RESEARCH PAPER
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Genetic variability, heritability and scope of genetic improvement for yield components in tomato (*Lycopersicon esculentum* Mill.)

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Genetic variability, heritability and genetic advance were studied among 20 agro-morphological traits of 31 genotypes of tomato (*Lycopersicon esculentum* Mill.) during *Rabi*, 2007-2008. Highest heritability estimate was recorded for average fruit weight (g), pericarp thickness (mm), days to 50 per cent flowering, number of fruits per plant, total fruit yield per plant, total soluble solids (%), indicating that these characters were highly heritable and governed by additive gene effects. High heritability coupled with high genetic advance was observed for number of seeds per fruit, average fruit weight (g), total number of fruits per plant, plant height, fruit set (%) indicating that most likely the heritability is due to additive gene effects. Thus, selection may likely to further improvement in these traits for varietal performance.

Key words : Tomato, Genetic variability, heritability, Genetic advance

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INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) is universally known important fruit vegetable and is one of the most widely grown. As a vegetable it is an important source of human nutrition with respect to vitamins, minerals and fibre content. It is a good source of vitamin A and C as well as providing antioxidant elements such as lycopen which prevents cancer (Bhutani and Kallo, 1983). Tomatoes are used either as fresh fruits or in the form of various processed products such as paste, whole peeled tomatoes, diced products and various forms of juices and soups. Before initiating any breeding programme, the knowledge of the genetic variability and its component being useful in designing selection procedure to a segregating and variable population.

RESEARCH METHODOLOGY

The experiment was conducted at Horticulture Research Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattishgarh during 2006-08. The experimental material comprised of thirty one genotypes of tomato collected from different agro-ecological regions of India. The genotypes grown during *Rabi* 2006 in Randomized Block Design in three replications. The observations for different characters *viz.*, days to 50 per cent flowering, plant height, number of primary branches per plant, number of flowers per cluster, number of fruits per cluster, fruit setting rate, number of fruits per plant, days to first fruit ripening, average fruit weight, fruit length, number of locules per fruit, number of calyx per fruit, pericarp thickness, number of seeds per fruit, total soluble solids, reducing sugar, acidity, pH, ascorbic acid and total fruit yield per plant were recorded on five plants basis in each replication. The following yield and quality traits were recorded from five randomly selected plants of genotypes, in each replication. The genetic variability was estimated by using the method suggested by Panse and Sukhatme (1967). The genotypic and phenotypic co-efficients of variability in percentage were computed according to Burton and De Vane (1953). The genotypic co-efficient of variation helps to measure the range of genetic variability in character and provides information about the genetic variability present for various quantitative characters. Genotypic co-efficient of variation along with heritability gives clear picture of gain to be expected from selection.

RESEARCH FINDINGS AND ANALYSIS

The ANOVA for revealed significant (P<5%) variation among genotypes for all the characters studied (Table 1). For improvement of crop characters the breeder has to select superior individuals from their phenotypic expression. Selection based on the phenotypic expression is sometime misleading, as the development of a character is the result of the heritable and non heritable factors. This highlights the imperative need for partitioning the overall variability in to its heritable and non heritable components. Thus, the components of variation such as genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation

Table 1: Analysis of variance for randomized block design for fruit yield and its component characters

Source	D.F.	Mean squares									
		1	2	3	4	5	6	7	8	9	10
Replication	2	0.14	0.13	0.15	0.038	0.14	0.68	0.11	0.12	0.61	0.06
Genotypes	38	174.32**	778.76**	16.49**	17.86**	12.45**	557.83**	1820.63**	988.93**	4.27**	2.82
Error	76	0.77	0.24	0.18	0.16	0.19	0.43	0.13	0.28	0.73	0.04
Source	D.F.	Mean squares									
		11	12	13	14	15	16	17	18	19	20
Replication	2	0.83	0.13	0.08	19.93	0.23	0.04	0.03	0.01	0.03	0.09
Genotypes	38	6.74**	1.47**	0.67	7869.18**	1.26**	1.86**	2.39**	0.58**	107.90**	1.14**
Error	76	0.14	0.06	0.02	139.97	0.04	0.03	0.03	0.01	0.17	0.03

*and** indicate significance of value at P=0.05 and P=0.01, respectively

1. Days to 50 % flowering
2. Plant height (cm)
3. No. of primary branches per plant
4. No of flowers per cluster
5. No of fruits per cluster
6. Fruit set (%)
7. No of fruits per plant
8. Average fruit weight (g)
9. Fruit length (cm)
10. Fruit width (cm)
11. No of locules per fruit
12. No of calyx per fruit
13. Pericarp thickness (mm)
14. No. of seeds per fruit
15. Total soluble solids (%)
16. Reducing sugar (%)
17. pH
18. Titrable acidity (%)
19. Ascorbic acid (mg/100 ml)
20. Total fruit yield/ plant (kg)

Table 2: Genotypic and phenotypic co-efficients of variations (GCV and PCV), heritability (h^2), genetic advance as % of mean and components of variance for fruit yield and its component characters

