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Study of Genetic Variability, Correlation and Path coefficient Analysis in F_2 Segregating Population of Tomato (*Solanum lycopersicum* L.)

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ABSTRACT: Different sources of creating the variability are mutation, recombinant DNA technology, natural variation and recombinational variability. Variation due to recombination will helps in selection of superior segregants in segregating generation. This study was done to know the magnitude to genetic variability due to recombination. From the segregating F_2 population of the cross DMT-2 × Line 38, genetic variability, correlation and path coefficient analysis were studied using 14 quantitative and qualitative traits. The study showed that existence of significant amount of genetic variability for all the characters studied viz., Plant height, number of clusters, number of fruits per clusters, number of fruits per plant, average fruit weight, number of locules, pH of fruit juice and fruit yield per plant exhibited higher values of genotypic and phenotypic coefficient of variation. Whereas, high heritability was shown by all characters except primary branches per plant, while days to 1st harvest and polar length of fruit showed low and moderate genetic advance as per cent mean. While, remaining characters showed high genetic advance. These characters can be effectively improved through selection. Correlation indicated that yield was significantly and positively associated with plant height, primary branches per plant, number of clusters, number of fruits per cluster, number of fruits per plant and average fruit weight. In path coefficient analysis the highest positive direct effect was recorded in number of clusters, average fruit weight, number of fruits per cluster and number of fruits per plant. Direct selection may be executed considering these traits as the main selection criteria to reduce indirect effect of other characters during development of high yielding tomato variety.

Keywords: Tomato, Variability, Heritability, F_2 Segregating Population, Correlation and Path analysis.

INTRODUCTION

Tomato (*Solanum lycopersicon* Mill.) is third most important *Solanaceous* vegetable crop after potato and onion, originated from Peru region which is grown widely all over the world. It is one of the most significant “Protective foods” because of its exceptional nutritional content. Because of its excellent standard and nutritional benefits, it is known as the "poor man's orange" in many nations. Lycopene, the red pigment in tomatoes, is currently regarded as the "world's most effective natural antioxidant." The F_2 generation, which results from the selfing of an F_1 hybrid, has all potential variants. Hence, selection with specific goals in F_2 generation is quite successful and selfing of those selected genotypes generation after generation aids in the development of inbred lines. Estimates of genotypic and phenotypic coefficients of variation give insight into the genotype-environment interaction that determines breeding results (Taiana *et al.*, 2015). A characteristic with a high heritability and genetic progress suggests that it is driven by additive gene action and so provides the most effective selection condition. Correlation studies between fruit yield and its components, as well as their proportional contribution to yield, are useful in developing a breeding programme. Path analysis makes it easier to divide the correlation coefficient into direct and indirect effects on yield and other variables (Islam *et al.*, 2010; Kumar *et al.*, 2013). Path coefficient analysis may also be used to establish breeding strategies for developing elite genotypes through selection in advanced generations. As a result, the current study was carried out to evaluate the performance of several economic features in tomato, as well as to measure the level of variability, heritability, predicted genetic progress, correlation and path coefficient analysis components.

MATERIAL AND METHODS

The material was sown during Rabi 2020-21 in unreplicated trial at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. Totally 300 F_2 tomato plants derived from the cross DMT-2 × Line 38 along with parents and F_1'S were evaluated for yield and yield contributing characters during the year 2020-2021. The F_2 progenies obtained by selfing from the F_1 cross were raised. Each plant in the cross was labelled for recording 14 quantitative and qualitative characters, which includes days to 1st harvest, plant height (cm), number of primary branches, number of clusters, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length (mm), fruit diameter (mm), rind thickness (mm), number of locules per fruit, TSS (°Brix), pH of fruit juice and fruit yield per plant (kg), Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance (GA) and genetic advance as percentage over mean were analyzed following the formula illustrated by Singh and Chaudhary (1985). The correlation coefficient was estimated according to formula given by Johnson *et al.* (1955). The direct and indirect paths were obtained according to the method of Dewey and Lu (1959).

Statistical analyses. The coefficient of range was calculated according to the following formula:

Coefficient of range= (Max.-Min.) Where, Max. is the highest value of the trait and Min. is the lowest one.

