



Research Article

COMPARATIVE STUDY OF COMPONENT AND GRAPHICAL ANALYSIS STUDIES FOR VARIOUS YIELD AND QUALITY TRAITS IN TOMATO (*Lycopersicon esculentum* Mill)

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Abstract- The study in a diallel fashion involving twelve parents and their sixty-six cross combinations was conducted at Vegetable Research farm of CCS HAU, Hisar during January to May, 2004. Observations were recorded on twenty-three yield and quality traits. The study revealed significant genotype differences for all characters except juice: pulp ratio and seed: pulp ratio. Significant variances due to general combining ability, and specific combining ability were observed for most of the characters. These estimates suggested the importance of both additive and non-additive gene action for the control of the characters investigated. Over dominance was observed for all the traits except number of seeds, total carotenoides and lycopene content for which partial dominance and complete dominance was observed respectively. The preponderance of additive and non-additive gene actions for yield, its components and quality parameters greatly suggested for both selection and heterosis breeding for the improvement of tomato crop.

Key words - Diallel, gene action, tomato, Inheritance, yield, quality.

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Introduction

Detailed information concerning the genetic control of the characters under selection is important if plant breeders are to conduct their programme efficiently by the choice of appropriate parents and selection methodology. Moreover, it is highly desirable that the information is obtained under the same conditions where selection is to take place. A breeding effort was initiated at CCH HAU, Hisar in 2003 and 2004 to complement existing programme, with the aim of producing hybrids of tomato (*Lycopersicon esculentum* Mill.) with particular emphasis as production problems and consumer preference including high yielding varieties having greater fruit number, weight, earliness, fruit size, other yield components and quality traits. The present diallel study was conducted to assist the breeding of high yield cultivars with better quality. A considerable number of diallel studies have been reported in tomato. Most have been heterosis and combining ability analysis since the development of commercial Knowledge of genetic architecture of the characters under improvement is essential for adopting appropriate breeding procedure. Such knowledge leads the plant breeder to develop new commercial varieties of the crop. Gardner (1963) stressed that information on variation attributable to genetic differences and also on the relationship among various quantitative traits is fundamentally significant in a crop improvement programme [1].

Therefore, the present study was undertaken with the objective to determine the mode of gene action in governing characters under high temperature stress. In addition, the accumulation of information in the literature is of considerable assistance with planning, executing and analyzing diallel experiments.

Materials and Methods

The twelve diverse genotypes of tomato (*Lycopersicon esculentum* Mill.) were chosen as representing a fixed sample of the best germplasm available for a range of characters of commercial importance, including yield, related components and quality traits. The parents were crossed by hand, reciprocal hybrids were excluded. The seeds of diallel set of crosses attempted, and selfed parental lines during February to March, 2003 and harvested in May, 2003 were sown in nursery beds on 20th November, 2003. The 40 days old seedlings were transplanted in the field on 10.01.2004. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Plot size was 60 cm spaced single rows of 3.15 m length for each genotype accommodating 7 plants spaced 45 cm from each other. In order to guard against the risk of frost injury, nursery was protected with white transparent polythene sheet till these were hardened enough for transplanting in the field. All other recommended cultural practices for the crop were followed. The parental (12 lines) and F₁ (66 lines) was grown in a furrow irrigated experiment at Vegetable Research Farm of CCS, HAU, Hisar, India, at an altitude of 215.2 metre above mean sea level and 29°10' N latitude north and 75°46' longitude east in spring summer 2004. The experiment received standard agronomic practices. The experiment consisted of three randomized complete blocks with 78 treatments consisting of 12 parents and 66F₁ hybrids. Genetic analysis of diallel data for graphical approach (Wr-Vr graph) as well as genetic components of variation was according to method of Hayman [2,6]. Plotting of Wr-Vr graph was done with the help of sigma plotting package.

