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Genetic variability studies in tomato (*Solanum lycopersicum* L.) under protected cultivation

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Abstract

A study on "Genetic variability in tomato (*Solanum lycopersicum* L.) for protected cultivation" was carried out during *rabi* season of 2022-23 under naturally ventilated polyhouse of Department of Vegetable Science, College of Horticulture, Bagalkot, Karnataka. The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications to investigate genetic variability for twenty-four genotypes. The analysis of variance revealed highly significant variation among the genotypes. Wide variation was observed for all the growth, earliness, yield and quality traits among genotypes under protected cultivation. The experimental results were indicated based on *per se* performance of genotypes and among these, AVTO1920, AVTO1464 and AVTO1706 were highly suitable for protected cultivation. Analysis of coefficient of variation revealed that the magnitude of phenotypic coefficient of variation (pcv) was almost similar to the genotypic coefficient of variation (gcv) for all the studied traits. Further, high estimates of heritability (h^2_{bs}) and genetic advance as percent mean over mean (GAM) were recorded for number of clusters per plant, number of fruits per cluster, number of fruits per plant, fruit polar diameter, plant height (cm) and number of branches. Thereby, suggesting that straight selection for these traits may bring worthwhile improvement in identifying the superior genotypes in tomato.

Keywords: Protected cultivation, RCBD, genetic variability, heritability, GAM, tomato

1. Introduction

The tomato, scientifically known as *Solanum lycopersicum* L., is a self-pollinating plant belonging to the Solanaceae family, originating from Central and South America. Commonly referred to as the 'Love Apple, with a chromosome number of (2n=2x=24). Recognized as a nutritional crop, tomatoes are rich in essential components such as vitamins A and C, minerals, sugars, organic acids, and lycopene (Waiba *et al.* 2021) [19]. Tomatoes are the third most cultivated vegetable in India, after potatoes and sweet potatoes. However, they are the most processed vegetable crop in the country (Kathayat *et al.* 2015) [4]. In India, tomatoes are grown on an area of 0.83 million hectares and produce 21.0 million tonnes annually, with a productivity of 25.32 tonnes per hectare (Anon., 2021) [1].

The purpose of protected cultivation is to produce crops in locations where the natural environment restricts or prevents plant growth, regardless of the climate (Mishra *et al.* 2010) [9]. Along with plant protection, protected tomato cultivation benefits growers by providing year-round production, pesticide residue-free produce, higher quality, greater yields, and higher returns to growers during the off-season. Because of their trailing behavior and high return from longer growth periods and suitable vertical space, indeterminate tomato varieties were well suited for polyhouse cultivation and yields higher yields (Mamta *et al.* 2022) [7].

Genetic variability is the possibility of a high degree of variation between individuals as a result of variations in their environment and genetic structure. Because yield is the ultimate goal and a complex character, it is essential to assess the genotypes genetic variability with respect to various characters. This aids in the planning of an effective breeding program that will produce hybrids fit for a protected environment. For the genetic improvement of the tomato crop, the basic requirement is to utilize genetic variability that provides better scope of selecting desirable genotypes. High amount of variability in the genotypes, greater is the scope for its improvement by selection (Waiba *et al.* 2021) [19].

Therefore, the present experiment was conducted to estimate coefficients of phenotypic and genotypic variations, heritability and genetic advance as percent over mean for studied horticultural traits based on yield and yield attributing characters and to evaluate tomato hybrids for high market yield.

