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Genetic Variability, Heritability and Genetic Advance for Yield Traits in Tomato (*Solanum lycopersicum* L.)

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ABSTRACT

Keywords

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The genetic parameters of variability were studied for ten yield traits in 66 genotypes of tomato. Highly significant genotypic differences were reported for all the traits. The maximum coefficient of range was reported for average fruit weight followed by fruit yield (Kg)/plant, number of seeds/fruit and total number of fruits/plant. The maximum estimate of phenotypic and genotypic variance was recorded for number of seeds/fruit followed by plant height, average fruit weight and total number of fruits/plant. The trait fruit yield (Kg)/plant recorded the maximum heritability followed by number of fruits/cluster. Important yield traits namely average fruit weight, number of fruits/plant, number of seeds/fruit and fruit yield (Kg)/plant revealed high heritability coupled with high Genetic Advance as percentage of mean. Simple selection or pure line selection following hybridization may be effective for improvement in yield traits.

Introduction

Tomato is one of the major vegetable crops cultivated throughout the world. It ranks 2nd among vegetable crops and 7th in the list of important crop species worldwide. In India, it is next only to potato and onion among vegetables in terms of production. Since its introduction in 16th century, it has spread to almost all the parts of the world and is being grown commercially in 159 countries (Saker *et al.*, 2011). The crop has become popular among farmers because of its short duration, high yield potential, high profitability and economic viability. On account of its high nutritive (Ram, 2005) and protective values (Chauhan *et al.*, 2014), it is one of the most consumed vegetables in different forms. It is highly valued in processing industries for its peculiar sensorial properties.

Tomato is a diploid species with 12 pairs of chromosomes. It is a member of solanaceae family and is close to several other important crops like brinjal, chilly, potato, tobacco. It has its primary center of diversity in a narrow belt along the Andean region of Ecuador and Peru (Carelli *et al.*, 2006). It was domesticated in 16th century and its consumption started in the later part of 18th century. Within short span of time, it has gained the major share of vegetable production across the world.

Tomato accounts for 15% of world vegetable production (FAO, 2013). China, India, USA, Turkey, Egypt, Iran, Italy, Brazil, Spain etc. are the major producers of tomato. India is the 2nd largest producer of tomato in terms of both area and production. In India, it is cultivated over an area of nearly 0.80 mha (DAC, 2016). Madhya Pradesh, Andhra Pradesh, Karnataka, Odisha are the major producing states of tomato in India. It has the share of nearly 8.3% of total vegetable area and 10.3% of total vegetable production in India. Though, Tomato is one of the major vegetables exported from India, per capita consumption in India is abysmally low (Srivastava *et al.*, 2016). In the year 2014-15, an estimated 0.22 mt of tomato worth 44 461.34 Lakh were exported from India.

Being an important vegetable crop, yield improvement is one of the major breeding objectives particularly in Indian context as the average Indian yield levels (21.2 t/ha) are far below the world average of 33.9 t/ha (National Horticulture Board, 2014). Being a complex trait, yield improvement is dependent on improvement in other traits contributing yield. Hence, the information on genetics of yield and yield traits is essential. Yield improvement of any crop is subject to formulation of efficient breeding programmes. Deployment of a particular breeding strategy needs an insight into the components of genetic variability. Genetic variability is estimated by phenotypic and genotypic coefficient of variation. Heritability estimates are indicative of transmissibility of a particular trait. This also gives an indication of environmental influences in the expression of a particular trait. Genetic advance refers to improvement of the selected progenies over the base population. The information on heritability in conjunction with genetic advance is needed for effective selection (Johnson *et al.*, 1955).

Many studies on genetic variability are available in tomato (Saeed *et al.*, 2007; Khanom *et al.*, 2008; Shashikanth *et al.*, 2010; Reddy *et al.*, 2013; Nwosu *et al.*, 2014). Most of these studies involved very small number of test genotypes. For a confirmative study, it is desirable to estimate the components of genetic variability using more number of test genotypes covering wide geographical distribution. Furthermore, it is essential to confirm the previous results using new accessions and at other locations. In this context, the present investigation was carried out to unravel the components of genetic variability, heritability and genetic advance of important yield traits in 66 genotypes tomato representing released varieties, improved lines, local collection and germplasm from India and abroad.

