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The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(4): 399-403

www.thepharmajournal.com
Received: 22-02-2021
Accepted: 24-03-2021

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Assessment of genetic variability in tomato (*Solanum lycopersicum* L.) for yield and yield attributing traits

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Abstract
The genetic parameters were studied to elucidate the genetic variability, heritability, genetic advance and genetic advance as *per cent* over mean in tomato (*Solanum lycopersicum* L.). Sixty diverse genotypes were evaluated during the year 2019-20 at experimental research farm of the Haweli campus, College of Horticulture, Bagalkot, and Karnataka. The analysis of variance revealed highly significant difference among 60 genotypes for all 24 characters under study. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for majority of the characters studied indicating influence of the environment on the trait expression. High heritability with high genetic advance as *per cent* of mean was observed for plant spread (98.2% and 35.76%), equatorial diameter (95.40% and 42.68%), polar diameter (96.00% and 38.97%), pericarp thickness (66.10% and 35.27%), fruit color (79.80% and 37.70%), fruit pH (91.40% and 31.99), lycopene (75.90% and 60.388%), titrable acidity (74.50% and 44.38%), ascorbic acid (75.40% and 26.80), fruit firmness (94.30% and 26.24%), average fruit weight (94.30% and 72.04), number of fruits per plant (63.40% and 57.23%). High heritability combined with high genetic advance indicates that additive gene action plays a major role in governing these traits and these traits can be improved by simple selection.

Keywords: genetic variability, heritability, genetic advance as per cent over mean, GCV, PCV

Introduction
Tomato, *Solanum lycopersicum* L. (2n = 2x = 24) is one of the versatile vegetable crops belonging to family solanaceae. Tomato is an important, popular and stands second only in most consumed vegetables after the potato. Tomato popularly known as 'love apple' in Europe is one of the most commonly grown vegetables in kitchen and homestead gardens. Tomato is a preferred crop of breeder as it provides excellent opportunity for plant genetic studies.

It is an unique crop as it is used in both fresh, processed forms and also for its nutritive value. It is a good source of vitamins like vitamin A and C, minerals like calcium, potassium and iron (Saleem *et al.*, 2013) [21]. Caretenoid, lycopene present in tomato a powerful antioxidant which confer health benefits to humans. Raw tomatoes and processed products are very good source of lycopene having an antioxidant property which quenches a single oxygen molecule produced by free oxy radicals. Thus, today it is one of the important raw material for many processing industries. Tomato is called as "poor man's apple" as the fruit is a very good source of nutritional components (Singh *et al.*, 2004) [25].

India is the second largest producer (11.5%) after China (30.7%) followed by U.S.A. (8.1%) (Anon., 2018) [3]. Tomato occupies 9.6 per cent area under vegetables and contributes 11.2 per cent towards national tomato production. In India area under tomatoes is about 0.78 million hectares with the production of 19.37 million tons and an average productivity of 28.10 t/ha (Anon., 2018) [3]. Andhra Pradesh is the leading state in tomato with respect area and production where as for the productivity *per se* Karnataka ranks first.

Being so much important crop with respect to its fresh consumption, usage for value added products and nutritive value, there is huge demand, which remains to be a challenge to meet with. It's very essential to meet the ever-increasing demand for this vegetable by increasing population and also important to meet nutritional security. Hence, there is a need to develop high yielding, improved, stable varieties and hybrids with respect to yield and quality in tomato. Development of hybrid is one prominent method among the others used for tomato improvement. The success of best hybrid depends on the extent of genetic variability present in the material used and the nature of inheritance and its extent (Allard, 1960) [1]. More the genetic divergence between the parental lines more will be the heterosis.

Hence, the present investigation is undertaken to assess the genetic variability present in the germplasm to the genetic value and further to be utilized in crop improvement of tomato.

Material and Methods

The experiment was conducted at experimental research farm of the Haweli campus, College of Horticulture, Bagalkot during the year 2019-20. Total 60 diverse tomato genotypes were collected and evaluated in randomized block design with two replicatons. The genotopes were analysed and studied for 24 different parameters *viz,* plant height, plant spread, number of branches, days to first flowering, days to 50 per cent flowering, days to fruit harvest, fruit color, fruit fiemness, pericarp thickness, number of locules, TSS, lycopene, pH, titrable acidity, ascorbic acid, flowers per cluster, fruit per cluster, fruit clusters per plant, equatorial diameter, polar diameter, average fruit weight, number of fruits per plant, yield per plant and yield per plot.