The environmental variance (Ve) was calculated as Ve = $(Vp_1 + Vp_2 + VF_1)/3$, where VP1, VP_2, and VF_1, is the variances of parent 1, parent 2, and the cross between them, respectively.

The Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated according to the formula suggested by Singh and Chaudhary (1985) as

PCV (%) = (σp / X) × 100

GCV (%) = (σg / X) × 100

Where, σp, σg, and X are the phenotypic standard deviation, genotypic standard deviation, and the grand mean of the trait, respectively.

Broad sense heritability (h^2b.s.) estimate of each trait was calculated according to Falconer (1981) as: h^2b.s. = GV/PV

Where h^2b.s. is the broad-sense heritability, GV is the genetic variance, and PV is the total phenotypic variance.

We adopted 5% as selection intensity to keep an adequate level of variability among selected individuals to agree with the long-term selection strategies. The Expected genetic advance was estimated according to the method outlined by Johnson *et al.* (1955) as follows:

Expected genetic advance (GA) = K× σp ×h^2b.s. where GA is the genetic advance, K is a constant = 2.06 at 5% selection intensity, σp is the square root of phenotypic variance, and h^2b.s. is the heritability in the broad sense.

GA as a percentage of the mean (GA %) = (GA/X) × 100; where X is the mean of the trait in the base population.

The analyses of phenotypic, genotypic and environmental correlations were estimated according to Miller *et al.* (1958) as follows: $rPxy=covpxy\sqrt{}$vpx.vpy

$rgxy$=cov$gxy\sqrt{}$vgx.vgy

Where rpxy = phenotypic correlation coefficient between traits x and y.

covpxy = phenotypic covariance between traits x and y.

vpx, vpy = phenotypic variance of a trait x and a trait y, respectively.

rgxy = genotypic correlation coefficient between traits x and y.

covgxy = genotypic covariance between traits x and y.

vgx, vgy= genotypic variance of a trait x and a trait y, respectively.

The significance of the correlation coefficients was tested at the probability levels of 0.05 using t test at n-2 degrees of freedom according to the following equation:

t= $r\times\sqrt{n}-21-r2$

where r is the correlation coefficient, and n is the number of F_2 individuals in the case of phenotypic correlation coefficient. Whereas for environmental correlation coefficient, the degrees of freedom will be n'-2, where n' is the average number of individuals from the generations used to estimate the environmental variance (P_1, P_2, and F_1). For the genotypic correlation coefficient, the degrees of freedom will be n''-2, where n'' is the average between n and n'. R software was adopted to analyze all data of the study.

RESULTS AND DISCUSSION

Variability plays a key role in vegetable breeding ensures the better chance of producing desirable crop plants. The results of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as percent mean (GA %) in F_2 population of cross DMT-2 × Line 38 are shown in the Table 1. High PCV and GCV were observed for the traits viz. Plant height (23.34; 21.57), number of clusters (44.52; 36.85), number of fruits per cluster (23.89; 22.26), number of fruits per plant (48.44; 41.63), average fruit weight (45.4; 44.58), number of locules (24.12; 21.18), pH of fruit juice (33.86; 33.57) and fruit yield per plant (49.75; 41.59) indicating higher magnitude of variability for these characters. Whereas, days to 1st harvest showed low PCV and GCV (5.38; 4.96), while the remaining characters viz. fruit length (12.10; 10.25), fruit diameter (12.44; 11.12) and rind thickness (18.61; 17.47) had shown moderate PCV and GCV. Primary branches per plant had shown high PCV (32.56) and moderate GCV (19.47). Higher phenotypic coefficient of variation was recorded than the genotypic coefficient of variation for all the traits but the difference is narrow indicating that less influence of environmental variation.

Table 1: Genetic parameters in F_2 population of the cross DMT-2 × Line 38.

