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Genetic Variability Studies in F_2 Segregating Population of Tomato (*Solanum lycopersicum* L.)

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ABSTRACT

The genetic parameters were studied in F_2 population of the cross IIHR-2201 X C-13-1-2-1 to elucidate the genetic variability, heritability and genetic advance in tomato (Solanum lycopersicum L.). The evaluation was carried out at experimental block, Department of Vegetable Science, College of Horticulture, UHS Campus, GKVK, Bengaluru during 2015-2016. Variability analysis showed the presence of sufficient amount of variability among all the traits studied in the segregating population. Very little differences were observed between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters except fruit firmness (kg/cm^2) and TSS (^{0}B) indicating that most of the traits were less influenced by environmental factors for their phenotypic expression. High heritability coupled with high genetic advance as per cent mean was observed for plant height, number of branches, number of fruits per plant, average fruit weight, pericarp thickness, number of locules, ascorbic acid and yield per plant indicating wide scope for improvement through selection of these traits. The exploration of genetic variability in the available germplasm is a prerequisite in a breeding programme for effective selection of superior genotype of tomato.

Key words: *Tomato, Genetic variability, GCV, PCV, Heritability, Genetic advance.*

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is an important remunerable vegetable of India and all over the world belongs to the family Solanaceae having diploid chromosome number of 24. It is grown for its edible fruit, which can be consumed, either raw, cooked or in the form of various processed products like juice, ketchup, sauce, pickle, pastes, puree and powder. It is universally referred as protective food and esteemed as an important source of minerals, organic acids and vitamins (A and C).

The cultivated tomato covers less than 5 per cent of the genetic variation of wild relatives[4]. Genetic variability is essentially the first step of plant breeding for crop improvement and it is the basic key to bring about genetic improvement to a crop by utilizing the available or created genetic variability[21].

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Phenotypic expression of the plant character is mainly controlled by the joint product of genetic makeup of the plant and environment. Hence, before venturing into a breeding programme, it is essential to study the variability and its heritable components for the yield contributing characters in the available genotypes. It is necessary to partition the observed overall phenotypic variation into heritable and non-heritable components with the help of suitable genetic parameters such as coefficients of variation, heritability estimates and genetic advance *etc.,* as these are useful biometrical tools for formulating appropriate breeding strategy and exploiting the inherent variability.

The present investigation was carried out to gather these information in F_2 segregating population of tomato which would be utilized for further improvement of tomato yield through an appropriate and sound breeding plan. The F_2 population obtained from the selfing of F_1 hybrid provides all possible variations. Hence, selection with particular objectives in F_2 generation is most effective and selfing of those selected genotypes generation after generation helps to develop inbred lines. These inbreds with desired characters including high yield potential can be used as high yielding variety (HYV) as well as the parents for hybrid variety[4]. Hence, the present study was conducted to study the genetic variability, heritability and genetic advance for yield and its contributing characters in F_2 segregating population of tomato.

MATERIAL AND METHODS

The study was conducted at the experimental block, Department of Vegetable Science, College of Horticulture, UHS Campus, GKVK, Bengaluru. The experimental material consisted of 305 plants of F_2 (IIHR-2201 X C-13-1-2-1) population, twenty plants of each F_1, parents and four commercial checks (Arka Rakshak, Arka Samrat, Arka Vikas and PTR-6) were planted in healthy plot to assess quality, yield and yield attributing traits. The experimental seed material was sown in protrays on 4th December 2015. Twenty eight days old seedlings were then transplanted to the main field with spacing of 75 cm x 60 cm. Before transplanting the plot was brought to fine tilth by ploughing and harrowing. The production aspects were followed as per the package of practices of UHS Bagalkot[1].

The traits studied in the experiment are provided in the table. The observations were recorded for each plant in F_2 population and five randomly selected plants in F_1 hybrid, parents and commercial checks. The genotypic and phenotypic coefficients of variation were calculated using the formula of Burton and Devane[2]. Heritability in broad sense was estimated according to the method of Hanson *et al*[6]. Genetic advance and genetic advance as per cent mean was calculated by the formula used by Johnson *et al*[8].

