

Estimation of Genetic Components and Heritability for Fruits Yield and Quality Characters in Tomato (*Solanum Lycopersicom*)

Badr L.A.A.; M.M.ELnager; M. H.M.Mohamed. and A.H. Halawa
Horticulture Dept., Faculty of Agriculture, Benha University, Benha, Egypt.

Abstract

Six parental genotypes of tomato (*Solanum Lycopersicom*), i.e. Castel ruck (p_1), Imperial (p_2), Crystal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6) were crossed in a half diallel fashion to produce F_1 in order to study some genetic components and ratios for some economic traits. The study consisted of twenty one genotypes; these genotypes were six inbred lines (parents) and fifteen F_1 crosses. These twenty one genotypes were subjected to evaluation trial at Moshtohor village, Kalyobiya Governorate, Egypt during summer seasons of 2016 in a randomized complete block design with three replications. Data on yield and its components and fruit traits were recorded and subjected to statistical analysis to investigate Hayman's approach were used to study genetic components and heritability which control these traits. Data indicated that the additive component (D) was insignificant for average fruit weight, number of fruits and total yield per plant traits indicating the importance of non-additive effect in the inheritance of these traits. Meanwhile, the dominance genetic variations H_1 and H_2 were significant or highly significant for all studied fruits traits, showing the importance of dominance genetic effects in the inheritance of these traits. The average degree of dominance $(H_1/D)^{1/2}$ showed over dominance for the average fruit weight, number of fruits and fruit yield per plant traits. The proportion of gene with positive and negative effects $(H_2/4H_1)$ in the parents was lower than one quarter proportion, indicating unequal distribution between the positive and negative alleles among the parents. The ratio of dominant to recessive alleles (K_D/K_R) in the parents was more than (one), indicating that the six parents used in the present study carried more dominant than recessive alleles. Heritability estimates in broad sense are very high for average fruit weight trait (100%), number of fruits (96%) and fruit yield per plant (92%), indicating the importance of genetic components of variation in the inheritance of these traits encouraging the usage of breeding programs to improve these traits. Meanwhile heritability estimates in narrow sense was low (2.7%, 1.4% and 0.7 %, respectively) clarifying the importance of non-additive genetic effects in the inheritance of these traits. These results indicate that a major of total phenotypic variances due to dominance and/or over-dominance and the environmental factor affects the inheritance of these traits. So it is of great importance to develop new hybrids in order to obtain maximum fruits number.

Key words: heritability, tomato, *Solanum Lycopersicom*, fruit, yield

Introduction

Tomato (*Lycopersicon esculentum* Mill.) is an important and widely grown solanaceous vegetable crop around the world including tropical, sub-tropical and temperate regions. The commercial exploitation of hybrid vigor has received greater importance on account of several advantages of hybrids over pure line varieties with response to marketable fruit yield and its component traits.

The diallel analysis techniques have been found to be the useful tools to obtain precise information about the types of gene actions involved in the expression of various traits and to predict the performance of the progenies in the latter segregating generations. Cross breeding and selection improved strains in succeeding generations would enable to sort out ideal genotypes of summer squash for which knowledge of its genetics is of priority importance.

Attempts have been made to determine the magnitude of heritable and non-heritable components and genetic parameters such as heritability and genetic advance as percentage of mean in some of the qualitative and quantitative characters of tomato (Ghosh *et al.* (2010), Kamel *et al.* (2010), Ankur *et*

al. (2014), Khapte and Jansirani (2014), Premalakshmi *et al.* (2014), Manjai Phom *et al.* (2015), Meena *et al.* (2017) and Singh and Kumar (2017)). The estimates of genetic variance and its components are of great importance as for the improvement of tomato by breeding programs. If the estimates of genetic variance indicate that the additive variance or general combining ability is the major importance the most effective breeding procedure will be the intra-population selection. While, hybrid vigour program may be the appropriate choice if the non-additive or specific combining ability is the major component (Cockerham, 1961).

In Egypt, most of the area of tomato crop nowadays is still under F_1 hybrids which their seeds are imported from developed countries. Therefore, there is dire need for developing high yielding tomato hybrids or suitable true breeding varieties. The objectives of this study are determining some useful genetic parameters and ratios such as the mean degree of dominance, the ratio of dominant to recessive alleles, heritability in broad sense and heritability in narrow sense, to understand genetic basis of some important traits in tomato in order to

develop superior hybrids suitable for Egyptian cultivation.

Materials and Methods

The present study was carried out in a private farm, Moshtohor village, Kalyobiya Governorate, Egypt during summer seasons of 2015 and 2016 to study the genetic behavior of some economic traits for six tomato cultivars. The experiment was a half diallel F_1 cross to study the type of gene action controlling the inheritance of different characters in tomato.

Six parental genotypes of tomato (*Solanum Lycopersicom*), i.e. Castel ruck (p_1), Imperial (p_2), Crystal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6) were used in making non- reciprocal diallel pattern of crosses during the summer season of 2015. Seeds of six parental genotypes were obtained from Horticultural Dept.; Faculty of Agricultural; Benha Univ. Seeds of these genotypes were sown on 1st of Jan. at nursery and transplanted on Feb. 27th, 2015. A half diallel crosses of the six parental line was conducted to produce fifteen F_1 hybrids.