Table 1 Following parents were included in the experiment

Name of Variety	Parent(s)/Source	Important characters
1. EC 31767	NBPGR	Indeterminate; small cherry round fruits
2. H 36	Hisar	Determinate; Medium round fruits
3. Pusa Ruby	Sioux and improved Meeruti (IARI)	Indeterminate; Early; Fruits flattened, grooved and medium sized
4. Punjab Chhuhara	EC 55055 and Punjab Tropic (PAU)	Determinate; Dwarf; High yielding; Pear Shaped Fruits; Thick Pericarp
5. Yashwant -A-2-8	Solan	Indeterminate; small cherry type orange round fruits
6. LA 1420	"P1379052" <i>L. esculentum</i> var. <i>cerasiforme</i>	Indeterminate; small cherry type orange round fruits; fruits with 2-3 locules, 2 cm in diameter, Red.
7. Merrol	Punjab, PAU	Determinate; Dwarf; High yielding; egg Shaped Fruits; Thick Pericarp
8. Sel-7 (Hisar Arun)	Pusa Early Dwarf and K1 (Hisar)	Determinate; Early; Dwarf; High yielding; Medium to Large Fruits; Round deep Red.
9. New Wonder	United States	Indeterminate; Medium to Large Fruits; Round deep Red.
10. Sel-15	Hisar	Determinate; High yielding; Medium to Large Fruits; Round deep Red.
11. Sioux	All Red and Stokesdale	Indeterminate; Medium late Maturity; Fruits Round Smooth Red.
12. Cul 29	Coimbatore	Determinate; Medium to Large Globular Fruits

The first three assumptions of the additive/ dominance genetic model underlying an analysis of the diallel cross (3) were tested as follows:

(1) diploid segregation; (2) homozygous parents each parent was maintained by inbreeding and was assumed to be homozygous; and (3) no reciprocal differences. The remaining assumptions of the simple additive dominance genetic model (4) are (4) independent effect of non- allelic genes (i.e. no epistasis); (5) no multiple allelism and (6) genes independently distributed between parents.

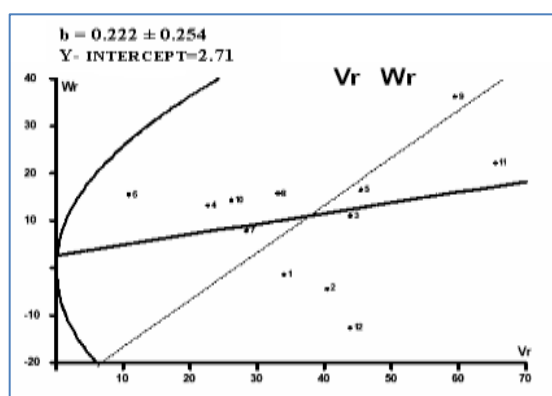
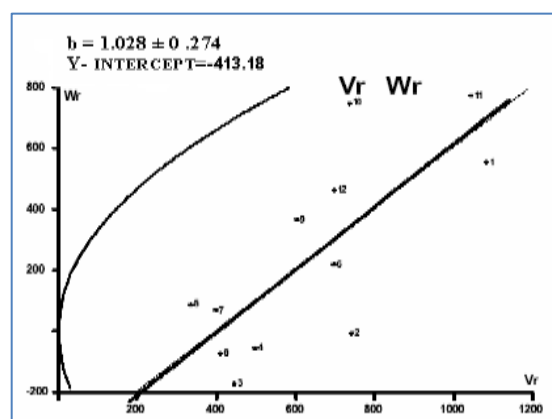
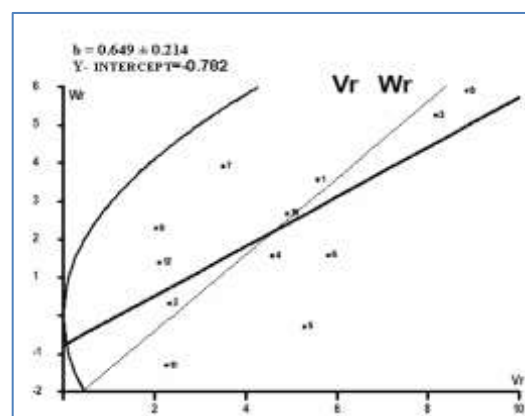
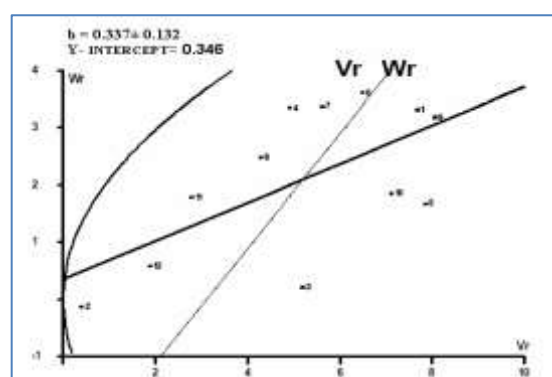
Result and Discussions