Characters	Grand mean (X)	Range		GCV %	PCV %	h^2 BS (%)	Genetic advance	Genetic advance as % of mean
		Minimum	Maximum					
Days to 50 % flowering	70.85	47.93	83.67	10.74	10.81	88.70	15.57	21.98
Plant height (cm)	79.42	56.88	111.78	20.28	20.29	59.90	33.17	41.76
No. of primary branches per plant	12.59	6.47	21.40	18.52	18.83	76.68	4.73	37.87
No of flowers per cluster	11.27	6.00	18.40	21.56	21.85	69.40	4.94	43.83
No of fruits per cluster	6.31	4.47	16.20	32.05	32.78	65.60	4.07	64.50
Fruit set (%)	56.77	36.38	85.74	24.01	24.04	72.80	28.05	49.40
No of fruits per plant	33.15	18.60	179.70	74.31	74.32	79.80	50.74	152.55
Average fruit weight (g)	58.59	28.05	92.35	30.98	31.00	93.00	37.38	63.80
Fruit length (cm)	4.39	1.80	6.22	26.93	27.63	35.00	2.38	54.21
Fruit width (cm)	4.32	2.48	6.17	22.31	22.83	48.50	1.94	44.91
No of locules per fruit	4.43	2.33	8.93	33.45	34.52	54.90	2.96	66.82
No of calyx per fruit	5.84	3.73	7.13	11.74	12.51	78.10	1.33	22.77
Pericarp thickness (mm)	0.14	0.26	0.08	34.34	36.33	89.30	0.09	69.23
No. of seeds per fruit	114.91	37.40	222.73	44.17	45.36	64.90	101.84	84.94
Total soluble solids (%)	4.42	3.33	5.76	14.33	14.96	76.70	1.25	28.22
Reducing sugar (%)	4.81	3.62	7.07	16.31	16.62	41.20	1.58	38.72
pH	4.15	2.73	6.13	21.39	21.80	56.63	1.80	43.37
Titrable acidity (%)	0.54	0.36	1.01	25.58	25.67	49.30	0.29	53.70
Ascorbic acid (mg/100 ml)	28.12	16.74	37.41	21.31	21.37	68.50	12.31	43.78
Total fruit yield/ plant (kg)	1.81	0.67	3.24	34.05	34.20	79.10	1.26	70.00

(PCV) were computed. The PCV was higher than the GCV for the characters under study.

The character, which exhibited high heritability, indicates the presence of additive gene action and such characters could be fixed by resorting to selection. According to Johnson *et al.* (1955), heritability estimates could not be alone guideline for improvement work, since high heritability does not mean high expected genetic gain. Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. Thus, the data of present investigation subjected to heritability in broad sense and genetic advance for all the characters under study and estimates of heritability grouped in to high (above 60 %), moderate (31 to 60 %) and low (below 30 %). In the same way the estimates of genetic advance as percentage of mean grouped in to high (above 20 %), moderate (10 to 20 %) and low (below 10 %) as suggested by Johnson *et al*. (1955). The results obtained on above genetical parameters are discussed (Table 2). High genotypic as well as phenotypic co-efficients of variation were recorded for traits *viz*., number of fruits per plant, number of seeds per fruit, number of locules per fruit, pericarp thickness (mm), total fruit yield per plant, number of fruits per cluster, titrable acidity (%), fruit set (%), fruit width (cm) and number of flowers per cluster.

Moderate genotypic and phenotypic co-efficients of variation were observed for pH, ascorbic acid (mg/ 100ml), plant height, number of primary branches, reducing sugar (%), total soluble solids (%), number of calyx per fruit and days to 50 per cent flowering. The estimates of GCV and PCV of the present study were closely in agreement with the findings of Rattan *et al.* (1983), Mohanty (2002), Singh *et al.* (2002), Singh and Narayan (2004), Joshi *et al.* (2004) and Kumari *et al.* (2007).

Among the characters studied, highest heritability estimate was recorded for average fruit weight (g) followed by pericarp thickness (mm), days to 50 per cent flowering, number of fruits per plant, total fruit yield per plant, total soluble solids (%), number of primary branches per plant, fruit set (%), number of fruits per cluster, number of seeds per fruit, number of flowers per cluster and ascorbic acid (mg/ 100 ml) indicating that these characters were highly heritable and governed by additive gene effects. These are closely follow the findings of Hasan *et al.* (2000), Singh *et al.* (2002), Kumar *et al.* (2004) and Singh *et al.* (2005).

Moderate broad sense heritability was observed for plant height, pH, number of locules per fruit, titrable acidity, fruit width (cm), reducing sugar (%) and fruit length (cm).

High heritability coupled with high genetic advance was observed for number of seeds per fruit, average fruit weight (g), total number of fruits per plant, plant height, fruit set (%) indicating that most likely the heritability is due to additive gene effects thus selection may be effective for these traits.

The number of fruits per plant recorded highest genetic advance as percentage of mean followed by number of seeds per fruit, total fruit yield per plant, pericarp thickness (mm), number of locules per fruit, number of fruits per plant, average fruit weight (g), fruit length (cm) and titrable acidity. Genetic advance in general was high for most of the characters studied except days to first flowering, days to first fruiting and plant height, which showed moderate genetic advance as percentage of mean. These findings are in close association with the study of Singh *et al.* (2002), Mariame *et al.* (2003), Joshi *et al.* (2004), Ahmed *et al.* (2006), Mahesha *et al.* (2006) and Kumari *et al.* (2007).

Thus, the present study suggested that good amount of variation was observed for various characters under study and recorded obvious breeding value as their heritability and genetic advance as a percentage of mean.

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