



## Research Article

# ASSESSMENT OF GENETIC VARIABILITY, CORRELATION AND PATH COEFFICIENTS FOR YIELD COMPONENTS AND QUALITY TRAITS IN TOMATO

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**Abstract-** The present study was carried out during the Autumn- winter period of 2014-2015 at Central Research Farm, Gayeshpur, Bidhan Chandra Krishi Viswavidyalaya, Nadia-West Bengal, with eighteen tomato genotypes including seven cultivars of *Solanum lycopersicum* viz., Berika, AC Aft, BCT-48, BCT-59, BCT-82, BCT 115dg, Pathurkuchi, five wild species namely *Solanum pimpinellifolium*, *Solanum chilense* (EC 513698), *Solanum cheesmaniae*, *Solanum lycopersicum* var. *cerasiformae* (EC 514013), *Solanum peruvianum* (EC251790), three inter specific hybrids (ISH) viz., ISH1- AC Aft x EC 514013, ISH2-Berika x EC 514013, ISH3-BCT 115dg x EC 514013 and three back cross progenies viz., ISH 1 XAC Aft, ISH2 X Berika, ISH 3 X BCT 115 dg. The characters that exhibited higher GCV and PCV values were for fruits per plant (119.35), polar diameter, fruit weight, number of cluster per plant, number of seed per fruit, test weight, plant height, number of primary branches per plant, number of fruits per cluster, locule number, flowers per cluster, equatorial diameter. High heritability along with high genetic advance as per cent of mean was observed for the traits like fruits per plant, number of cluster per plant, fruit weight, number of seed per fruit, test weight. The association studies indicated that fruit yield had significant positive correlation with fruits per cluster and fruits per plant.

**Keywords-** Tomato, Wild relatives, GCV, PCV, Correlation and Path Coefficient

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## Introduction

Tomato (*Solanum lycopersicon* Mill.) is the second most important vegetable crops of Peru-Ecuador origin after potato. Ripe fresh fruits are consumed as salads, stew and various processed products such as juice, paste, powder, ketchup, sauce and canned whole fruits [1]. Unripe green fruits are used for preparation of pickles and chutney [1, 2]. Nutritionally, tomato is a good source of vitamin A and vitamin C [3] Fruits are also a good source of lycopene, ascorbic acid and  $\beta$ -carotene, all of which are antioxidants and valued for their colour and flavour. For successful crop improvement programme, information on the nature and magnitude of genetic variability, degree of transmission of the traits is of immense importance [4]. The variability available in the population can be partitioned into heritable and non heritable component viz., phenotypic and genotypic coefficient of variation, heritability and genetic advance on which selection can be effectively carried out. The relative values of these types of coefficients give an idea about magnitude of variability present in the genetic population [5]. High phenotypic and genotypic coefficient of variation values indicates the presence of ample variation among the germplasm under study and facilitates the selection of desirable genotypes for improving the particular character [1]. However, presence of sufficient variation is not enough unless the character is additively inherent. Heritability and genetic advance are important selection parameters. High heritability alone is not enough for rewarding selection, unless accompanied by substantial amount of genetic advance [6]. High

heritability accompanied with high genetic advance confirms the additively inherent nature of a particular character. Correlation coefficient analysis is a method to estimate the mutual relationship between yield and various component characters based on which selection can be done for improvement in yield [7]. Path coefficient analysis reveals whether the association of each individual character with yield is due to their own direct effect or an indirect effect via other component traits [8]. Keeping in view of this, an attempt was made to estimate the genetic variability exists; degree of association among various yield components; and their direct and indirect effect on yield in a combined population of tomato which consists cultivated types, wild relatives, inter-specific hybrids and back cross progenies.

## Material and Methods

The field experiments were carried out during the autumn-winter of 2014-2015 at Central Research Farm, Gayeshpur, Bidhan Chandra Krishi Viswavidyalaya, Nadia-West Bengal. Topographic situation of the experimental site comes under Gangetic new alluvial plains of West Bengal with sandy loam soil. In this study, eighteen tomato genotypes including seven cultivars viz., Berika, AC Aft, BCT-48, BCT-59, BCT-82, BCT 115dg, Pathurkuchi, five wild species viz., *Solanum pimpinellifolium*, *Solanum chilense* (EC 513698), *Solanum cheesmaniae*, *Solanum lycopersicum* var. *cerasiformae* (EC 514013), *Solanum peruvianum* (EC251790), three Interspecific hybrids (ISH) viz., ISH1- AC Aft x EC 514013, ISH2-Berika x EC

514013, ISH3-BCT 115dg x EC 514013 and three Back cross progenies ISH 1 XAC Aft, ISH2 X X Berika, ISH 3 X X BCT 115 dg, were grown in randomized block design with 3 replications keeping 20 plants in each replication at 70 x 70 spacing to study the manifestation of different characters in them.

