



# Graphical Analysis (Vr-Wr) for Fruit Yield and Its Component Traits in Eggplant

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**Abstract:** The objectives of this study were to determine the gene action in all the way for fourteen fruit yield and biochemical traits in eggplant that can be used in targeted breeding program. The experiment was conducted at Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, (SKUAST-J), Jammu, India. A total 29 progenies including the seven parental lines, 21 hybrid F<sub>1</sub>'s generated through 7 × 7 half diallel mating design, and one standard check were arranged in a randomized complete block design. The results demonstrated that existence of both additive and non-additive genetic variation for the inheritance of most of the studied traits. The Vr-Wr graphical analysis exhibited that higher proportion of dominance alleles for days to 50% flowering, days to first picking, fruit girth, fruit weight, branches per plant, plant height, fruit yield per plant, ascorbic acid content and total phenol content. The higher proportion of recessive alleles recorded for number of fruits per cluster, fruit length, number of fruits per plant and crop duration.

**Keywords:** *Solanum melongena* L., Half diallel, Genetic analysis

Eggplant is a versatile vegetable crop and has been widely cultivated in India as well as in the world (Rani et al 2018). Aside from being observed as an important vegetable crop, it is exploited for medicinal purposes owing to its high antioxidant properties viz., anthocyanins, phenolic compounds and alkaloids that have beneficial effects on human health (Mistry et al 2016, Dranca and Oroian 2017). It is an economic crop that provides a great income source for small-scale farmers globally (Datta et al 2021). Most of the inter-varietal F<sub>1</sub> hybrids of eggplant exhibited considerable vigor in economic traits; mainly fruit yield (Kaushik et al 2018). The parental selection to get high yielding hybrid F<sub>1</sub>'s is most important footstep in any crop breeding program (Boyaci et al 2020). Genetic analysis furnishes a direction for the appraisal of relative breeding potential of the genitors or identifies best combiners (Akpan et al 2016). Diallel analysis assists in understanding the genetic control of trait, which escort crop breeder to forward and select segregating generations. The nature of gene action involved in the inheritance of different traits is most important to decide the breeding strategy for improvement of the crop (Meena et al 2020). It could be estimated by graphical approach (Vr-Wr graph). The graphical statistic offers an estimate of the associate number of dominance to recessive genes existing in the common arrays of the parents, with the Vr and Wr statistics, calculated from diallel tables, graphs can be drawn and the geometric representation of these statistics could be

interpreted. The position of the regression line in the graph indicates the degree of dominance and assembles parabola limits in the graph. The elucidations of graphical analysis results are simple and genuine if the principal assumptions of the diallel analysis are fulfilled (Hussain et al 2018, Patel and Kathiria 2018). Thus, the current research was conducted with the objective to assess the gene action in all the ways for various horticultural traits to provide appropriate information that could be utilize in the eggplant breeding programs aimed at improving fruit yield and its components.

## MATERIAL AND METHODS

Seven genetically diverse parental lines of eggplant viz., Pusa Purple Cluster (PPC), IC 261797, IC 261767, IC 354611, IC 203585, IC 104101 and IC 310886 (received from National Bureau of Plant Genetic Resources, New Delhi, India) were included in the research. Twenty F<sub>1</sub> hybrids were generated through 7 × 7 half diallel mating design (excluding reciprocals) at Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, (SKUAST-J), Jammu, India. The resultant 21 F<sub>1</sub> hybrids along with their parents and one standard check (Pusa Hybrid-5) were arranged in randomized complete block design with three replications. The seedlings were transplanted on ridges, and the row × the plant spacing was maintained at 75 cm × 60 cm. Standard cultural practices, such as fertilization, irrigation, weeding, diseases and insect-pests control were performed

whenever required (Anonymous 2016). Fourteen fruit yield and biochemical traits were studied by recording observations on five plants from each replication. The traits included plant height (cm), number of primary branches per plant, days to 50% flowering, days to first picking, number of fruits per cluster, fruit length (cm), fruit girth (cm), number of fruits per plant, average fruit weight (g), crop duration (days from transplanting to final harvesting of fruits), fruit yield per plant (g), total fruit yield (q/ ha ), ascorbic acid content (mg/ 100 g) and total phenols content (mg/ 100 g). The graphical analysis was done according to Hayman (1954). The data collected were analyzed by using computer software Windostat (Indostat services Ltd. Hyderabad, India).

