

### Original Research Article

## Genetic Variability, Correlation and Path Coefficient analysis in Multi-parent Derived F<sub>2</sub> Population of Tomato (*Solanum lycopersicum* L.)

### Abstract

Genetic variability, correlation and path coefficient analysis for 8 yield contributing traits were studied in multi-parent derived F<sub>2</sub> population obtained from crossing 4 commercial hybrids (S-85×IndamRohini) × (Mahyco-701×Indus-1105). For the current study, 285 multi-parent derived F<sub>2</sub> plants were used. The study indicated the presence of immense variability for all the traits under study viz, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of fruits per plant, average fruit weight and fruit yield per plant. High variability was witnessed due to the higher values of PCV and GCV and large variation in the F<sub>2</sub> range for all the traits in comparison with the parental range of all the traits. This might be due to the involvement of the genome constitution from multiple parents. All the characters exhibited high estimates of heritability coupled with high genetic advance, hence all the characters can be improved through selection. Correlation indicated that yield per plant was significantly and positively associated with average fruit weight and number of fruits per plant. Average fruit weight and number of fruits per plant showed the highest positive direct effect on fruit per plant. Direct selection can be executed considering these traits as the main selection criteria to minimize the indirect effect of other traits. The genetic variability displayed in the present study can be well exploited to broaden the genetic base of the crop. Meantime, the efficient use of significant correlation and the relatedness in the commercially target traits can yield fruits of rapid trait improvement in near future.

Keywords: Genetic variability, Segregating population, Heritability, Genetic advance, GCV and PCV.

### INTRODUCTION:

Tomato (*Solanum lycopersicum* L.) is one of the most economically important vegetables grown all over the world, belongs to the family Solanaceae and the genus *Solanum* having the chromosome number of  $2n = 2x = 24$ . It is native to Peru Ecuador Bolivia Region of the Andes, South America Rick [1]. Tomato occupies a distinct place in the world of vegetables because of its high nutritive value and large-scale utilization. It is universally treated as “protective food” due to its special nutritional value and widespread production. Tomatoes are a very good source of lycopene, an antioxidant, the principal carotenoid, which causes the characteristic red color of tomatoes and is used to cure several chronic diseases such as cancer, cardiovascular disease, *etc.* In many crops including the tomato usually been a significant loss in variability because of the domestication process and plant breeding programs Arrons [2]. There will be a higher risk for yield loss and quality deterioration whenever we are facing threats like various kinds of biotic and abiotic stresses due to a lack of genetic variability. The same plant breeding tool can be used for recovering the part of the lost variability.

Genetic variability can be created by various strategies, geneticists and plant breeders found one of the best ways to genetic variability *i.e.*, multi-parent derived population. The multi-parent population scheme is mainly to derive progenies from distant

crosses for exploitation of variation. Multi-parent derived  $F_2$  population results from the multi-parent derived  $F_1$  population which has all potential variants. Selection in this early segregating generation with a specific goal and selfing those selected genotypes generation after generation creates an advanced inbred population called MAGIC (Multi-parent Advanced Generation Inter-cross) population, which can be further utilized for various purposes *viz.*, QTL detection, directly released as a variety with a required desirable trait or used in further crossing program. The amount of genetic variation present and the heritability of the traits serve as the main determinants of selection efficiency. MAGIC can help in development of variety which can adopt several diverse regions of the world and suitable for diverse climatic condition. MAGIC population can be used directly as a source material for the extraction and development of breeding lines and varieties. And it can help to create a novel diversity.

A study of the correlation between different quantitative characters provides an idea of the degree of association among themselves as well as with the yield. So, it would be desirable to consider the relative magnitude of the association of various characters with yield for any effective selection program. The technique of path coefficient facilitates the partitioning of correlation coefficients into direct and indirect contributions of various characters on yield Kumar [3]. Considering all the facts described above the present investigation was undertaken with the objective of assessing the level of variability, correlation and path coefficient analysis components.

## **MATERIAL AND METHODS:**

This experiment was conducted at the Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The material under investigation comprised of multi-parent derived  $F_2$  population derived from 4 commercial hybrids (S-85×IndamRohini) × (Mahyco-701×Indus-1105). During the *Rabi* 2021-22 planting season, 285 multi-parent derived  $F_2$  plants and 20 plants from each parent were planted in an un-replicated design, following 60 cm x 60cm spacing and evaluated for yield and yield-related parameters. Each plant in the population was labeled for recording 8 quantitative characters *viz.*, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of fruits per plant, average fruit weight (g) and fruit yield per plant (kg). The methods illustrated by Singh and Choudhary [4] were used for the calculation of the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability ( $h^2$ ), genetic advance (GA) and genetic advance as percent over mean (GAM). The Johnson [5] suggested method was used to calculate the correlation coefficient. Dewey and Lu's [6] technique was used to determine the direct and indirect effects.