2. Materials and Method

The experiment was conducted in naturally ventilated polyhouse of the Department of Vegetable Science, College of Horticulture, Bagalkot, Karnataka, India during *rabi* season 2022-23 (September-February). It is located at an altitude of 533 meters above mean sea level (MSL) at 16°18’N latitude and 75°07’ E longitude in the Northern Dry Zone of Karnataka (Zone-III) with North-South direction of polyhouse having 560 m^2 area. The experimental polyhouse consists raised beds of red sandy loam soil (Alfisol) with a uniform soil fertility. Twenty-four genotypes of tomato were calculated in Randomized Complete Block Design (RCBD) with two replications inside the protected structure. The genotypes collected from different sources *viz*., 15 lines from world vegetable center (WVC), Taiwan, eight lines developed at College of Horticulture, Bagalkot (COH BGK) and one genotype from KAU, Vellanikkara (Table 1) were evaluated for protected cultivation. At a distance of 60 cm × 45 cm, eight plants of each treatment were planted. To protect a healthy crop development, the intercultural procedures-hoeing, earthing up, irrigation, fertigation, weeding, cutting, training, pruning, and staking—were carried out in line with the suggested package of practices. Using a drip irrigation system, irrigation was carried out two or three times a week depending on the needs of the crop. Using nylon and jute twine, the plants were trained on two stems. Five randomly chosen plants from each replication were observed for various growth, earliness, yield, and quality parameters. R-Studio was used to statistically analyze the data for the various characters in order to calculate the mean performance and an analysis of variance in accordance with the methodology.

Table 1: Tomato genotypes details used in the experiment with their source of collection

Sl. No	Genotypes	Entry	Source
1.	AVTO1706	AVTO1	WVC, Taiwan
2.	AVTO1920	AVTO2	WVC, Taiwan
3.	AVTO1429	AVTO3	WVC, Taiwan
4.	AVTO1954	AVTO4	WVC, Taiwan
5.	AVTO1914	AVTO5	WVC, Taiwan
6.	AVTO1915	AVTO6	WVC, Taiwan
7.	AVTO2017	AVTO7	WVC, Taiwan
8.	AVTO1701	AVTO8	WVC, Taiwan
9.	AVTO0301	AVTO9	WVC, Taiwan
10.	III-5	III-5	Line developed at COHBGK
11.	AVTO1907	AVTO11	WVC, Taiwan
12.	AVTO2014	AVTO12	WVC, Taiwan
13.	AVTO1906	AVTO13	WVC, Taiwan
14.	AVTO1424	AVTO14	WVC, Taiwan
15.	AVTO1909	AVTO15	WVC, Taiwan
16.	II-154	II-154	Line developed at COHBGK
17.	IV-109	IV-109	Line developed at COHBGK
18.	I-173	I-173	Line developed at COHBGK
19.	IV-49	IV-49	Line developed at COHBGK
20.	III-45	III-45	Line developed at COHBGK
21.	II-107	II-107	Line developed at COHBGK
22.	Anagha	Anagha	KAU, Vellanikkara
23.	AVTO1464	AVTO10	WVC, Taiwan
24.	IV-106	IV-106	Line developed at COHBGK

3. Results and Discussion

3.1 Analysis of variance

The Mean sum of squares values of analysis of variance (ANOVA) in Table 2 revealed highly significant differences among the genotypes for all the 20 traits studied *viz*., plant height, number of branches, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit firmness, Number of locules, pericarp thickness, shelf life, TSS, number of clusters per plant, Number of fruits per cluster, Number of fruits per plant, average fruit weight, polar diameter, equatorial diameter, fruit yield per plant, yield per square meter and fruit yield per hectare. The significance variations among the genotypes presented in Table 2, showed the presence of adequate variability which can be exploited through selection and also observed in (Dar and Sharma, 2011; Kaushik *et al.*, 2011; Meena and Bahadur, 2015; Sanchez *et al.*, 2019; Sinha *et al.*, 2020) [21, 5, 8, 14, 16].