Characters	MEAN	MAX	MIN	Vp	Ve	Vg	h^2 (bs)	GCV	PCV	GA	GAM
Days to 1st harvest	87.64	94.00	82.00	22.20	3.28	18.92	85.23	4.96	5.38	8.27	9.44
Plant height (cm)	76.40	130.00	5.00	317.95	46.46	271.49	85.39	21.57	23.34	31.36	41.05
Primary branches per plant	1.18	2.00	1.00	0.15	0.09	0.05	35.78	19.47	32.56	0.28	24.00
Number of clusters	11.63	32.00	1.00	26.79	8.43	18.35	68.52	36.85	44.52	7.31	62.83
Number of fruits per clusters	2.50	4.00	1.00	0.36	0.05	0.31	86.80	22.26	23.89	1.07	42.71
Number of fruits per plant	29.63	70.00	6.00	205.91	53.82	152.09	73.86	41.63	48.44	21.83	73.70
Average fruit weight (g)	62.60	320.50	27.29	807.84	29.01	778.83	96.41	44.58	45.40	56.45	90.17
Fruit length (mm)	41.11	71.30	25.00	24.76	7.01	17.74	71.67	10.25	12.10	7.35	17.87
Fruit diameter (mm)	45.07	58.64	27.00	31.44	6.32	25.12	79.88	11.12	12.44	9.23	20.47
Rind thickness (mm)	4.09	6.00	1.00	0.58	0.07	0.51	88.18	17.47	18.61	1.38	33.80
Number of locules	4.48	7.00	2.00	1.17	0.27	0.90	77.11	21.18	24.12	1.72	38.32
TSS (^{0} brix)	4.30	6.40	2.40	0.24	0.02	0.22	91.97	10.85	11.32	0.92	21.44
pH of fruit juice	4.32	28.00	1.90	2.14	0.04	2.10	98.31	33.57	33.86	2.96	68.58
Yield per plant (Kg)	1.62	4.73	0.31	0.65	0.20	0.45	69.86	41.59	49.75	1.16	71.60

These findings were similar to Firas Al- Aysh *et al.* (2012); Reddy *et al.* (2013); Sharanappa and Mogali (2014), Ullah *et al.* (2015); Rai *et al.* (2016); Anuradha *et al.* (2020); Eppakayala *et al.* (2021); Hussain *et al.* (2021) in tomato. Fig. 1 depicts the level of PCV and GCV for all the studied traits. High value of heritability was noticed in days to 1st harvest (85.23) followed by plant height (85.39), number of clusters (68.52), number of fruits per cluster (86.80), number of fruits per plant (73.86), average fruit weight (96.41), fruit length (71.67), fruit diameter (79.88), rind thickness (88.18), number of locules (77.11), pH of fruit juice (91.97) and fruit yield per plant (98.31). Whereas, primary branches per plant (35.78 %) exhibited moderate heritability, similar results were observed by Salim *et al.* (2020); Islam *et al.* (2022).

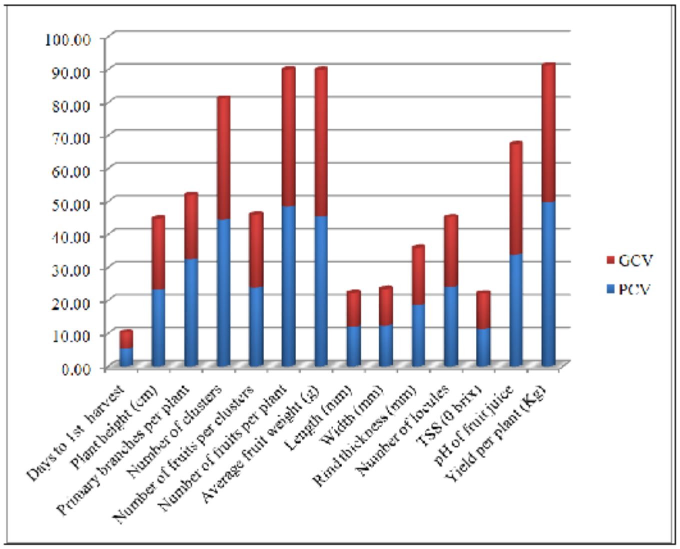

Fig. 1. PCV and GCV for yield and yield attributing traits in segregating F_2 population of tomato.