RESULTS AND DISCUSSION

The extent of variability with respect to fourteen quantitative and qualitative characters in F_2 population measured in term of mean performance, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, genetic advance as per cent mean and expected mean in next generation are given in table. It was observed that the material assessed in the present investigation possesed wide range of variation for various characters observed (Fig. 1, 2 and 3).

The PCV was slightly higher than the corresponding GCV for all the traits which might be due to the interaction of the genotypes with the environment to some degree or other denoting environmental factors influencing the expression of these characters. High level of PCV and GCV were recorded for number of fruits per plant (31.07 %, 30.60 %) and yield per plant (31.72 %, 31.15 %). The estimate of high level of PCV was observed for number of branches per plant (21.72 %). Moderate levels of PCV and GCV were obtained for plant height (14.90 %, 14.70 %), pericarp thickness (17.62 %, 17.33 %), number of locules (13.41 %, 12.16 %), average fruit weight (18.10 %, 17.58 %) and ascorbic acid

(17.78 %, 15.97 %). High and moderate levels of GCV and PCV indicate moderate degree of variability as they are segregating population and good scope for improvement. Low PCV and GCV were noticed in case of days to first anthesis (5.15 %, 4.59 %), TSS (5.48 %, 2.84 %), pH (2.74 %, 2.08 %), fruit length (8.86 %, 7.77 %) and fruit width (9.01 %, 7.96 %). The low values indicate narrow range of variation for these characters and provides very least scope for improvement through selection. These findings are similar to that of Joshi and Singh[9], Mohanty[14], Kumar *et al*.[11], Shashikanth *et al*.[19], Mayavel *et al*.[12] and Khanom *et al*[10].

High heritability was observed for plant height (97.38 %), number of branches (81.00 %), days to first anthesis (79.51 %), fruit length (76.89 %), fruit width (78.10 %), number of fruits per plant (97.04), average fruit weight (94.38 %), pericarp thickness (96.75 %), number of locules (82.18 %), ascorbic acid (80.62 %) and yield per plant (96.39 %). Moderate heritability has been recorded for pH (57.78 %). High heritability indicates the traits were less influenced by environment and selection of such traits are effective. The moderate values shows the characters were influenced by the environmental effects and the selection for the improvement of such characters may not be effective. Moderate values also indicate the role of non-additive gene action which includes dominance and epistasis, therefore selection is not advisable. Similar results were reported by Natarajan[16], Gadekar *et al*.[3], Singh *et al*.[20] and Golani *et al*[5]. Heritability was found to be low for characters such as fruit firmness (21.57 %), TSS (26.82 %) and selection for such traits may not be rewarding. High level of GA have been observed for average fruit weight (26.44), plant height (23.79) and number of fruits (32.63) while GA was low for all other traits. Low values of expected genetic advance indicate the presence of both additive and non-additive gene action.

High level of genetic advance as per cent mean noticed for plant height (29.88 %), number of branches (36.24 %), fruits per plant (62.10 %), average fruit weight (35.19 %),

Table: Genetic parameters of variability for different characters in F$_2$ population of cross IIHR-2201 X C-13-1-2-1

