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Genetic studies in tomato (*Solanum* spp.) under temperate conditions

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Abstract

In this study, fifty tomato genotypes were tested for various yield and yield contributing characters. For all of the characteristics studied, analysis of variance indicated huge significant differences among all of the genotypes. The presence of sufficient genetic diversity for all of the traits was demonstrated by range values. The phenotypic coefficients of variance were found to be greater than their genotypic counterparts. The phenotypic and genotypic coefficients of variation for the majority of the characteristics were both high. All of the characters except one had strong heritability estimates as well as high genetic progress as a percentage of the mean.

Keywords: Tomato, variability, coefficients of variation, genetic advance, heritability

Introduction

Tomato (Solanum lycopersicum) having chromosomal number 2n = 2x = 24, is a member of the Solanum genus in the Solanaceae (Nightshade) family. There are around 1,500-2,000 species in the genus, all of which are not edible. It's a South American native (Peru Equador region) (Rick 1969)^[8]. Tomato is a berry with an ovary and seeds inside, botanically. Tomato, Solanum lycopersicum var. lycopersicum L., is one of the most widely consumed vegetables in the world, with an estimated production of 180.77 million metric tonnes produced annually (Statista, 2020) ^[11]. In India, the cultivable area available is 813 thousand hectares and production is 21 million metric tonnes (Statista, 2019-2020)^[11]. It is one of the most important vegetable crops farmed around the world due to consumer desire and its variety in terms of usage. Due to its self-pollinated nature (Bernatzky and Tanksley, 1986)^[2] and a comparatively short size of the genome (950 Mb), it has been employed in both conventional and molecular genetics. It also has a wider range of adaptability, ease of culture, a short life cycle, suitability as an intercrop with pulses and plantation crops, high self-fertility and homozygozity, ease of use for controlled pollination and hybridization, a large number of genetic stocks, high reproductive potential, and high yielding potential. Tomatoes are designated as 'Protective Food' because they are high in lycopene, ascorbic acid, and beta-carotene. Carotenoids, which are capable of reducing arteriosclerosis and cataract formation, are often credited with the positive effects of tomato consumption (Weisburger, 1998)^[13]. Due to the above stated merits of the crop, it presents a wider scope of improvement. The crop improvement programme largely depends on the extent of variability present. In order to make selection and improvement programmes effective, it is essential to partition the total variability existing in a germplasm into genetic, phenotypic and environmental components. The potential for improvement in crops is proportional to the magnitude of genetic variability present in the germplasm. Heritability has been widely used in determining the degree to which a character may be transmitted from parents to off springs. High heritability along with high genetic advance is important for making effective selections.

Materials and Methods

The present investigation was conducted at Experimental farm of the Division of Vegetable Science, SKUAST-K, and Shalimar in the year 2019. Fifty genotypes of tomato were collected from different agro climatic regions of the world and evaluated for various yield and yield attributing traits. The germplasm was collected from National Bureau of Plant Genetic Resources (NBPGR), Indian Institute of Vegetable Research (IIVR), Indian Institute of

Horticultural Research (IIHR) and Indian Agricultural Research Institute (IARI). The single factor experiment was laid out in randomized complete block design (RCBD) with three replications. Standard cultural and plant protection practices were followed to ensure a healthy crop growth. Observations were recorded on various yield and yield attributing traits. The data thus generated was subjected to standard statistical procedures. The analysis of variance was calculated as per Gomez and Gomez (1983). Phenotypic and genotypic coefficient of variation was estimated according to Burton and De Vane (1953). Heritability in broad sense and genetic advance as per cent of mean were calculated as per formula given by Allard (1960) and Jhonson *et al.* (1955) respectively.

Results and Discussion

For all characteristics, analysis of variance found huge variations among all genotypes significant under investigation, indicating a high level of variability in the existing material. Similar results with respect to analysis of variance were also reported by Meena et al. (2015)^[3], Prajapati et al. (2015)^[5]. The genetic variability estimates, heritability (bs) and genetic advance as a per cent of mean are shown in Table-1. The presence of significant genetic diversity for all of the traits was demonstrated by range values, which is a requirement for generating improvements through selection. Range values in different characters reflect the amount of phenotypic variability in those characters, but they aren't very dependable because they encompass genotypic, environmental, and genotype-environment interaction components and don't reveal which character has the most variability. As a result, it's required to divide the observed variability into phenotypic and genotypic coefficients of variation, which finally represent the degree of variability for different characteristics. With a little discrepancy in the values, phenotypic coefficients of variation were found to be larger than comparable genotypic coefficients of variation. This revealed that genetic differences were the primary source of diversity, with little influence from the environment on the expression of the traits under study. This was in agreement with the study of Ullah et al. (2015)^[12] and Nalla et al. (2016)^[4]. No of fruits/plant, average fruit weight, fruit yield, no of flowers/truss, no of fruits/truss and plant height recorded high phenotypic and genotypic coefficients of variation, indicating that genotypes had broad genetic base for these characters. Similar results

