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Genetic analysis for growth and yield character association in different genotypes of tomato (*Solanum lycopersicum* L.)

Sateesha HD and Anita KerkettaDOI: <https://doi.org/10.22271/chemi.2021.v9.i1s.11410>**Abstract**

The present study was carried out at the Experimental Research Field, Department of Horticulture, Naini Agriculture Institute, SHUATS, Prayagraj. The material for the present study comprised of 15 genotypes of tomato. The experiment was laid out in a randomized block design (RBD) with three replications for each treatment. Quantitative character were recorded such as plant height (cm), Days to 1st flowering, days to 50% flowering, Number of branches per plant, number of flowers per cluster, number of fruit set per cluster, number of flower cluster per plant, number of fruits per plant, days to first fruit set, fruit yield per plot, fruit weight (g), fruit length, fruit diameter (cm), TSS, ascorbic acid, pericarp thickness (mm), number of locules per fruit, fruit yield plant⁻¹ (kg). On the basis of Analysis of variance, significant differences were observed among the genotypes for all the characters under study. The high (> 30%) Phenotypic Coefficient of Variation (PCV) were observed fruit weight (30.25%) and all other remaining parameters are comes under moderate and low PCV and Genotypic Coefficient of Variation (GCV). The presence of high PCV and moderate GCV for fruit weight suggested the possibility of improving and fixing these characters through employing selection breeding.

Keywords: Tomato, genetic variability and correlation**Introduction**

Tomato (*Solanum lycopersicum* L.) is belongs to the nightshade family Solanaceae with chromosome number $2n=2x=24$. It is an herbaceous, annual to perennial, prostrate, sexually propagated, and typical day neutral plant, It is self-pollinated crop but a certain percentage of cross-pollination also occurs. It has taproot and growth habit of the plant is determinate or indeterminate. Scientific information indicates that the cultivated tomato originated in a wild in the Peru-Ecuador-Bolivia area of the Andes (South American). However, the domestication of tomato took place in Mexico. The most likely ancestor of cultivated tomato is the cherry type (*Lycopersicon esculantum* var. *creasiforme*). There are several species of tomato but the fruits are edible only of two species namely (*Lycopersicon esculantum* and *L. pimpinellifolium*) and third popular widely grown and consumed vegetable in the world after potato and sweet potato. In India, tomato occupies an area of 7.7 million hectare with a production of 193.97 million ton and productivity of tonnes per hectare (FAO, 2012) [5]. It is a rich source of vitamins, minerals and organic acids those imparts considerable amounts of antioxidant property in human body (Tomlekova *et al.*, 2007; Glogovac *et al.*, 2010) [6, 7] that alleviate chronic diseases such as cancer and coronary heart disease (Canene-Adams *et al.*, 2005; Omoni and Aluko, 2005; Kun *et al.*, 2006) [8, 14, 9]. Being a self-pollinated crop, it has a tremendous potential for heterosis breeding and it is used in different breeding programme for genetic studies. Potent variability can be expected in tomato with respect to plant stature, fruit shape, size, quantity and quality (Bhardwaj and Sharma, 2005) [10]. In order to meet the demands of alarming increasing population of the world, plant breeders exerting great toil to improve genetic potential of yield and quality traits of tomato crop. Thus for improving the productivity of tomato primary concern should be on development of elite genotype by employing selection among and/or within the population through the utilization of existing genetic variability. Yield is attributed as complex polygenetically controlled character, closely associated with direct effect of other individually contributing characters and their complex interactions among themselves for ultimate manifestation of yield.

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Materials and Methods

The experiment was conducted at farm of Department of Horticulture, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology & Sciences Naini, Prayagraj Uttar Pradesh in rabi season during 2019-2020. The genotype was consisted of 15 tomato genotypes. The experiment was laid out in Randomized block design (RBD) with 3 replications. An inter-row spacing of 60 cm and inter-plant distance of 45 cm was mentioned. All the package of practices was followed to get a healthy crop. The data collected on different parameters during the course of investigation were subjected to statistical analysis as per method of analysis of variance (Panse and Sukhatme 1957)^[15]. The significance and non-significance of the treatment effect were judged with the help of 'F' variance ratio test. Calculated 'F' value (variance ratio) was compared with the table value of 'F' at 5% level of significance. If calculated value exceeded the table value, the effect was considered to be significant.