The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications. Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) [5] based on estimate of genotypic and phenotypic variance. The broad sense heritability was estimated by following the procedure suggested by Hanson *et al.*, 1956. Genetic advance as percent of mean was categorized as low, moderate and high as given by Johnson *et al.* (1955) [11].

Results and discussion

In the present investigation, analysis of variance was calculated for 24 characters. The analysis of variance revealed highly significant difference among 60 genotypes for all 24 characters (Table 1). All the genotypes exhibited considerable amount of differences in their mean performance with respect to all the characters studied which indicated that, the germplasm under present study was genetically diverse.

Estimates of Phenotypic Coefficient of Variation (PCV) were higher than that of the Genotypic Coefficient of Variance (GCV) for majority of the characters studied implying that greater role was played by the environment for expression of characters (Table 2). Considerable differences between the phenotypic and genotypic coefficient of variations observed for number of branches (12.84 and 17.03), days to first flowering (5.84 and 11.49) and days to 50 per cent flowering (5.70 and 10.07), total soluble solids (9.73 and 18.98), number of locules (21.72 and 31.71), flowers per cluster (9.81 and 15.43), fruits per cluster (9.39 and 17.33), fruit cluster per plant (12.91 and 17.09), number of fruits per plant (34.89 and 43.08), yield per plant (12.64 and 23.64) and yield per plot (14.52 and 27.15). In tomato, similar results were also observed for characters like number of branches (Mehta and Asati, 2008) [14], days to first flowering (Hasan *et al*. 2016; Haydar *et al*. 2007) [8, 9], days to 50 per cent flowering (Veershetty, 2004; Narolia *et al.* 2012; Rawat *et al.* 2020) [28, 15, 19], for TSS (Sunilkumar *et al*. 2016; Hasan *et al.* 2016) [26, 8], number of locules (Sherpa *et al*. 2014; Renuka *et al.* 2017) [23, 20], flowers per cluster (Joshi and Singh,2003) [12], for fruits per cluster (Basavaraj *et al*. 2015) [4], fruit clusters plant (Kumar *et al.* 1980; Joshi and Singh, 2003) [12], number of fruits per plant (Mehta and Asati, 2008; Basavaraj *et al.* 2015) [14, 4], for yield per plant (Prashanth *et al*. 2006; Al-Aysh *et al*. 2012) [18, 2], for yield per plot (Shashikanth *et al*. 2010) [22]. Higher values for PCV than that of GCV suggesting that the characters are sensitive to environmental fluctuations. Thus, selection based on phenotypic performance of these characters would be ineffective to bring about considerable genetic improvement of these traits in the genotypes included in the present study.

Differences observed between GCV and PCV were of lesser magnitude for the characters like, plant height, plant spread, days to first harvest, polar diameter, equatorial diameter, pericarp thickness, fruit color, fruit firmness, fruit pH, lycopene content, titrable acidity, ascorbic acid, average fruit weight. The estimates of GCV and PCV were low in the present study for days to first harvest (7.665%, 8.769%). Similar kind of results were reported by Henareh (2015) [10], Singh and Janeja (2018) [24] and Rawat et al. 2020 [19]. This indicates that there was little influence of environmental factors on the phenotypic expression on above mentioned characters. Thus, selection based on phenotypic performance of these characters would be effective to bring about considerable genetic improvement.

In general, a high coefficient of variability indicated that there is a scope for selection and improvement of these traits. Further estimation of heritability is useful for the prediction of response of a genotype for selection. Estimate of heritability assists breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955) [11].

High estimates of broad sense of heritability (>60%) was observed in the present study for plant height (71.20%), plant spread (84.80%), days to first harvest (76.4%), polar diameter (95.40%), equatorial diameter (96.00%), pericarp thickness (66.10%), fruit color(79.80%), fruit pH (91.40%), fruit firmness (94.30%), Lycopene (75.90%), TA (74.50%), ascorbic acid (75.40%), average fruit weight (94.30%), Number of fruits per plant (63.40%). This indicates the improvement can be made through simple selection for these traits. Low heritability (0-30%) was observed for days to first flowering, days to 50% flowering, TSS, fruits per cluster, yield per plant, yield per plot in the present study and similar were the observations of earlier workers also. Low heritability indicates greater role of environment on the expression of the traits. Therefore, methods of selection based on families and progeny testing are more effective and efficient. Similar results were also reported earlier Rawat *et al.* 2020 [19]; Sureshkumara *et al.* 2018 [27]; Mehta and Asati, 2008 [14]; Joshi and Singh, 2003 [12], Lekshmi and Celine, 2017 [13]; Basavaraj *et al.* 2015 [4].

