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Genetic variability, heritability and genetics advance studies for yield and its contributing traits in tomato (*Solanum lycopersicum* L.)

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Abstract
The presence of adequate genetic variability and its critical analysis are needed for initiating any crop improvement program and for adopting appropriate selection techniques. An investigation was carried out to know the extent of genetic variability present in thirty genotypes of tomato during *rabi* season. Analysis of variance revealed highly significant differences for all the 20 quantitative traits, indicating the presence of genetic variability among the genotypes. The magnitude of PCV was slightly higher than GCV for the traits *viz.,* days to first flowering, days to 50% flowering, days to 50% fruiting, primary branches, secondary branches, plant height, clusters/plant, flowers/cluster, fruits/cluster, fruits/plant, pericarp thickness, locule number, seed index, average fruit weight, fruit shape index, juice-pulp ratio, total soluble solids, yield/plant, lycopene and Carotene indicating the considerable influence of the environment on the expression of the traits. The estimates of PCV and GCV were moderate to high for the traits *viz.,* days to first flowering, primary branches, secondary branches, plant height, clusters/plant, flowers/cluster, flowers/cluster, fruits/cluster, fruits/plant, pericarp thickness, locule number, seed index, average fruit weight, fruit shape index, juice-pulp ratio, fruit yield/Plant, lycopene and carotene indicating the influence of the environment rather than the genotype alone. Moderate high to medium broad-sense heritability estimates observed for most of the traits suggests that selection for these traits can be achieved directly based on their phenotypic performance. The low broad sense heritability observed for total soluble solids indicative of the influence of the environment on this trait. The low heritability of this trait indicates the ineffectiveness of direct selection for this trait. The heritability and genetic advance estimates were moderate for most of the traits indicating the influence of additive gene action; as such selection would likely be effective for improvement of these traits.

Keywords: Genetic variability, heritability, genetic advance, *Solanum lycopersicum* L.

Introduction
Tomato (*Solanum lycopersicum* L.) is one of the most important *Solanaceous* vegetable crops grown widely all over the world. It is a very versatile vegetable for culinary purpose. It is a member of *Solanaceous* family with chromosome numbers 2n = 24 (Jenkins, 1948). It is a tropical day neutral plant and predominantly self-pollinated but a certain percentage of cross-pollination also occurs. Peru Ecuador region is considered to be the center of its origin (Rick, 1969) [18]. It is a warm season crop reasonably resistant to heat and drought and grows under wide range of soil and climatic conditions. Tomato cultivation has become increasingly popular since the mid-nineteenth century because of its varied climatic tolerance and high nutritive value. In India tomato is grown in an area of about 25.66 mha which accounts about with the estimated production of 320.48 million tones **(**Anonymous, 2019-20) [2]. The production of tomato is very low in India due to non-availability of high yielding varieties. Development of high yielding varieties require the existence of variability therefore, the knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Estimation of genetic variability parameters such as genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV) are useful in detecting the amount of variability preset in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in detecting the influence of environment on the expression the genotypic and phenotypic reliability of traits. With the above background information the present investigation was undertaken to study the genetic parameters among the thirty tomato genotypes.

Materials and Methods

The present experiment was carried out during *rabi* season at vegetable research farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental material consisted of 30 tomato genotypes (Table 1). The recommended agronomic practices were followed. Fertilizers were applied at the rate of 120 kg N, 80 kg P_2O_5 and 70 kg K_2O per hectare, of which basal application of half of nitrogenous and entire quantities of phosphatic and potassium fertilizers were given at sowing time. The remaining half amount of nitrogen was divided into two parts and was applied after each of two irrigations. Thirty genotypes were grown in a randomized block design (RBD) with three replications. Observations were recorded on for 20 traits *viz.*, days to first flowering, days to 50% flowering, days to 50% fruiting, primary branches, secondary branches, plant height, clusters/plant, flowers/cluster, fruits/cluster, fruits/plant, pericarp thickness, locule number, seed index, average fruit weight, fruit shape index, juice-pulp ratio, total soluble solids, yield/plant, lycopene and Carotene. Each entry in a replication was represented by one row, each row having 10 plants. Row to row distance was kept at 60 cm and plant to plant distance within the row was maintained at 45 cm. The data were analysed by Analysis of Variance technique of Randomized Block Design given by Ostle (1966) [16] and the genotypic and phenotypic variances were calculated as per the formulae suggested by Burton, (1952). Heritability in broad sense and expected genetic advance as % of mean were estimated as per suggested by Allard (1960) [1].

