the regression line for node number of 1st male flower initiation was less than one but greater than 0.5 ($b = 0.84 \pm 0.28$) indicating presence of additive-additive nature of genetic system (Fig. 3). The Vr-Wr graph indicated the regression line intercepted for Wr axis below the origin which suggested over-dominance gene action for the inheritance of node number at 1st male flower initiation (Fig. 3). The order of dominance of parent for this character was P₂, P₁, P₆, P₇, P₃, P₅ and P₄. Array point P₂ was nearer to the origin and contained high

frequency of dominant alleles as it held closest to the point of origin, while P₄ and P₅ were away from the origin contained the maximum frequency of recessive alleles. The remaining parents P₁, P₃, P₆ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominance gene action in snake gourd and Dubey and Ram (2007) observed over dominance gene action in bottle gourd for node order to 1st male flower initiation. Banik (2003) found partial dominance gene action in snake gourd and Dubey and Ram (2007) observed over dominant gene action in bottle gourd for node order to 1st male flower initiation.

The slope of the regression line for node number of 1st female flower initiation, was less than 0.5 ($b = 0.09 \pm 0.39$) indicating absence of additive-additive nature of genetic system (Fig. 4). For node number of 1st female flower initiation, the regression line passed above the origin, indicating the presence of partial dominance gene action for the trait (Fig. 4). The order of dominance of parent for this character was P₆, P₁, P₇, P₃, P₅ and P₄. The parent P₆ occupied the closest position to the point of origin in Vr-Wr graph indicating preponderance of dominant gene, while the parents P₂ and P₄ possessed farthest suggesting recessive gene action for the expression of the trait. The parents P₁, P₃, P₅ and P₇ were at intermediate position suggesting almost equal control of dominant and recessive gene. Banik (2003) found over dominance gene action for node order to 1st female flower initiation in snake gourd.

The Vr - Wr graph (Fig. 5) for main vine length gave a slope $b = 0.65 \pm 0.22$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line for main vine length cut the Wr axis below the point of origin suggesting over dominance gene action (Fig. 5). The order of dominance of parent for this character was P₄, P₃, P₇, P₂, P₅, P₁ and P₆. The parent P₆ was farthest from the origin exhibiting higher proportion of recessive genes, whereas the parent P₄ was closest to the origin as it had highest proportion of dominant genes. The other parents P₁, P₂, P₃, P₅ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found over dominance gene action in snake gourd and Dubey and Ram (2007) observed over dominant gene action in bottle gourd for vine length in bottle gourd.

The Vr - Wr graph (Fig. 6) for number of primary branches per plant gave a slope $b = -0.14 \pm 0.07$ which was less than 0.5 and negative indicating presence of non-allelic interaction i.e. epistasis playing role for this trait. Intersection of regression line above the origin on Wr axis clearly indicated the presence of partial dominance for number of primary branches/ plant (Fig. 6). The order of dominance of parent for this character was parent P₅, P₄, P₁, P₆, P₇, P₂ and P₃. The parent P₃ was farthest from the origin and thus possessed higher proportion of recessive genes, whereas the parent possessed equal number of dominant and recessive genes as it was lying intermediate position. The parents P₅, P₄, P₁, P₆ and P₇ were closest to the origin

and thus it revealed more proportion of dominant genes. Banik (2003) was found partial dominance gene action for primary branches/ plant in snake gourd.

The Vr - Wr graph (Fig. 7) for number of nodes on main vine gave a slope $b = 0.52 \pm 0.22$ which was less greater than 0.5 and less than 1.0 indicating presence of additive-additive nature of genetic system. The regression line for number of nodes on main vine intersected the Wr axis above the origin which revealed partial-dominance gene action to regulate the trait (Fig. 7). The parent P₅ exhibited greater proportion of recessive alleles being furthest from the origin, whereas the parent P₄ exhibited greater proportion of dominant alleles for the trait, being closest to the origin. The remaining parents P₁, P₂, P₃, P₆ and P₇ possessed nearly equal proportion of dominance and recessive genes as they fell nearly in the middle of the regression lines. Dubey and Ram (2007) observed partial dominant gene action in bottle gourd for this trait.

The Vr - Wr graph (Fig. 8) for days to 1st fruit harvest gave a slope $b = -0.03 \pm 0.10$ which was negative indicating presence of non-allelic interaction i.e. epistasis playing role for this trait. The regression line for days to 1st fruit harvest intersected Wr-axis above the point of origin, indicating partial dominance gene action to influence the trait (Fig. 8). The order of dominance of parent for this character was parent P₆, P₇, P₄, P₁, P₃, P₂ and P₅. Parents P₂ and P₅ possessed higher proportion of recessive alleles, being furthest from the origin, whereas parent P₆ revealed more proportion of dominant alleles as it fell nearest to the origin. The remaining parents P₁, P₃, P₄, and P₇ occupied intermediate positions and hence, contained nearly equal frequencies of dominant and recessive alleles. Dubey and Ram (2007) observed partial dominance gene action for days to 1st harvest in bottle gourd. Krishnamoorthy and Marxmathi, 2019 observed similar findings in pumpkin.