The observations were recorded on a randomly selected five competitive plants from each replication for morphological and biochemical characters viz. (1) plant height (cm), (2) number of primary branches per plant, (3) number of clusters per plant, (4) number of flower per cluster (5) Days to 1<sup>st</sup> flowering (6) number of fruits per cluster, (7) number of fruits per plant, (8) fruit weight (g), (9) equatorial diameter of fruit (mm), (10) polar diameter of fruit (mm), (11) pericarp thickness (mm), (12) locule number, (13) number of seeds per fruit, (14) test weight(g), (15) yield per plant (kg). The analysis of variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability in broad sense ( $h^2_{bs}$ ), genetic advance (GA) and genetic advance as percent over mean (GAM) for all

the characters were calculated following the formulae illustrated by Cochran and Cox [9] for ANOVA; Burten [4] for genotypic and phenotypic coefficients of variability; Hansen [10] for heritability; Jhonson [6] for genetic advance; Al-jibouri et al. [11] for genotypic and phenotypic correlations; and Dewey and Lu [8] for path coefficients.

## Results and Discussion

The analysis of variance indicated the existence of significantly greater variability among the genotypes for all the 15 characters at 1% and 5% probability level [Table-1]. The genotypes exhibited highly significant differences for all the characters studied. Number of fruits per plant, plant height, and number of seeds per fruit, fruit weight and clusters per plant were showed highly significant variation. The significant variation among the genotypes exposed that presence of adequate variability, which is sufficient to carry out further analysis.

**Table-1 Analysis of Variance for Selected characters of Tomato genotypes.**

Source of variance	Plant height	Primary branches / plant	Cluster / plant	Flower per cluster	Days to 1 <sup>st</sup> flowering	Fruits per cluster	Fruits per plant	Fruit weight (g)	Equatorial diameter (mm)	Polar diameter (mm)	Pericarp thickness (mm)	Locule number	Seeds per fruit	Test weight (g)	Yield per plant (kg)
Replication	29.24	0.27	3.34	0.12	1.44	0.09	707.54	3.71	3.22	10.91	0.03	0.02	6.83	0.01	0.01
Treatment	7228**	74.08**	2594.9**	18.09**	21.69**	19.11**	9897 24.5**	2644.74**	354.08**	717.1**	8.58**	1.8**	3107.3**	5.07**	1.90**
Error	8.49	0.08	1.05	0.04	0.50	0.03	223.13	1.74	1.12	8.67	0.01	0.01	2.55	0.01	0.01

\*\* Significant at  $P \leq 0.01$ ; \* Significant at  $P \leq 0.05$

The mean performance and range of the genotypes and different genetic variability parameters are presented in [Table-2]. The range of genotype means was highest for fruits per plant (35.26-1923.41), plant height (33.30-187.89), fruit weight (3.16-109.07), number of seed per fruit (19.69-124.428) and number of cluster per plant (10.71-110.95),

The nature and extent of genetic variability is one of the most important criteria in formulating an efficient breeding programme and knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is much helpful in predicting the amount of variation present in a given genetic stock. The highest phenotypic coefficient of variance was recorded for fruits per plant (119.36%), polar diameter (106.11%), fruit weight (88.13%), number of clusters per plant (72.06%), number of seeds per fruit (57.92%), test weight (51.32%),

plant height (43.1%), number of primary branches per plant (43.5%), number of fruits per cluster (34.2%), locule number (30.75%), flowers per cluster (28.9%), equatorial diameter (28.35%) and yield per plant (27.79%) whereas the lowest phenotypic coefficient of variation was observed for days to 1<sup>st</sup> flowering (9.19%). Genotypic coefficient of variation was high for all the characters, except days to 1<sup>st</sup> flowering (8.88%). Similar results were previously found by Agong et al. [12]. Generally PCV values were higher than GCV values for all traits but the difference between values of PCV and GCV were very less. It means that these traits were less influenced by environment. A very high PCV and GCV values (> 100%) for fruits per plant and polar diameter were due to the high standard deviation (574.38 for fruits per plant and 53.90 for polar diameter) of genotype mean values from the grand mean [Table-2].