Materials and Methods

Experimental site and Environment

The present investigation was carried out at Vegetable Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental site is located in the middle Ganges valley in the Eastern part of the state of Uttar Pradesh at 25°19′59″N latitude, and longitude: 83°00′00″E longitude and at elevation of 77 m above mean sea level. The climate of the location is characterized as humid subtropical climate with large variations between summer and winter temperatures. The average annual rainfall is 1,110 mm (44 in). Fog is common in the winters, while hot dry winds, blow in the summer. .

Experimental material, Experimentation and observation

The experimental material comprised of 66 genotypes of tomato collected from different institutes and agricultural universities across India and abroad and maintained at Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The test genotypes are listed in table 1.

The nursery was raised in 2nd fortnight of August-2014. Due care was taken to get the healthy seedlings. The 25-day-old crop was transplanted in the main field. The experiment was laid out in Randomized Complete Block design (RCBD) with three replications. An inter-row spacing of 60 cm and inter-plant distance of 45 cm was maintained. All the recommended package of practices was followed to get a healthy crop. Data were recorded from five randomly selected plants for ten yield traits *viz*., days to 50% flowering, plant height, number of primary branches per plant, number of flowers/cluster, number of fruits/cluster, number of fruits per plant average fruit weight, number of locules/fruit, number of seeds/fruit and yield/plant.

Statistical Analyses

Analysis of variance was done based on RCBD as suggested by Panse and Sukhatme (1985) for each of the characters separately. The total variation was split into variation due to replication, genotypes and error. The phenotypic and genotypic coefficient of variance was estimated according to Burton and De Vane (1953). The heritability in broad sense and genetic advance was calculated as per Johnson *et al.*, (1955). Coefficient of range was calculated using following formula:

$$Coefficient\ of\ range = \frac{H - L}{H + L}$$

Where,

H is the highest value in a set of observation and
L is the lowest value in a set of observation.

Results and Discussion

The analysis of variance revealed highly significant differences among genotypes for all the traits indicating presence of considerable variability for the traits under study among the test genotypes (Table 3).

The different genetic parameters like range, mean, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as a percentage of mean are presented in table 2.

The range was the maximum for number of seeds/fruit (172.7) followed by number of fruits/plant (92.5), average fruit weight (71.8) and plant height (58.8). This is in agreement with reports of Golani *et al.*, (2007) who reported wide variability for average fruit weight, fruit yield(Kg) /plant, and plant height. Patel *et al.*, (2013) also reported higher range for average fruit weight in tomato. Meena *et al.*, (2015) also reported high estimates of range for fruit yield/ plant and plant height. The range is not a very robust measure of dispersion.

Hence, coefficient of range (a relative measure of dispersion) was calculated as it is a more precise estimate of variability.

The maximum coefficient of range was reported for average fruit weight (0.97) followed by fruit yield(Kg) /plant (0.94), number of seed/fruit (0.73) and total number of fruits/plant (0.66) indicating existence of sufficient variability among the test genotypes for the traits. The least coefficient of range was noted for days to 50% flowering. The existing wide variability can be efficiently employed in direct selection for improved plant type as a short term strategy.

The data indicated that phenotypic variance was greater than genotypic variance for all the traits under study. The maximum estimate of phenotypic and genotypic variance, respectively was recorded for number of seeds/fruit (770.30 and 721.94) followed by plant height (186.59 and 160.11), average fruit weight (181.12 and 176.89) and total number of fruits/plant (174.58 and 170.11).

The least estimate of phenotypic and genotypic variance was recorded for fruit yield(Kg) /plant (0.28 and 0.27). Mohamed *et al.,* (2012) also reported higher estimates of genotypic variance for plant height and average fruit weight. Meena and Bahahdur (2014) also recorded high estimates of phenotypic and genotypic variance for plant height. Narrow difference between the estimates of phenotypic and genotypic variance indicated higher contribution of genetic component towards total variability.