The Vr - Wr graph (Fig. 9) for fruit fly infestation gave a slope $b = 20 \pm 11$. The regression line for fruit fly infestation passed through the point of origin, which revealed complete dominance for controlling this trait (Fig. 9). The order of dominance of parent for this character was parent P₃, P₁, P₆, P₇, P₅ and P₄. The parents P₃, P₁, P₆, and P₇ exhibited greater proportion of dominant alleles as they fell closest to the origin, whereas P₄ exhibited greater proportion of recessive alleles for the trait as it occupied a position furthest away from the origin. The remaining P₂ and P₅ possessed nearly equal proportion of dominance and recessive genes as they fell nearly in the middle of the regression lines.

The Vr - Wr graph (Fig. 10) for individual fruit weight gave a slope $b = 0.85 \pm 0.39$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line for individual fruit weight intersected Wr axis below the point of origin, suggesting over dominance gene action for controlling the trait (Fig. 10). The order of dominance of parent for this character was parent P₄, P₅, P₆, P₃, P₇ and P₁. The parent P₄ occupied the nearest position to the point of origin hence possessed maximum number of dominant

genes. On the contrary the parents, the parent P₁, P₇ and P₃ occupied far away from the origin, which indicated that it contained maximum number of recessive genes among them. The other parents P₂, P₅ and P₆ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found over dominance gene action for individual fruit weight in snake gourd. Singh *et al.*, 2019 revealed over dominant gene action for this trait in pumpkin.

The Vr - Wr graph (Fig. 11) for number of fruits /plant gave a slope $b = 0.24 \pm 0.36$ which was less than 0.5 indicating absence of additive-additive nature of genetic system. The regression line for number of fruits/ plant intersected Wr-axis above the point of origin, which implied partial dominance gene action to influence the trait (Fig. 11). The order of dominance of parents for this character was parent P₃, P₁, P₄, P₅, P₆, P₇ and P₁. The parent P₁ and P₃ fell close to the origin and hence provided with a maximum frequency of dominant alleles, while the parent P₂ occupied a position furthest away from the origin, and thus it contained maximum frequency of recessive alleles. The other parents P₄, P₅, P₆ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found over dominant gene action in snake gourd. Dube and Ram (2007) also observed over dominant gene action in bottle gourd for number of fruits/plant.

The Vr - Wr graph (Fig. 12) for fruit yield /plant gave a slope $b = 0.52 \pm 0.26$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line of unit slope intercepted Wr axis below the origin and this suggested over-dominance gene action for controlling fruit yield per plant (Fig. 12). The order of dominance of parents for this character was parent P₁, P₃, P₄, P₅, P₆, P₇ and P₂. None of the parent fell close to the origin and hence not provided with a maximum frequency of dominant alleles, while the parent P₂, occupied a position furthest away from the origin, and thus it contained the maximum frequency of recessive alleles. The other parents P₁, P₃, P₄, P₅, P₆ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominance gene action in snake gourd. Dubey and Ram (2007) observed over dominant gene action in bottle gourd for the yield of fruits/plant. Quamruzzaman *et al.*, 2022 revealed over dominant gene action for this trait in bottle gourd.

The regression of Wr on Vr for yield of fruits/ ha (Fig. 13) gave a slope $b = 0.52 \pm 0.26$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line intersected below the point of origin which indicated the presence of over dominance for this trait. The order of dominance of parents for this character was parent P₁, P₃, P₄, P₅, P₆, P₇ and P₂. None of the parents fell close to the origin and hence not provided with a maximum frequency of dominant alleles, while the parent P₂, occupied a position furthest

away from the origin and thus it contained the maximum frequency of recessive alleles. The other parents P₁, P₃, P₄, P₅, P₆ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Dubey and Ram (2007) observed over dominant gene action in bottle gourd for the yield of fruits/ ha. Quamruzzaman *et al.*, 2022 revealed over dominant gene action for this trait in bottle gourd.

The regression of W_r on V_r for fruit length (Fig. 14) gave a slope $b = 0.94 \pm 06$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line intersected above the point of origin which indicated the presence of partial dominance for fruit length. The order of dominance of parents for the fruit length P₄, P₅, P₇, P₃, P₆, P₂ and P₁. The distribution of array points in the graph suggested that the parental genotypes P₄ and P₅ apparently contained maximum frequency of dominant alleles as they fell more or less close to the origin, while P₁ had the most recessive alleles as it fell far away to the point of origin. The other parents P₂, P₃, P₆ and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominant gene action in snake gourd. Dubey and Ram (2007) observed partial dominant gene action in bottle gourd for fruit length.