For obtaining information about allelic constitution of the parents used in diallel cross, Graphical analysis was recorded. In the present study, regression coefficient values (b , w_r , v_r) for twenty three characters viz; Days to 50% flowering, Plant height (cm), Number of branches per plant, Number of flower clusters per plant, Number of fruit per truss, Number of fruits per plant, Fruit size (length/breadth ratio), Fruit weight (g), Early fruit yield of first two pickings (Kg), Total fruit yield (Kg), Number of locules per fruit, Pericarp thickness (mm), Number of seeds per fruit, Dry matter content (%), Juice : pulp ratio, Seed : pulp ratio, Total soluble solids (%), Total Sugars (%), Reducing sugars (%), Titrable acidity (g of citric acid/100 ml of juice), Ascorbic acid (mg/100 g of fruit), Total carotenoides (mg/100 g of fruit) and Lycopene content (mg/100 g of fruit) did not differ significantly from unity indicating the absence of epistasis and hence fulfill the assumption that epistasis is absent for these characters. The W_r - V_r graphs for these characters have been presented in Figures [Fig-1-11]. But for the rest characters regression value differs significantly. So, for these characters epistatic gene action may be present. For almost all the characters, the parental array points were scattered all along the regression line in the W_r - V_r graph. This indicates the genetic diversity among the parents for all the traits studied. Distribution of array points in W_r - V_r graph also decides relative proportions of dominant and recessive alleles present in parent.

Test of homogeneity

Hayman's homogeneity test i.e., t^2 - test of W_r - V_r indicated that for all the characters except number of fruits per truss, number of locules per fruits, pericarp thickness, juice-pulp ratio, seed-pulp ratio, Titrable acidity, TSS and reducing sugars, the array mean squares were not significant at 0.05 probability level [6]. This indicated the probability fulfillment of the postulated hypothesis. The

characters for which t^2 - test significant suggested that some of the postulated assumptions of the diallel might have not been fulfilled.

**Fig -1** Days to 50% flowering**Fig-2** Plant height (cm)**Fig-3** Number of branches per plant**Fig-4** Number of flower clusters per plant

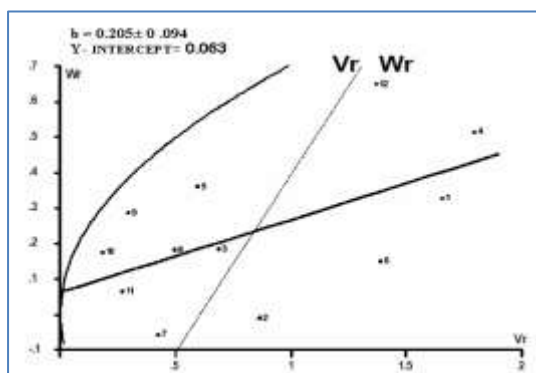


Fig-5 Number of Fruit per truss

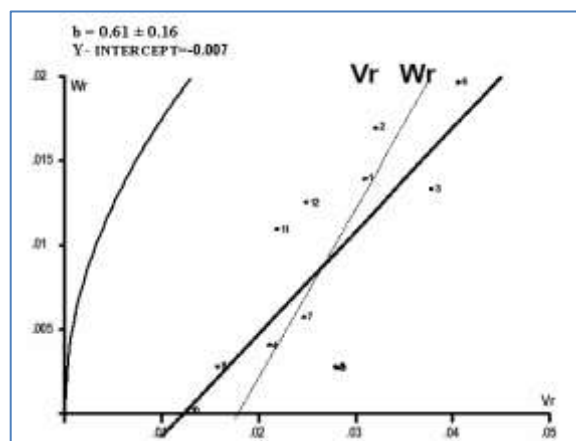


Fig-9 Early fruit yield (Kg)

