

Genetic Variability Studies in F₁ Generation of Tomato (*Solanum lycopersicon* L.)

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Abstract: Twenty four hybrids along with their 11 parents (8 lines and 3 testers) were subjected to study the genetic variability indicated that genetic material in the present investigation possessed variability which provides sufficient basis for selection by breeder. High estimates of PCV and GCV were obtained for plant height, number of fruits per cluster, average fruit weight, yield per plant, titrable acidity, ascorbic acid and lycopene indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement. High heritability assisted with high genetic advance as per cent of mean was observed for plant height, number of primary branches per plant, number of fruits per cluster, fruit length, fruit width, average fruit weight, number of locules per fruit, pericarp thickness, titrable acidity, ascorbic acid, lycopene and shelf life. Hence, simple selection based on phenotypic performance of these traits would be more effective.

Key words: Genetic variability, Heritability, Genetic advance, F₁ generation, Tomato

I. Introduction

Tomato (*Solanum lycopersicon* L.) is one of the most important vegetable crops grown throughout the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. The red pigment in tomato (lycopene) is now being considered as the “world’s most powerful natural antioxidant” [1]. Therefore, tomato is one of the most important ‘protective foods’ because of its special nutritive value. However, the average national productivity is very low (19.5 tonnes/ha as compared to other countries like USA (81 t/ha), Spain (74 t/ha) and Brazil (60.7 t/ha) [2]. This indicates that there is a need to increase the productivity of this crop by developing high yielding varieties through appropriate breeding work to meet the demand of domestic and export markets.

The development of an effective plant breeding programme is depending upon the assessment of polygenic variation, selection of elite genotypes, choice of parents and breeding procedures. Crop improvement depends upon the magnitude of genetic variability and the extent to which desirable characters are heritable. Genetic variability for yield and yield components is essential in the base population for successful crop improvement [3]. Yield and yield components are quantitative characters and are poly genetically inherited which are greatly influenced by environment. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. Genetic parameters such as Genotypic, Phenotypic coefficient of variation (PCV and GCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection [4]. The total variability can be partitioned into heritable and non heritable components with the help of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance. Heritable variation can be effectively studied in conjunction with genetic advance. High heritability alone is not enough to make efficient selection in segregation, unless the information is accompanied for substantial amount of genetic advance [5]. Tomato, being self pollinated crop in general, we can create genetic variability through hybridization which could be favorably utilized in developing a genotype with all desirable characters. The 24 F₁'s and their 11 parents differed significantly for all the characters. The results obtained on Variability, Heritability and Genetic Advance as per cent of Mean (GAM) are discussed here.

II. Materials And Methods

The present investigation was undertaken during *Kharif*, 2010 at Vegetable Research Station, Rajendranagar, Dr. Y.S.R. Horticultural University, Andhra Pradesh. The experimental material consisted of 24 F₁ hybrids, 11 parents (8 lines and 3 testers) and two commercial checks (Lakshmi and US-618). The

experiment was laid out in Randomized Block Design with three replications. Each entry was grown in two rows with 10 plants in each row by adopting inter row spacing of 60cm and intra row spacing of 45cm. All recommended agronomic package of practices were followed to grow a healthy crop. The observations were recorded on various growth, yield and quality parameters from 10 randomly selected plants in each replication as per standard procedures. The analysis of variance for testing the variance among treatments was carried out as per the method suggested by Panse and Sukhatme (1967)[6]. The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1982)[7]. Categorization of the range of variation was proposed by Sivasubramaniam and Madavamenon (1973)[8]. Heritability (h^2) in the broad sense was calculated according to the following formula given by Burton (1952)[9]. The range of heritability and genetic advance as per cent of Mean (GAM) were classified as suggested by Johnson *et al.* (1955) [5].

III. Results And Discussion

3.1 Variability

The analysis of variance (Table 1) revealed that highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement. However, the absolute variability in different characters does not permit identification of the characters showing the highest degree of variability. Therefore, PCV and GCV values were estimated. The coefficient of variation whether it is genotypic or phenotypic, both are useful in studying the extent of variability in different characters as it measures the range of variability.

The PCV values were slightly higher than the respective GCV for all the characters denoting little influence of environmental factors on their expression. The difference between values of PCV and GCV were less for all traits except titrable acidity in present investigation. It means that these traits were less influenced by environment and hence, they could be improved by following different phenotypic selections like directional, disruptive and stabilized selections. The PCV and GCV values were very high particularly for lycopene, yield per plant and ascorbic acid due to very high variability available in these traits (Table 2).

Higher estimates of PCV and GCV are obtained for plant height [10], number of fruits per cluster [11], Average fruit weight [12], yield per plant [13], titrable acidity [14], ascorbic acid content [15] and lycopene [14] indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement.

Moderate PCV and GCV values for number of primary branches, fruit length, fruit width, number of locules per fruit, pericarp thickness and shelf life indicated the presence of moderate genetic variability for these characters [11], [16], [14], [17] respectively in Tomato. Whereas, moderate PCV and low GCV was recorded for number of flower per cluster and TSS [18].