Table 1: Show the table of Genotype symbol and source

Sl. No.	Genotype symbol	Genotype	Source
1	G1	Narendra tomato-1	NDAU, Faizabad
2	G2	Narendra tomato-2	NDAU, Faizabad
3	G3	Narendra tomato-3	NDAU, Faizabad
4	G4	Narendra tomato-5	NDAU, Faizabad
5	G5	Narendra tomato-6	NDAU, Faizabad
6	G6	Narendra tomato-7	NDAU, Faizabad
7	G7	Narendra tomato-8	NDAU, Faizabad
8	G8	Pusa ruby	IARI, New Delhi
9	G9	Pant tomato-1	GBPUAT, Pantnagar
10	G10	Pant tomato-3	GBPUAT, Pantnagar
11	G11	Arka Vikash	IIHR, Bangalore
12	G12	Arka Abha	IIHR, Bangalore
13	G13	Kashi Hemant	IIVR, Varanasi
14	G14	Angoorlata	CSAU, Kanpur
15	G15	Kashi Sharad	IIVR, Varanasi

Result and Discussion

Analysis of variance

The mean sum of square in ANOVA revealed high variability among 15 genotypes for all the characters at 5% and 1% level of probability. Analysis of variance revealed that significant difference among the genotypes for all the traits under study indicating the presence of substantial genetic variability in tomato (Table-2). Similar results proposed Shashi Kanth *et al.*, (2010)^[18], Patel *et al.*, (2013)^[16] and Bhandari *et al.* (2017)^[2].

Genetic Parameters

One of the important considerations in any crop improvement is the detailed study of genetic variability. Variability is a measure by estimation of Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h^2) in the broad sense, genetic advance, and genetic advance as per cent of the mean.

Range

The highly significant differences might be endorsed to their genetic makeup of germplasm lines and various regions from where they have been collected. The results of present investigation are in accordance with jaiswa *et al.*, (2015), Gowher *et al.*, (2013) and Kumar *et al.*, (2017). The mean performance of various genotypes has also showed good range of variability for various characters, which were studied in present investigation (Table 3). The Range record for plant

height (74.06 cm to 120.67 cm), Days to First Flowering (24.83 to 29.80), Days to 50% Flowering (41.66 to 47.62), Number of branches per plant (6.60 to 10.73), Number of flower per cluster (5.20 to 5.86), Number of flowers cluster per plant (10.53 to 18), Number of fruit set per cluster (2.80 to 4.06), Number of fruits per plant (37.96 to 65.61), Days to first fruit set (48.46 to 50.13), Fruit yield per plant (2.02 kg to 4.60 kg), Fruit yield per plot (6.66 kg to 10.66 kg), Fruit weight (50.00 g to 124.33 g), Fruit length (4.13 to 5.70), Fruit diameter (3.30 cm to 4.30 cm.), Total Soluble Solid (TSS) (3.52 Brix to 5.83 Brix.), Ascorbic acid (12.62 to 18.75), Pericarp thickness (3.22 mm to 5.10 mm), Number of locules per fruit (2.36 to 4.56.).

Genotypic and Phenotypic Coefficient of Variation

The highest value of genotypic coefficient of variation (GCV) was recorded for average fruit weight (27.46%) followed by fruit yield per plant (24.52%), moderate coefficients of variation was recorded for number of locules per fruit (17.13%), number of flower cluster per plant (12.92%), Number of fruits per plant (12.77%), pericarp thickness (12.39%), plant height (11.48%), days to first flowering (11.04%), fruit yield per plot (10.16%), number of fruit cluster per plant (10.03%), and genotypic coefficient of variation was recorded for fruit set per cluster (9.02%), TSS (8.58%), fruit length (6.72%), number of branches per plant (6.00%), Days to 50% flowering (5.81%), number of flower per cluster (5.43%), fruit diameter (4.80%), ascorbic acid (3.59%) and days to first fruit set (0.71%).

Similar result was also observed by Ahemed *et al.* (2006)^[11] for plant height, for TSS⁰Brix and Manna and Paul (2012)^[12] for ascorbic acid who reported that relative magnitude of phenotypic coefficient of variation is greater than corresponding genotypic coefficient of variation which indicates the effect of environment.

Heritability (h^2 in broad sense), Genetic Advance and Genetic advance as percent of mean:

Heritability and genetic advance are the important genetic parameters for selecting a genotype that permit greater effectiveness of selection by separating out environmental influence from total variability. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. Heritability and genetic advance estimated for different characters under study are presented in Table 2 and its summary are presented also in (Figure 1).