**Table-2 Mean performance and parameters of variability for selected characters of Tomato genotypes**

	Mean	S.D.	Range		PCV %	GCV%	Heritability (bs)%	GA	GAM
			Min	Max					
Plant height (cm)	114.04	49.09	33.30	187.89	43.09	43.02	99.65	100.88	88.46
Primary branches / plant	11.43	4.97	4.90	19.18	43.5	43.46	99.68	10.22	89.39
Clusters / plant	40.83	29.41	10.72	110.95	72.06	72.01	99.88	60.54	148.25
Flowers per cluster	8.50	2.46	4.92	13.19	28.9	28.86	99.41	5.04	59.27
Days to 1 <sup>st</sup> flowering	29.94	2.69	23.53	35.51	9.19	8.88	93.35	5.29	17.67
Fruits per cluster	7.39	2.52	3.93	13.19	34.2	34.13	99.56	5.18	70.15
Fruits per plant	481.33	574.38	35.26	1923.41	119.36	119.32	99.93	1182.68	245.71
Fruit weight (g)	33.71	29.69	3.16	109.07	88.13	88.05	99.80	61.08	181.20
Equatorial diameter (mm)	38.44	10.86	22.72	60.17	28.35	28.21	99.06	22.24	57.85
Polar diameter (mm)	50.85	53.90	20.74	75.08	106.11	105.95	99.70	110.82	217.94
Pericarp thickness (mm)	3.90	1.69	0.42	7.59	43.49	43.41	99.61	3.48	89.25
Locule number	2.56	0.78	1.93	4.20	30.75	30.63	99.25	1.61	62.87
Seeds per fruit	55.61	32.18	19.69	124.43	57.92	57.85	99.75	66.19	119.02
Test weight (g)	2.54	1.30	1.18	5.30	51.32	51.25	99.72	2.67	105.42
Yield per plant (kg)	2.88	0.80	1.38	4.72	27.79	27.66	99.04	1.63	56.69

(PCV= Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, GA= Genetic Advance & GAM= Genetic Advance as percent of Mean)

High heritability estimates were observed for all the traits and ranged from 99 to 100 per cent, suggesting that high inheritance capacity of these traits and direct selection based on phenotypic expression could be effective for the improvement of these characters. The highest heritability was recorded in average fruits per plant (99.93%) with an expected genetic advance over per cent of mean 245.71% followed by number of clusters per plant 99.88% with a GAM of 148.25%, fruit weight 99.80% with a GAM of 181.20%, number of seeds per fruit 99.75% with a GAM of 119.02%, test weight 99.72% with a GAM of 105.2% indicating that these

traits are controlled by additive gene action, hence, direct selection is effective for improving these characters. Remaining traits except days to 1<sup>st</sup> flowering were also having high heritability coupled with sufficiently high genetic advance depicting the possibility of their improvement through the selection. Days to 1<sup>st</sup> flowering had high heritability (93.35%) coupled with low GAM (17.67%). This indicated those days to 1<sup>st</sup> flowering was under the influence of non-additive gene action.

The genotypic and phenotypic correlation coefficients were worked out among 14

characters [Table-3]. The genotypic correlation coefficient values were greater than the of phenotypic correlation coefficient values for majority of the characters, which indicated a strong inherent association among various traits that were quite influenced by the environment. Among all quantitative traits, yield per plant displayed highly significant and positive correlation with traits viz., number of fruits per plant (0.307, 0.308) followed by number of fruits per cluster (0.296, 0.292) at

both phenotypic and genotypic level. Similar kinds of results were obtained by Premalakshmi et al. [13] and Indu Rani et al. [14]. Plant height was having significant correlation with all the traits under study except with yield per plant. Significant positive association was observed between seeds per fruit and test weight and negative association was observed between fruits per plant and fruit weight.

