

Genetic Variability, Heritability and Genetic Advance In Tomato (*Solanum Lycopersicon* Mill.)

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Abstract

In the present study an attempt has been made to germplasm evaluation in 39 diverse genotypes of tomato at Vegetable Research Farm, Rewa (Madhya Pradesh) during the *Rabi* session of 2011. Analysis of variance showed significant variation among the genotypes for all evaluated traits. Number of fruits plant⁻¹ showed the highest genotypic and phenotypic variance (1282.0 and 1287.6) whereas test weight showed the lowest (0.03 and 0.08). High genotypic variance was observed for most of the characters indicating more contribution of genetic components for the total variation. Genotypic coefficients of variations (GCV) and phenotypic coefficient of variation (PCV) were highest for average fruit weight (48.85 and 48.87), number of seeds fruit⁻¹ (44.54 and 45.29) whereas the lowest were recorded for days to 50% fruit setting (1.984 and 2.81). Higher GCV and PVC were recorded for most of the characters indicating higher magnitude of variability for these characters. The highest heritability (broad senses) estimates were observed for average fruit weight (99.92) number of secondary branches (99.65%), while the lowest was for the test weight (45.29%). Highest genetic advance as per cent of mean was recorded for average fruit weight (100.59%) and lowest for days to 50% fruit setting (2.89). The exploration of genetic variability in the available germplasm is a prerequisite in a breeding programme for effective selection of superior genotype of tomato.

Highlights

- Thirty nine cultivars were selected for the study of genetic variability, heritability, genetic advance in tomato. Highest phenotypic and genotypic variances were observed number of fruits plant⁻¹.
- Maximum heritability and genetic advance was recorded for average fruit weight, number of seeds fruit⁻¹ respectively.
- Genotypes VS-404, H-86, MHT-256 and Santury were estimated higher yield performance in central plateau of India.
- Genotypes H-86, DT-10, Arka Vikash, GT-2 and Arkha Meghali were observed higher pericarp thickness which is desirable character for transportation and storage life.

Keywords: Tomato, *Solanum Lycopersicon*, GCV, PCV, heritability, genetic advance



Tomato (*Solanum Lycopersicon* Mill.) is the second most important vegetable crops of Peru-Ecuador origin (Singh *et al.* 1969) after potato. Nutritionally, tomato is a good source of vitamin A and vitamin C (Gould *et al.* 1983). Tomato plays a major role in human nutrition, fruit contain Water 93.1%, Protein 1.9%, Fat 0.3g, Fiber 0.7%, Carbohydrates 3.6%, Calorie 23, Vitamin A 320 I.U., Vitamin B₁ 0.07mg, Vitamin B₂ 0.01mg, Vitamin C 31mg, Calcium 20mg, Phosphorus 36mg and iron 0.8mg. Tomato also a good source of lycopene (an antioxidant), ascorbic acid and β -carotene and valued for their colour and flavour. In India it occupies an area of 879.6 thousand hectare with a production of 18227.0 thousand metric tonnes and average productivity is 20.7 metric tonnes per hec. Major tomato growing states in India are Bihar, Karnataka, Orissa, Maharashtra and Andhra Pradesh. In Madhya Pradesh, it is grown in 62.59 thousand hec of land with the annual production of 1845.0 thousand metric tonnes and productivity of 29.5 metric tonnes hec⁻¹ (Anonymous 2014).

Tomato genotype varies not only in the morphological features but also in the quality (Abhusita *et al.* 1997). Most of the quality traits in tomato show continuous variation and is strongly influenced by environmental conditions (Lecome *et al.* 2004). The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epistasis (non-allelic interaction) therefore, it essential to partition the estimated phenotypic variability into its heritable and non-heritable components with suitable parameters such as genetic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, genetic advance, and heritability. Partitioning of variance into various components provides information regarding breeding value and nature and magnitude of variability in the expression of a particular trait. Systematic study and evaluation of tomato germplasm is of great importance for current and future agronomic and genetic improvement of the crop, evaluation of germplasm is imperative in order to understand the genetic background and the

breeding value of the available germplasm (Agong *et al.* 2000). Hence, the present investigation will be carried out to generate information in respect of some genetic parameter related to fruit yield and its attributing traits in tomato.