Parental genotype and their F_1 s hybrids were planted in successive summer plantings of 2016 under open field conditions. A randomized complete block design (RCBD) with three replicates was used, each replicate consisted of twenty-one plots (six parents and fifteen hybrids). Each experimental plot was one ridge of 11.5 meter in length and the distance between plants was 50 cm apart, therefore, the plot area consisted of twenty-one plants. Treatments in each replicate (parents + F_1 s) were randomly assigned to plots.

Three plants were selected excluding border plants for recording the observation. For studying different genetic parameters, yield and its components characters as well as fruit traits were taken viz., average fruit weight (g), average fruit length (cm), average fruit diameter (cm), total soluble solids percentage and ascorbic acid content (according to **A.O.A.C., 1990**), total sugars content in the fruit (**Flood and Priestly, 1973**), fruits number and total yield (kg/plant) per plant.

Data from parents and the related F_1 generation for the different traits were analyzed using the diallel cross method of **Jinks (1958)** and **Hayman (1954)**. The analysis of homogeneity of W_r-V_r over arrays was performed to test the validity of the assumption required for Jinks-Hayman analysis. The genetic components estimated under this analysis were:

$(H_1 / D)^{1/2}$ = Average degree of dominance.

$H_2 / 4H_1$ = Measures the proportion of genes with positive and negative effects in the parents.

$((4DH_1)^{1/2} + F) / ((4DH_1)^{1/2} - F)$ = the ratio of the total number of dominant to recessive genes in all the parents. Where:

D = Component of variation due to the additive effects of genes.

H_1 = Component of variation due to the dominance effects of genes.

$H_2 = H_1 (1 - (U-V)^2)$

Where:

u = Proportion of positive genes in the parents.

V = Proportion of negative genes in the parents.

F = the covariance of dominance and additive effects in a single array.

The previously mentioned estimates were obtained from the variance and covariance by removing the environmental variance (E) which, in this experiment, was estimated from the parents and F_1 block differences.

Narrow and broad-sense heritabilities for the genotypes used in the present study were calculated from the genetic components according to the formulas proposed by **Mather and Jinks (1971)**.

Results and Discussion

Data obtained were subjected to the genetic analysis of half diallel table described by **Hayman (1954)** to obtain more information about the genetic behavior of the traits involved in the study. The mean values of each cross were used to estimate the genetic parameters D, H_1 , H_2 , h^2 , and F as defined by **Hayman (1954)**.

1. Fruit characteristics.

Data presented in the Table 1 show the proportions of the genetic components for fruits characters, i.e., fruit length, fruit diameter, total soluble solids (T.S.S. %), Vitamine-C and total sugars in 15 tomato F_1 hybrids according to Jinks-Hayman analysis. Results indicate that the additive component (D) was significant for fruit length and diameter as well as vitamine - C traits, indicating the importance of additive effect in the inheritance of these fruit traits. While, the additive component (D) was insignificant for total soluble solids (T.S.S. %) and total sugars trait, indicating the importance of non-additive effect in the inheritance of these traits. The dominance genetic variations H_1 and H_2 were significant for all studied fruits traits, showing the importance of dominance genetic effects in the inheritance of these traits. In this respect, **Dhaliwal et al. (2004)**, **Rai et al. (2005)**, **Pandey et al. (2006)**, **Sharma et al. (2007)**, **Palash et al. (2014)**, **Diklesh et al. (2016)** suggested the role of additive and non-additive gene effects in the inheritance of these characters.

Regarding (F) value, it is apparent that fruit length, total soluble solids (T.S.S. %) and total sugars traits were not significant and this might indicate that there is symmetric gene distribution or the equality in the relative frequencies of dominant and recessive genes in the parents. Meanwhile, Examination of the (F) value is apparent that the fruit diameter and vitamine-C contain traits were highly

significant and this might indicates that there were more dominant than recessive genes in the parents used in this study.

Concerning to h^2 parameter, which indicates the dominance variance over all the heterozygous loci in the genetic constitution, was insignificant in the all fruit traits except vitamin-C trait, this indicates that dominance variances over all the heterozygous loci is not important except in the case of vitamin-C trait. The average degree of dominance (H_1/D)^{0.5} showed

over dominance for all fruit traits. This can be considered that the over-dominance was towards parent with high fruit length and fruit diameter as well as high content of total soluble solids (T.S.S. %), vitamin-C and total sugars.

The proportion of gene with positive and negative effects ($H_2/4H_1$) in the parents were not close to one quarter (0.25) proportion for all studied fruit traits, showing that the positive and negative alleles among the parents are not equally distributed.

Table 1. The proportions of the genetic components for fruits characters in 15 tomato F₁ hybrids according to Jinks-Hayman analysis.

Traits Components	Fruit length	Fruit diameter	Total soluble solids (T.S.S. %)	Vitamine - C	Total sugars
E	0.04	8.05	0.083**	5.931	0.024
D	0.61*	328.36**	0.139	205.254**	0.477
F	0.82	243.12**	0.155	392.65**	1.352
H ₁	1.34*	661.93**	0.801**	570.282**	6.867**
H ₂	1.01*	542.21**	0.681**	375.547**	5.761**
h^2	0.01	12.73	0.091	161.875*	0.023
S ²	0.05	845.8	0.006	1469.291	0.737
(H_1/D) ^{0.5}	1.48	1.42	2.402	1.667	3.794
$H_2/4H_1$	0.19	0.20	0.213	0.165	0.21
K_D/K_R	2.65	1.71	1.606	3.693	2.192
r	0.79	0.72	0.312	-0.838	-0.962
r ²	0.62	0.51	0.097	0.702	0.926
h^2/H_2	0.01	0.02	0.134	0.431	0.004
Mean of F _r	1.93	800.17	0.645	793.929	4.142
H ² (n.s)	0.18	0.42	0.17	0.035	0.073
H ² (b.s)	0.89	0.97	0.73	0.94	0.99

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

The ratio of dominant to recessive alleles (K_D/K_R) in the parents was more than one for fruit length (2.65), fruit diameter (1.71), total soluble solids (1.60), vitamin-C (3.69) and total sugars (2.19), indicating that the six parents used in the present study carried more dominant than recessive alleles.