**Table-3** Genotypic (G) and Phenotypic (P) Correlation coefficients among the Characters of Tomato

		A	B	C	D	E	F	G	H	I	J	K	L	M	N
B	G	0.884**													
	P	0.884**													
C	G	0.680**	0.854**												
	P	0.680**	0.854**												
D	G	0.724**	0.852**	0.725**											
	P	0.725**	0.852**	0.724**											
E	G	0.438**	0.527**	0.520**	0.611**										
	P	0.437**	0.522**	0.510**	0.608**										
F	G	0.803**	0.870**	0.678**	0.916**	0.577**									
	P	0.804**	0.871**	0.679**	0.916**	0.573**									
G	G	0.768**	0.712**	0.575**	0.629**	0.241 <sup>NS</sup>	0.814**								
	P	0.768**	0.712**	0.575**	0.628**	0.237 <sup>NS</sup>	0.813**								
H	G	-0.818**	-0.807**	-0.624**	-0.580**	-0.312*	-0.711**	-0.739**							
	P	-0.814**	-0.803**	-0.623**	-0.575**	-0.292*	-0.707**	-0.737**							
I	G	-0.653**	-0.709**	-0.551**	-0.542**	-0.360**	-0.701**	-0.758**	0.738**						
	P	-0.644**	-0.700**	-0.545**	-0.531**	-0.323*	-0.690**	-0.753**	0.737**						
J	G	0.113 <sup>NS</sup>	0.086 <sup>NS</sup>	0.001 <sup>NS</sup>	-0.269*	-0.369**	-0.187 <sup>NS</sup>	0.007 <sup>NS</sup>	-0.100 <sup>NS</sup>	-0.071 <sup>NS</sup>					
	P	0.115 <sup>NS</sup>	0.088 <sup>NS</sup>	0.002 <sup>NS</sup>	-0.266 <sup>NS</sup>	-0.346*	-0.184 <sup>NS</sup>	0.008 <sup>NS</sup>	-0.099 <sup>NS</sup>	-0.068 <sup>NS</sup>					
K	G	-0.415**	-0.363**	-0.228 <sup>NS</sup>	-0.158 <sup>NS</sup>	-0.154 <sup>NS</sup>	-0.378**	-0.572**	0.458**	0.716**	-0.063 <sup>NS</sup>				
	P	-0.410**	-0.359**	-0.226 <sup>NS</sup>	-0.152 <sup>NS</sup>	-0.134 <sup>NS</sup>	-0.373**	-0.570**	0.459**	0.717**	-0.061 <sup>NS</sup>				
L	G	-0.604**	-0.641**	-0.487**	-0.462**	-0.246 <sup>NS</sup>	-0.535**	-0.549**	0.801**	0.652**	-0.076 <sup>NS</sup>	0.269*			
	P	-0.596**	-0.633**	-0.483**	-0.452**	-0.215 <sup>NS</sup>	-0.526**	-0.545**	0.801**	0.655**	-0.072 <sup>NS</sup>	0.272*			
M	G	-0.505**	-0.687**	-0.636**	-0.522**	-0.308*	-0.572**	-0.475**	0.686**	0.433**	-0.035 <sup>NS</sup>	0.088 <sup>NS</sup>	0.828**		
	P	-0.502**	-0.684**	-0.634**	-0.516**	-0.286*	-0.568**	-0.474**	0.686**	0.435**	-0.034 <sup>NS</sup>	0.090 <sup>NS</sup>	0.827**		
N	G	-0.759**	-0.830**	-0.687**	-0.690**	-0.586**	-0.740**	-0.656**	0.790**	0.700**	0.104 <sup>NS</sup>	0.409**	0.834**	0.754**	
	P	-0.754**	-0.825**	-0.684**	-0.684**	-0.553**	-0.734**	-0.654**	0.790**	0.700**	0.106 <sup>NS</sup>	0.411**	0.834**	0.755**	
Yield	G	0.110 <sup>NS</sup>	0.162 <sup>NS</sup>	0.151 <sup>NS</sup>	0.247 <sup>NS</sup>	0.092 <sup>NS</sup>	0.292*	0.308*	0.235 <sup>NS</sup>	-0.179 <sup>NS</sup>	-0.155 <sup>NS</sup>	-0.154 <sup>NS</sup>	0.111 <sup>NS</sup>	-0.002 <sup>NS</sup>	-0.139 <sup>NS</sup>
	P	0.115 <sup>NS</sup>	0.166 <sup>NS</sup>	0.153 <sup>NS</sup>	0.252 <sup>NS</sup>	0.113 <sup>NS</sup>	0.296*	0.307*	0.238 <sup>NS</sup>	-0.168 <sup>NS</sup>	-0.151 <sup>NS</sup>	-0.147 <sup>NS</sup>	0.118 <sup>NS</sup>	0.002 <sup>NS</sup>	-0.134 <sup>NS</sup>

A=Plant height(cm); B=Primary branch / plant; C=Cluster /plant; D=Flower/cluster; E=Days to 1<sup>st</sup> flowering; F=Fruits /cluster; G=Fruits /plant; H=Fruit weight(g); I=Equatorial diameter (mm); J= Polar diameter (mm); K=Pericarp thickness(mm); L=Locule number.; M=Seeds / fruit; N=Test weight (g).