The regression of W_r on V_r for fruit diameter (Fig. 15) gave a slope $b = 0.83 \pm 0.39$ which was less than 1.0 but greater than 0.5 indicating presence of additive-additive nature of genetic system. The regression line for fruit diameter intersected W_r axis below the point of origin, which implied over dominance gene action for controlling fruit diameter (Fig. 15). The order of dominance of parent for fruit diameter P₃, P₂, P₂, P₁, P₄, P₆, P₅ and P₇. The parent P₂ and P₃ fell more or less close to the origin and hence provided with a maximum frequency of dominant alleles, while the parent P₅ and P₇ occupied a position furthest away from the origin, and thus it contained maximum frequency of recessive alleles. The other parents P₁, P₄ and P₆ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominance gene action in snake gourd for fruit diameter. Dubey and Ram (2007) observed over dominant gene action in bottle gourd for the same trait. Singh *et al.*, 2019 revealed over dominant gene action for this trait in pumpkin. Krishnamoorthy and Marxmathi, 2019 observed identical findings in pumpkin.

The V_r - W_r graph (Fig. 16) for fruit flesh thickness gave a slope $b = 0.13 \pm 0.26$ which was less than 0.5 indicating absence of additive-additive nature of genetic system. The regression line intersected through the point of origin which indicated the presence of complete dominance for fruit flesh thickness. The order of dominance of parent for the fruit length P₂, P₃, P₅, P₆, P₄, P₇ and P₁. None of the parents fell close to the origin and hence not provided with a maximum frequency of dominant alleles, whereas the parents P₁, P₇, and P₄ occupied a position furthest away from the origin and thus it contained maximum frequency of recessive

alleles. The remaining parents P₂, P₃, P₅ and P₆ were in intermediate position and hence contained more or less equal frequencies of dominant and recessive alleles.

The regression of W_r on V_r for number of locules/ fruit (Fig. 17) gave a slope $b = 0.024 \pm 0.31$ which was far away from 0.5 indicating absence of additive-dominance nature of genetic system. The regression line intersected above the point of origin suggested partial dominance gene action for controlling the trait. The order of dominance of parent for the fruit length P₆, P₁, P₇, P₅, P₂, P₃ and P₄. The distribution of array points indicated that among five parents P₆ and P₁ contained the maximum frequency of dominant alleles as they held the closest position to the point of origin. The parent P₄ contained the maximum frequency of recessive alleles as it occupied a position furthest away from the origin. The other parents P₂, P₃, P₅, and P₇ occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles.

The regression of W_r on V_r for number of seeds per fruit (Fig. 18) gave a slope $b = 0.21 \pm 0.11$ which was less than 0.5 indicating absence of additive-dominance nature of genetic system. The regression line intercepted the W_r axis below the origin in number of seeds per fruit showing a clear cut case of over dominance. The order of dominance of parent for the fruit length P₁, P₇, P₂, P₃, P₅, P₆ and P₄. The relative position of array points on V_r-W_r graph indicated that parental genotypes P₁ and P₇ contained high frequency of dominant alleles as they fell close to the origin. However, both dominant and recessive alleles were approximately of equal proportion in the genetic makeup of the other parents P₂, P₃, P₅ and P₆ for this trait because they occupied intermediate positions and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found over dominant gene action for seeds/fruit in snake gourd. Krishnamoorthy and Marxmathi, 2019 found partial dominance gene action in pumpkin.

The regression of W_r on V_r for 100-seed weight (Fig. 19) gave a slope $b = 0.041 \pm 0.09$ which was less than 0.5 indicating absence of additive-dominance nature of genetic system. For 100-seed weight (Fig. 19) partial dominance was found to control this trait, as the regression line passed above the point of origin. The order of dominance of parent for the fruit length P₅, P₇, P₁, P₂, P₆, P₃ and P₄. The parent P₅ fell close to the origin and hence provided with maximum frequency of dominant alleles, while the parent P₄ occupied a position furthest away from the origin, and thus it contained maximum frequency of recessive alleles. The other parents P₂, P₃, P₆ and P₇ occupied intermediate position and hence contained more or less equal frequencies of dominant and recessive alleles. Banik (2003) found partial dominant gene action for 100-seed weight in snake gourd.

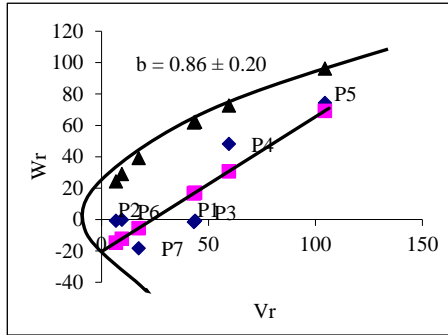


Fig. 1. Vr-Wr graph for days to 1st male flower open.

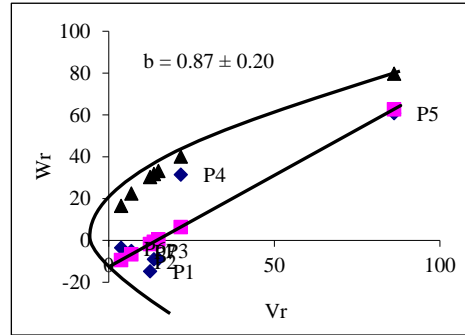


Fig. 2. Vr-Wr graph for days to 1st female flower open.

