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

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A B S T R A C T

The present research programme, Genetic variability, heritability and genetic advance for yield and yield attributes in tomato (*Solanum lycopersicum* L.) was carried out at experimental farm of college of horticulture, Department of vegetable science, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad, Telangana, kharif, 2017-18. Forty tomato genotypes were evaluated in Randomized Block Design with three replications. Significant differences among genotypes were noticed in all characters. In the present investigation the high genetic variability observed for the characters number of primary branches per plant, number of fruits per plant, average fruit weight, fruit yield per plant and yield per hectare reveal the significance of these characters to be used for selecting superior genotypes. High heritability coupled with high genetic advance as per cent of mean shows operation of additive gene action which was observed in character's plant height, number of primary branches per plant, days to 50% flowering, days to fruit set, number of fruits per plant, average fruit weight, fruit yield per plant, yield per hectare, ascorbic acid content, TSS, beta carotene and lycopene content which may be exploited for improvement through phenotypic selection for yield improvement.

Introduction

Tomato (*Solanum lycopersicum* L.), originated from South America, is one of the most important and widely grown crop in Solanaceae family. Tomato is also called Love apple, Poor man's orange and it is universally treated as Protective food. It is rich in Vit-C and it is an important source of lycopene, which is a powerful antioxidant and it prevents certain types of cancer.

The magnitude of variability and its genetic components are the most pivotal aspects of breeding material. Variability in tomato is anticipated to be immense as the fruits vary greatly in shape and size (Dixit and Dubey, 1985; Bhardwaj and Sharma, 2005). Studies

on genetic parameters and character associations provide to choose and help to develop optimum breeding procedure. Many researchers (Kamruzzahan *et al.,* 2000) have noticed different genetic parameters in tomato based on few traits. As yield is the prime object of a breeder, it is essential to know the relationship between various characters that have direct and indirect effect on yield. Generally, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are measured to study the variability.

Heritability and genetic advance are important selection parameters. However, the character showing high heritability needs not exhibit high genetic advance (Johnson *et al.,* 1955). High heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection.

Materials and Methods

The experimental material comprised of forty germplasm lines, of tomato 34 genotypes and 6 released varieties as checks (Arka Vikas, Pusa Ruby, PKM-1, Marutham, Arka Meghali, Arka Alok) which were obtained from NBPGR, Regional Station, Hyderabad, IARI, New Delhi, IIHR, Bengaluru which were evaluated systematically during the research period.

The research was carried out at the experimental farm of college of horticulture, Department of vegetable science, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad, Telangana, *kharif,* 2017-18. The experiment was laid out with forty genotypes of tomato in Randomized Block Design (RBD) with three replications. Each germplasm line was grown in a plot of 1.8 m × 3.15 m (5.67 Sq. meters) accommodating 21 plants per plot, 7 plants per row with spacing of 60×45 cm^2 per replication. Broad sense heritability was calculated as per Lush (1940) and genetic advance assessed by the method of Johnson *et al.,* (1955).

Genotypic and phenotypic coefficients of variation were deliberated by using the formulae of Burton (1952). Categorization of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance (GA) were done as per Sivasubramanian and Menon (1973) and heritability categorized as by Johnson *et al.,* (1955).

Results and Discussion

Plant growth characters

The data regarding plant height showed very high phenotypic and genotypic variances (994.66 and 961.95) which were combined with high PCV (28.78%) and GCV (28.30%) respectively (Table 1). This trait exhibited high heritability (96.70%) with high genetic advance (62.83) and high GA as per cent mean (57.34).

The outcome for the trait plant height are in proof with the results of Sajjan *et al.,* (2016), Somraj *et al.,* (2017), Vijay Bahadur *et al.,* (2017), Kumar Nitish *et al.,* (2018) and Sritama Kundu *et al.,* (2018).