Data in Table 1 show that heritability estimates in broad sense are very high or high for fruit length (89%), fruit diameter (97%), total soluble solids (73%), vitamin-C (94%) and total sugars (99%), indicating the importance of genetic components of variation in the inheritance of these traits encouraging the usage of breeding programs to improve these traits. Concerning heritability estimates in narrow sense, data show that this value are low in fruit length (18%), total soluble solids (17%), vitamin-C (0.3%) and total sugars (0.7%) or moderate in fruit diameter (42%), this clarify the importance of non-additive genetic effects in the inheritance of these trait, consequently establishing hybrids will be suggested to obtain high quality of tomato fruits. The high heritability in broad sense and low heritability in narrow sense indicate that a major part of total phenotypic variances are due to dominance and/or over-dominance and the environmental influences affected these traits.

Furthermore, the additive genetic variance components is relatively large comparing to the non-additive genetic variance indicating high progress which can be achieved by selection individual plants in segregating generations to improve fruit traits for tomato plants. In this regard, **Khapte and Jansirani (2014)**, **Basavaraj et al. (2015)**, **Diklesh et al. (2016)**, **Choudhury et al. (2017)**, **Meena et al. (2017)** and **Singh and Kumar (2017)** observed high heritability for most fruit traits.

The information obtained in Table 1 could be described in Figures 1,2,3,4 and 5 for fruit length, fruit diameter, total soluble solids (T.S.S. %), Vitamine-C and total sugars, respectively in 15 tomato F₁ hybrids.

Concerning the figure 1, the regression line of Vr-Wr intersected the Wr axis above the origin as shown in Fig.1. This indicated the presence of partial dominance in the inheritance of this trait. The relative values of the Vr and Wr showed that the parental cultivars Perso (p₄), Imperial (p₂), Valcum valentime (p₆) and Pascal (p₅) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the cultivars Castel Ruck (p₁) and Cristal (p₃) had the highest values and hence, contained the most recessive genes. Moreover, the parental cultivars Castel Ruck

(p₁) and Cristal (p₃) which had high values of Vr and Wr, had a distinguished genotypes concerning fruit length. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. The positive value of (r) (+0.79) (Table 1) indicates that

the parents are containing the most decreasing genes. The value of (r²) (0.62) could suggest the existence of (yr) and (Wr ± Vr) and hence, prediction on completely dominant and recessive parents is possible.

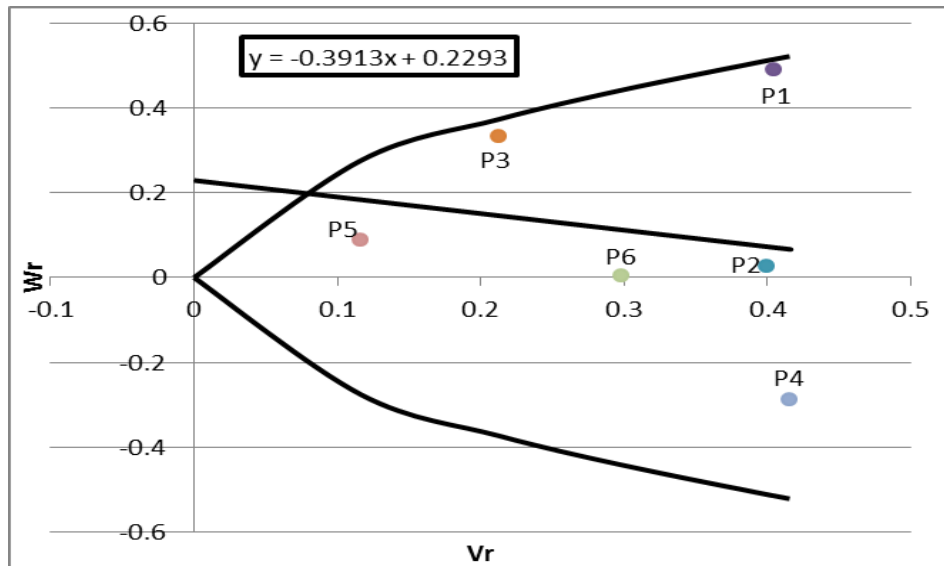


Fig. 1. Variance (Vr) and covariance (Wr) graph of fruit length in F₁ generation of tomato genotypes. [Castel Ruck (p₁), Imperial (p₂), Cristal (p₃), Perso (p₄), Pascal (p₅) and Valcum valentime (p₆)]

Regarding fruit diameter, the regression line of Vr-Wr intersected the Wr axis in the origin as shown in Fig.2. This indicated the presence of partial dominance in the inheritance of fruit diameter. he relative values of the Vr and Wr show that the parental cultivars Castel Ruck (p₁) and Pascal (p₅) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivars Cristal (p₃), Imperial (p₂), Perso (p₄) and Valcum valentime (p₆) had the highest values and hence contained the most recessive genes. Moreover, these parental cultivars

which had high values of Vr and Wr, had a distinguished genotypes concerning fruit diameter. Such infomation is of great value especially in the stage of selecting parental tomato cultivars which will inter in a cenain breeding programs. The positive value of (r) (+0.72) (Table 1) indicates that the parents are containing the most decreasing genes. The value of (r²) (0.51) could suggest the existence of (yr) and (Wr ± Vr) and hence, prediction on completely dominant and recessive parents is possible.