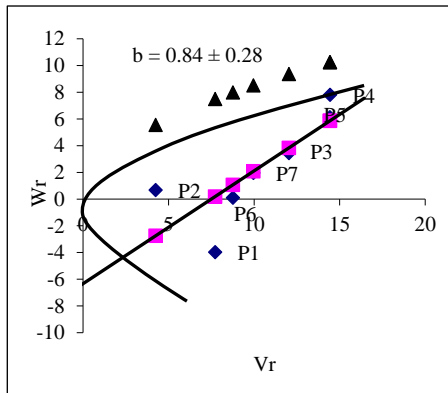


Fig. 3. Vr-Wr graph for node number to 1st male flower initiation.

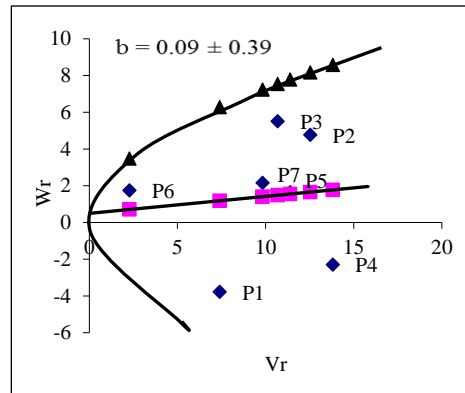


Fig. 4. Vr-Wr graph for node number to 1st female flower initiation.

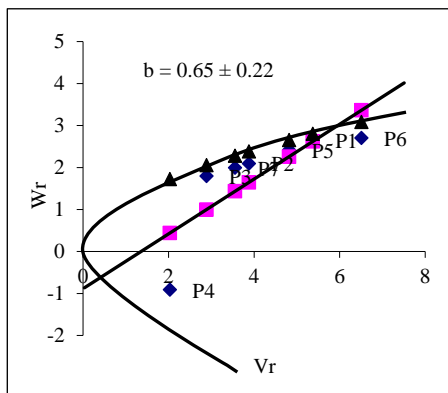


Fig. 5. Vr-Wr graph for main vine length.

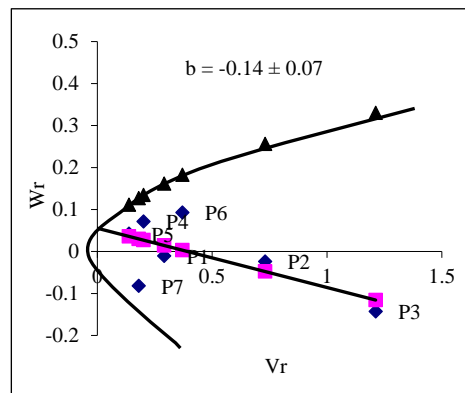


Fig. 6. Vr-Wr graph for primary branches per plant.

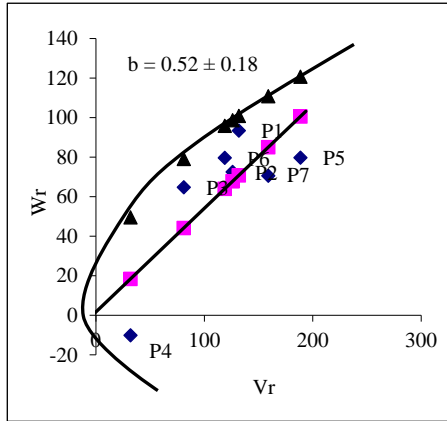


Fig. 7. Vr-Wr graph for nodes on main vine.

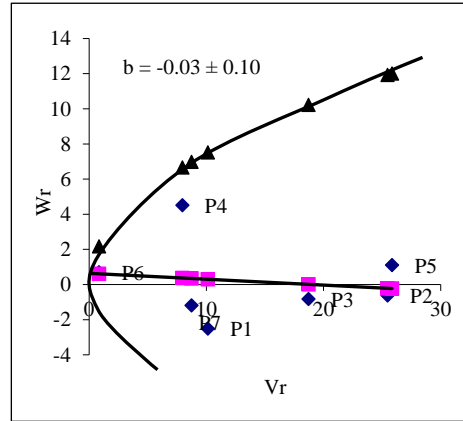


Fig. 8. Vr-Wr graph for days to 1st harvest.

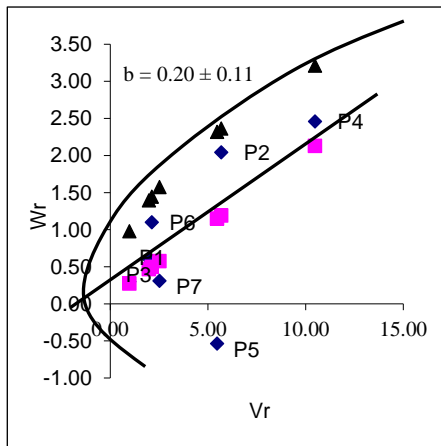


Fig. 9. Vr-Wr graph for fruit fly infestation (%).