Sl. No.	Characters	Grand mean	Range		PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	EMNG
			Minimum	Maximum						
1	Plant height (cm)	79.62	48.00	106.00	14.90	14.70	97.38	23.79	29.88	103.42
2	Number of branches/plant	8.27	4.00	14.00	21.72	19.55	81.00	3.00	36.24	11.27
3	Days to first anthesis	28.87	22.00	33.00	5.15	4.59	79.51	2.44	8.44	31.31
4	Fruit length (cm)	4.95	3.17	6.13	8.86	7.77	76.89	0.70	14.03	5.65
5	Fruit width (cm)	4.93	3.60	6.07	9.01	7.96	78.10	0.71	14.49	5.64
6	Fruit firmness (kg/cm^2)	2.51	1.43	3.87	10.20	4.74	21.57	0.11	4.53	2.62
7	Number of fruits/plant	52.54	14.00	95.00	31.07	30.60	97.04	32.63	62.10	85.16
8	Average fruit weight (g)	75.15	36.67	111.33	18.10	17.58	94.38	26.44	35.19	101.59
9	Pericarp thickness (mm)	5.60	2.98	8.36	17.62	17.33	96.75	1.97	35.12	7.57
10	Number of locules/fruit	3.12	2.00	4.67	13.41	12.16	82.18	0.71	22.70	3.82
11	TSS (^{0}Brix)	4.54	3.91	5.10	5.48	2.84	26.82	0.14	3.03	4.67
12	pH	4.22	4.00	4.50	2.74	2.08	57.78	0.14	3.26	4.36
13	Ascorbic acid (mg/100g)	24.26	15.60	36.40	17.78	15.97	80.62	7.16	29.53	31.43
14	Yield/plant (kg)	3.26	1.00	6.120	31.72	31.15	96.39	2.06	63.00	5.32

PCV- Phenotypic co-efficient of variation
GCV- Genotypic co-efficient of variation
EMNG- Expected mean in next generation
h^2 - Broad sense heritability
GA- Genetic advance
GAM – Genetic advance as per cent mean

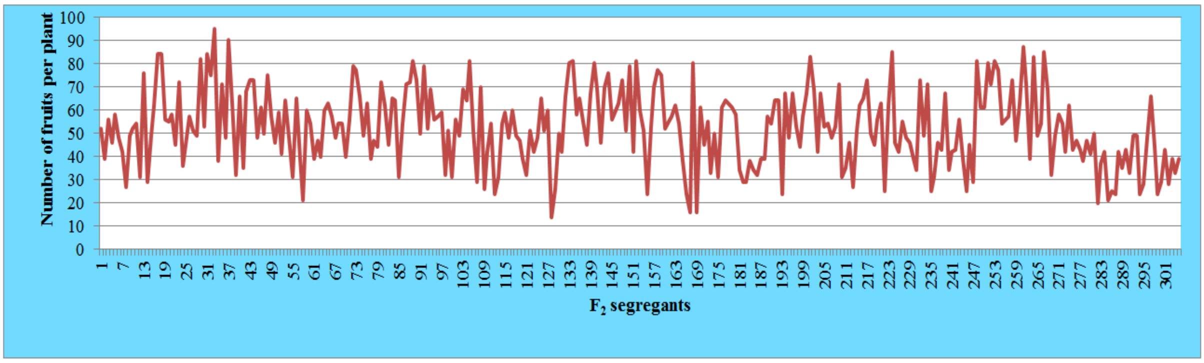

Fig. 1: Variability for number of fruits per plant in F_2 population of IIHR-2201 X C-13-1-2-1