The data regarding number of primary branches per plant revealed low phenotypic and genotypic variances of 4.83 and 4.71 respectively with high PCV (37.30%) and GCV (36.86%). The high heritability (97.70%), low genetic advance (4.42) and high GA as per cent mean (75.05) were also noticed for this trait. Comparable results were reported by Mehta and Asati (2008), Anitha *et al.,* (2013), Arun *et al.,* (2016), Shankar *et al.,* (2016), Kumar Manish *et al.,* (2017) and Somraj *et al.,* (2017).

Table.1 Estimation of variability, heritability and genetic advance as % of mean for thirteen characters in forty genotypes of tomato

S. No	Characters	Range		Mean	Variance		PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic Advance	GA as % of mean
		Minimum	Maximum		Phenotypic	Genotypic					
1	**Plant height (cm)**	68.60	191.56	109.56	994.66	961.95	28.78	28.30	96.70	62.83	57.34
2	**Number of primary branches per plant**	2.43	9.83	5.89	4.83	4.71	37.30	36.86	97.70	4.42	75.05
3	**Days to first flowering**	21.26	43.86	31.62	22.45	14.26	14.98	11.94	63.50	6.20	19.61
4	**Days to 50% flowering**	29.00	52.00	37.13	26.94	21.85	13.98	12.59	81.10	8.67	23.35
5	**Days to fruit set**	37.60	63.13	45.40	44.20	29.38	14.64	11.94	66.50	9.10	20.05
6	**Number of fruits per plant**	10.58	323.00	54.45	6038.11	6026.12	142.69	142.54	99.80	159.75	293.35
7	**Average fruit weight (g)**	0.96	194.44	53.87	1645.41	1625.22	75.29	74.82	98.80	82.53	153.19
8	**Fruit yield/plant (kg)**	0.26	2.28	1.17	0.28	0.27	45.30	44.82	97.90	1.07	91.38
9	**Yield /ha (t)**	9.66	85.96	43.44	385.61	379.12	45.20	44.81	98.30	39.77	91.54
10	**Ascorbic acid content (mg/100g)**	11.76	59.43	31.25	103.27	101.00	32.51	32.16	97.80	20.47	65.51
11	**TSS (^{0}Brix)**	2.96	8.16	4.31	1.35	1.31	26.92	26.57	97.40	2.33	54.03
12	**Beta-carotene (mg/100g)**	1.06	2.63	1.70	0.19	0.18	25.87	25.50	97.20	0.88	51.79
13	**Lycopene content (mg/100g)**	0.00	6.12	3.31	1.61	1.59	38.37	38.07	98.50	2.58	77.83

PCV and GCV: Phenotypic and genotypic coefficient of variation, h^2_{bs}: Heritability in broad sense, GA: Genetic Advance

Moderate phenotypic and genotypic variances (22.45 and 14.26 respectively) with moderate PCV (14.98%) and GCV (11.94%), high heritability (63.50%), low genetic advance (6.20) and moderate GA as per cent mean (19.61) were revealed for the character days to first flowering.

The data regarding days to 50 per cent flowering exhibited high phenotypic and genotypic variances (26.94 and 21.85 respectively) with moderate PCV (13.98%) and GCV (12.59%). High heritability (81.10%), moderate genetic advance (8.67) and high GA as per cent mean (23.35) estimates were noticed for this trait. The results are similar with findings of Anitha *et al.,* (2013), Arun *et al.,* (2016) and Shankar *et al.,* (2016).

High Phenotypic and genotypic variance values of 44.20 and 29.38 with moderate PCV and GCV of 14.64 % and 11.94 %, very high heritability (66.50%), moderate genetic advance (9.10) and high GA as per cent mean (20.05) respectively were noticed for the days to fruit set.