Genetic advance as percent of mean was high for the traits like plant height (41.05), primary branches per plant (24.0), number of clusters (62.83), number of fruits per cluster (42.71), number of fruits per plant (73.70), average fruit weight (90.17), fruit diameter (20.47), rind thickness (33.80), number of locules (38.32), pH of fruit juice (68.58) and fruit yield per plant (71.60) respectively. Lowest genetic advance as percent of mean was observed by days to 1st harvest (9.44). While, moderate genetic advance as percent of mean was recorded by fruit length (17.87). High estimates of heritability with high genetic advance as percent over mean were recorded for all traits except days to 1st harvest, primary branches per plant and fruit length. These findings are similar to Mehta and Asati (2008); Reddy *et al.* (2013); Ullah *et al.* (2015); Rai *et al.* (2016); Maurya *et al.* (2020); Akhter and Nanjine (2022). It might be assigned to be under the control of additive genes and phenotypic selection for their improvement could be achieved by simple breeding methods.

Correlation coefficients. The correlation between fruit yield per plant with different yield attributes are presented in (Table 2). The correlation coefficient among different characters indicated that yield per plant was significant and positively associated with plant height (0.32), primary branches per plant (0.0.29), number of clusters (0.72), number of fruits per cluster (0.38), number of fruits per plant (0.78) and average fruit weight (0.17). These results are in agreement with findings of Meena *et al.* (2015); Phom *et al.* (2015); Ullah *et al.* (2015); Meena and Bahadur (2015);

Rahman *et al.* (2015); Hazim *et al.* (2016); Maurya *et al.* (2020); Nevani and Sridevi (2021) in tomato. Days to 1^{st} harvest has showed negative and significant association with number of clusters (-0.23), number of fruits per clusters (-0.12) and number of fruits per plant (-0.2). The plant height had shown positive and significant correlation with number of clusters (0.3), number of fruits per clusters (0.15) and number of fruits per plant (0.3). Positive and significant correlation was shown by primary branches per plant with number of cluster (0.27), number of fruits per cluster (0.12), number of fruits per plant (0.32), average fruit weight (0.1) and fruit length (0.12). Similar results were also obtained by Mayavel *et al.* (2005); Akhtar and Najnine (2022). Number of clusters recorded positive and significant correlation with number of fruits per cluster (0.1) and number of fruits per plant (0.81). While, number of fruits per cluster exhibited positive and significant correlation with number of fruits per plant (0.4) and TSS (0.12). These results are in conformity with the findings of Sherpa *et al.* (2014) and Nevani and Sridevi (2021). The fruit length had positive and significant correlation with fruit diameter (0.54) and rind thickness (0.14). The result is in agreement with the findings of Mahapatra *et al.* (2013); Rahman *et al.* (2015); Venkadeswaran *et al.* (2021). Fruit diameter noticed positive and significant correlation with rind thickness (0.17) and number of locules (0.16). Other studies reported by Mahapatra *et al.* (2013); Kumar *et al.* (2013); Chernet *et al.* (2013) are also same with this findings. Correlation heatmap is graphical representation of correlation matrix representing correlation between different variables. The value of correlation can take any values from -1 to 1. Correlation between two random variables or bivariate data does not necessary imply causal relationship. Characters showing high positive correlation are shown in intense red colour, whereas characters showing negative correlation are presented in blue colour, remaining characters are in between these colours (Fig. 2).

Table 2: Correlation coefficient between fruit yield and yield components traits in F_2 generation of DMT-2 × Line 38.