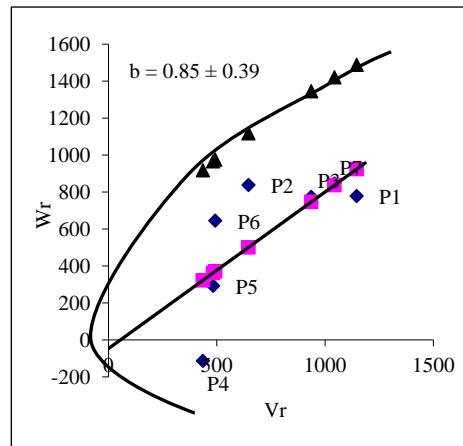


Fig. 10. Vr-Wr graph for individual fruit weight.

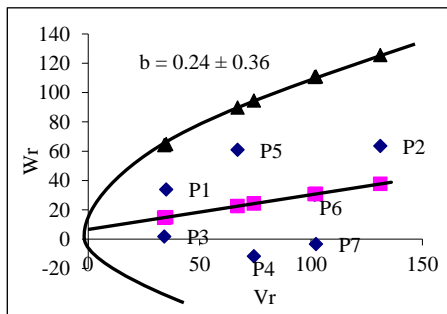


Fig. 11. Vr-Wr graph for fruits per plant.

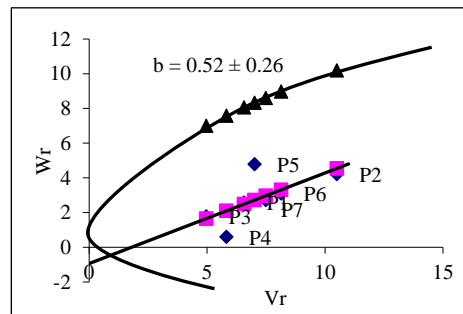


Fig. 12. Vr-Wr graph for fruit yield per plant.

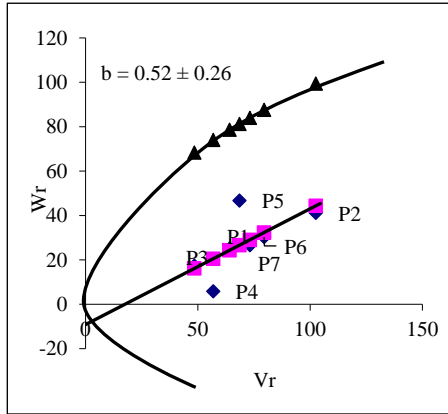


Fig. 13. V_r - W_r graph for yield of fruits per hectare.

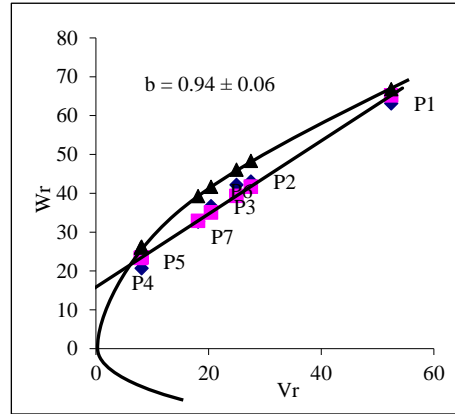


Fig. 14. V_r - W_r graph for fruit length.

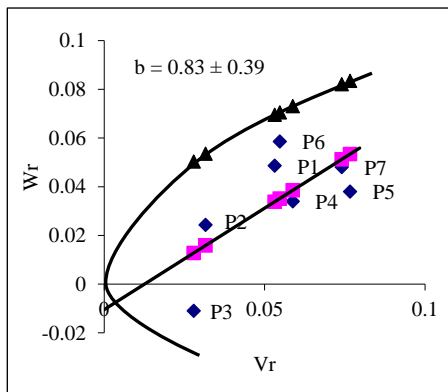


Fig. 15. V_r - W_r graph for fruit diameter.

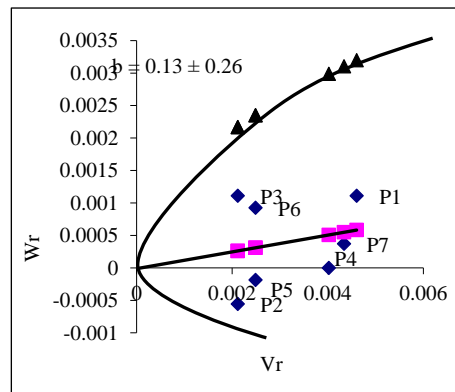


Fig. 16. V_r - W_r graph for fruit flesh thickness.