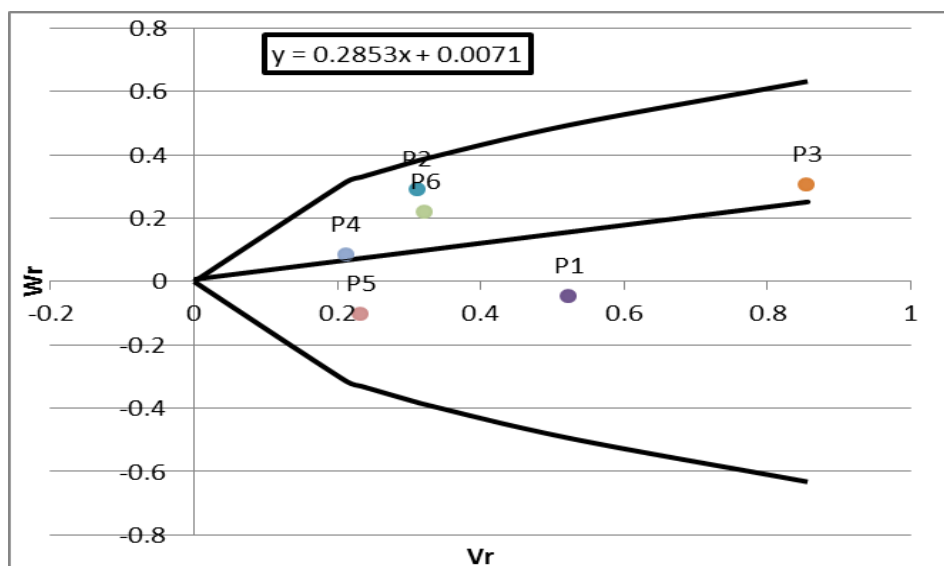


Fig. 2 Variance (V_r) and covariance (W_r) graph of fruit diameter in F_1 generation of tomato genotypes. [Castel Ruck (p_1), Imperial (p_2), Cristal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6)].

In concern of the figure 3, regression line of V_r - W_r intersected the W_r axis below the origin. This indicated the presence of over-dominance in the inheritance of the total soluble solids. The relative values of the V_r and W_r show that the parental cultivars Imperial (p_2), Perso (p_4) and Valcum valentime (p_6) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivar Castel Ruck (p_1), Cristal (p_3), and Pascal (p_5) had the highest values and hence contained the most recessive genes. Moreover, the values of V_r and W_r associated with the parental cultivars P_3 and P_5 were

close to each other which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, these parental cultivars which had high values of V_r and W_r , had a distinguished genotypes concerning T.S.S. %. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. The positive value of (r) (0.31) (Table 1) indicates that the parents are containing the most decreasing genes. The value of (r^2) (0.097) could suggest the existence of (y_r) and ($W_r \pm V_r$) and hence, prediction on completely dominant and recessive parents is possible.