## **RESULTS AND DISCUSSION:**

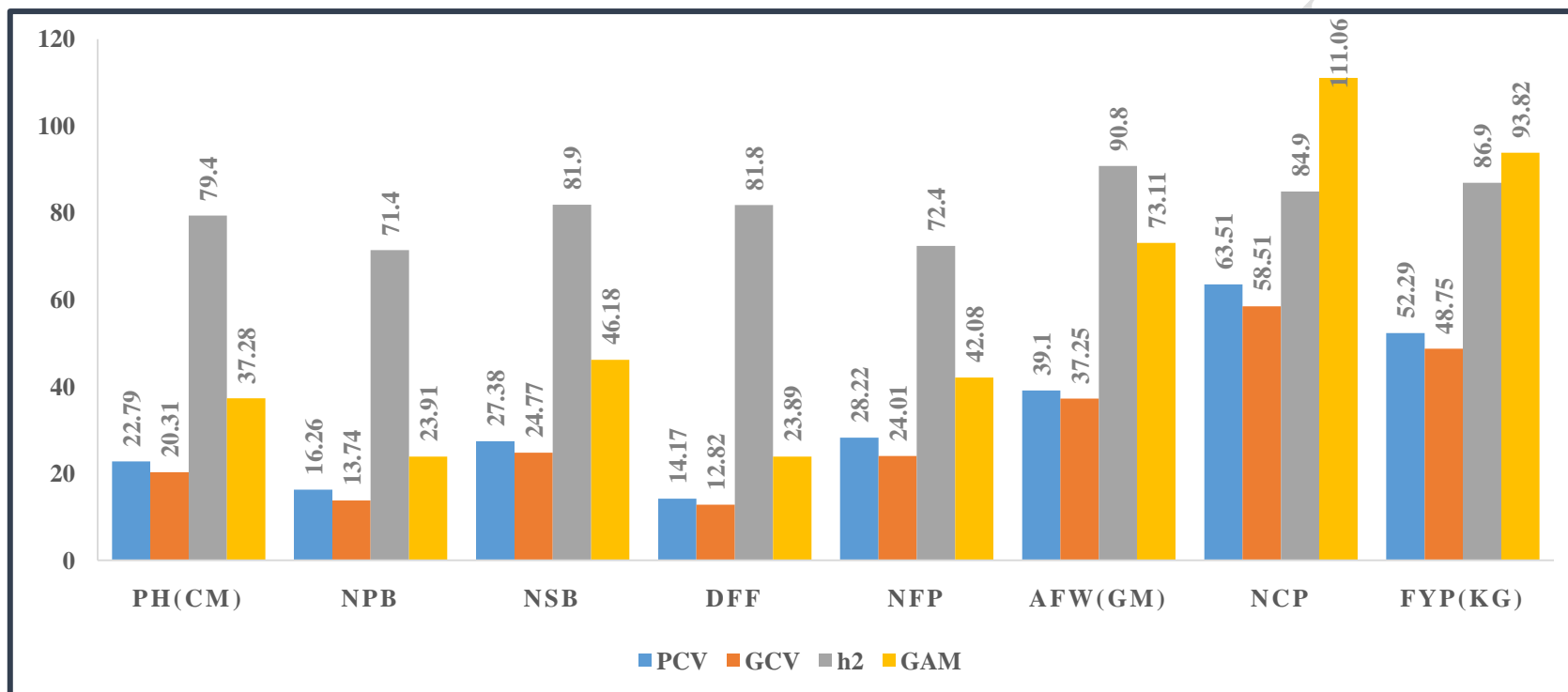
*Variability:* The estimation of genotypic (GCV) and phenotypic (PCV) coefficients of variation indicates the presence of an immense amount of variability among the genotypes. The estimates of descriptive statistics for a multi-parent derived  $F_2$  population comprising 8 characters are presented in Table 1. The range of variation was more pronounced in almost all the characters. The PCV was higher than the GCV, but the difference between them was very narrow indicating environmental influence was much less. The traits with the highest PCV and GCV observed were; number of clusters per plant (63.51; 58.51) followed by fruit yield per plant (52.29; 48.75), average fruit weight (39.10; 37.25), number of fruits per plant (28.22; 24.01), number of secondary branches (27.38; 24.77) and plant height (22.79; 20.31). Whereas, moderate PCV and GCV were observed for