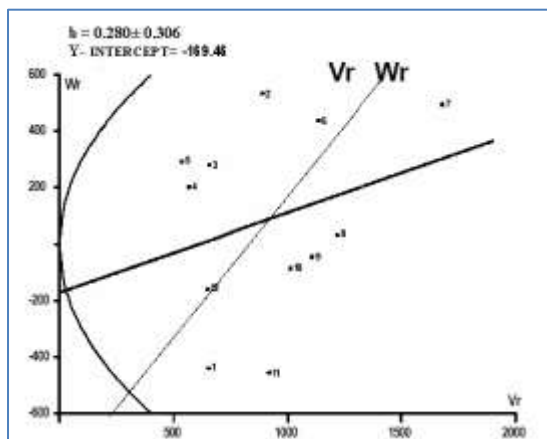


Fig-6 Number of Fruits per plant

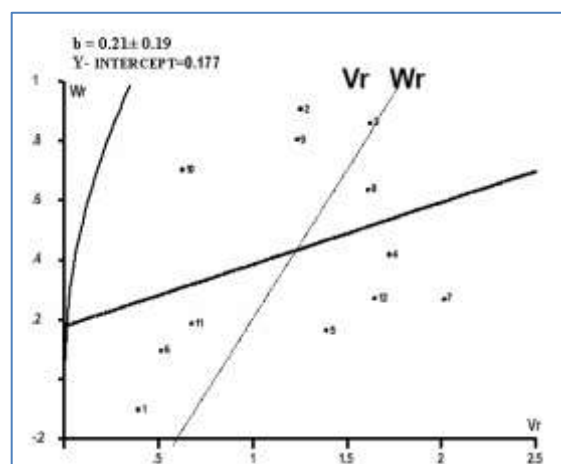


Fig-10 Total fruit yield (Kg)

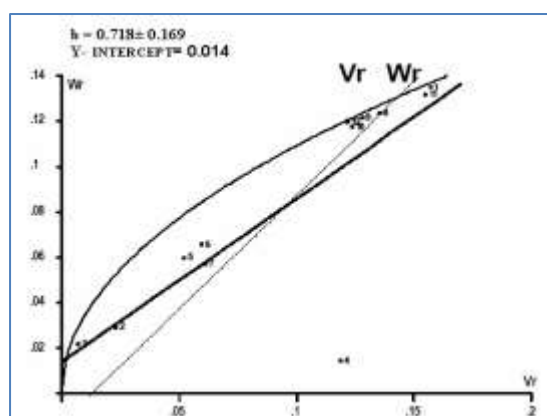


Fig-7 Fruit size (length/breadth ratio)

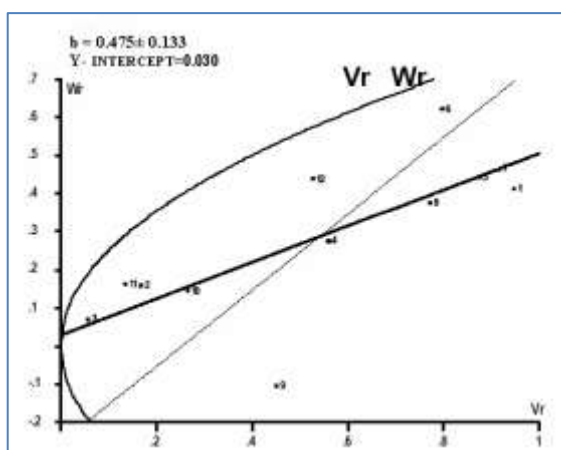


Fig-11 Number of locules per fruit

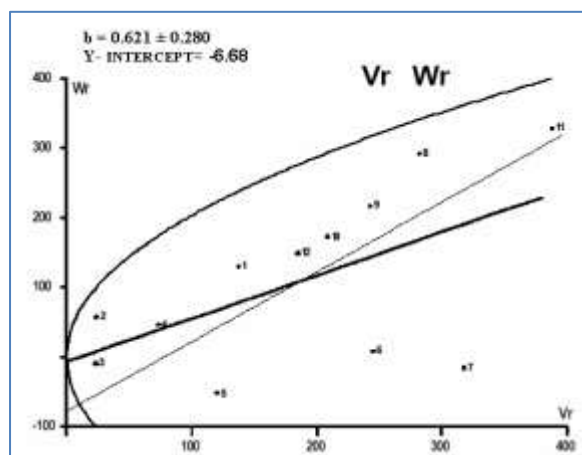


Fig-8 Fruit weight (g)

Plotting of Wr-Vr graph

Wr-Vr graph have been plotted and presented in [Fig-1 to 23]. Array points, in all these figures, for parents EC-31767, H-36, Pusa Ruby, Punjab Chhuhara, Yashwant A-2-8, LA-1420, Merrol, Sel-7, New Wonder, Sel-15, Sioux and Cul-29 have been designated as 1,2,3,4,5,6,7,8,9,10,11 and 12 respectively.

The Wr-Vr graph for days to 50% flowering, plant height, number of branches per plant, number of flower cluster per plant, number of fruits per plant, fruit size, early fruit yield of first two pickings, total fruit yield, dry matter content, total sugar and ascorbic acid revealed that regression coefficient were significantly different from 0 and approaching unity and thereby indicated the absence of epistatic gene interaction. The regression line intercepted the Wr-axis below the origin and thus suggesting over dominance for these characters. These findings are in line with results of Ghosh, *et al.*, (1995) [2] and Vallejo and Huepa, (1999) [3].