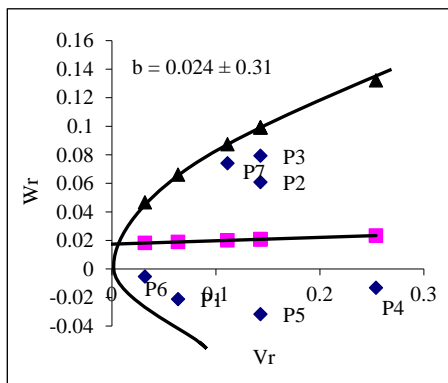


Fig. 17. V_r - W_r graph for locules per fruit.

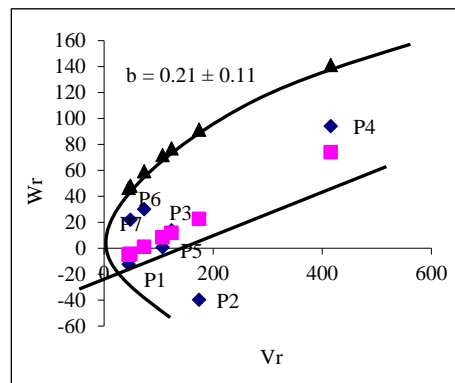


Fig. 18. V_r - W_r graph for seeds per fruit.

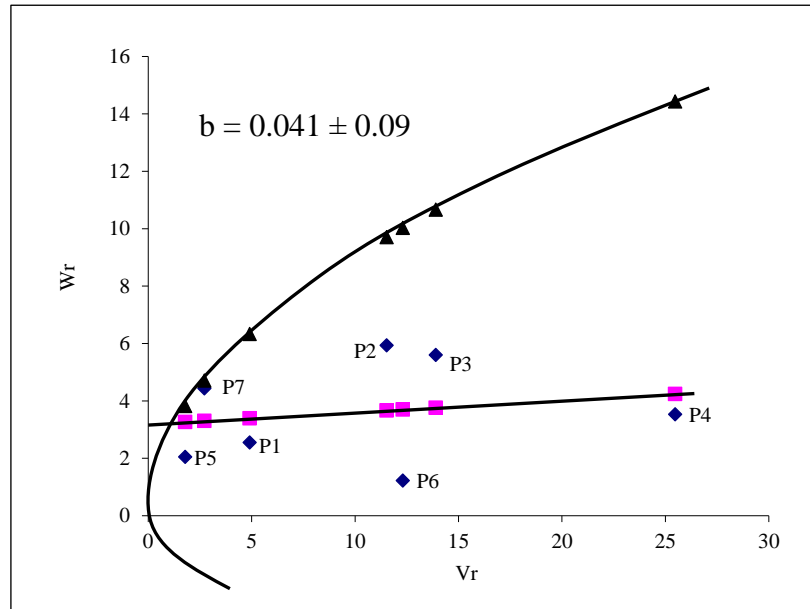


Fig. 19. Vr-Wr graph for 100-seed weight.

Genetic Components

The Influence of Additive (D) and Dominance (H_1)

The component D, which reflect the additive genetic variance was highly significant for all the characters studied, indicating the importance of additive gene effects in their inheritance. The component H_1 , which measures the dominance variation, was highly significant for all the traits (Table 1) indicating the importance of dominance gene effects in controlling them. The estimation of D was higher than H_1 in case of fruit length, indicating the predominance of additive components over dominance components. So that selection based on these traits may be useful for improvement program. However, in other characters viz., days to 1st male flower open, days to 1st female flower open, node number of 1st male flower open, node number of 1st female flower open, main vine length, node number on main vine, number of primary branches/ plant, days to 1st fruit harvest, fruit fly infestation (%), number of fruits/ plant, fruit yield/ plant, fruit yield/ ha, individual fruit weight, fruit diameter, fruit flesh thickness, number of locules/ fruit, number of seeds/ fruit and 100-seed weigh, the estimates of H_1 was higher than D, indicating the predominance of dominance effect over additive effects in their expression (Table 1). Therefore, hybridization may be effective for these traits. The results agreed with the findings of Banik (2003) in the same crop.

Gene Distribution in the Parents

Distribution of genes in the parents can be observed from the value of H_2 . The genes controlling the inheritance of all characters studied were not spread evenly in the parents, because the values of the H_2 against all characters indicated significant differences (Table 1). The proportion of positive genes will be seen from the value of H_1 against H_2 . If $H_1 > H_2$ then the genes were more positive genes, on the other hand, if $H_1 < H_2$ then the genes were more negative genes. Genes involved more heavily in determining all the characters were positive genes reflected in the value of $H_1 > H_2$ (Table 1).

Dominance Level

The amount of dominance effects can be seen from the value $(H_1/D)^{1/2}$. The value $(H_1/D)^{1/2}$ of number of fruits per plant and fruit length was less than one indicating a partial dominance, while the value of $(H_1/D)^{1/2}$ of other remaining characters viz., days to male flower open, days to female flower open, node number of first male flower open, main vine length, fruit yield/ plant, fruit yield/ ha, individual fruit weight and fruit diameter was more than one indicating over-dominance in the heritance of those characters in the parents (Table 1).