the traits viz., number of primary branches (16.26; 13.74) and days to 50% flowering (14.17; 12.82), these findings are in parallel with the findings of Anuradha[7], Al-Araby [8], Neavani and Sridevi [9], Kadyan[10] and Mahrtale[11]. A comparison of the F<sub>2</sub> range and parental mean range revealed that all the traits recorded a high F<sub>2</sub> range in comparison with the parental mean range. For plant height(cm) 25 to 75 and 47.12 to 59.89 indicate F<sub>2</sub> range and parental mean range respectively were observed. Similarly for the number of fruits per plant 6 to 27 and 10.14 to 12.30, for average fruit weight (g) 22.5 to 105.9 and 56.60 to 79.80, for the number of clusters per plant 3 to 18 and 3.69 to 5.75 and for the yield per plant (kg) 0.2 to 2.9 and 0.54 to 1.10 F<sub>2</sub> range and parental mean range respectively was observed indicating the higher magnitude of variability was observed for all traits in multi-parent derived F<sub>2</sub> population when we compare the F<sub>2</sub> range with the parental mean ranges.

The highest heritability was observed for average fruit weight (90.80 %) followed by fruit yield per plant (86.90 %), number of clusters per plant (84.90 %), number of secondary branches per plant (81.90 %), days to 50 % flowering (81.80 %), plant height (79.40 %), number of fruits per plant (72.40 %) and number of primary branches per plant (71.40 %). The number of clusters per plant (111.06 %) had highest genetic advance as percent of mean followed by fruit yield per plant (93.82 %), average fruit weight (73.11 %), number of secondary branches per plant (46.18 %), number of fruits per plant (42.08 %), plant height (37.28 %), number of primary branches per plant (23.91 %) and days to 50 % flowering (23.89 %). High heritability (>60%) coupled with high genetic advance as a percent of the mean (>20%) were recorded for all the traits under the study. With this outcome, higher heritability along with high genetic advance can be regarded under the control of additive genes. Hence, phenotypic selection for these trait improvement can be achieved by simple breeding methods. These findings are similar to the findings of Gopinath and Vethamoni [12], Anuradha *et al.* [7] and Nevani and Sridevi [9].

**Table 1: Mean, range and variability parameters for yield and yield related component traits in multi-parent derived F<sub>2</sub> population of tomato**

Sl. No.	Character	Mean	Range		h <sup>2</sup> (%)	GCV (%)	PCV (%)	GA	GAM (%)	Parental Mean Range	
			Min.	Max.						Min.	Max.
1	Days to 50% flowering	38.86	28.0	49.0	81.8	12.82	14.17	9.28	23.89	36.09	39.04
2	Plant height(cm)	44.34	25.0	75.0	79.4	20.31	22.79	16.53	37.28	47.12	59.89
3	Number of primary branches	2.13	2.0	4.0	71.4	13.74	16.26	0.51	23.91	2.31	2.70
4	Number of secondary branches	5.49	2.0	9.0	81.9	24.77	27.38	2.53	46.18	3.95	4.30
5	Number of clusters per plant	4.49	3.0	18.0	84.9	58.51	63.51	4.98	111.06	3.69	5.75
6	Number of fruits per plant	14.18	6.0	27.0	72.4	24.01	28.22	5.96	42.08	10.14	12.30
7	Average fruit weight (gm)	55.33	22.5	105.9	90.8	37.25	39.10	40.45	73.11	56.60	79.80
8	Yield per plant (kg)	0.80	0.2	2.9	86.9	48.75	52.29	0.75	93.82	0.54	1.10



**Fig. (1): Genetic variability parameters for yield and yield related traits in multi-parent derived F<sub>2</sub> Population**

*Correlation studies:* The correlation between the yield per plant and other yield-attributing traits are presented in Table 2. Correlation coefficients among different characters indicated that yield per plant was significantly and positively associated with average fruit weight (0.8154) and number of fruits per plant (0.6501). Selection of these two traits helps in direct improvement of yield. The number of secondary branches per plant showed a significant and positive correlation with number of primary branches per plant (0.1480). The number of clusters per plant had a positive and significant correlation with the number of secondary branches per plant (0.4296). The number of fruits per plant was positively and significantly correlated to the number of secondary branches per plant (0.1767) and the number of clusters per plant (0.2045). Similar results were also obtained by Nevani and Sridevi [9], Akther [13], Joshi [14], Reddy[15], Kadyan[10] and shubha[16].