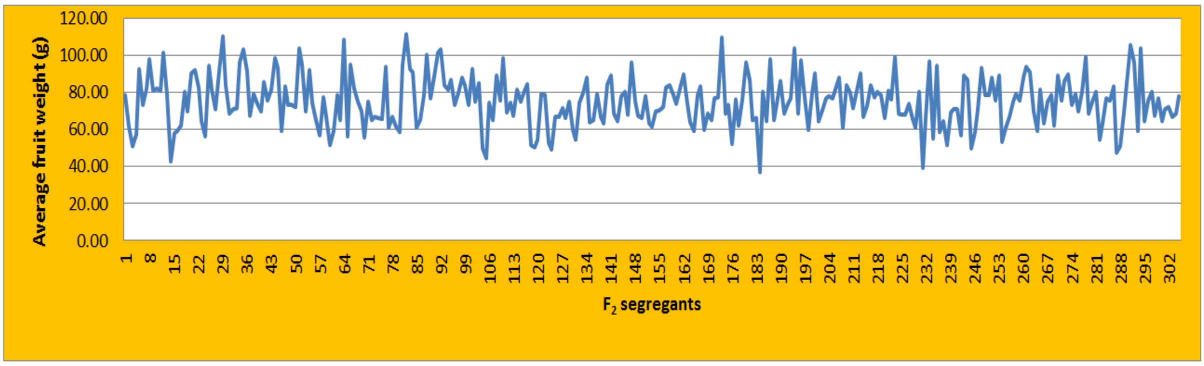

Fig. 2: Variability for average fruit weight in F_2 population of IIHR-2201 X C-13-1-2-1

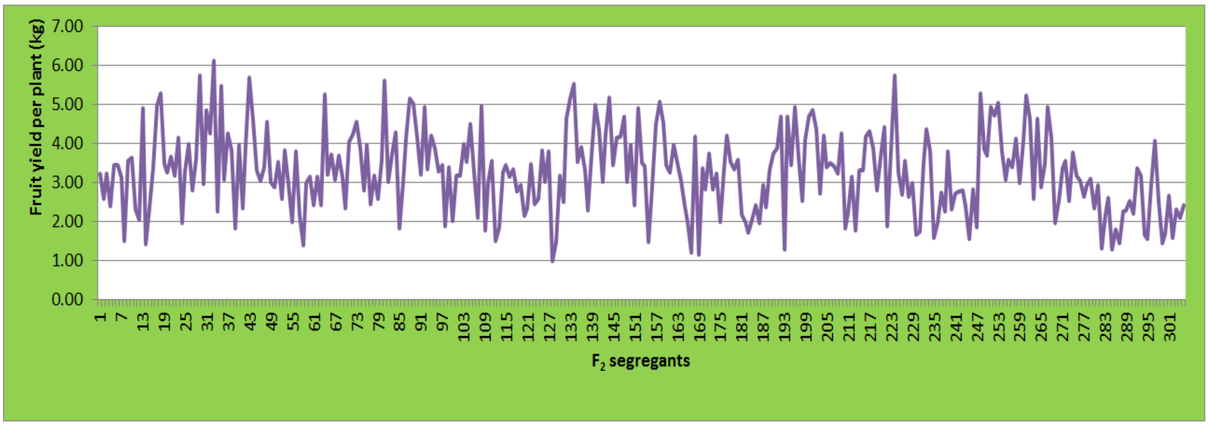

Fig. 3: Variability for fruit yield per plant in F_2 population of IIHR-2201 X C-13-1-2-1

Pericarp thickness (35.12 %), number of locules (22.70 %), ascorbic acid (29.53 %), yield per plant (63.00 %) and selection for such traits may be economic. These results are in conformity with the findings of Mohanty[15], Veershetty[22], Ghosh *et al.*[4], Reddy and Reddy[18], Shashikanth *et al.*[19] and Meena and Bahadur[13]. Moderate GAM has been observed for fruit length (14.03 %), fruit width (14.49%) followed by low GAM for days to first anthesis (8.44 %), fruit firmness (4.53 %), total soluble solids (3.03 %) and pH (3.26 %). The low value provides very least scope for improvement through selection. Similar results have also been reported by Islam *et al.*[7] and Reddy *et al*[17].

CONCLUSION

Heritability coupled with genetic advance as per cent mean were more useful than heritability alone in predicting the resultant effect for selecting the best individual as explained by Singh *et al.*[20] and Kumar *et al*[11]. High heritability coupled with high genetic advance as per cent mean for plant height, number of branches, number of fruits per plant, average fruit weight, pericarp thickness, number of locules, ascorbic acid, yield per plant (Table) noticed might be assigned to additive gene effects governing their inheritance and phenotypic selection for their improvement could be achieved by simple breeding methods. So, the findings suggested that for getting higher yield, selection should be practiced for yield related traits giving equal importance to plant height, number of branches, number of fruits per plant and average fruit weight.

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