Proportion of Dominant to Recessive Genes.

Table 1 shows that all the characters except main vine length, node number on main vine length, fruit fly infestation (%) and 100-seed weight had a value of $K_d/K_r > 1$. This result indicated that the genes were more dominant in these characters, mainly days to male flower open, days to female flower open, node number of first male flower open, node number of first female flower open, number of primary branches/plant, days to 1st fruit harvest, fruit yield/plant, fruit yield/ha, individual fruit weight, fruit diameter, fruit flesh thickness, number of locules/fruit and number of seeds/fruit in the parents. Meanwhile, main vine length, node number on main vine, fruit fly infestation (%) and 100-seed weight had a value of $K_d/K_r < 1$ (0.25, 0.44, 0.52 and 0.80, respectively), showing that the recessive genes were more in the parents.

Distribution of positive and negative alleles

The ratio of $H_2/4H_1$ provides an estimation of the average frequency of positive and negative alleles in all the parents (Table 1). The values of this ratio for all the characters studied were less than i.e. far away from 0.25 indicating unequal distribution of positive and negative alleles.

Number of Genes Controlling Characters.

The degree of controlling genes was reflected in the value h^2/H_2 . The ratio of h^2/H_2 estimates the number of gene or group of genes which control the character

exhibiting the degree of dominance to some extent. The estimated number of factors (h^2/H_2) for all characters studied having this ratios smaller than 1 indicated the involvement of single dominant gene or one group of genes which are responsible for their genetic control (Table 1).

Frequency of dominant and recessive alleles

In the present study, the values of F for all the characters except main vine length, primary branches/ plant, nodes on main vine, percentage of fruit fly infestation and 100-seed weight were positive (Table 1), which expressed that dominant alleles were more frequent than recessive alleles in these characters. In case of vine length, primary branches /plant, nodes on main vine, percentage of fruit fly infestation and 100-seed weight were negative, which expressed that recessive alleles were more frequent than dominant alleles in the character.

Environmental effect

The environmental component E exhibited significant value for all the traits indicating the influence of environmental factors in the expression of those traits (Table 1). However, the magnitude of E for each character was much lower than their respective value of D and H_1 . Such results indicated that the environmental influence upon the character was comparatively lower than that of additive and dominant effects. However, E was higher than D for primary branches /plant and locule number, indicating environmental effects exist on these characters.

Narrow sense heritability

The narrow sense heritability (h^2_n) was found moderately high in days to 1st male flower open (0.54) and high for days to 1st female flower open (0.81) and fruit length (0.91) (Table 1). These values were more than 50% for these characters, indicating major part of additive gene action in phenotypic variability in nature and selection should be effective for improvement of these characters in snake gourd. Estimates of narrow sense heritability were less than 0.5 for node number of first male flower open, node number of first female flower open, main vine length, node number on main vine, number of primary branches/ plant, days to 1st fruit harvest, fruit fly infestation (%), number of fruits/ plant, fruit yield/ plant, fruit yield/ ha, individual fruit weight, fruit diameter, fruit flesh thickness, number of locules/ fruit, number of seeds/ fruit and 100-seed weight, indicating low heritability of these traits. Therefore, given the high contribution of non-additive effect of genes on controlling these traits, selection potential for these traits would not be high; therefore, hybridization and selection based breeding methods in advanced generations may be useful (Zare *et al.*, 2011).

Table 1. Estimation of genetic components of variation and ratios for nineteen traits in snake gourd

Components of variation/ traits	D	H ₁	H ₂	F	h ²	E	(H ₁ / D) ^{1/2}	H ₂ /4H ₁	$\frac{\{(4DH_1)^{1/2} + F\}}{\{(4DH_1)^{1/2} - F\}}$	h ² /H ₂	h ² (ns)
Days to 1st male flower open	88.20** ±0.10	191.84** ±0.23	-41704.59** ±0.20	118.89** ±0.23	-98.019** ±0.13	0.57** ±0.03	1.47	-54.35	2.68	0.002	0.54
Days to 1st female flower open	73.41** ±0.08	134.57** ±0.19	-46987.69** ±0.17	117.82** ±0.19	-102.72** ±0.11	0.44** ±0.03	1.35	-87.29	3.91	0.002	0.81
Node number to 1 st male flower initiation	6.55** ±0.01	36.98** ±0.03	-2368.25** ±0.03	4.31** ±0.03	-20.03** ±0.02	0.73** ±0.01	2.38	-16.01	1.32	0.008	0.16
Node number to 1 st female flower initiation	3.84** ±0.03	34.52** ±0.07	-5022.15** ±0.06	2.95** ±0.07	-25.98** ±0.04	1.49** ±0.01	3.00	-36.38	1.29	0.005	0.09
Vine length (m)	1.34** ±0.01	10.44** ±0.01	-680.03** ±0.01	-4.53** ±0.01	-7.13** ±0.01	0.12** ±0.002	2.79	-16.28	0.25	0.01	0.08
Primary branches per plant	-0.07** ±0.003	1.47** ±0.006	-212.09** ±0.006	-0.02* ±0.006	-5.60** ±0.004	0.16** ±0.001	-4.55	-36.13	1.06	0.03	-0.03
Nodes on main vine	71.45** ±0.18	282.23** ±0.45	-37707.65** ±0.40	-111.27** ±0.45	-70.55** ±0.27	5.83** ±0.07	1.99	-33.4	0.44	0.002	0.146
Days to 1 st harvest	4.96** ±0.06	59.02** ±0.14	-68901.15** ±0.13	9.59** ±0.14	-126.1** ±0.08	0.63** ±0.02	3.45	-291.88	1.78	0.002	0.087
Fruit fly infestation (%)	0.73** ±0.02	13.41** ±0.04	-381.93** ±0.03	-1.98** ±0.04	-6.25** ±0.02	0.25** ±0.006	4.28	-7.12	0.52	0.02	0.04
Individual fruit weight (g)	1911.52** ±1.54	2511.73** ±3.71	-647512.5** ±3.26	1515.59* ±3.69	-302.11** ±2.19	23.03** ±0.54	1.15	-64.45	2.06	0.001	0.64