3.2 Genetic variability

The genetic variation through mean, range, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h2), and genetic advance as a percentage of the mean (GAM) were calculated for 20 plant traits (Table 2). The coefficient of variation of genotypic and phenotypic components are both useful measures of the extent of variability in different characters that gives the range of variability. Burton and De Vane (1953) [20] suggested that considering both genetic variability (GV) and heritability (h^2) is essential to determine the maximum and most precise effects of selection. Using both heritability and genetic advance as a percent of over mean can help breeders to select for traits that are both heritable and have a high potential for genetic improvement. This can lead to more effective breeding programs and the development of new hybrids with improved traits (Reddy *et al*. 2019) [13]. The read through data of range and average values of 24 genotypes for various traits presented in Table 2. For growth parameters like Height of plant at final harvest (cm) and branches number (counts) at last harvest, the ranges and average values were recorded by using statistical data analysis. The genotypes, AVTO1429 and AVTO1464 were recorded significant for plant growth and number of branches traits. In case of earliness parameters like days to first flowering, days to 50 percent flowering and days to first harvest, their different ranges and mean values were computed and genotypes, AVTO1915 and AVTO1706 were best for earliness traits. For quality parameters like pericarp thickness (mm), number of locules (counts), TSS (ºBrix), shelf-life and fruit firmness (N), the range and average values were estimated from data analyzer. The genotype, AVTO2014 was significant for the studied quality parameters. Yield parameters like days to last harvest, number of clusters / plant, number of fruits / cluster, number of fruits / plant, average fruit weight (g), fruit diameter (polar & equatorial), fruit yield / plant (kg), square meter (kg) and hectare (t), the highest and lowest data with mean values of 24 genotypes were calculated. For this yield traits, AVTO1920, AVTO1464 and AVTO1706 were significant in positive direction and suitable for protected cultivation. Estimates of PCVs were almost similar to the GCVs for majority of the characters studied and implied that the influence of the environment for expression of characters was nill. Therefore, the observed differences in traits are likely to be heritable & selection of genotypes based on these traits lead to development of new hybrids.

Differences observed between the coefficients of genetic and phenotypic variation (GCV and PCV) have shown lesser magnitude for all the characters studied. Identical results have also obtained by Sureshkumara *et al*., (2018) [18], Lekshmi and Celine (2017) [6]. Highest level of GCV and PCV were recorded in fruit polar diameter, number of clusters / plant, number of fruits / cluster, number of branches, plant height, number of fruits / plant fruit firmness, fruit yield / hectare, fruit yield / m^2, fruit yield per plant (kg) and number of locules (n). High degree for PCVs and GCVs were also reported by Lekshmi and Celine (2017) [6] and Panchbhaiya *et al*., (2018) [11]. Moderate level of variations in genotypes and phenotypes were recorded in fruit weight (g), shelf life (Days) and TSS (ºBrix) which shows these traits were controlled by both additive type and non-additive type of gene action and also recorded by Lekshmi and Celine (2017) [6] and Panchbhaiya *et al*., (2018) [11]. Low level of both type of genetic variations have found in pericarp thickness (N), equatorial diameter, last harvest (days), days to 1st flowering, days to 50 percent flowering. Similar kind of results were reported by Henareh (2015) [3], Singh and Janeja (2018) [15]. This indicates that there was little influence of environmental factors on the phenotypic expression of above mentioned characters. Thus, selection based of phenotypic performance of these characters would be effective to bring about considerable genetic improvement.

Broad sense heritability of all genotypes have recorded more than 60 percent for 20 traits, indicating a strong genetic determination passed on to the next generation. Similar results were reported by Sunilkumar *et al.* (2013) [17], Sureshkumara *et al.* (2018) [18]. High estimates of genetic Advance as a percentage of mean (GAM) were recorded in plant growth parameters such as plant height (cm) and number of branches, as well as in yield-attributing traits like number of clusters / plant, fruit polar diameter, number of fruits / cluster and number of fruits / plant. High estimates of GAM indicated that the preponderance of additive genetic effects in expression of these traits and heritable over generations. Therefore, selection for these characters in genotypes based on phenotypic performance would likely be effectively more. Similar outputs were obtained by Namita *et al.* (2021), (Sunilkumar *et al*., 2013) [17], Sureshkumara *et al*. (2018) [18].

The parameters like number of clusters / plant, fruit polar diameter, number of fruits / cluster, number of fruits / plant, height of plant and number of branches after 90 days have shown highest percentage of both heritability & GAM which suggested that the observed variation in the trait is largely influenced by genetic factors and there is potential for effective selection to improve the trait in future generations. Similar reports were obtained by Sunilkumar *et al*. (2013) [17], Sureshkumara *et al*. (2018) [18]. Whereas days to 1st flowering, days to 50% flowering and days to first harvest (counts) have scored less percentage of both that indicated they are largely influenced by environmental factors. The traits like average fruit weight, fruit yield per plant, fruit yield per hectare, fruit firmness, and number of locules were found to have high heritability and moderate genetic advance as a percentage of mean values. This suggests that the expression of those attributes was influenced by both the environment and non-additive gene action. Each of these traits could be taken advantage of by dominance expression and by using heterosis to produce epistatic components.