Results and Discussion

Variability in the population is a prerequisite especially for characters where improvement is required. Success of plant breeding programmes largely depends on the amount of genetic variability present in a given crop species for the character under improvement. The analysis of variance for all characters (Table 2) revealed highly significant differences among all the 30 genotypes for all the characters *viz*., days to first flowering, days to 50% flowering, days to 50% fruiting, primary branches, secondary branches, plant height, clusters/plant, flowers/cluster, fruits/cluster, fruits/plant, pericarp thickness, locule number, seed index, average fruit weight, fruit shape index, juice-pulp ratio, total soluble solids, yield/plant, lycopene and Carotene. The result indicated that high variability among the genotypes providing ample scope of selection for different quantitative traits. Significant variation for various quantitative traits were also reported by Brar *et al*. (2000) [5], Kumar *et al.* (2001) [12], Singh *et al.* (2002) [19], Hidayatullah *et al.* (2008) [9], Ara *et al.* (2009) [3], Bernousi *et al.* (2011) [4]. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters.

The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study.

Estimates of phenotypic variances were higher than genotypic variance for all the studied quantitative traits indicating the influence of environmental factors on these traits (Table 2). These results are in conformity with the earlier findings of Phookan *et al.* (1998) [17], Dar and Sharma (2011) [7], Maurya *et al.* (2011) [14]. Moderate to high for the traits *viz.*, days to first flowering, primary branches, secondary branches, plant height, clusters/plant, flowers/cluster, flowers/cluster, fruits / cluster, fruits/plant, pericarp thickness, locule number, seed index, average fruit weight, fruit shape index, juice-pulp ratio, fruit yield/Plant, lycopene and carotene, indicating the possibilities for direct phenotypic selection under sodicity, similar results were reported by Singh (2002) [19] and Ara *et al.* (2009) [3]. The difference between PCV and GCV was less for all traits under study. This suggested that the traits were less influenced by environment and predominance of genetic factor controlling variability in these traits hence, they could be improved by following phenotypic selection. Heritability estimates indicate the relative degree at which a character is transmitted from parents to off-spring. High heritability values indicated that the characters under study were less influenced by environment in their expression. The traits exhibiting high heritability could be improved by adopting simple selection methods. The magnitude of broad-sense heritability ranged from 26.80% (total soluble solids) to 98.9% (carotene). Heritability is grouped as low (<40%), moderate (40-60%) moderate high (60-80%) and high (> 80%). Moderate high heritability were observed for characters like days to 50% flowering, primary branches, clusters/plant, flowers/cluster, fruits /cluster, average fruit weight, fruit shape index and juice-pulp ratio Similar finding were reported by Manna and Paul (2012) [13]. Mohanty (2002a) [15]. Low heritability observed for total soluble solids (26.80) might be due to the variation of environmental component involved for this trait and vice versa. High heritability estimated traits indicated a high response to selection for particular traits. Heritability itself alone is not very much useful because it includes the effect of both additive and non-additive gene. The genetic advance is therefore a useful indicator to achieve expected result on the trait of interest of a population after selection. Genetic advance in percentage of mean give more precise result in comparison to only genetic advance. Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and high (≥20%). Moderate Genetic advance in percent mean (10-20%) were observed for days to 50% flowering and days to 50% fruiting other traits showed high genetic advances (≥20%) except total soluble solids (3.15). This indicates observed characters among tested genotypes governed by non-additive gene action and thus heterosis breeding, family selection and progeny testing methods is used for improvement on such traits. These results are in conformity with the earlier findings of Das *et al.* (1998) [8], Kumar and Tiwari (1999) and Singh (1999) [11, 21].

Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. In the present study, moderately high heritability along with moderate genetic advance as percent of mean were exhibited by days to first flowering, Plant height, Fruits / Plant and Fruit yield / Plant. The present finding is in corresponding to the work of Mohanty (2002a) [15] and suggesting the presence of both additive and non-additive gene actions and simple selection offers best possibility of improvement of these traits.

Table 1: List of Tomato genotypes collected from different region of India

Sr. No.	Genotype/Code	Sr. No.	Genotype/Code
1	EC - 168283	16	Angurlata
2	EC - 20510	17	Azad T-5
3	EC - 538148	18	Co-3
4	EC - 538380	19	DT-10
5	EC - 538408	20	H-86
6	EC - 538419	21	Kajela
7	EC - 538422	22	Kashi Amrit
8	EC - 538423	23	Kashi Sharad
9	EC - 538455	24	Pant T-3
10	EC - 62025	25	PM-1
11	EC - 620530	26	Punjab Upama
12	EC - 620536	27	Selection-7
13	EC - 620538	28	Shalimar-2
14	EC - 620541	29	Superbug
15	EC - 620578	30	Swarna Naveen

Table 2: Analysis of variance for yield and quality traits in 30 genotypes of tomato