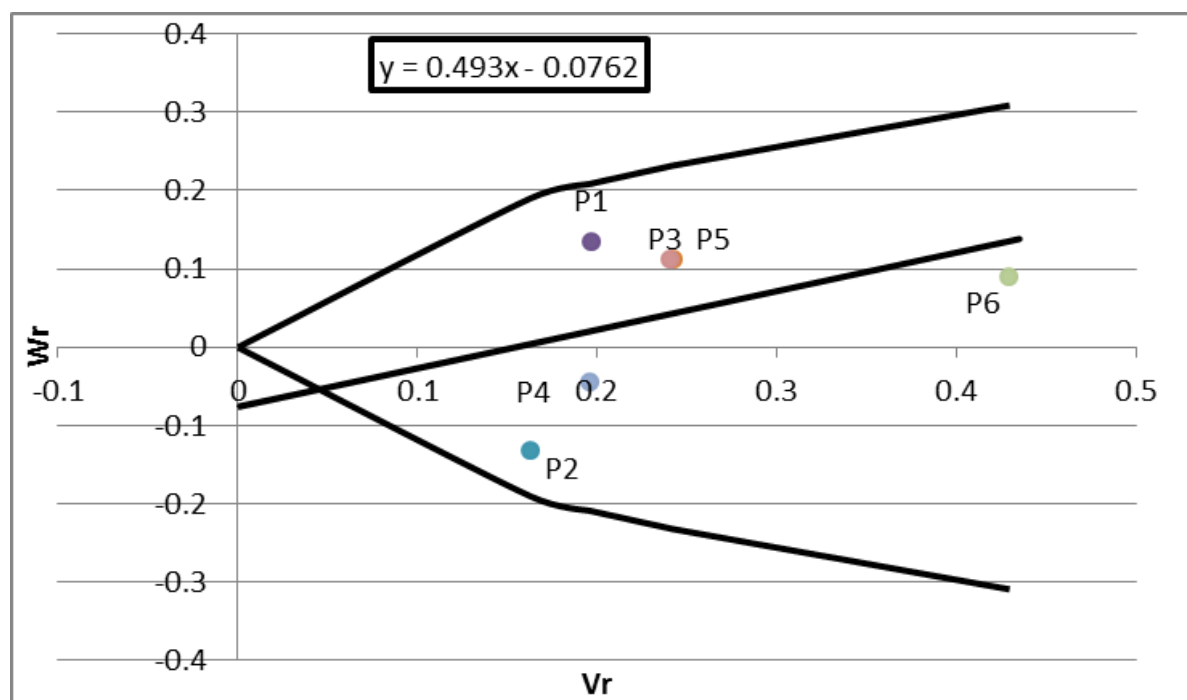


Fig.3: Variance (V_r) and covariance (W_r) graph of T.S.S.% for tomato fruits in F_1 generation of tomato genotypes. [Castel Ruck (p_1), Imperial (p_2), Cristal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6)]

In concern of the figure 4 for ascorbic acid content trait, the regression line of Vr-Wr intersected the Vr axis blew the origin. This indicated the presence of over-dominance in the inheritance of this trait. The relative values of the Vr and Wr show that the parental cultivars Imperial (p₂), Perso (p₄) and Valcum valentime (p₆) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivars Castel Ruck (p₁) and Cristal (p₃) had the highest values and hence contained the most recessive genes. Moreover, the values of Vr and Wr associated with the parental cultivars Imperial (p₂),

Perso (p₄) and Valcum valentime (p₆) were close to each other (Fig.4) which indicate that these cultivars have similar genotypes concerning the studied character. Such infomation is of great value especially in the stage of selecting parental tomato cultivars which will inter in a cenain breeding programs. The negative value of (r) (- 0.838) (Table, 1) indicates that the parents are containing the most increasing genes. The value of (r²) (0.70) could suggest the existence of (yr) and (Wr ± Vr) and hence, prediction on completely dominant and recessive parents is possible.

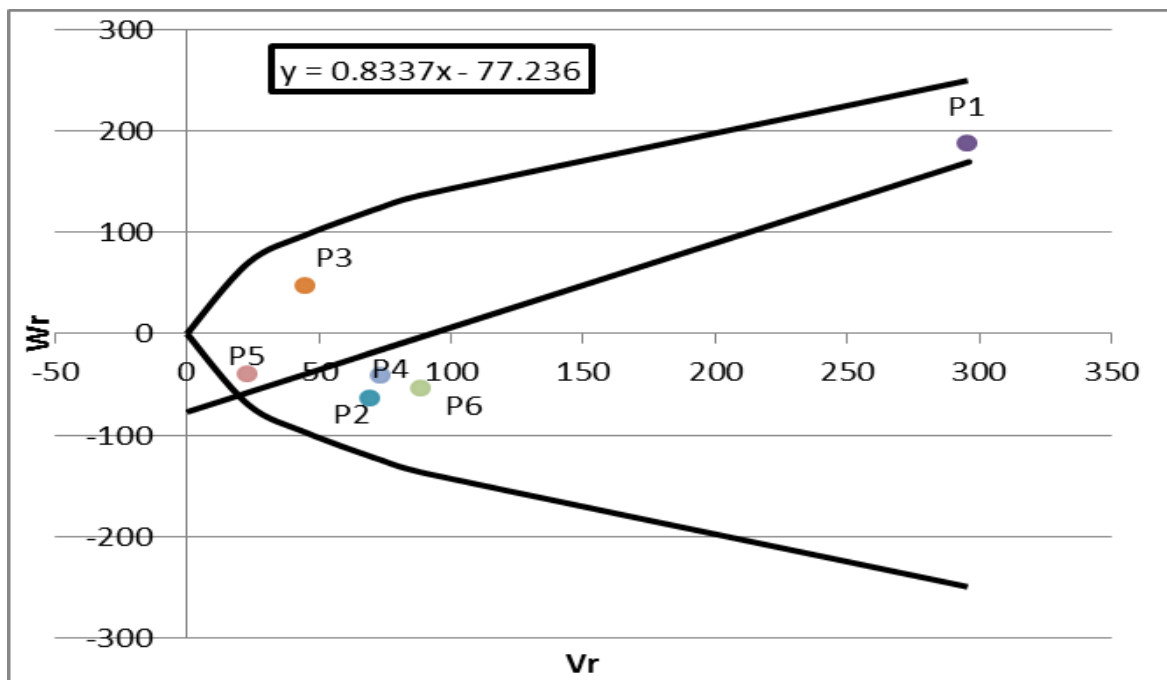


Fig. 4: Variance (Vr) and covariance (Wr) graph of ascorbic acid content for fruit in F₁ generation of tomato genotypes. [Castel Ruck (p₁), Imperial (p₂), Cristal (p₃), Perso (p₄), Pascal (p₅) and Valcum valentime (p₆)]

For total sugars content trait as shown in Fig.5, The regression line of Vr-Wr intersected the Vr axis above the origin. This indicated the presence of partial-dominance in the inheritance of total sugars content of tomato fruits. The relative values of the Vr and Wr showed that the parental cultivars Imperial (p₂) and Valcum valentime (p₆) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the cultivars Castel Ruck (p₁) and Cristal (p₃) had the highest values and hence, contained the most recessive genes. Moreover, the parental cultivars Castel Ruck

(p₁) and Cristal (p₃) which had high values of Vr and Wr, had a distinguished genotypes concerning total sugars content. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. The negative value of (r) (-0.96) (Table 1) indicates that the parents are containing the most decreasing genes. The value of (r²) (0.926) could suggest the existence of (yr) and (Wr ± Vr) and hence, prediction on completely dominant and recessive parents is possible.