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1	-0.07	-0.03	-0.23*	-0.12*	-0.2*	0.08	0.01	0	-0.07	-0.01	0.04	-0.01	-0.15*
X2		1	0.09	0.3*	0.15*	0.3*	-0.05	0.08	0.05	-0.05	-0.03	-0.05	-0.02	0.32*
X3			1	0.27*	0.12*	0.32*	-0.04	-0.05	0.05	-0.04	0.1*	0.02	0.12*	0.29*
X4				1	0.1*	0.81*	-0.22*	0.01	-0.01	-0.04	0.04	0	0	0.72*
X5					1	0.4*	-0.22*	0.02	-0.01	-0.03	0.04	0.12*	-0.06	0.38*
X6						1	-0.16*	0	-0.03	-0.02	0.05	0.02	-0.03	0.78*
X7							1	0.06	0.05	0.01	0.03	-0.06	-0.03	0.17*
X8								1	0.54*	0.14*	-0.04	-0.09	-0.17*	0.04
X9									1	0.17*	0.16*	-0.1*	-0.13*	0.01
X10										1	-0.05	0.05	0.06	-0.04
X11											1	0.01	0.06	0.04
X12												1	-0.02	0.05
X13													1	-0.05
X14														1

X_1= Days to 1^{st} harvest
X_2= Plant height (cm)
X_3= Number of Primary branches
X_4= Number of clusters per plant
X_5= Number of fruits per cluster
X_6= Number of fruits per plant
X_7= Average fruit weight (g)
X_8= Fruit length (mm)
X_9=Fruit Diameter (mm)
X_{10}= Rind thickness (mm)
X_{11}= Number of locules
X_{12}= Total soluble solids (TSS) (^{0} brix)
X_{13}=pH of fruit juice
X_{14}=Fruit yield per plant (kg)

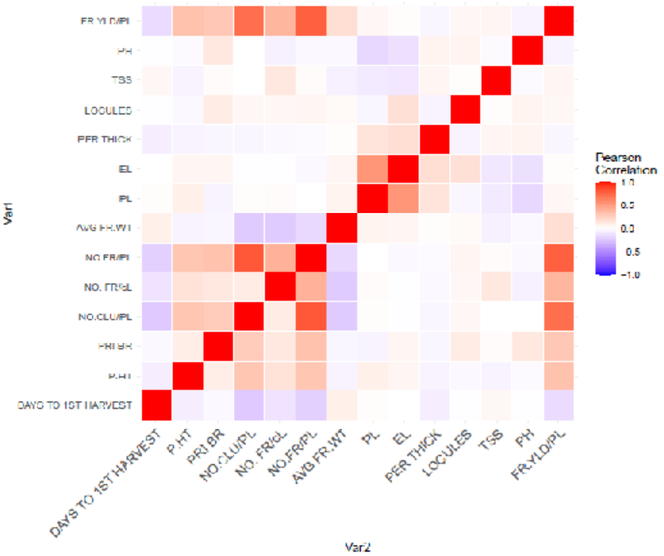

Fig. 2. Heat map showing the correlation analysis between traits in segregating F_2 population of tomato.

Path coefficient analysis. Although correlation studies are helpful in determining components of yield, with the inclusion of more variables in correlation studies, the indirect association becomes more complex. Two characters may show a correlation because they correlate with a common third one. Under such circumstances, path analysis helps in partitioning of correlation coefficients into direct and indirect effects, permitting a critical examination of the relative importance of each trait. The path coefficient analysis in (Table 3) revealed that high positive direct effect on fruit yield per plant was exerted by number of clusters (0.5562), average fruit weight (0.4022), number of fruits per cluster (0.2993) and number of fruits per plant (0.2539). The highest negative direct effect on fruit yield per plant was noted by number of locules per fruit (-0.0222). The fruit diameter recorded lowest positive direct effect of 0.0091 on fruit yield. The lowest negative direct effect on fruit yield per plant was exerted by fruit length (-0.0025). The characters showing high direct effect on yield per plant indicated that direct selection for these traits might be effective and there is a possibility of improving yield per plant through selection based on these characters. Similar results of direct positive effects for those traits were reported by Meena and Bahadur (2015); Ullah *et al.* (2015); Nagariya *et al.* (2015); Gopinath and Vethamoni (2017); Nevani and Sridevi (2021). On the other hand, positive indirect effects of plant height, primary branches per plant, number of cluster per plant and number of fruits per cluster through number of fruits per plant to yield per plant was also observed. Similar results for indirect effects were recorded by Islam *et al.* (2010); Meena and Bahadur (2015). Lower residual error of 0.195 was observed indicating the sufficient numbers of characters are considered while calculating direct and indirect effects.