Materials and Methods

The present experiment was conducted at Vegetable Research Farm, College of Agriculture Rewa, JNKVV, Jabalpur (Madhya Pradesh). Under study thirty nine tomato genotypes viz., Nandi, Arka Meghali, DVRT -1, Salimar -2, PKM -1, Roma, GT-2, CO-3, T.L.B.R.-3, Utkal Urvashi, H-88-78-1, H-88-78-2, Arka Saurabh, Arka Vikas, Shankarmit, Utkal Raja, Palam Pink, Selection-7, Arka Alok, Utkal Kumari, Dhanashree, DT-10, DVRT-2, Vaibhav, Christmas Grape, Madan Tomato, F1-Bhasker, Santury Research, Ujvork Udham, MHT-301, Mahalaxmi, MHT-256, T-99, MST-256, Bhagya, H-86, VS -44, VS -312 and VS-404, were evaluated for different plant and fruit characters during 2010-11. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Rewa is situated in the North, Eastern part of Madhya Pradesh, the climatic region comes under the semi-arid and subtropical having extreme winter and summer. It is situated at the latitude of 24°31 N, longitude 81°15 E altitude of 306 meter above the sea level. Appropriate agronomic practices were followed to raise a good crop. Ten randomly taken plants were used to record observations on quantitative and qualitative traits, as days to first flowering, days to 50% flowering, days to 50% fruit setting, days to 100% fruit setting, days to fruit maturity, number of flowers per cluster, number of fruits cluster-1, number of fruiting clusters plant-1, plant height (cm), number of primary branches, number of secondary branches, fruit length (cm), fruit diameter (cm), test weight (g), average fruit weight (g), T.S.S.(%), number of fruits plant-1, pericarp thickness (mm), number of locules fruits-1, fruit yield plant-1 (kg.), number of seeds fruit-1, which included analysis of variance, genotypic variance (a2g), phenotypic variances (a3p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability in broad sense (h2bs), genetic advance (GA) and genetic advance as% over mean were analyzed following the formula illustrated (Singh *et al.* 1985).

**Table 1: Analysis of variance for different characters in thirty nine tomato genotypes**

Characters	RMS	GMS	EMS	SEm±	CD @ 1%	CD@ 5%
Days to first flowering	1.5	08.50**	0.77	0.5	1.89	1.42
Days to 50% flowering	5.49	06.69**	1.35	0.67	2.5	1.89
Days to 50% fruit setting	14.5	05.96**	1.49	0.7	2.64	1.99
Days to 100% fruit setting	0.2	16.74**	2.18	0.85	3.19	2.4
Days to fruit maturity	10.74	14.20**	1.85	0.78	2.93	2.21
Number of flowers per cluster	0.0	01.54*	0.09	0.17	0.65	0.49
number of fruits per cluster	0.18	01.34*	0.05	0.13	0.48	0.36
No. of fruiting clusters per plant	7.62	216.07**	1.99	0.81	3.04	2.29
Plant height (cm)	3.64	999.22**	5.36	1.33	4.99	3.76
Number of primary branches	0.16	11.46**	0.09	0.18	0.67	0.5
Number of secondary branches	0.19	18.14**	0.02	0.08	0.31	0.23
Fruit length (cm)	0.06	01.97*	0.01	0.06	0.22	0.17
Fruit diameter (cm)	0.04	02.59**	0.01	0.06	0.22	0.17
Test weight (g)	0.19	00.15	0.04	1.12	0.45	0.34
Average fruit weight (g)	0.39	836.66**	0.21	0.26	1	0.75
T.S.S. (%)	0.5	02.07*	0.05	0.13	0.51	0.38
Number of fruits per plant	29.91	3852.5**	5.23	1.32	4.93	3.72
Pericarp thickness (mm)	0.07	04.80**	0.07	0.16	0.59	0.45
Number of locules per fruits	0.03	00.90	0.51	0.13	0.49	0.36
Fruit yield per plant (kg.)	0.04	02.74**	0.04	0.11	0.43	0.32
Number of seeds per fruit	74.52	3195.3**	35.5	3.44	12.8	9.69