The W_r - V_r graph for number of fruits per truss, number of locules per fruit, pericarp thickness, juice: pulp ratio, seed: pulp ratio, total soluble solids, reducing sugar and titrable acidity revealed that regression coefficient were not significantly different from 0 and approaching unity and thereby indicated the presence of epistatic gene interaction. The regression line intercepted the W_r - axis below the origin and thus suggesting over dominance for these characters. Gunasekera and Perera, 1999 [4] has also observed epistasis for these characters.

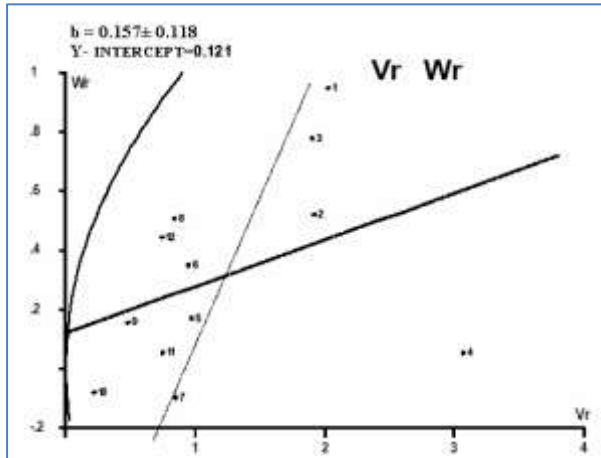


Fig-12 Pericarp thickness (mm)

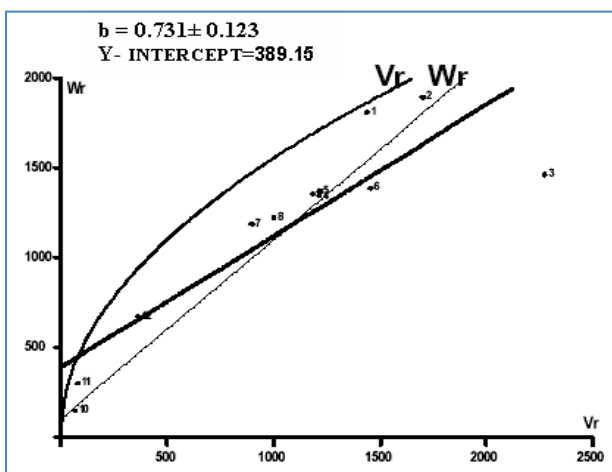


Fig-13 Number of seeds per fruit

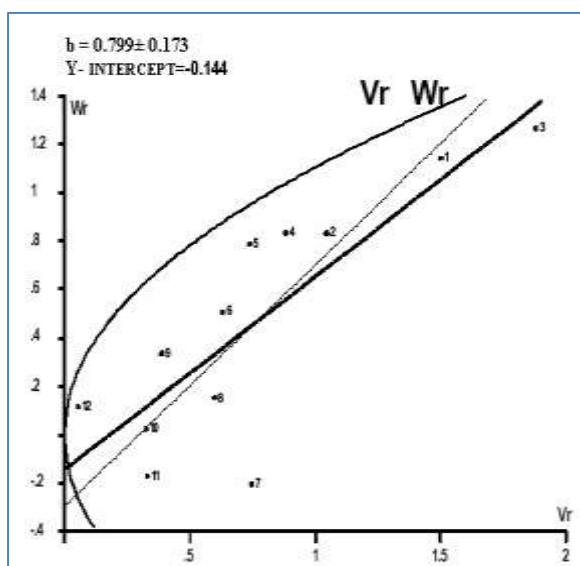


Fig-14 Dry matter content (%)