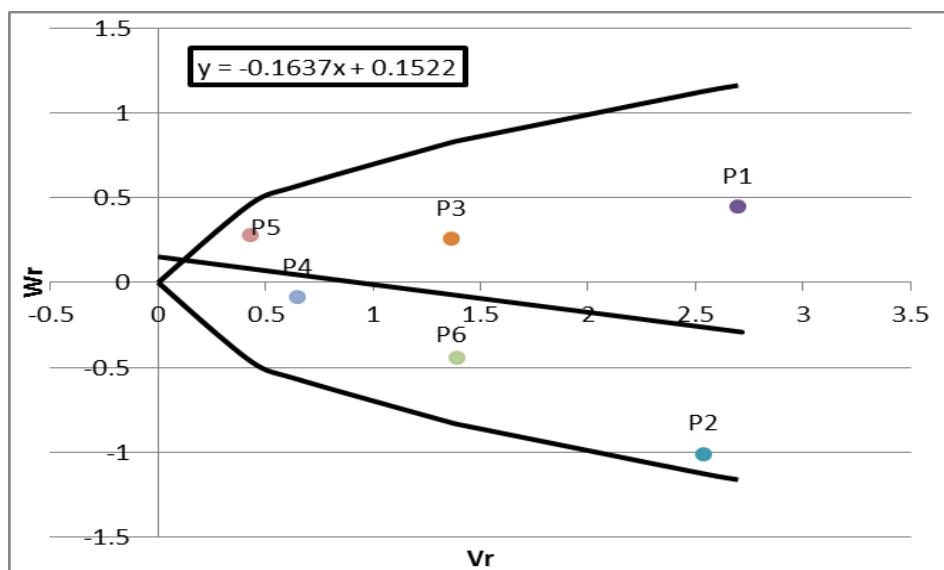


Fig. 5 Variance (Vr) and covariance (Wr) graph of total sugars content in F₁ generation of tomato genotypes. [Castel Ruck (p₁), Imperial (p₂), Cristal (p₃), Perso (p₄), Pascal (p₅) and Valcum valentime (p₆)]

4.1.4. Yield and its components

Data presented in the Table 2 show the proportions of the genetic components for yield and its components, i.e., average fruit weight, fruits number and yield per plant in 15 tomato F₁ hybrids according to Jinks-Hayman analysis. Results show that the additive component (D) was insignificant for these traits indicating the importance of non-additive effect in the inheritance of these traits. The dominance genetic variations H₁ and H₂ were significant or highly significant for all studied fruits traits, showing the importance of dominance genetic effects in the inheritance of these traits. This is in agreement with Chadha *et al.* (2001), Makesh *et al.* (2002), Dhaliwal *et al.* (2004), Rai *et al.* (2005), Pandey *et al.* (2006), Kansouh and Masoud (2007),

Rattan *et al.* (2007), Saidi *et al.* (2008), Hazra *et al.* (2009) and Bhattarai *et al.* (2016) who reported that both additive and non-additive gene actions were involved in the expression of number of fruits per plant. Examination of F value, show that the studied yield and its components trait traits were insignificant and this might indicate that there is symmetric gene distribution or the equality in the relative frequencies of dominant and recessive genes in the parents. Concerning to h² parameter which indicates the dominance variance over all the heterozygous loci in the genetic constitution, was significant only for fruits yield per plant trait. This indicates that dominance variance over all the heterozygous loci is important only in the inheritance of fruits yield per plant trait.

Table 2. The proportions of the genetic components for number of fruits and total yield per plant traits in 15 tomato F₁ hybrids according to Jinks-Hayman analysis.

Components	Traits		
	Average fruit weight	No. of fruit/ plant	Fruit yield/ plant
E	2.94	1.84	0.02
D	1030.55	11.9	0.08
F	799.36	11.05	0.23
H ₁	3608.9*	156.75**	1.1**
H ₂	3226.24*	145.37**	0.92**
h ²	116.45	20.15	0.5**
S ²	434555.8	205.18	0.01
(H ₁ /D) ^{0.5}	1.87	3.63	3.67
H ₂ /4H ₁	0.22	0.23	0.21
K _D /K _R	1.52	1.29	2.28
r	-0.15	0.32	-0.62
r ²	0.02	0.1	0.38
h ² /H ₂	0.04	0.14	0.55
Mean of F _r	3035.81	77.04	0.71
H ₂ (n.s)	0.27	0.14	0.07
H ₂ (b.s)	1	0.96	0.92

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

The average degree of dominance $(H_1/D)^{1/2}$ showed over dominance for the average fruit weight, number of fruits and fruit yield per plant traits since these values were greater than one i.e., 1.87, 3.63 and 3.67, respectively. The proportion of gene with positive and negative effects $(H_2/4H_1)$ in the parents was lower than one quarter proportion, indicating unequal distribution between the positive and negative alleles among the parents. The ratio of dominant to recessive alleles (K_D/K_R) in the parents was more than (one) i.e. 1.52, 1.29 and 2.28, indicating that the six parents used in the present study carried more dominant than recessive alleles. In this concern, **Dhaliwal et al. (2004)** and **Saleba et al. (2004)** who reported that additive and non-additive gene effects were found to be more or less equally important.