** Significant at $p=0.01$, * Significant at $p=0.05$

Results and Discussion

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all 21 characters at 1% and 5% probability level (Table 1). The mean performance and range of the genotypes for variability and estimates of different genetic variability parameters are presented in (Table 2). The range of variability was highest for number of fruits per plant (34.63-163.46), followed by number of seeds per fruit (20.9-157.66), plant height (43.4-123.66), days to fruit maturity (78.5-87.7), days to 100% fruit setting (69.4-79.4), average fruit weight (8.33- 69.3), days to 50% fruit setting (57.66-66.4), days to 50% flowering (50.7-59.3) number of fruiting cluster per plant (8.26-42.6), number of secondary

branches (8.6-17.43), number of primary branches (4.26-12.63), number of flowers per cluster (5.6-8.6), T.S.S.(5.4-9.43), pericarp thickness(2-7), fruit diameter (2.7-5.8), fruit yield per plant (0.76 - 5.45 kg), number of fruits per cluster (2.53-5.43), fruit length (2.2-5.3cm), number of locules per fruits (2-5), test weight (1.56 - 2.66g). The variability among the 39 genotypes of tomato is presented through pictures in (Plate 1).

The highest genotypic variance recorded for number of fruits per plant (1282.0), followed by number of seed per fruit (1053.2), plant height (331.2), average fruit weight (278.8), number of fruiting cluster per plant (71.35) whereas the lowest genotypic variance were estimated for test weight (0.03), followed by

Table 2: Different genetic parameters for twenty two quantitative traits in tomato