### RESULTS AND DISCUSSION

The estimates of component of analysis indicated significant additive (D) and non-additive ( $H_1$  and  $H_2$ ) effects were observed for days to 50% flowering, days to first picking, number of fruits per cluster, fruit length, fruit girth, plant height. Non-additive ( $H_1$  and  $H_2$ ) effects were higher in magnitude than additive (D) effects. The graphical analysis (Vr-Wr) of research data recorded in order to get knowledge on allelic constitution of parents utilized in diallel cross. In the current study, the regression coefficient (b) was non-significant for all the traits depicting presence of non-allelic interactions, and the results of studied traits presented as Vr-Wr graphs (Figs. 1-8). The  $t^2$  values were not significant for any of the characters hence the basic assumptions of diallel analysis are fulfilled and were further analyzed. Hayman's approach known as graphic analysis based on variance-covariance matrices (Vr-Wr) was used for testing the validity of assumptions of diallel analysis. Graphical analysis depicted partial dominance for all the traits except for days to first picking and average fruit weight for which no dominance was recorded. The graphical analysis revealed partial dominance as the regression line intersected the Wr-axis above the point of origin. Scattering of array points along the regression line indicated wide genetic diversity among parents for the studied traits. The graphical analysis revealed no dominance for days to first picking and average fruit weight as the regression line did not intersect the Wr-axis. The relative position of the parental points along the regression line indicated the distribution of dominant and recessive genes in the parents. The location of array points nearer to the point of origin and far away from the point of origin suggested higher proportion of dominant and recessive genes in the parents, respectively. The line of regression intercepted Wr axis passed below the origin indicating the presence of over-dominance in the control of expression of the respective trait. For days to 50% flowering, parent IC 261767 had excess of

dominant genes and IC 203585 had excess of recessive alleles, while all other parents had more or less equal proportion of dominant and recessive genes. Parent IC 261797 having mostly recessive genes for days to first picking as it was lying far from the point of origin. The rest of the parents possessed almost equal proportions of dominant and recessive genes. For number of fruits per cluster, the parent IC 261767 exhibited maximum frequency of dominant genes being nearest to the origin point. However, IC 354611 had the greater number of recessive genes, being farthest from the origin; and remaining parents had mostly equal proportion of dominant and recessive genes. Distribution of parental arrays near to the regression line exhibited that parent IC 104101 had more number of dominant genes for fruit length while rest all the parents were having recessive genes as they are lying away from the point of origin. For Fruit girth, parent IC 261767 had higher number of dominant genes. While all other parents had maximum frequency of recessive genes except for PPC which was having more or less equal proportion of dominant and recessive genes. The parent IC 203585 and PPC had high number of dominant genes and remaining all the parents were having recessive genes, as they were lying far away from point of origin for average fruit weight. In case of number of fruits per plant, all the parents had balanced proportion of dominant and recessive genes, as they were lying far away from the point of origin. For primary branches per plant, parent IC 261797, IC 354611, PPC and IC 104101 had more number of dominant genes, as they were lying close to the point of origin. Rests of the parents were having maximum number of recessive genes.

Parents Pusa Purple Cluster, IC 354611, IC 104101 and IC 261767 had excess of dominant genes for plant height, whereas, rest of the parents had greater number of recessive genes. The distribution of parental arrays along the regression line suggested that IC 310886 and IC 104101 had the maximum number of dominant genes, and the parent IC 261767 and IC 203585 had the maximum number of recessive genes for crop duration. The rest of parents had more or less equal proportion of dominant and recessive genes. For fruit yield per plant, the parent IC 104101 had maximum number of dominant genes as it was found near the point of origin. Rests of the parents carried the maximum number of recessive alleles being farthest from the origin. The parents IC 310886 and IC 203585 had more recessive genes for ascorbic acid content as they were lying far from the point of origin and remaining parents were having more or less equal proportion of dominant and recessive genes. For total phenol content (mg/100g), the parents IC 261767, IC 354611 and IC 310886 possessed more number of dominant genes,