High heritability with high genetic advance as per cent of mean was observed for plant spread, equatorial diameter, polar diameter, pericarp thickness, fruit color (L*a*b*), fruit pH, lycopene, titrable acidity, ascorbic acid, fruit firmness, average fruit weight, number of fruits per plant. Similar results were obtained by Sunilkumar *et al.* (2016) [26], Patel *et al.* (2017) [17], Sureshkumara *et al.* (2018) [27] and Pandey *et al.* (2019). This indicates that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Low heritability and low genetic advance as per cent over mean was observed for days to first flowering, days to 50 per cent flowering. Similar results reported by Joshi and Singh (2003) [12]. Low heritability and moderate genetic advance as per cent over mean for yield per plant and yield per plot were observed and similar results were also reported by Veershetty (2004) [28] and this indicated

that, the characters are governed by non-additive gene action and heterosis breeding will be useful.

Heritability in broad sense may mislead in judging the effectiveness of selection for the trait. As only additive component of genetic variance is efficiently transferred from generation to generation. Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggests reliability of crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters.

High heritability with high genetic advance as per cent of mean was observed for plant spread (98.2% and 35.76%), equatorial diameter (95.40% and 42.68%), polar diameter (96.00% and 38.97%), pericarp thickness (66.10% and 35.27%), fruit color (L*a*b*) (79.80% and 37.70%), fruit pH (91.40% and 31.99), lycopene (75.90% and 60.388%), titrable acidity (74.50% and 44.38%), ascorbic acid (75.40% and 26.80), fruit firmness (94.30% and 26.24%), average fruit weight (94.30% and 72.04), number of fruits per plant (63.40% and 57.23%). Similar results were obtained by Sunilkumar *et al.* (2016) [26], Patel *et al*. (2017) [17], Sureshkumara *et al.* (2018) [27] and Pandey *et al*. (2019) [16]. This indicates that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Low heritability and low genetic advance as per cent over mean was observed for days to first flowering (25.88% and 6.11%), days to 50 per cent flowering (32.00% and 6.64%). Similar results reported by Joshi and Singh (2003) [12]. Low heritability and moderate genetic advance as per cent over mean for yield per plant and yield per plot were observed and similar results were also reported by Veershetty (2004) [28] and this indicated that, the characters are governed by non-additive gene action and heterosis breeding will be useful.

Table 1: Analysis of variance (ANOVA) for growth, yield and quality parameters in tomato

Sl. No.	Source of Variations	Replicate	Treatments	Error
	DF	1	59	59
1	Plant height (cm)	36.3	112.971**	18.991
2	Plant Spread (cm)	30.261*	75.433**	6.207
3	Nuber of branches	4.84**	1.249**	0.344
4	Days to first flowering	36.3*	15.057*	8.876
5	Days to 50% flowering	39.675*	15.367**	7.912
6	Days to first harvest	29.008	79.195**	10.602
7	Fruit color (L*)	8.603	85.258**	9.605
8	Fruit color (a*)	2.892	51.546**	9.059
9	Fruit color (b*)	2.868	88.709**	13.66
10	Fruit Firmness (N)	110.4**	496.431**	14.528
11	Number of locules	0.919	1.63**	0.589
12	Pericarp Thickness (mm)	7.435**	2.665**	0.544
13	TSS ^{o}Brix	3.156*	0.983*	0.574
14	pH	0.041	1.223**	0.055
15	Lycopene	1.135	20.616**	2.818
16	Titrable acidity (%)	0.021	0.055**	0.008
17	Ascorbic acid (mg)	0.638	24.841**	3.476
18	Flowers per cluster	0	0.915**	0.388
19	Fruits per cluster	0.662	0.788*	0.43
20	Fruit cluster per plant	4.74	13.801**	3.775
21	Polar Diameter(cm)	0.127	1.53**	0.036
22	Equatorial Diameter (cm)	0.403**	1.476**	0.03
23	Average Fruit weight (g)	43.032	865.126**	25.26
24	Number of fruits per plant	136.811	416.925**	93.318
25	Yield per plant(Kg)	0.27	0.325*	0.181
26	Yield per plot(Kg)	6.03	32.549*	18.074

Table 2: Estimates of mean, range, components of variance, heritability and genetic advance for growth, yield and quality parameters in tomato