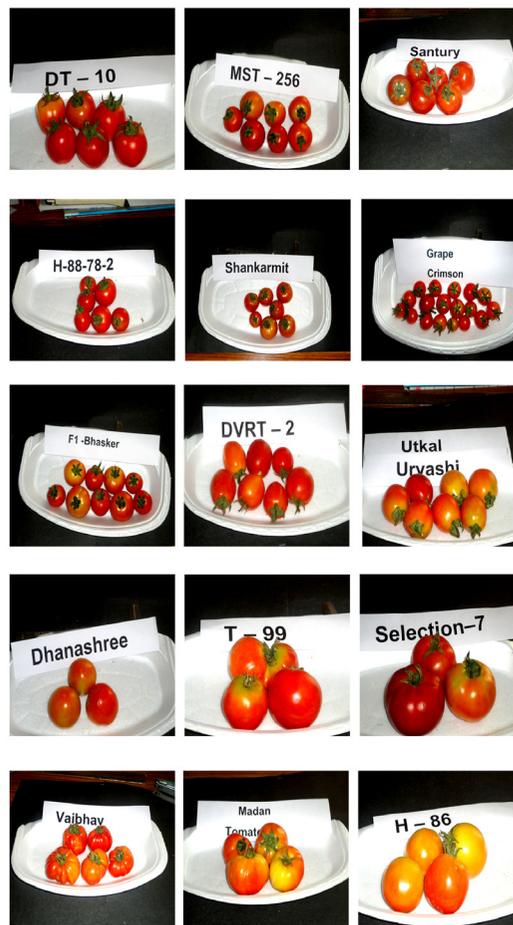
Characters	Range		Mean	Variance		PCV (%)	GCV (%)	H ² (bs)	GA (%)	GA as% of mean (%)
	Min.	Max		$\sigma^2 p$	$\sigma^2 g$					
Days to first flowering	40.2	49.73	43.03	3.34	2.57	4.25	3.72	76.94	2.9	6.73
Days to 50% flowering	50.7	59.3	53.88	3.13	1.78	3.28	2.47	56.82	2.07	3.84
Days to 50% fruit setting	57.66	66.4	61.36	2.98	1.48	2.81	1.98	49.85	1.77	2.89
Days to 100% fruit setting	69.4	79.4	74.42	7.03	4.85	3.56	2.95	68.94	3.76	5.06
Days to fruit maturity	78.5	87.7	82.97	5.97	4.11	2.94	2.44	68.92	3.46	4.18
Number of flowers per cluster	5.6	8.6	6.22	0.57	0.48	12.18	11.17	84.07	1.31	21.1
Number of fruits per cluster	2.53	5.43	3.64	0.48	0.42	19.02	17.99	89.41	1.27	35.04
Number of fruiting cluster per plant	8.26	42.6	27.77	73.35	71.35	30.83	30.41	97.28	17.16	61.79
Plant height(cm)	43.4	123.6	66.9	336.6	331.2	27.42	27.2	98.41	37.19	55.59
Number of primary branches	4.26	12.63	6.9	3.88	3.79	28.56	28.2	97.48	3.95	57.35
Number of secondary branches	8.6	17.43	13.24	6.06	6.04	18.59	18.55	99.65	5.05	38.16
Fruit length(cm)	2.2	5.3	3.86	0.66	0.65	21.11	20.93	98.34	1.65	42.77
Fruit diameter (cm)	2.7	5.8	4.24	0.87	0.86	21.99	21.85	98.74	1.9	44.73
Test weight (g)	1.56	2.66	2.36	0.08	0.03	12.12	8.16	45.29	0.26	11.31
Average fruit weight (g)	8.33	69.3	34.17	279.03	278.8	48.87	48.85	99.92	34.38	100.59
T.S.S. (%)	5.4	9.43	7.17	0.72	0.67	11.88	11.41	92.22	1.62	22.58
Number of fruits per plant	34.63	163.46	75.74	1287.6	1282	47.37	74.27	99.59	73.62	97.19
Pericarp thickness(mm)	2.0	7.0	4.23	1.65	1.57	30.4	29.68	95.35	2.52	59.71
Number of locules per fruit	2.0	5.0	3.29	0.33	0.28	17.6	16.2	84.67	1.01	30.7
Fruit yield per plant (kg)	0.76	5.45	2.29	0.94	0.9	42.2	41.27	95.63	1.91	83.14
Number of seeds per fruit	20.9	157.66	72.85	1088.8	1053.2	45.29	44.54	96.74	65.75	90.25



Plate: 1 Variability for fruit characters in tomato



Plate:1-Variability for fruit characters in tomato



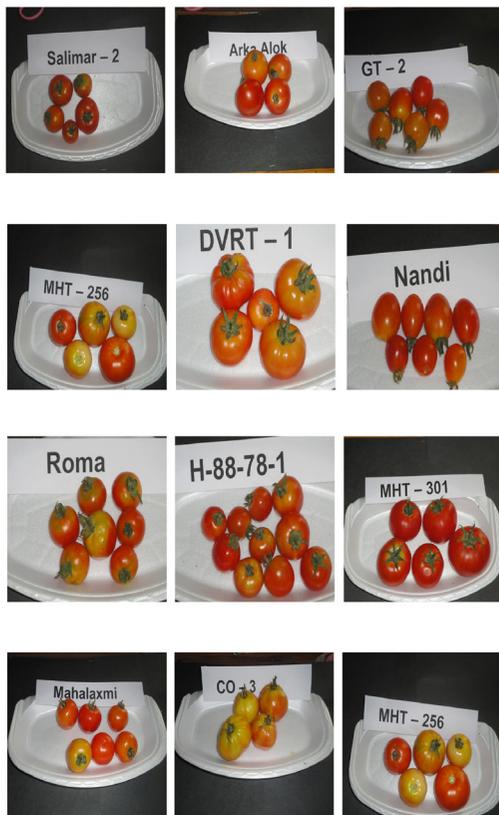
number of locules per fruits (0.28), number of fruits per cluster (0.42), number of flowers per cluster (0.48). Similarly, phenotypic variance were also the highest for number of fruits per plant (1287.6), followed by number of seeds per fruit (1088.8), plant height (336.65), average fruit weight (279.03), number of fruiting clusters per plant (73.35), whereas the lowest phenotypic variance was test weight per fruit (0.08), followed by number of locules per fruit (0.33), number of fruits per cluster (0.48), number of flowers per cluster (0.57). High genotypic variance was observed for most of the characters indicating more contribution of genetic component for the total variation. Therefore, these characters (Table