The data regarding number of fruits per plant exhibited very high phenotypic and genotypic variances of (6038.11 and 6026.12 respectively) were recorded with very high PCV and GCV of 142.69% and 142.54%. Very high heritability (99.80%), very high genetic advance (159.75) and very high GA as per cent mean (293.35) were recorded for this trait. The results are similar with findings of Kumari and Sharma (2013), Vinod Kumar *et al.,* (2013), Sajjan *et al.,* (2016), Bhandari *et al.,* (2017), Dixit and Pandey *et al.,* (2017), Vijay Bahadur *et al.,* (2017), Kumar Nitish *et al.,* (2018) and Sritama Kundu *et al.,* (2018). The data regarding average fruit weight revealed high phenotypic and genotypic variances (1645.41 and 1625.22) along with high PCV (75.29%) and GCV (74.82%), very high heritability (98.80%), high genetic advances (82.53) as well as high GA as per cent mean (153.19) were recorded for this trait. Comparable results are noticed by Lal *et al.,* (1991), Brar and Singh (1998), Mohanty (2002), Sharma *et al.,* (2006), Islam *et al.,* (2012) and Mohamed *et al.,* (2012), Rahaman *et al.,* (2012), Sajjan *et al.,* (2016), Bhandari *et al.,* (2017), Somraj *et al.,* (2017), Vijay Bahadur *et al.,* (2017) and Kumar Nitish *et al.,* (2018).

The data regarding fruit yield per plant revealed very low phenotypic and genotypic variances (0.28 and 0.27) with high PCV (45.30%), GCV (44.82%) and high heritability (97.90%) but very low genetic advance (1.07) and high GA as per cent mean (91.38). The results are in line with the findings of Singh *et al.,* (1973), Kumar *et al.,* (1980), Supe (1985) and Sharma *et al.,* (2006), Ranjodh *et al.,* (2005), Anoop *et al.,* (2013), Meena and Bahadur (2014), Umesh *et al.,* (2015), Arun *et al.,* (2016) and Shankar *et al* (2016), and Dixit and Pandey *et al.,* (2017).

The data regarding yield per hectare showed high phenotypic and genotypic variances (385.61 and 379.12) with high PCV (45.20%) and GCV (44.81%), high heritability (98.30%) coupled with high genetic advance (39.77) and high GA as per cent mean (91.54).

Quality characters

Very high phenotypic (103.27) and genotypic (101.00) variances and high PCV (32.51%) and GCV (32.16%) were noted for ascorbic acid. High heritability (97.80%), high genetic advance (20.47) and high GA as per cent mean (65.51) estimates were noticed for this trait. The results are in line with Kumar *et al.,* (2006), Anitha *et al.,* (2013), Shankar *et al.,* (2013), Arun *et al.,* (2016) and Shankar *et al.,* (2016), Vijay Bahadur *et al.,* (2017).

With regards to total soluble solids, low phenotypic and genotypic variances (1.35 and 1.31), moderate PCV (26.92%) and GCV (26.57%), high heritability (97.40%), low genetic advance (2.33), and high GA as per cent mean (54.03) estimates were noted. The results are in similar with the findings of Arun and Veeraraghavatham *et al.,* (2005), Kumar and Thakur (2007), Anitha *et al.,* (2013), Shankar *et al.,* (2013), Arun *et al.,* (2016) and Shankar *et al.,* (2016). The data regarding beta carotene showed very low phenotypic and genotypic variances (0.19 and 0.18), moderate PCV (25.87%) and GCV (25.50%), high heritability (97.20%), very low genetic advance (0.88), and high GA as per cent mean (51.79) estimates were noted.

With regards to lycopene, low phenotypic and genotypic variances (1.61 and 1.59), high PCV (38.37%) and GCV (38.07%), high heritability (98.50%), low genetic advance (2.58), and high GA as per cent mean (77.83) which are in line with the findings of Kumar *et al.,* (2006), Anitha *et al.,* (2013), Shankar *et al.,* (2013), Arun *et al.,* (2016) and Shankar *et al.,* (2016).

Thus, it may be concluded that high genetic variability demonstrated directional selection could be essential for desired genetic improvement. High heritability coupled with high genetic advance as per cent of mean specify the significance so, that these characters can be utilized for choosing superior genotypes. Moderate genetic advance as per cent of mean with high heritability suggests the action of both additive and non-additive genes and favorable influence of environment in the expression. The same was reported in case of days to first flowering. Therefore, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes.

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