Sl. No.	Traits	Range		General Mean	Var Genotypical	GCV	Var Phenotypical	PCV	h2 (Broad Sense)	Genetic Advancement 5%	Gen.Adv as per cent Mean 5%
		MIN	MAX								
Growth and earliness parameters:											
1	Plant height (cm)	46.38	80.21	59.77	46.99	11.47	65.98	13.59	71.2	11.92	19.94
2	Plant Spread (cm)	27.83	59.92	41.22	34.61	14.27	40.82	15.50	84.8	11.16	27.07
3	Primary Branches	4.06	8.25	5.24	0.45	12.84	0.80	17.03	56.8	1.044	19.93
4	Days to first flowering	24.00	36.50	30.12	3.09	5.84	11.97	11.49	25.8	1.84	6.11
5	Days to 50% flowering	27.50	40.50	33.88	3.73	5.70	11.64	10.07	32	2.25	6.64
6	Days to first harvest	61.00	86.50	76.41	34.30	7.67	44.90	8.77	76.4	10.54	13.8
7	Fruit color (L*)	15.78	52.13	30.01	37.83	20.49	47.43	22.95	79.8	11.31	37.7
8	Fruit color(a*)	9.69	38.12	30.97	21.24	14.88	30.30	17.78	70.1	7.95	25.67
9	Fruit color(b*)	21.01	61.71	29.40	37.52	20.84	51.19	24.34	73.3	10.81	36.76
10	Fruit Firmness	91.80	139.76	118.33	240.95	13.12	255.48	13.51	94.3	31.05	26.24
11	Number of locules	2.00	5.25	3.32	0.52	21.72	1.11	31.71	46.9	1.02	30.65
12	Pericarp Thickness (cm)	2.24	7.71	4.89	1.06	21.06	1.60	25.90	66.1	1.73	35.27

13	TSS ºBrix	1.78	6.53	4.65	0.20	9.73	0.78	18.98	26.3	0.48	10.27
14	Fruit pH	3.78	7.12	4.71	0.58	16.24	0.64	16.98	91.4	1.51	31.99
15	Lycopene	1.93	15.47	8.87	8.90	33.64	11.72	38.60	75.9	5.36	60.39
16	TA (%)	0.35	1.12	0.61	0.02	24.95	0.032	28.92	74.5	0.27	44.36
17	Ascorbic acid (mg/100g)			21.82	10.68	14.98	14.16	17.24	75.4	5.85	26.80
Yield parameters:											
18	Flowers per cluster	4.17	7.75	5.23	0.26	9.81	0.65	15.44	40.4	0.67	12.85
19	Fruits per cluster	3.17	6.75	4.50	0.18	9.39	0.61	17.33	29.4	0.47	10.48
20	Fruit cluster per plant	13.54	24.60	17.35	5.01	12.91	8.79	17.09	57	3.48	20.08
21	Polar Diameter(cm)	22.12	63.13	4.08	0.75	21.21	0.78	21.72	95.4	1.74	42.66
22	Equatorial Diameter (cm)	23.54	57.09	4.40	0.72	19.31	0.75	19.72	96	1.72	38.98
23	Average Fruit weight (g)	7.86	102.92	56.91	419.93	36.01	445.19	37.08	94.3	41.00	72.04
24	Number of fruits per plant	18.25	89.75	36.46	161.80	34.89	255.12	43.80	63.4	20.87	57.23
25	Yield per plant	1.24	3.41	2.13	0.07	12.64	0.25	23.64	28.6	0.30	13.92
26	Yield per plot	9.65	31.35	18.53	7.24	14.52	25.31	27.15	28.6	2.96	15.99

GV = Genotypic variance PV = Phenotypic variance GCV = Genotypic coefficient of variance
GA= Expected genetic advance PCV= Phenotypic coefficient of variance h^2 = Heritability (broad sense)
GAM = Genetic advance (per cent mean)

Conclusion

From the findings of the present investigation, it is realised that sufficient quantum of genetic variability for different traits was assessed in diverse genotypes of tomato, which indicates the existence of considerable scope for the improvement of these genotypes for these traits through selection and hybridization. The parallelism between the magnitude of heritability and degree of genetic gain has been due to the additive gene playing a predominant role and therefore, these were more reliable for effective selection. Furthermore, moderate to high GCV together with moderate to high heritability and genetic advance as percent of mean was reported for many characters under study which indicated predominant additive gene action and thus these traits has ample scope for the improvement of concerned traits through selection.

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