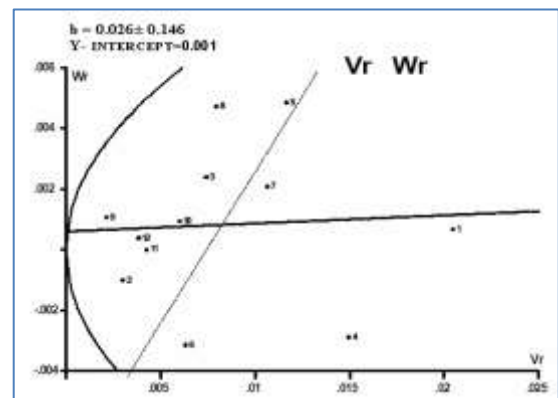


Fig-15 Juice: pulp ratio

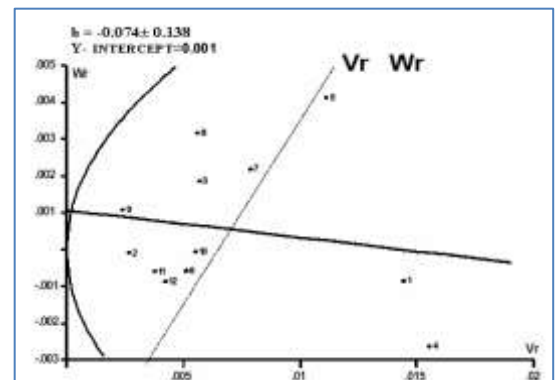


Fig-16 Seed : pulp ratio

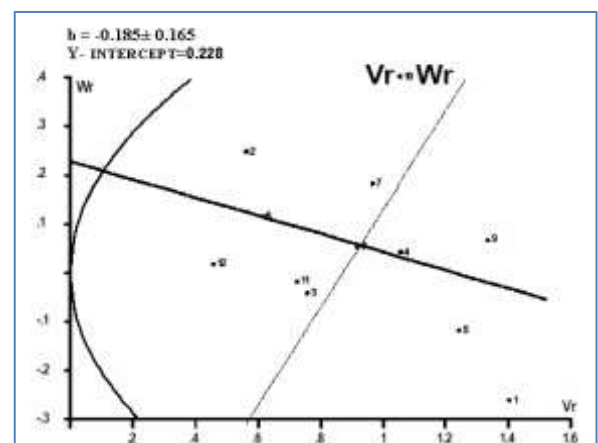


Fig-17 Total soluble solids (%)

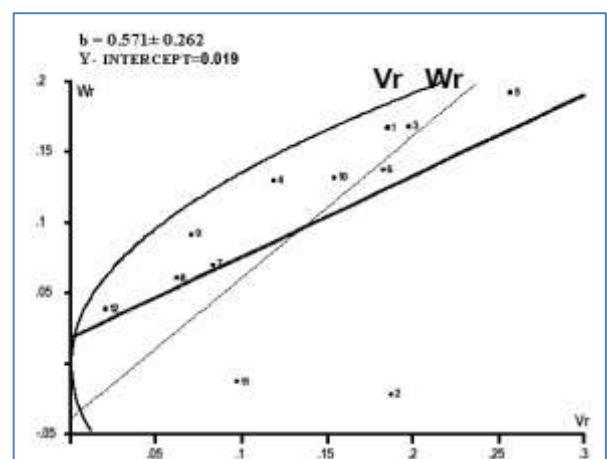


Fig-18 Total Sugars (%)

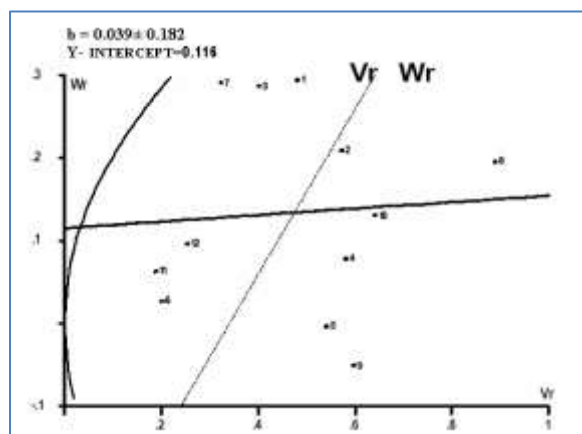


Fig-19 Reducing sugars (%)

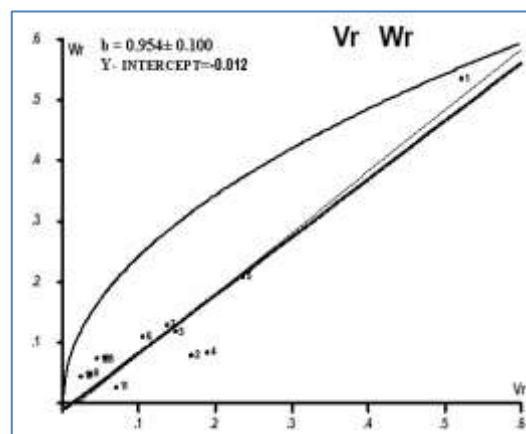


Fig-23 Lycopene content (mg/g of fruit)