2) could be considered and exploited for selection purpose. These results were in accordance of the results obtained by Mohanty *et al.* (2002), Lecome *et al.* (2004), Hyder *et al.* (2007), Ghosh *et al.* (2010), Bernousi *et al.* (2011), Manna *et al.* (2012), Naik *et al.* (2012). Patel *et al.* (2013), Agrawal *et al.* (2014) and Khapte *et al.* (2014).

The highest phenotypic coefficient of variation was observed for average fruit weight (48.87), number of fruits per plant (47.37), number of seeds per fruit (45.29), and number of fruiting clusters plant-1 (30.83). Similarly, the highest genotypic coefficient of variation (GCV) were reported for number of fruits per plant (74.27), average fruit weight (48.85),

number of seeds per fruit, fruit yield per plant (41.27), number of secondary branches (18.55). Similar results also reported by Lecomte *et al.* (2004), Shashikant *et al.* (2010), Bernousi *et al.* (2011) Mohamed *et al.* (2012), Patel *et al.* (2013), Santader *et al.* (2013) and Agrawal *et al.* (2014).

Genotypic coefficient of variation, which is the true indicator of the extent of genetic variability in a



population, was high for all the characters, except days to 50% fruit setting (1.98). Similar results were obtained (Agong *et al.* 2000). Generally, PCV values were higher than GCV values for all traits. Higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PVC) were recorded for characters like average fruit weight, number of fruits per plant, number of seeds per fruit, number of fruiting cluster per plant, number of seed per fruit, fruit yield per plant, number of secondary branches, indicating higher magnitude of variability for these characters. The results are in conformity

with the findings of Hyder *et al.* (2007), Ghosh *et al.* (2010), Shashikant *et al.* (2010), Bernousi *et al.* (2011) Manna *et al.* (2012), Shrishail *et al.* (2013) in Okra, Agrawal *et al.* (2014) and Khapte *et al.* (2014).

The highest heritability was recorded in average fruit weight (99.92%), with an expected genetic advance over per cent of mean (100.59%), followed by number of secondary branches (99.65%) with an expected genetic advance over% of mean (38.16%), number of fruits per plant (99.59%) with an expected genetic advance over per cent of mean (97.19%), fruit diameter (98.74%) with an expected genetic advance over% of mean (44.73%), plant height (98.41%) with an expected genetic advance (55.59%) indicating that these traits are controlled by additive gene action which is very useful in selection. While the lowest heritability were that test weight per fruit (45.29) with an expected genetic advance over per cent of mean of (11.31), days to 50% fruit setting (49.85), with an expected genetic advance over% of mean of (2.89). These results agreed with those of Agong *et al.* (2000) Mohanty *et al.* (2002), Hyder *et al.* (2007) and Shasikant *et al.* (2010). Thus, heritability estimates appear to be more essential when accompanied by estimates of genetic advance and as% of mean (%).

The genotypes expressed high genotypic and phenotypic coefficient of variation, heritability (h^2) and genetic advance for fruit yield per plant (kg), number of fruits per cluster, and number of fruit per plant, average fruit weight, number of secondary branches, revealed these characters are under the control of additive gene action. This indicated high response to selection for genetic improvement of tomato genotypes under study.

Conclusion

Analysis of variance revealed the presence of considerable amount of genetic variability for yield and its components studied in all the environments. The genotypes expressed high genotypic and phenotypic coefficient of variation, heritability (h^2) and genetic advance for fruit yield plant⁻¹ (kg), number of fruits cluster⁻¹, and number of fruit plant⁻¹, average fruit weight, number of secondary



branches, revealed these characters are under the control of additive gene action. This indicated high response to selection for genetic improvement of tomato genotypes under study.

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