Components of variation/ traits	D	H ₁	H ₂	F	h ²	E	(H ₁ / D) ^{1/2}	H ₂ /4H ₁	$\frac{\{(4DH_1)^{1/2} + F\}}{\{(4DH_1)^{1/2} - F\}}$	h ² /H ₂	h ² (ns)
Number of fruits/ plant	117.42** ±0.23	323.72** ±0.56	-31933.31** ±0.50	136.31** ±0.56	-73.92** ±0.33	2.97** ±0.08	1.66	-24.66	2.07	0.002	0.37
Fruit yield/ plant (kg)	9.73** ±0.01	27.02** ±0.02	-1515.92** ±0.02	8.25** ±0.02	-12.16** ±0.01	0.15** ±0.002	0.15	-14.02	1.68	0.008	0.33
Fruit yield/ ha (t)	95.06** ±0.8	263.88** ±0.19	-14803.95** ±0.16	80.54** ±0.19	-38.50** ±0.11	1.46** ±0.03	1.67	-14.02	1.68	0.003	0.33
Fruit length (cm)	84.23** ±0.01	24.69** ±0.03	-17692.81** ±0.03	19.78** ±0.03	-60.51** ±0.01	0.88** ±0.005	0.54	-	1.55	0.003	0.91
Fruit diameter (cm)	0.08**	0.15** ±0.0002	-235.76** ±0.0002	0.03** ±0.0002	-6.91** ±0.0002	0.008**	1.33	-	1.35	0.029	0.36
Fruit flesh thickness (cm)	0.002**	0.012**	-4.180**	0.002**	-0.876**	0.001**	2.69	-89.77	1.59	0.21	0.117
Locules/Fruit	0.030**	0.391** ±0.001	-149.38** ±0.001	0.001 ±0.001	-5.08**	0.038**	3.58	-95.49	1.01	0.034	0.053
Seeds/ fruit	39.19** ±0.62	525.81** ±1.49	-48863.1** ±1.31	21.50** ±1.49	-79.82** ±0.88	8.81** ±0.22	3.66	-23.23	1.16	0.002	0.07
100-seed weight (g)	5.05** ±0.05	26.69** ±0.11	-11627.1** ±0.10	-2.59** ±0.11	-49.93** ±0.07	3.13** ±0.02	2.30	-	0.8	0.004	0.11

** Significant at 1% level, * Significant at 5% level, Without star indicates non-significant, h² (ns)= heritability in narrow sense

Conclusion

Hayman's graphical approach to diallel analysis is based on monogenic additive model. The regression line for days to 1st male flower open, days to 1st female flower open, node number of 1st male flower initiation, main vine length, individual fruit weight, fruit yield/ plant/ ha, fruit diameter and number of seeds/ fruit were below the origin indicating the presence of over-dominance, while for node number of 1st female flower initiation, number of primary branches/ plant, days to 1st fruit harvest, number of fruits/ plant, fruit length, number of locules/ fruit and 100-seed weight was above the origin suggesting the presence of partial dominance. The regression lines for nodes on main vine, fruit flesh thickness and fruit fly infestation percentage were through the origin indicating the presence of complete dominance. The additive component (D) and dominance component (H₁) of genetic variance were found highly significant for all the characters. The estimation of narrow sense heritability is a very useful selection parameter in plant breeding. It was found moderately high for days to 1st male flower open (0.54) and high for days to 1st female flower open (0.81) and fruit length (0.91). For other characters narrow sense heritability was found low. Based on this genetic information in this study, hybridization, selection-based breeding method, evaluation and isolation of superior genotypes in advanced generation are suggested for snake gourd crop improvement.

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