Source of Variation	d.f.	Mean sum of squares									
		Days to first flowering	Days to 50% flowering	Days to 50% fruiting	Primary branches	Secondary branches	Plant height	Clusters / Plant	Flowers / Cluster	Fruits / Cluster	Fruits / Plant
Replication	2	3.811	7.878	3.900	2.396**	1.083	170.093**	2.859**	0.244	0.824*	22.660
Treatment	29	74.793**	66.136**	70.606**	1.307**	15.890**	804.575**	2.763**	3.744**	1.725**	249.748**
Error	58	4.202	5.154	3.164	0.192	1.164	20.231	0.332	0.324	0.248	8.866
Source of Variation	**d.f.**	**Mean sum of squares**									
		Pericarp thickness	**Locule number**	**Seed index**	**Average fruit weight**	**Fruit shape index**	**Juice-pulp ratio**	**Total soluble solids**	**Fruit Yield / Plant**	**Lycopene**	**Carotene**
Replication	2	0.003	0.120	0.0003	42.842	0.004	0.012	0.126	0.055	0.000003	0.001
Treatment	29	0.028**	1.940**	0.012**	438.422**	0.065**	0.147**	0.777**	1.192**	0.067**	0.329**
Error	58	0.001	0.136	0.001	56.884	0.006	0.018	0.370	0.044	0.001	0.001
* Significant at p=0.05											
** Significant at p=0.01											

Table 3: Estimates of genetic parameters for various traits of 30 tomato genotypes

Parameters Characters	Mean ±S.E.	Range		$Ϭ^2_p$	$Ϭ^2_g$	PCV (%)	GCV (%)	h^2_{bs} (%)	GA (%)	GA as % of Mean
		Min	Max							
Days to first flowering	40.66 ± 1.18	28.33	49.00	27.73	23.53	12.95	11.93	84.8	9.21	22.64
Days to 50% flowering	48.24 ± 1.31	39.67	56.33	25.48	20.33	10.46	9.35	79.8	8.30	17.20
Days to 50% fruiting	60.63 ± 1.03	53.00	68.33	25.65	22.48	8.35	7.82	87.7	9.15	15.08
Primary branches	3.43 ± 0.25	2.07	4.70	0.56	0.37	21.91	17.79	66.0	1.02	29.76
Secondary branches	6.17 ± 0.62	2.33	13.03	6.07	4.91	39.95	35.92	80.8	4.10	66.52
Plant height	80.71 ± 2.6	46.17	116.20	281.68	261.44	20.79	20.03	92.8	32.09	39.76
Clusters / Plant	4.89 ± 0.33	3.83	8.53	1.14	0.81	21.84	18.39	71.0	1.56	31.92
Flowers / Cluster	5.29 ± 0.33	3.50	8.85	1.46	1.14	22.89	20.20	77.9	1.94	36.72
Fruits / Cluster	3.58 ± 0.29	2.16	6.14	0.74	0.49	24.04	19.61	66.5	1.18	32.93
Fruits / Plant	31.71 ± 1.72	19.00	54.67	89.16	80.29	29.78	28.26	90.1	17.52	55.24
Pericarp thickness	0.5 ± 0.02	0.24	0.71	0.01	0.01	20.29	18.80	85.8	0.18	35.88
Locule number	3.03 ± 0.21	2.00	4.40	0.74	0.60	28.30	25.56	81.6	1.44	47.56
Seed index	0.27 ± 0.01	0.13	0.40	0.004	0.004	25.24	23.65	87.8	0.12	45.65
Average fruit weight	39.26 ± 4.35	21.00	71.67	184.06	127.18	34.56	28.73	69.1	19.31	49.19
Fruit shape index	0.98 ± 0.04	0.69	1.28	0.03	0.02	16.28	14.31	77.3	0.25	25.92
Juice-pulp ratio	0.65 ± 0.08	0.32	1.11	0.06	0.04	38.04	31.93	70.4	0.36	55.21
Total soluble solids*	4.66 (12.44±0.35)	3.88 (11.32)	5.47 (13.52)	0.51	0.14	5.71	2.96	26.8	0.39	3.15
Fruit yield / Plant	1.47 ± 0.12	0.63	3.20	0.43	0.38	44.39	42.02	89.6	1.21	81.95
Lycopene	0.19 ± 0.01	0.01	0.61	0.02	0.02	80.19	79.23	97.6	0.30	161.25
Carotene	0.56 ± 0.02	0.06	1.20	0.11	0.11	59.02	58.71	98.9	0.68	120.30

$Ϭ^2_p$ – phenotypic variance; $Ϭ^2_g$ – genotypic variance; PCV – Phenotypic coefficient of variance; GCV – Genotypic coefficient of variance; h^2_{bs} – heritability in broad sense; GA – Genetic advance (at 5% selection intensity i.e. K = 2.06)
*Values in parenthesis are transformed values.

Conclusion

The estimate of heritability was moderately high with low genetic advance as percentage of mean for number of locules per fruit pericarp thickness and yield per plant which indicated that high heritability was due to non-additive gene effects and influence of environment. Hence, there was a

limited scope for selection. The present finding is in corresponding to the work of Singh *et al.* (2006) [20].

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Competing Interests
Authors have declared that no competing interests exist.

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