Table 2: Estimates of range, mean, coefficient of variation, heritability and genetic advance (percent mean) for growth, earliness, yield and quality traits in tomato

SI No.	Traits	Range	Mean	GCV (%)	PCV (%)	h^2bs (%)	GAM (%)
I	**Growth parameters**						
1	Plant height (cm) at final harvest	103.80-237.57	139.16	25.04	25.26	98.28	51.14
2	Number of branches at final harvest	4.97-13.84	8.57	25.86	26.03	98.75	52.94
II	**Earliness parameters**						
3	Days to first flowering	27.97-34.36	31.79	5.07	5.50	85.04	9.64
4	Days to 50% flowering	28.65-33.61	31.55	4.37	5.14	72.42	7.67
5	Days to first harvest	76.14-87.90	82.75	3.40	4.02	71.21	5.90
III	**Quality parameters**						
6	Fruit firmness (N)	2.17-6.21	4.51	22.69	22.90	98.21	46.32
7	Number of locules	2.21-5.61	3.87	21.48	21.64	98.69	43.98
8	Pericarp thickness (mm)	4.51-6.29	5.60	9.45	9.85	92.09	18.70
9	Shelf life	5.83-11.06	8.44	13.43	13.66	97.09	27.30
10	TSS ^{0}Brix	4.00-5.39	4.70	10.19	10.36	95.04	20.30
IV	**Yield parameters**						
11	Days to last harvest	124.49-160.20	137.40	7.06	7.57	87.88	13.54
12	Number of clusters per plant	20.02-60.83	43.01	30.23	30.36	99.12	62.00
13	Number of fruits per cluster	2.11-5.87	3.81	25.60	26.72	99.14	52.52
14	Number of fruits per plant	28.96-80.37	47.00	24.83	25.00	99.45	51.03
15	Average fruit weight (g)	42.73-112.02	87.06	17.69	18.01	98.90	35.88
16	Fruit polar diameter (cm)	4.35-6.69	4.99	31.39	31.51	99.24	64.42
17	Fruit Equatorial diameter (cm)	4.03-6.07	5.12	8.87	9.25	92.00	17.51
18	Fruit yield per plant (kg)	2.44-5.73	3.85	22.15	22.42	97.66	45.10
19	Fruit yield per sq.mt. (kg)	7.34-17.29	11.53	22.49	22.60	99.03	46.11
20	Fruit yield per hectare (t)	73.55-175.27	114.87	22.64	22.80	98.58	46.30

GCV= Genotypic coefficient of variance
PCV= Phenotypic coefficient of variance
H^2 = Heritability (broad sense)
GAM = Genetic advance (percent mean)

4. Conclusion

Under protected conditions, the current investigation assisted in quantifying the variability among tomato genotypes for growth, earliness, quality and yield related characters. The study conducted under protected conditions showed that GAM together with simultaneous selection based on several characters with high estimates of heritability may be significantly helpful in crop improvement. The analysis of the 24 genotypes revealed that tomato genotypes can function better in protected environments and the three promising genotypes-AVTO1920, AVTO1464, and AVTO1706-can move forward for future trials.

5. Future Scope

Genetic variability studies of tomato hybrids for protected cultivation can help to identify high-performing tomato genotypes. This information can be used to develop new tomato cultivars with improved yield, quality, and resistance to pests and diseases. In addition, genetic variability studies can help to understand the genetic basis of tomato traits. This information can be used to develop new breeding strategies for improving tomato crops.

6. Conflict of interest: Authors have declared that there is no competing interests exist.

7. Author contribution

Volaguthala Sairam: Wrote the paper
Namita Raut: Performed the analysis
Arun kumar Bhavidoddi: Collected the data
Rekha Chittapur: Contributed data analysis tools
Veeresh Mallayya Hiremath: Conceived and designed the analysis
Raveendra S. Jawadagi: Contributed data analysis tools

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