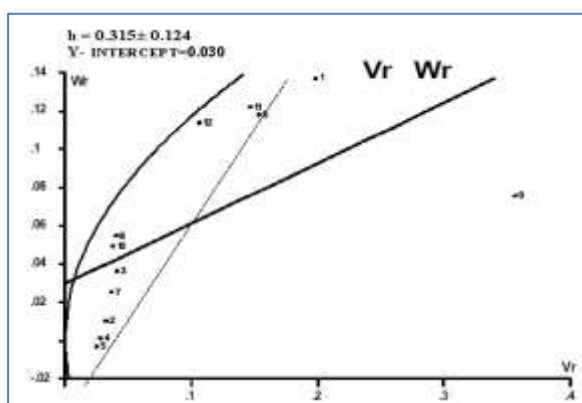


Fig-20 Titrable acidity (g of citric acid/100 ml of juice)

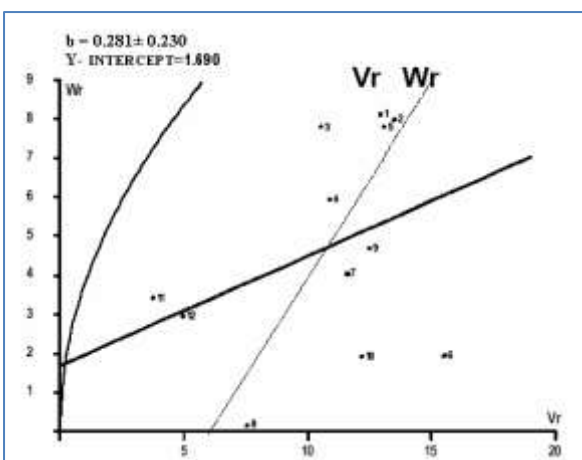


Fig-21 Ascorbic acid (mg/100 g of fruit)

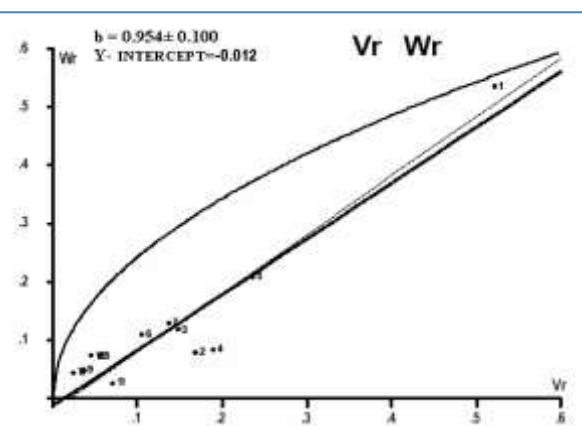


Fig-22 Total carotenoides (mg/g of fruit)

Parents			
1	EC-31767	7	Merrol
2	H-36	8	Sel-7
3	Pusa Ruby	9	New Wonder
4	Punjab Chhuhara	10	Sel-15
5	Yashwant A-2-8	11	Sioux
6	LA-1420	12	Cul-29

The Vr-Wr graph for number of seeds per fruits was significantly different from 0 and approaching unity and thereby indicated the absence of epistatic gene interaction. The regression line intercepted the Vr - axis above the origin and thus suggesting partial dominance.

The Vr-Wr graph for total carotenoides and lycopene content of fruits was significantly different from 0 and approaching unity and thereby indicated the absence of epistatic gene interaction. The regression line passes through the origin and thus suggesting complete dominance.

These results are in agreement with findings of Ghosh, *et al.*, (1996) [2] and Dilip, *et al.*, (2015) [5].