Accordingly, phenotypic coefficient of variance was greater than genotypic coefficient of variance for all the traits. The narrow difference between phenotypic coefficient of variation and genotypic coefficient of variation was indicative of lesser influence of environment on expression of these traits.

Similar findings were reported by Khapte and Jansirani (2014), Patel *et al.,* (2013) and Golani *et al.,* (2007). The difference between phenotypic and genotypic coefficient of variance was comparatively larger for number of locules/fruit and days to 50% flowering. Heritability in broad sense estimate ranged from 80.02 to 98.92%.

The trait fruit yield (Kg) /plant recorded the maximum heritability (98.92%) followed by number of fruits/cluster (98.69%). All the traits with the exception of days to 50% flowering and number of locules/fruit recorded heritability of more than 90%. Days to 50% flowering and number of locules/fruit recorded heritability of 80.02 and 88.68%, respectively. This is in agreement with the reports of Nwosu *et al.,* (2014) and Reddy *et al.,* (2013) who reported higher estimates of heritability for important yield traits like fruit weight, number of fruits/cluster etc.

Genetic advance as a per cent of mean (GAM) ranged from 15.91 to 71.93. The least GAM was observed for days to 50% flowering (15.91) followed by plant height (32.14), number of flowers/cluster (36.38) and number of primary branches/plant (37.44). Moderate GAM (<60) was observed for number of fruits/cluster (40.29) and number of locules/fruit (42.26).

High estimates of GAM (>60) was observed for average fruit weight (62.88), number of seeds/fruit (70.23), fruit yield(Kg) /plant (70.68) and number of fruits/plant (71.93). Khapte and Jansirani (2014) also reported low GAM for plant height and number of primary branches/plant and high GAM for fruit yield(Kg) /plant.

Present study indicated that phenotypic selection may be fruitful for the traits showing higher GAM *viz.,* average fruit weight, number of fruits/plant number of seeds/fruit and fruit yield(Kg) /plant.

GAM must be considered in conjunction with heritability. Important yield traits namely average fruit weight, number of fruits/plant, number of seeds/fruit and fruit yield(Kg) /plant revealed high heritability coupled with high GAM. This indicated the additive gene effect in determination of these traits. Comparatively low heritability coupled with low GAM for days to 50% flowering revealed the influence of environment on the trait.

Table.1 List of genotypes included in genetic variability study

S. No.	Genotype	Source/Origin	S. No.	Genotype	Source/Origin
1	EC 620578	IIVR, Varanasi	34	EC 538423	IIVR, Varanasi
2	EC 521087	IIVR, Varanasi	35	Punjab Upma	PAU, Ludhiana
3	EC 520061	IIVR, Varanasi	36	Kajela	-
4	EC 20510	IIVR, Varanasi	37	DT-2	IIVR, Varanasi
5	EC 620541	IIVR, Varanasi	38	DVRT1-2	IIVR, Varanasi
6	EC 531803	IIVR, Varanasi	39	DT-10	IARI, New Delhi
7	Nandi	IIHR, Bangalore	40	HT-4	-
8	EC 528374	IIVR, Varanasi	41	TLC-1	-
9	EC 538156	IIVR, Varanasi	42	T- Local	Tripura
10	EC 620530	IIVR, Varanasi	43	Selection-7	HAU, Hissar
11	Kashi Sharad	IIVR, Varanasi	44	NDT-3	NDUA&T, Faizabad
12	EC 620536	IIVR, Varanasi	45	NDTVR-60	NDUA&T, Faizabad
13	EC 538411	IIVR, Varanasi	46	VR-20	-
14	EC 620538	IIVR, Varanasi	47	Angurlata	-
15	EC 605694	IIVR, Varanasi	48	Azad T-5	CSUA&T, Kanpur
16	CLN 2116	AVRDC, Taiwan	49	Flawery	USA
17	EC 538434	IIVR, Varanasi	50	Superbug	USA
18	EC 538380	IIVR, Varanasi	51	GT	Gujarat
19	EC 620419	IIVR, Varanasi	52	FLA 7171	USA
20	EC 168283	IIVR, Varanasi	53	Co-3	TNAU, Coimbatore
21	EC 538155	IIVR, Varanasi	54	Arka Vikas	IIHR, Bangalore
22	EC 521069	IIVR, Varanasi	55	Kashi Amrit	IIVR, Varanasi
23	EC 620438	IIVR, Varanasi	56	NDT 8	NDUA&T, Faizabad
24	BS-24-2	-	57	PM-1	IARI, New Delhi
25	EC 538440	-	58	H-88-78-1	IIVR, Varanasi
26	PS-1	IARI, New Delhi	59	Swarna Naveen	-
27	BS-31-3	-	60	Floradel	Florida, USA
28	BS-18-7	-	61	Feb-04	-
29	Columbia	USA	62	Kashi Anupam	IIVR, Varanasi
30	B-S-2-5	-	63	Pusa Sadabahar	-
31	Pant-T-3	GBPUA&T	64	Shalimar-2	-
32	H-24	-	65	BT-120	--
33	Kashi Vshesh	IIVR, Varanasi	66	NDTVR-73	NDUA&T, Faizabad