**Table-4** Path Analysis using genotypic correlations

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	Correlation with yield
A	0.59	0.44	-0.10	-0.52	-0.21	0.39	0.28	-1.58	0.51	-0.03	-0.12	-0.42	0.25	0.65	0.110
B	0.52	0.50	-0.13	-0.61	-0.26	0.42	0.26	-1.56	0.55	-0.02	-0.11	-0.44	0.33	0.71	0.162
C	0.40	0.43	-0.15	-0.52	-0.25	0.33	0.21	-1.21	0.43	0.00	-0.07	-0.34	0.31	0.59	0.151
D	0.43	0.43	-0.11	-0.72	-0.30	0.44	0.23	-1.12	0.42	0.07	-0.05	-0.32	0.25	0.59	0.247
E	0.26	0.26	-0.08	-0.44	-0.49	0.28	0.09	-0.60	0.28	0.10	-0.05	-0.17	0.15	0.50	0.092
F	0.47	0.44	-0.10	-0.66	-0.28	0.48	0.29	-1.37	0.54	0.05	-0.11	-0.37	0.28	0.63	0.292*
G	0.45	0.36	-0.09	-0.45	-0.12	0.39	0.36	-1.43	0.59	0.00	-0.17	-0.38	0.23	0.56	0.308*
H	-0.48	-0.41	0.09	0.42	0.15	-0.34	-0.27	1.93	-0.57	0.03	0.14	0.55	-0.33	-0.68	0.235
I	-0.39	-0.36	0.08	0.39	0.18	-0.34	-0.27	1.42	-0.77	0.02	0.21	0.45	-0.21	-0.60	-0.179
J	0.07	0.04	0.00	0.19	0.18	-0.09	0.00	-0.19	0.06	-0.27	-0.02	-0.05	0.02	-0.09	-0.155
K	-0.25	-0.18	0.03	0.11	0.08	-0.18	-0.21	0.88	-0.55	0.02	0.30	0.19	-0.04	-0.35	-0.154
L	-0.36	-0.32	0.07	0.33	0.12	-0.26	-0.20	1.55	-0.50	0.02	0.08	0.69	-0.40	-0.71	0.111
M	-0.30	-0.35	0.10	0.37	0.15	-0.27	-0.17	1.32	-0.33	0.01	0.03	0.57	-0.49	-0.65	-0.002
N	-0.45	-0.42	0.10	0.49	0.29	-0.36	-0.24	1.52	-0.54	-0.03	0.12	0.58	-0.37	-0.86	-0.139

A=Plant height (cm); B=Primary branch / plant; C=Cluster /plant; D=Flower/cluster; E=Days to 1<sup>st</sup> flowering; F=Fruits /cluster; G=Fruits /plant; H=Fruit weight(g); I=Equatorial diameter (mm); J= Polar diameter (mm); K=Pericarp thickness(mm); L=Locule number.; M=Seeds / fruit; N=Test weight (g).

The result of genotypic path coefficient analysis is presented in [Table-4]. In the present study, the residual value was 0.06239, which showed that the characters studied contributed 99.4% variation towards fruit yield in tomato and only 0.6 % variation in fruit yield remained unaccounted. Among all the traits under study, fruit weight (1.93) had very high direct positive effect on fruit yield per plant followed by number of locules (0.69), plant height (0.59), primary branches per plant (0.50), fruits per cluster (0.48), fruits per plant (0.36). Therefore, direct selection of

segregants based on fruit weight, plant height, primary branches per plant, fruits per cluster, fruits per plant, fruit weight and number of locules would result in higher breeding efficiency for improving fruit yield. Thus, these traits might be estimated as the most important component trait for fruit yield per plant. Similar results have been obtained by Indu Rani et al. [14].

The highest negative direct effect were observed for test weight followed by equatorial diameter, number of flowers per cluster, days to first flowering, number

of seeds per fruit and polar diameter suggesting for selection of lower values for these traits. These results are similar to Premalakshmi et al. [13].

### Conclusion

A wide range of tomato germplasm including local cultivars, wild relatives and inter-specific segregants and backcross progeny were employed and it resulted in the greater amount of variability. High variation was observed for fruits per plant, polar diameter and plant height. Fruits per plant and fruits per cluster had significant positive association with the yield per plant and fruit weight, plant height, primary branches per plant, fruits per cluster, fruits per plant, fruit weight and number of locules was having high direct effect on fruit yield. Hence direct selection based these characters would be effective in these progenies.

### Conflict of Interest: None declared

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