Data in Table 2 show that heritability estimates in broad sense are very high for average fruit weight trait (100%), number of fruits (96%) and fruit yield per plant (92%), indicating the importance of genetic components of variation in the inheritance of these traits encouraging the usage of breeding programs to improve these traits. Meanwhile heritability estimates in narrow sense was low (2.7%, 1.4% and 0.7 %, respectively) clarifying the importance of non-additive genetic effects in the inheritance of these traits. These results indicate that a major of total phenotypic variances due to dominance and/or over-dominance and the environmental factor affects the inheritance of these traits. So it is of great importance to develop new hybrids in order to obtain maximum fruits number. This is in accordance with **Ghosh et al. (2010)**, **Kamel et al. (2010)**, **Ankur et**

al. (2014), **Khapte and Jansirani (2014)**, **Premalakashmi et al. (2014)**, **Manjai Phom et al. (2015)**, **Meena et al. (2017)** and **Singh and Kumar (2017)** who observed high heritability for fruits number and yield.

The information obtained in Table 2 could be described in Figures 6, 7 and 8 for average fruit weight, fruits number and yield per plant, respectively in 15 tomato F₁ hybrids.

Concerning the figure 6 for average fruit weight trait, the regression line of Vr-Wr intersected the Vr axis above the origin as shown in Fig.6. This indicated the presence of partial dominance in the inheritance of this trait. The relative values of the Vr and Wr show that the parental cultivars P₁ and P₅ had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivar P₃ and P₄ had the highest values and hence contained the most recessive genes. Moreover, the values of Vr and Wr associated with the parental cultivars P₄, P₆ and P₂ were close to each other which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, the parental cultivars P₃ and P₄ which had high values of Vr and Wr, had a distinguished genotypes concerning average fruit weight. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. The negative value of (r) (- 0.15) (Table 2) indicates that the parents are containing the most increasing genes. The value of (r²) (0.02) could suggest the existence of (yr) and (Wr ± Vr) and hence, prediction on completely dominant and recessive parents is possible.

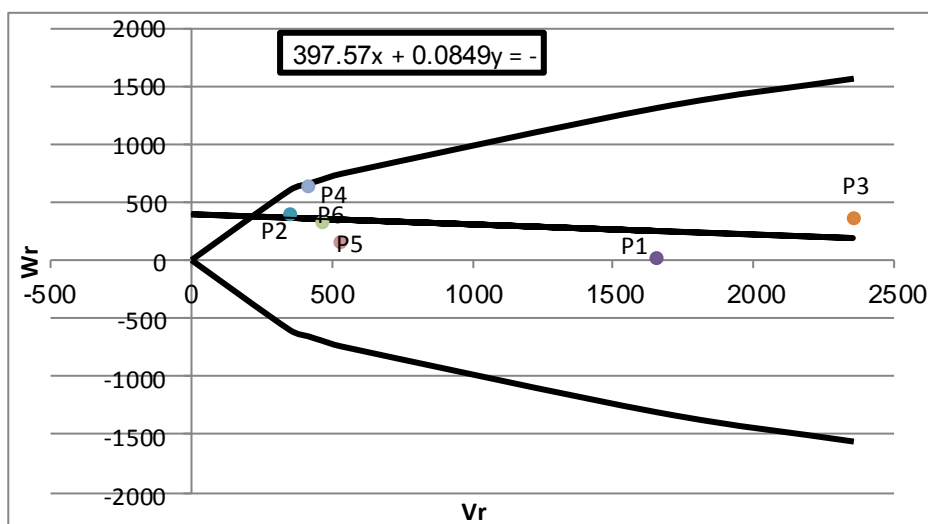


Fig. 6: Variance (Vr) and covariance (Wr) graph of average fruit weight in F₁ generation of tomato genotypes. [Castel Ruck (p₁), Imperial (p₂), Cristal (p₃), Perso (p₄), Pascal (p₅) and Valcum valentime (p₆)]

In concern of the figure 7 for fruits number per plant trait. The regression line of Vr-Wr intersected the Vr axis below the origin as shown in Fig.7. This indicated the presence of over-dominance in the

inheritance of number fruits per plant. The relative values of the Vr and Wr show that the parental cultivars Cristal (p₃), Perso (p₄) and Pascal (p₅) had the lowest values which indicate that these cultivars

contained the most dominant genes. On the other hand, the parental cultivars Castel Ruck (p_1), Imperial (p_2) and Valcum valentime (p_6) had the highest values and hence contained the most recessive genes. Moreover, the values of V_r and W_r associated with the parental cultivars Imperial (p_2) and Castel Ruck (p_1) were close to each other (Fig.7) which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, these parental which had high values of

V_r and W_r , had a distinguished genotypes concerning number of fruits per plant. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. As shown in Table 2, the positive value of r (0.32) indicates that the parents are containing the most decreasing genes. The value of (r^2) (0.01) could suggest the existence of (y_r) and $(W_r \pm V_r)$ and hence, prediction on completely dominant and recessive parents is possible.