Low PCV and GCV for days to 50% flowering [19] suggesting less variability existed in these characters. This moderate to low variability indicates the need for improvement of base population through intercrossing in F₂ generation followed by recurrent selection to increase the gene flow and to fix favorable alleles.

3.2 Heritability and Genetic advance

Perusal of results on heritability and genetic advance as per cent of mean (GAM) revealed that heritability estimates were high for all the characters studied. This suggested the greater effectiveness of selection due to less influence of environment and improvement to be expected for these characters in future breeding programme.

Johnson *et al.* (1955) [5] suggested that high heritability coupled with high genetic advance as percentage of mean (GAM) were more useful than heritability alone in predicting the resultant effect during selection of best individual genotype. Genetic advance is the measure of genetic gain under selection and expression in percentage of mean.

In the present experiment high heritability and genetic advance as per cent of mean (GAM) was recorded for plant height [10], number of primary branches [18], number of fruits per cluster [20], fruit length and fruit width [10], average fruit weight [21], number of locules per fruit [16], pericarp thickness [22], titrable acidity and ascorbic acid [18], lycopene [14] and shelf life [23] indicating predominance of additive gene action for these characters. Simple selection based on phenotypic performance of these characters would be more effective.

Table 1. Analysis of variance for yield, yield contributing and quality characters in tomato

Source of Variations	df	Mean sum of squares										
		Plant height (cm)	No. of primary branches/plant	Days to 50% flowering	No. of flowers/ cluster	No. of fruits/ cluster	fruit length (cm)	fruit width (cm)	Average Fruit Weight (g)	Yield / plant (kg)	No. of locules/ fruit	Pericarp thickness (mm)
Replications	2	263.49	2.38	0.25	0.14	0.14	0.25	0.02	9.59	0.93	0.28	0.00
Treatments	36	1694.07**	4.76**	12.21**	0.70**	0.88**	1.18**	1.57**	832.18**	1.76**	1.89**	1.76**
Error	72	88.10	0.25	0.63	0.12	0.07	0.08	0.03	2.80	0.01	0.18	0.07

Source of Variations	df	Mean sum of squares				
		TSS (^o Brix)	Titration Acidity (%)	Ascorbic acid (mg/100g)	Lycopene (mg/100g)	Shelf life (days)
Replications	2	0.0025	0.0285	417.9233	0.0620	1.1244
Treatments	36	0.4796**	0.0532**	135.2445**	16.3514**	8.1671**
Error	72	0.0481	0.0045	0.0395	0.1653	0.6605

* Significant at 5 per cent level ** Significant at 1 per cent level

Table 2: Estimates of Genetic parameters for yield, yield contributing and quality characters in Tomato

S.No.	Characters	Range		Mean	PCV (%)	GCV (%)	Heritability (Broad Sense %)	Genetic Advance (%)	GAM
		Min.	Max.						
1	Plant height (cm)	48.33	153.63	99.86	25.00	23.17	0.86	44.17	44.23
2	No. of primary branches/ plant	5.33	10.60	8.11	16.32	15.11	0.86	2.34	28.83
3	Days to 50% flowering	28.00	37.00	32.62	6.49	6.02	0.86	3.75	11.51
4	No. of flowers/ cluster	4.53	6.37	5.45	10.31	8.05	0.61	0.71	12.95
5	No. of fruits/ cluster	1.17	3.60	2.57	22.73	20.11	0.78	0.94	36.65
6	fruit length (cm)	3.00	6.10	4.33	15.47	13.97	0.82	1.13	25.98
7	fruit width (cm)	3.43	6.97	5.28	13.95	13.56	0.95	1.43	27.18
8	Avrg. Fruit Wt. (gm)	40.20	105.53	73.04	22.88	22.76	0.99	34.08	46.66
9	Yeild/ plant (kg)	1.00	3.90	2.44	31.65	31.29	0.98	1.55	63.70
10	No. of locules/ fruit	2.33	6.50	4.40	19.65	17.13	0.76	1.35	30.77
11	Pericarp thickness (mm)	3.83	6.70	5.29	14.99	14.19	0.90	1.46	27.67
12	TSS (Brix)	3.17	5.00	4.12	10.63	9.20	0.75	0.68	16.41
13	Titration Acidity (%)	0.27	0.77	0.49	29.66	26.25	0.78	0.23	47.88
14	Vit-C (mg/100g)	14.67	40.67	24.42	27.50	27.49	1.00	13.82	56.61
15	Lycopene (mg/100g)	2.07	11.73	5.65	41.73	41.11	0.97	4.71	83.41
16	Shelf life (days)	6.00	12.00	9.03	19.70	17.52	0.79	2.90	32.10

High heritability and moderate genetic advance as per cent of mean values were observed for the characters, days to 50 per cent flowering [24], number of flowers per cluster [11], TSS [14]. This indicates the influence of non-additive gene action and considerable influence of environment in the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis.

Hence, 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 especially in case of tomato.

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