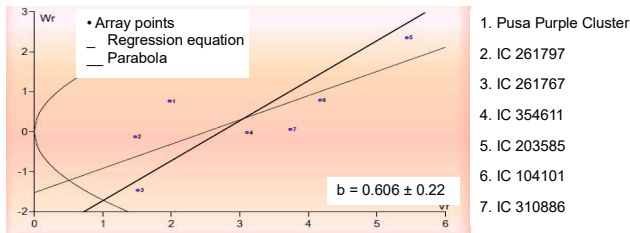


Fig. 1. Vr-Wr graph for days to 50% flowering

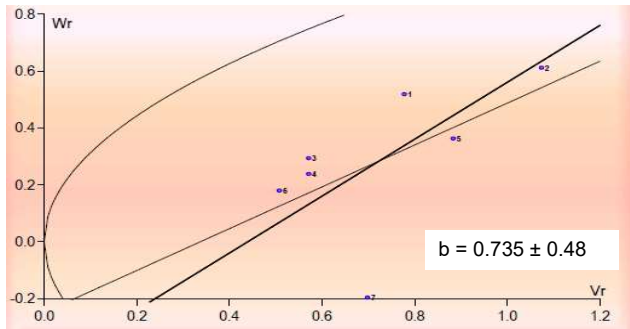


Fig. 2. Vr-Wr graph for days to first picking

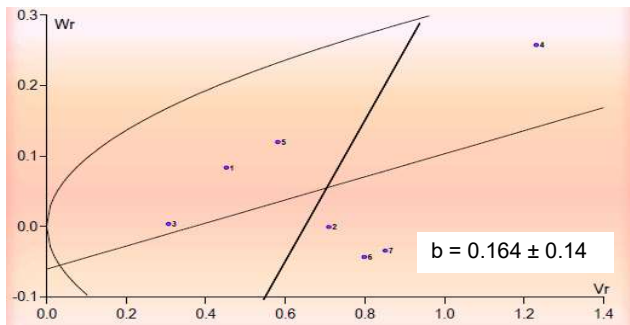


Fig. 3. Vr-Wr graph for number of fruits per cluster

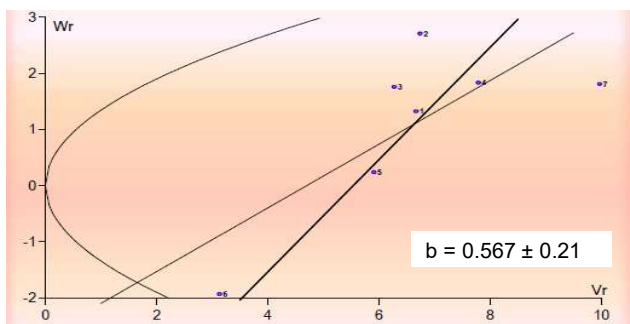


Fig. 4. Vr-Wr graph for fruit length (cm)

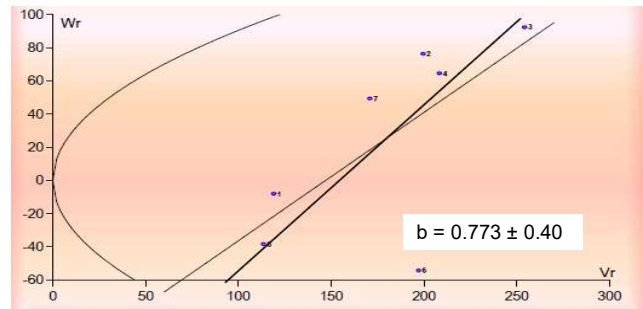


Fig. 5. Vr-Wr graph for average fruit weight (g)

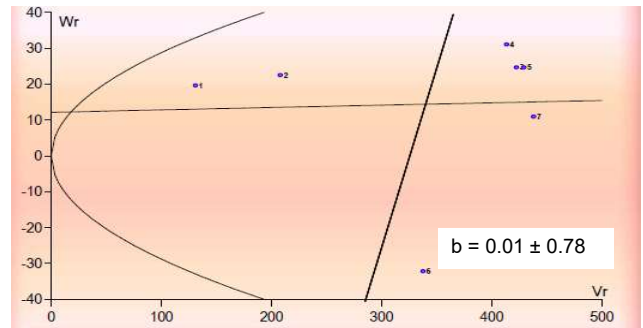


Fig. 6. Vr-Wr graph for number of fruits per plant

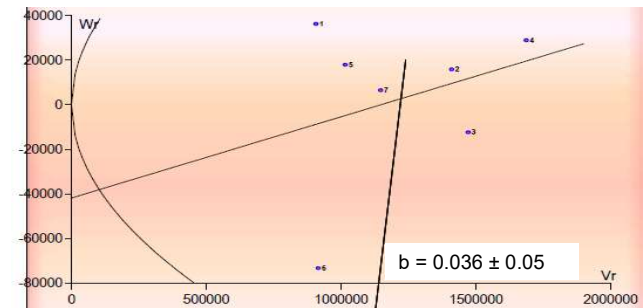


Fig. 7. Vr-Wr graph for fruit yield per plant (g)

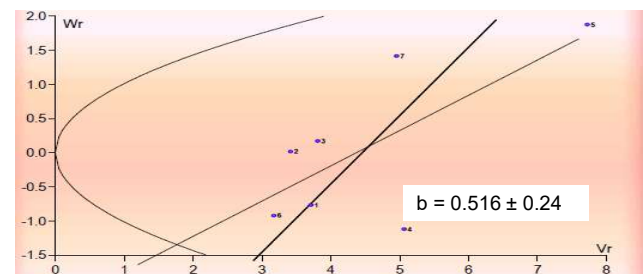


Fig. 8. Vr-Wr graph for ascorbic acid content (mg/100g)

and maximum number of recessive genes was shown by IC 104101. The parents namely Pusa Purple Cluster, IC 261797, IC 203585 and IC 310886 which had a balanced proportion of dominant and recessive genes. Most of the findings results have also been corroborated with observation of Biswajit et al (2004), Quamruzzaman et al (2006), Samlindsujin et al (2020) for various traits in eggplant.

**CONCLUSIONS**

In the current study, the estimates of component of analysis indicated significant additive and non-additive effects were observed for days to 50% flowering, days to first picking, number of fruits per cluster, fruit length, fruit girth, plant height. The regression coefficient (b) was non-significant for all the traits depicting presence of non-allelic interactions. Graphical analysis depicted partial dominance for all the traits except for days to first picking and average

fruit weight for which no dominance was recorded. The parents possessed higher proportion of dominant genes than recessive ones for all the traits except for number of fruits per cluster, fruit length, number of fruits per plant and crop duration.

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