The highest heritability estimate was observed for days to first flower (86.9%), fruit weight (82.4%), days to 50% flowering (79.9%), pericarp thickness (74.1%), fruit yield per plant (70.4%), plant height (54.8%), followed by TSS (99.28%), number of locules per fruit (53.8%), number of fruit set per cluster (53.7%), number of flower cluster per plant (40.2%), fruit length (34.6%), number of flower per cluster (32.4%), number of fruits per plant (31.2%), fruit yield per plot (29.1%), TSS (20.2%), fruit diameter (17.1%), Number branches per plant (12.6%), and Ascorbic acid (7.00%). The high values of heritability estimates in broad sense indicated that sustainable improvement can be made using standard selection procedures. Similar results were noticed by Phookan *et al.* (1998) for number of fruits per plant, fruit set per cent and average fruit weight; Ahmed *et al.* (2006)^[11] for all traits; Mahesha *et al.* (2006)^[11] for plant height, fruit weight and fruits per plant and Darand Sharma (2011)^[4] for ascorbic acid. On the other hand the highest genetic advance as percent of mean observed for fruit weight (51.36) followed by fruit

yield per plant (42.38), number of locules per fruit (0.90), pericarp thickness (0.87), days to first flower (21.20), plant height (17.50), numbers of flowers per cluster (0.34), number of fruits per plant (14.49), number of flower cluster per plant (2.47), number of fruit set per cluster (13.62), fruit yield per plot (11.30), days to 50% flowering (10.69), fruit length (8.14), TSS (7.65), number of flower per cluster (6.36), number of branches per plant (4.38), fruit diameter (4.08), ascorbic acid (1.96), days to first fruit set (0.48). Tasisa *et al.* (2011) [19] recorded high genetic advance as per cent of mean for fruits per plant, plant height, yield per plant and fruit diameter, which indicate that selection would be more useful to improve crops. Similar finding were also reported by Ahmed *et al.* (2006) [1] and Mahesha *et al.* (2006) [11] for plant height, number of fruits per plant, fruit weight and fruit yield per plant and Pandit *et al.* (2010) for fruit weight.

Conclusion

From the above discussion it could be concluded that there were sufficient variability among the genotypes for all the characters under study that justified the incorporation of local genotype in the present experiment and expression of characters was less influenced by the environment. Higher magnitude for genotypic as well as phenotypic coefficient of variation for fruit yield per plant and fruit weight suggested effectiveness of selection breeding in fixation and improvement of these characters. High heritability coupled with high genetic advance as per cent of mean for all the characters under study was evident for existence of additive gene effect, suggested significance of selection breeding for improvement of these characters.

Table 2: Analysis of variance for different characters in different genotypes of Tomato

Sl. No.	Characters	Mean sum of square		
		Replication (df=2)	Genotype (df=24)	Error (df=28)
1	Plant height	31.59	488.73 **	105.36
2	Days to first flowering	1.25	34.13 **	1.6
3	Days to 50% flowering	0.68	24.96 **	1.94
4	Number of branches per plant	1.08	2.69 **	1.88
5	Number of flowers per cluster	0.08	0.09 *	0.35
6	Fruit set per cluster	0.52	0.4 *	0.08
7	Flower cluster per plant	8.45	16.11 **	5.34
8	Number of fruits per plant	74.63	230.94 **	97.71
9	Days to first fruit set	1.39	0.91 *	1.28
10	Fruit yield per plot	0.76	2.38 **	0.29
11	Fruit yield per plant	6.46	4.81 **	2.15
12	Fruit weight	310.48	1232.92**	81.91
13	Fruit length	0.26	0.47 *	0.18
14	Fruit diameter	0.10	0.23 *	0.14
15	TSS	0.55	0.96 **	0.54
16	Ascorbic acid	18.11	5.11 **	4.16
17	Pericarp thickness	0.03	0.81 **	0.08
18	Number of locules per fruit	0.32	1.39 **	0.31

Significant at 5% level of probability, **Significant at 1% level of probability

Table 3: Mean, Range, Heritability, Genetic advance as percent of mean and coefficient of variations (GCV and PCV), for 18 characters of tomato genotypes