*Path coefficient analysis:* Path coefficient analysis enables the division of the correlation coefficients into the effects of a group of independent variables on the dependent variable and provides a more accurate picture of the relationship between the independent variables and the dependent variable determining the effective elements and the character's relationship. Path coefficient analysis (Table 3) revealed that a high positive direct effect on yield per plant was exerted by average fruit weight (0.7366) and number of fruits per plant (0.5481), these results are in parallel with the results of Reddy[15], Kadyan[10] and Shubha[16]. The highest negative direct effect on yield per plant was exerted by the number of clusters per plant (-0.0128). The lowest direct positive effect on yield per plant was indicated by number of secondary branches per plant (0.0042). The lowest negative direct effect on yield per plant was shown by plant height (-0.0082). The traits with a higher direct effect on yield per plant indicate direct selection for these traits might be effective and there is a possibility of improving yield. The results of direct effects on yield per plant were in parallel with the results of Gopinath and Vethamoni [12], Joshi [14] and Neavani and Sridevi [9].

**Table 2: Phenotypic correlations among yield and yield related traits in multi-parent derived F<sub>2</sub> population of tomato**

	<b>Days to 50% flowering</b>	<b>Plant height</b>	<b>Number of primary branches</b>	<b>Number of secondary branches</b>	<b>Number of clusters per plant</b>	<b>Number of fruits per plant</b>	<b>Average fruit weight</b>	<b>Yield per plant</b>
Days to 50% flowering	1							
Plant height	-0.0012	1						
Number of primary branches	0.0135	-0.0785	1					
Number of secondary branches	-0.0127	-0.1101	0.1480*	1				
Number of clusters per plant	-0.0724	0.0750	0.0531	0.4296**	1			
Number of fruits per plant	0.0271	0.0790	0.0519	0.1767**	0.2045**	1		
Average fruit weight	-0.1374*	0.0826	0.0340	-0.0725	-0.1121	0.1414*	1	
Yield per plant	-0.0943	0.0946	0.0143	0.0398	0.0180	0.6501**	0.8154**	1

\*, \*\* indicates significant at 5 per cent and 1 per cent level of probability, respectively.

**Table 3: Direct and indirect effects of different yield related traits on fruit yield in multi-parent derived F<sub>2</sub> population of tomato**

	<b>Days to 50% flowering</b>	<b>Plant height</b>	<b>Number of primary branches</b>	<b>Number of secondary branches</b>	<b>Number of clusters per plant</b>	<b>Number of fruits per plant</b>	<b>Average fruit weight</b>	<b>Yield per plant</b>
<b>Days to 50% flowering</b>	<b>-0.0087</b>	0.0000	-0.0001	-0.0001	0.0009	0.0149	-0.1012	-0.0943
<b>Plant height</b>	0.0000	<b>-0.0082</b>	-0.0008	0.0005	-0.0010	0.0433	0.0608	0.0946
<b>Number of primary branches</b>	0.0001	-0.0006	<b>-0.0100</b>	0.0006	-0.0007	-0.0284	0.0250	0.0143
<b>Number of secondary branches</b>	0.0001	-0.0009	-0.0015	<b>0.0042</b>	-0.0055	0.0968	-0.0534	0.0398
<b>Number of cluster per plant</b>	0.0006	-0.0006	-0.0005	0.0018	<b>-0.0128</b>	0.1121	-0.0826	0.0180
<b>Number of fruits per plant</b>	-0.0002	-0.0006	0.0005	0.0007	-0.0026	<b>0.5481</b>	0.1042	0.6501
<b>Average fruit weight</b>	0.0012	-0.0007	-0.0003	-0.0003	0.0014	0.0775	<b>0.7366</b>	0.8154

Diagonal values indicate direct effects, off-diagonal value- indirect effect

Residual =0.2071

## Conclusion:

In this present study variability parameters, heritability, genetic advance, correlation and path analysis for yield and yield contributing traits in multi-parent derived F<sub>2</sub> were assessed. The results indicated that a wide range of variability was seen in all traits under the study, which was witnessed by the results comparison of the F<sub>2</sub> range and parental mean range, as well as variability parameters such as PCV and GCV. So, the multi-parent derived F<sub>2</sub> population holds high variability since it involves genome constitution from multiple parents and the result is reflected as maximum variability values observed in the characters under the present investigation. Concerning fruit yield per plant, a very important trait in crop improvement programme, high heritability coupled with high genetic advance was recorded for this trait. A significant level of correlation with fruit yield per plant in a desirable direction was observed in the characters such as average fruit weight followed by number of fruits/plant. The number of fruits per plant and average fruit weight performed the highest positive direct effect on fruit yield per plant. Hence, these traits can be subjected to the selection for genetic improvement as well as the development new advanced population called MAGIC (Multi-parent Advanced Generation Intercross) can be developed which can be utilized as a mapping population for QTL mapping.

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