Table 3: Path co-efficient on fruit yield per plant in F_2 generation of the cross DMT-2 × Line 38

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**	**X12**	**X13**	**Phenotypic Correlation with yield per plant**
X1	**0.0352**	-0.0036	-0.0011	-0.1279	-0.0359	-0.0508	0.0322	0.0000	0.0000	0.0003	0.0002	0.0014	0.0001	-0.15*
X2	-0.0025	**0.0516**	0.0034	0.1669	0.0449	0.0762	-0.0201	-0.0002	0.0005	0.0002	0.0007	-0.0017	0.0002	0.32*
X3	-0.0011	0.0046	**0.0374**	0.1502	0.0359	0.0812	-0.0161	0.0001	0.0005	0.0002	-0.0022	0.0007	-0.0015	0.29*
X4	-0.0081	0.0155	0.0101	**0.5562**	0.0299	0.2057	-0.0885	0.0000	-0.0001	0.0002	-0.0009	0.0000	0.0000	0.72*
X5	-0.0042	0.0077	0.0045	0.0556	**0.2993**	0.1016	-0.0885	0.0000	-0.0001	0.0001	-0.0009	0.0041	0.0007	0.38*
X6	-0.0070	0.0155	0.0120	0.4506	0.1197	**0.2539**	-0.0644	0.0000	-0.0003	0.0001	-0.0011	0.0007	0.0004	0.78*
X7	0.0028	-0.0026	-0.0015	-0.1224	-0.0658	-0.0406	**0.4022**	-0.0001	0.0005	0.0000	-0.0007	-0.0021	0.0004	0.17*
X8	0.0004	0.0041	-0.0019	0.0056	0.0060	0.0000	0.0241	**-0.0025**	0.0049	-0.0006	0.0009	-0.0031	0.0021	0.04
X9	0.0000	0.0026	0.0019	-0.0056	-0.0030	-0.0076	0.0201	-0.0013	**0.0091**	-0.0008	-0.0036	-0.0034	0.0016	0.01
X10	-0.0025	-0.0026	-0.0015	-0.0222	-0.0090	-0.0051	0.0040	-0.0003	0.0015	**-0.0045**	0.0011	0.0017	-0.0007	-0.04
X11	-0.0004	-0.0015	0.0037	0.0222	0.0120	0.0127	0.0121	0.0001	0.0015	0.0002	**-0.0222**	0.0003	-0.0007	0.04
X12	0.0014	-0.0026	0.0007	0.0000	0.0359	0.0051	-0.0241	0.0002	-0.0009	-0.0002	-0.0002	**0.0344**	0.0002	0.05
X13	-0.0004	-0.0010	0.0045	0.0000	-0.0180	-0.0076	-0.0121	0.0004	-0.0012	-0.0003	-0.0013	-0.0007	**-0.0124**	-0.05

Residual error: 0.1956

X_1= Days to 1st harvest
X_2= Plant height (cm)
X_3= Number of Primary branches
X_4= Number of clusters per plant
X_5= Number of fruits per cluster
X_6= Number of fruits per plant
X_7= Average fruit weight (g)
X_8= Fruit length (mm)
X_9=Fruit Diameter (mm)
X_{10}= Rind thickness (mm)
X_{11}= Number of locules
X_{12}= Total soluble solids (TSS) (^{0} brix)
X_{13}=pH of fruit juice

CONCLUSION

In respect of fruit yield, which is the most important character in any crop improvement programme, high heritability coupled with high genetic advance was the important parameter. It indicates the chances for wide range for selection in F_2 population of the cross DMT-2 × Line 38 and the yield per plant was positively and significantly correlated with plant height, primary branches per plant, number of clusters, number of fruits per cluster, number of fruits per plant and average fruit weight. In path coefficient analysis the highest positive direct effect was recorded in number of clusters, average fruit weight, number of fruits per cluster and number of fruits per plant. Hence, these traits can further be exploited by direct selection for genetic improvement in tomato to bring about the improvement in yield, from this study we obtained important transgressive segregants which can be selfed upto they attain homozygosity and can be released as new variety.

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Conflict of interest. None.

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