were observed by Rai et al. (2016)^[6] for number of fruits per plant, average fruit weight, fruit yield per plant. Days to emergence, seedling length and no of primary branches exhibited moderate phenotypic and genotypic coefficients of variation suggesting the existence of moderate variability in the genetic stock studied. Similar findings were reported by Reddy et al., 2013 [7] for no of primary branches. Low phenotypic and genotypic coefficients of variation were observed for fruit size index, no of days to fruit set, duration of harvest and no of days to first harvest. Similar results were obtained by Reddy et al. (2013) [7], Singh et al. (2000) [10], and Ara et al. (2009)^[1] for days to first fruit set and days to first fruit harvest. Characters with moderate to high coefficients of variation indicated that there was a greater chance of improvement through selection. A wide range of variability, as well as high estimates of phenotypic and genotypic coefficients of variation, suggests that these traits would be responsive to selection.

For all the characters under study, heritability (b.s.) was high, ranging from 78 to 99 percent, indicating that they are less influenced by environmental factors and that they are effectively transferred to the progeny. This shows that genetic constitution plays a significant influence in the expression of a character, and that selection based on phenotypic expression can be relied upon. High heritability was also reported by Reddy et al. (2013)^[7] for plant height, number of flowers per cluster, days to first fruit set, number of fruits per cluster, number of fruits per plant, and fruit yield. Rai et al. (2016)^[6] observed high heritability for average fruit weight. All the characters showed the high estimates of heritability coupled with high genetic advance as per cent of mean except no. of days to first harvest indicating the preponderance of additive gene action for control of these traits. This suggests that real progress in improvement through selection could be made for yield. These results are in conformity with work of several workers viz. for number of fruits per plant, average fruit weight and yield per plant; Rai et al. (2016) ^[6]. For plant height, number of flowers per cluster, number of fruits per cluster, fruit weight and fruit yield per plant similar results were obtained by Reddy *et al.*, (2013)^[7]. Fruit yield plant⁻¹ is an important character, which decides the commercial viability of the hybrid/variety. The high heritability of this character, as well as the strong genetic progress as a percentage of the mean, showed that high yielding cultivars may be selected from the current collection.

S. No.	Parameters	Range	Environmental variance (EV)	Phenotypic variance (PV)	Genotypic variance (GV)	Environmental coefficient of variation (ECV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV	Heritability (bs)	Genetic advance (as%) of mean)
1	Days to emergence	5.5-16.4	0.30	5.56	5.25	6.30	27	26.25	0.94	52.59
2	Seedling length (cm)	7.3-25.9	0.63	18.49	17.85	4.52	24.36	23.94	0.96	48.46
3	Plant height (cm)	33.3-198.3	95	1994.9	1898.9	8.30	37.86	36.94	0.95	74.24
4	No of primary branches	2-5.3	0.205	1.06	0.85	12.95	29.48	26.49	0.81	49.02
5	No of flowers/truss	2.6-12.7	0.31	4.64	4.33	11.44	44.31	42.81	0.93	85.19
6	No of days to fruit set	24.7-54.3	0.77	34.26	33.49	2.35	15.70	15.53	0.97	31.63
7	No of days to first harvest	86-95.6	0.65	3.04	2.39	0.87	1.89	1.68	0.78	3.07
8	No of fruits/truss	2.3-9	0.35	2.75	2.40	14.58	41.01	38.33	0.87	73.79
9	Fruit size index (cm ²)	0.53-1.4	0.001	0.03	0.03	2.96	17.60	17.35	0.97	35.22
10	Average Fruit weight (g)	0.95-127.4	6.59	747.83	741.23	6.71	71.42	71.10	0.99	145.83
11	Fruit yield (kg/ plant)	0.19-4.14	0.01	0.39	0.38	8.90	57.82	57.13	0.97	116.28
12	No of fruits/plant	3.3-210.6	10.45	2329.50	2319.05	6.14	91.65	91.45	0.99	187.95
13	Duration of harvest	94.8-133.3	1.83	164.22	162.38	1.20	11.38	11.322	0.98	23.18

Table 1: Estimates of range, environmental variance, phenotypic variance, genotypic variance, environmental, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as% of mean) for different characters in Tomato (*Solanum* spp.)

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