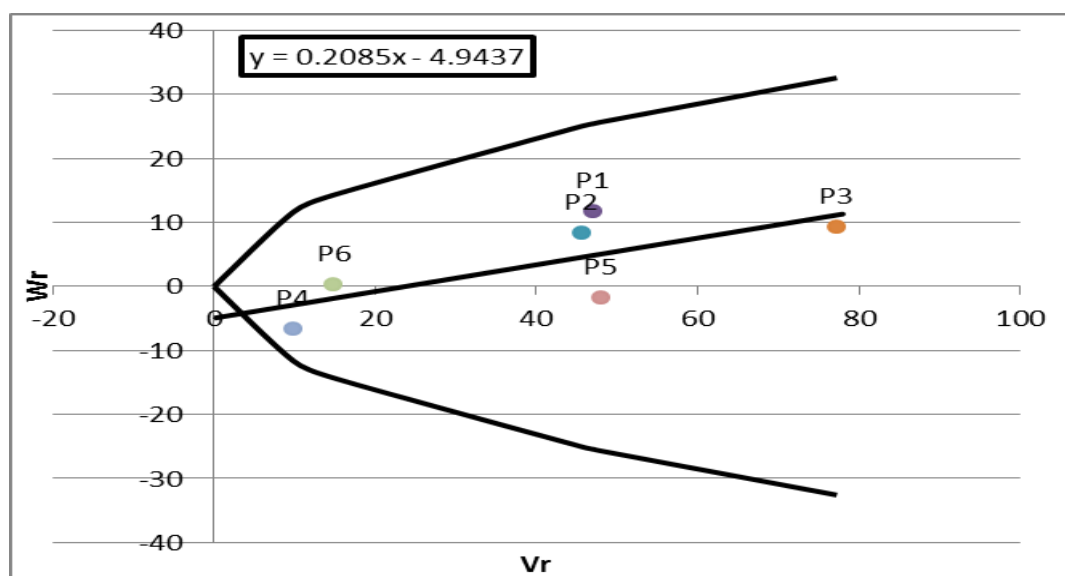


Fig. 7: Variance (V_r) and covariance (W_r) graph of fruits number per plant in F_1 generation of tomato genotypes. [Castel Ruck (p_1), Imperial (p_2), Cristal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6)].

In concern of the figure 8 for fruit yield per plant trait, the regression line of V_r - W_r intersected the W_r axis below the origin as shown in Fig.8. This indicated the presence of over-dominance in the inheritance of this trait. The relative values of the V_r and W_r show that the parental cultivars Imperial (p_2), Cristal (p_3), Perso (p_4) and Valcum valentime (p_6) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivars Castel Ruck (p_1), and Pascal (p_5) had the highest values and hence contained the most recessive genes. Moreover, the values of V_r and W_r associated with the parental cultivars Castel Ruck (p_1) and Pascal (p_5) were close

to each other (Fig.8) which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, the parentals Castel Ruck (p_1), and Pascal (p_5) which had high values of V_r and W_r , had a distinguished genotypes concerning fruits yield per plant. Such information is of great value especially in the stage of selecting parental tomato cultivars which will inter in a certain breeding program. As shown in Table 2, the negative value of r (-0.62) indicates that the parents are containing the most increasing genes. The value of (r^2) (0.38) could suggest the existence of (y_r) and $(W_r \pm V_r)$ and hence, prediction on completely dominant and recessive parents is possible.

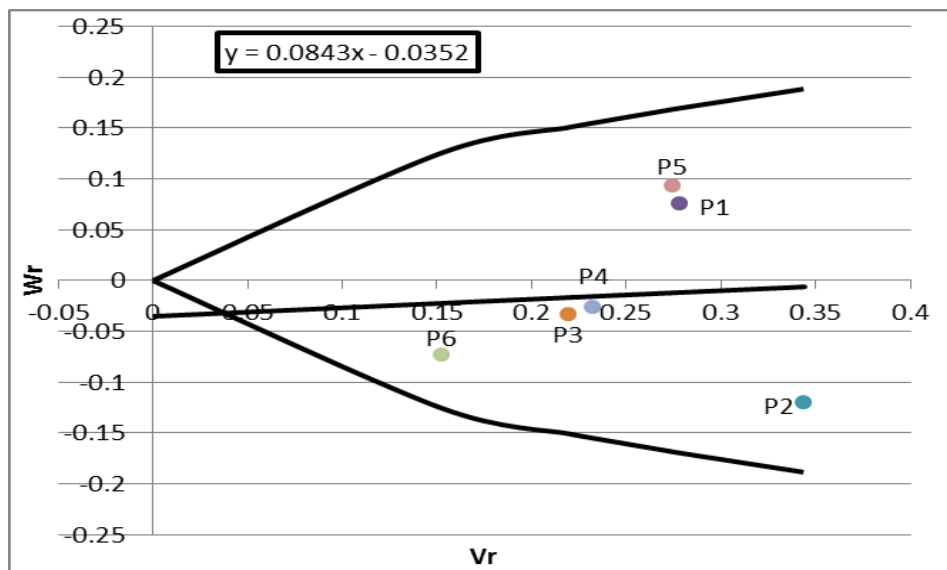


Fig. 8: Variance (V_r) and covariance (W_r) graph of fruits yield per plant in F_1 generation of tomato genotypes. [Castel Ruck (p_1), Imperial (p_2), Cristal (p_3), Perso (p_4), Pascal (p_5) and Valcum valentime (p_6)].

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