The parent LA-1420 carries the highest number of (over) dominant alleles and New Wonder possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for days to 50% flowering; the parent Pusa Ruby carries the highest number of (over) dominant alleles and Sioux possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for plant height; parent Sioux carries the highest number of (over) dominant alleles and Sel-7 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for number of branches per plant; the parent H-36 carries the highest number of (over) dominant alleles and New Wonder possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for number of flower cluster per plant; the parent Merrol carries the highest number of (over) dominant alleles and Punjab Chhuhara possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles number of fruit/truss; the parent EC-31767 carries the highest number of (over) dominant alleles and Merrol possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for number of fruits/plant; the parent Pusa Ruby carries the highest number of (over) dominant alleles and EC-31767 possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for fruit size; the parent Pusa Ruby carries the highest number of (over) dominant alleles and Sioux possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for fruit weight; the parent Sel-15 carries the highest number of (over) dominant alleles and LA-1420 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for early yield of first two pickings; the parent EC-31767 carries the highest number of (over) dominant alleles and Pusa Ruby possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for total fruit yield: the parent Pusa Ruby carries the highest number of (over)

dominant alleles and LA-1420 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for number of locules per fruit; the parent Sel-15 carries the highest number of (over) dominant alleles and Punjab Chuhara possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for pericarp thickness; the parent Sel-15 carries the highest number of (partial) dominant alleles and Pusa Ruby possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for number of seeds per fruit; the parent Sioux carries the highest number of (over) dominant alleles and Pusa Ruby possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for dry matter content; the parent H-36 carries the highest number of (over) dominant alleles and EC-31767 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for juice-pulp ratio; the parent H-36 carries the highest number of (over) dominant alleles and Yashwant A-2-8 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for seed-pulp ratio; the parent Cul-29 carries the highest number of (over) dominant alleles and Sel-15 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for total soluble solids; the parent Cul-29 carries the highest number of (over) dominant alleles and Yashwant A-2-8

possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for total sugars; the parent LA-1420 carries the highest number of (over) dominant alleles and Sel-7 possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for reducing sugars; the parent Yashwant A-2-8 carries the highest number of (over) dominant alleles and New Wonder possesses large number of recessive alleles. All others have symmetrical distribution of dominant and recessive alleles for titrable acidity; the parent Sioux carries the highest number of (over) dominant alleles and H-36 possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles ascorbic acid and the parent Sel-5, New Wonder, Sioux and Cul-29 carry the highest number of (complete) dominant alleles and EC-31767 possesses large number of recessive alleles. All others have asymmetrical distribution of dominant and recessive alleles for total carotenoides and lycopene content.

From the three sets of analyses [Table-2], namely combining ability, component and graphical, the preponderance of non-additive type of gene effects for most of the characters with few exceptions, have been recorded. However, for a few characters, significant additive gene action appears to be important. The combining ability and component analysis proved to be similar to a great extent for type of gene action involved in almost all the quality and yield characters under study.

Table-2 Comparative evaluation of different analyses used to study the genetic architecture of different character in tomato

Sr. No.	Characters	Pre-dominant component of genetic variation		Average degree of dominance	
		Combining ability analysis	Component analysis	Component analysis	Graphical analysis
1	Days to 50% flowering	NA	NA	OD	OD
2	Plant height (cm)	NA	NA	OD	OD
3	Number of branches per plant	NA	NA	OD	OD
4	Number of flower clusters per plant	NA	NA	OD	OD
5	Number of Fruit per truss	NA	NA	OD	OD
6	Number of Fruits per plant	NA	NA	OD	OD
7	Fruit size (length/breadth ratio)	A	NA	OD	OD
8	Fruit weight (g)	NA	NA	OD	OD
9	Early fruit yield (Kg)	NA	NA	OD	OD
10	Total fruit yield (Kg)	NA	NA	OD	OD
11	Number of locules per fruit	NA	NA	OD	OD
12	Pericarp thickness (mm)	NA	NA	OD	OD
13	Number of seeds per fruit	A	A	PD	PD
14	Dry matter content (%)	NA	NA	OD	OD
15	Juice : pulp ratio	NA	NA	OD	OD
16	Seed : pulp ratio	NA	NA	OD	OD
17	Total soluble solids (%)	NA	NA	OD	OD
18	Total Sugars (%)	NA	NA	OD	OD
19	Reducing sugars (%)	NA	NA	OD	OD
20	Titrable acidity (g of citric acid/100 ml of juice)	NA	NA	OD	OD
21	Ascorbic acid (mg/100 g of fruit)	NA	NA	OD	OD
22	Total carotenoides (mg/g of fruit)	NA	A	CD	CD
23	Lycopene content (mg/g of fruit)	NA	NA	CD	CD

A=Additive, NA=Non-additive
OD= Over-dominance, PD= Partial-dominance
CD= Complete dominance

Application of research: Genetics and Plant Breeding

Research Category: Vegetable Breeding

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Research project name or number: PhD Thesis

Author Contributions: All author equally contributed

Author statement: All authors read, reviewed, agree and approved the final manuscript

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

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