Table.2 Genetic parameters of different yield traits

Parameter/ Trait	**General Mean**	**Range**	**Coefficient of range**	**PV**	**GV**	**PCV**	**GCV**	**h^2 (bs)**	**Genetic Advance**	**Genetic Advance as % of mean**
DF (50%)	44.78	35.3-55.7	0.22	29.15	18.67	12.06	9.65	80.02	7.12	15.91
Plant Height (cm)	75.12	46.2-105.0	0.39	186.59	160.11	18.18	16.85	92.68	24.15	32.14
No of primary branches	4.52	2.0-6.7	0.54	0.91	0.78	21.07	19.57	92.88	1.69	37.44
No of flowers/cluster	5.23	3.5-8.7	0.43	1.05	0.95	19.59	18.60	94.95	1.90	36.38
No of fruits/cluster	4.26	2.5-6.7	0.46	0.99	0.83	23.32	21.36	91.60	1.71	40.29
Total no of fruits/plant	36.87	23.5-116.0	0.66	174.58	170.11	35.84	35.37	98.69	26.52	71.93
Average fruit weight (g)	43.06	1.2-73.0	0.97	181.12	176.89	31.25	30.89	98.85	27.08	62.88
No of seeds/fruit	76.30	32.0-204.7	0.73	770.30	721.94	36.38	35.22	96.81	53.58	70.23
No of locules/fruit	3.21	1.8-5.6	0.51	0.70	0.55	26.07	23.12	88.68	1.35	42.26
Fruit yield (Kg/ha)	1.51	0.1-3.2	0.94	0.28	0.27	35.07	34.69	98.92	1.07	70.68

Table.3 Analysis of variance for different economic traits

Trait/ Source of variation	Replication MSS	Genotype MSS	Error MSS	CV	SE (d)±
Degree of freedom	2	65	130	-	-
DF (50%)	38.87*	66.49***	10.48	7.23	2.64
Plant Height	6.1	506.8***	26.48	6.85	4.20
No of primary branches	0.74**	2.47***	0.12	7.81	0.29
No of flowers/ cluster	0.12	2.94***	0.10	6.15	0.26
No of fruits/ cluster	0.18	2.64***	0.16	9.37	0.33
Total no of fruits/ plant	11.97	514.79***	4.47	5.74	1.73
Average fruit weight	0.28	534.91***	4.23	4.78	1.68
No of seeds/ fruit	131.17	2214.18***	48.37	9.12	5.68
No of locules/ fruit	0.13	1.80***	0.15	12.03	0.32
Fruit yield/ ha	0.02	0.83***	0.01	5.17	0.06

MSS: Mean sum of squares; CV: Coefficient of variation; SE(d): Standard Error of difference; *: Significant at 5% probability; **: Significant at 1% level of probability; ***: Significant at 0.1% level of probability

This trait can be improved by hybridization. The study revealed that simple selection or pure line selection following hybridization in early generations may be rewarding for improvement in improvement of important yield traits.

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