Sl. No	Characters	Mean	Min	Max	Heritability (%)	Genetic advance (%)	Genetic advance as percentage of mean	GCV (%)	PCV (%)
1	Plant height	98.48	74.06	120.66	54.8	17.24	17.50	11.48	15.50
2	Days to first flowering	29.80	24.83	38.13	86.9	6.31	21.20	11.04	11.85
3	Days to 50% flowering	47.62	41.66	50.80	79.9	5.09	10.69	5.81	6.51
4	Number of branches per plant	8.67	6.60	10.73	12.6	0.38	4.38	6.00	16.92
5	Number of flowers per cluster	5.45	5.20	5.86	32.4	0.34	6.36	5.43	9.54
6	Fruit set per cluster	3.56	2.80	4.06	53.7	0.48	13.62	9.02	12.31
7	Flower cluster per plant	14.65	10.53	18.93	40.2	2.47	16.87	12.92	20.39
8	Number of fruits per plant	52.04	37.96	65.61	31.2	7.64	14.49	12.77	22.89
9	Days to first fruit set	49.40	48.46	50.13	10.7	0.23	0.48	0.71	2.18
10	Fruit yield per plot	9.267	6.66	10.66	29.1	1.04	11.30	10.16	18.82
11	Fruit weight	71.31	50.00	124.33	82.4	36.62	51.36	27.46	30.25
12	Fruit length	4.62	4.13	4.13	34.6	0.37	8.14	6.72	11.44
13	Fruit diameter	3.62	3.30	4.20	17.1	0.14	4.08	4.80	11.61
14	TSS	4.34	3.52	5.83	20.2	0.34	7.95	8.58	19.10
15	Ascorbic acid	15.63	12.62	18.75	7	0.30	1.96	3.59	13.54
16	Pericarp thickness	3.98		3.22	74.1	0.87	21.97	12.39	14.40
17	Number of locules per fruit	3.50	2.36	4.56	53.8	0.90	25.88	17.13	23.37
18	Fruit yield per plant	3.40	2.02	4.60	70.4	1.44	42.38	24.52	29.22

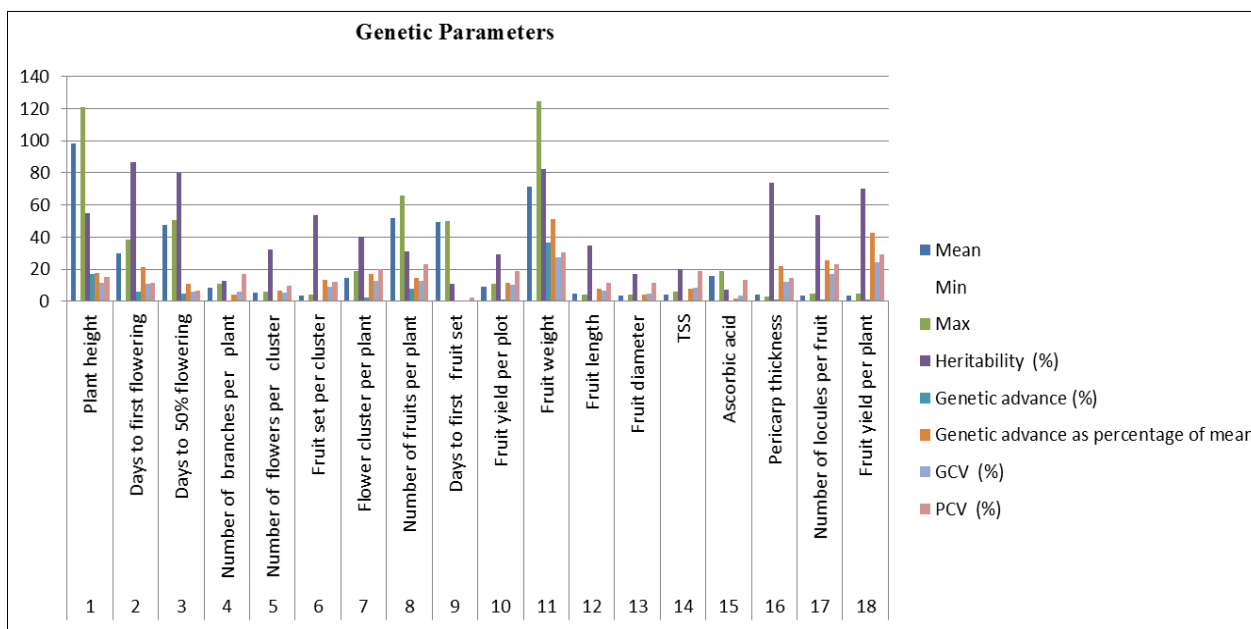


Fig 1: Mean, Range, Heritability, Genetic advance as percent of mean and coefficient of variations (GCV and PCV), for 18 characters of tomato genotypes

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