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Chethan Kumar S

Department of Vegetable Science, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Jawadagi RS

Department of Vegetable Science, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Fakrudin B

Department of Biotechnology and Crop Improvement, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Hanchinamani CN

Department of Vegetable Science, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Kulkarni MS

Department of Plant Pathology, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Lakshmidevamma TN

Department of Biotechnology and Crop Improvement, University of Horticultural Sciences, Bagalkote, Karnataka, India

#### Vijayakumar R

Department of Vegetable Science, University of Horticultural Sciences, Bagalkote, Karnataka, India

Corresponding Author: Chethan Kumar S Department of Vegetable Science, University of Horticultural Sciences, Bagalkote, Karnataka, India

### Evaluation of recombinant inbred line population derived from FBT-27 × Sankranti cross for genetic parameters in tomato (*Solanum lycopersicum* L.)

## Chethan Kumar S, Jawadagi RS, Fakrudin B, Hanchinamani CN, Kulkarni MS, Lakshmidevamma TN and Vijayakumar R

#### Abstract

The present study was carried out to investigate yield and quality traits in tomato, in order to generate information regarding the extent of genetic variability, heritability and genetic gain. The experiment was laid out during *kharif* 2021-2022 in augmented design at Department of Vegetable Science, K.R.C.C.H., Arabhavi Belagavi. Genetic variability was estimated among 220 developed recombinant inbred lines derived from FBT-27 × Sankranti cross of tomato. Analysis of variation revealed that there is a significant difference between all the traits and the magnitude of phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the studied traits. Further, high estimates of heritability and genetic gain were recorded for all the characters except the quality traits TSS and pH. Thereby, suggesting that straight selection for these traits may bring worthwhile improvement in identifying superior genotypes in tomato.

Keywords: Variability, heritability, genetic gain, yield, tomato

#### Introduction

Tomato (*Solanum lycopersicum* L.) are native to Western South America (Rick, 1976) and it is the most important vegetable crop over the world. It's belongs to the family solanaceae and having chromosome number 2n=24. It is having most of the health benefits due to presence of antioxidants, vitamins and mineral. It is grown as an annual or short-lived perennial herbaceous plant with a taproot system and determinate, semi-determinate and indeterminate growth habits. Tomato cultivation in India occupies an area of 0.81 million hectares with a production of 21.17 million tons and productivity of 25.32 metric tons per hectare. Karnataka, occupies third place in the country with an area of 64.25 thousand hectares and production of 2081 thousand tons and productivity 32.40 metric tons per hectare (NHB, 2018)<sup>[2]</sup>.

Achievement of plant breeding depends upon the nature and magnitude of variability present in the genotypes. Likewise, the assessment of heritable and non-heritable components of total variability will have enormous value in the choice of suitable breeding procedures. But the production and productivity of this crop in India is far below compare to the global scenario. There is a need to develop superior hybrids or varieties suitable for diverse agro-ecological conditions with specific end use. Success and speed of conventional breeding is predominantly conditioned by the availability of desired genetic variability for the target traits (Ara et al., 2009)<sup>[4]</sup>. Genetic resources empower plant breeders to create novel plant gene combinations and select crop varieties more suitable to the needs of diverse agricultural systems (Glaszmann et al., 2010)<sup>[10]</sup>. The importance of genetic variability was perceived for the first time by a Russian scientist, Vavilov (1951) <sup>[19]</sup>, who advocated that a wide range of variability offers better scope for selecting a desirable genotype. The proficiency of selection depends on the nature and extent of genetic variability, degree of transmissibility of desirable characters and actual expected genetic gain for the character in a population (Golani et al., 2007) [11]. An insight into the magnitude of variability and the extent of heritability present in the gene pool of a crop species for desirable traits is of ultimate prominence to a plant breeder for initiate a judicious plant breeding programme.

#### **Material and Method**

The experiment was conducted at Kittur Rani Channamma College of Horticulture, Arabhavi, Belagavi, during *Kharif* season of 2021-2022 with 220 developed recombinant inbred lines

derived from FBT-27 × Sankranti cross. The experiment was conducted in augmented design with six checks. Seeds from each recombinant inbred line populations were sown in portrays and after four weeks, seedlings were transplanted with the  $60 \times 60$  cm spacing in field with light irrigation. Irrigation, weeding and other intercultural operations were done as and when necessary. Fifteen plants per each line were transplanted in the field and five plants were selected randomly from each line for collecting data on growth and yield attributes for statistical analysis. The analysis of variance for each of the characters was performed using R software. The data of the experiment was subjected to Fischer's method of analysis of variance given by Federer and Raghavrao (1975)<sup>[9]</sup> for analysis and interpretation of data. The level of significance used in 'F' was 5 per cent. The genotypic and phenotypic variances were estimated as per Johnson *et al.* (1955) <sup>[12]</sup>. Genotypic and phenotypic coefficients of variation were calculated following Burton and Devane (1953)<sup>[7]</sup>. The expected genetic advance for different characters was estimated as per Johnson et al. (1955)<sup>[12]</sup>.

#### **Result and Discussion**

#### Analysis of variance

Analysis of variation revealed that significant variations for the all character were observed in the developed recombinant inbred lines which could be due to the genetic background and morphological variability present in the parents used for development (Table 1). This trend was also reported by Bhandari *et al.* (2017) <sup>[6]</sup>, Aralikatti *et al.* (2018) <sup>[5]</sup> and Tsagaye *et al.* (2020) <sup>[17]</sup>, which confirms our findings. Thus, considerable amount of genetic variability was present in the experimental material which can be exploited for improvement of fruit yield and yield attributes in tomato.

#### **Genetic parameters**

Genetic parameters revealed that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits observed (Table 2). This revealed that the existing variation is due to the genetic constitution of genotypes and added with environmental variance. Anuradha *et al.* (2020) <sup>[3]</sup>; Rawat *et al.* (2020) <sup>[14]</sup> and Venkadeswaran *et al.* (2020) <sup>[19]</sup> also reported broad genetic variation in the germplasm of tomato. This will help in further selection of promising types. The estimates of phenotypic and genotypic coefficient of variation was higher than that of the genotypic

coefficient of variation for all the characters studied and there was a narrow difference between GCV and PCV implying that greater role was played by recombinant inbred line populations, rather than environment for expression of characters. Similar results were obtained by Debnath et al. (2021)<sup>[8]</sup>. In the present investigation, among all the characters studied, the maximum genotypic and phenotypic coefficient of variation was observed for total yield per plant followed by number of fruits per plant, which indicated the presence of wide variation for these characters, which reflected that these traits were governed by additive gene action. So, there is scope for improvement of these traits through selection and selection for these traits will be rewarding. Lower PCV and GCV were observed for TSS and pH indicating that these traits are governed by non-additive gene action and hence there is less scope for improvement of these traits through selection. Because the traits are qualitative in nature and controlled by one or two genes, so there is not much variation present. Moreover the recombinant inbred lines which were developed from the FBT-27  $\times$  Sankranti were homozygous.

In the present study, high heritability was observed for all the characters studied. This indicates that good correspondence between genotypic and phenotypic values and thereby a low environmental effect on the expression of all characters. High heritability coupled with high genetic advance as per cent of mean observed for all the traits except TSS and pH which suggested the preponderance of additive genes. It also indicated a higher response for the selection of high yielding genotypes as these characters are governed by additive gene actions. High heritability along with high expected genetic advance as per cent of mean for the characters controlled by polygenes might be useful for the plant breeders for making effective selection. High heritability coupled with high expected genetic advance as per cent of mean for plant height and number of branches per plant was reported by Akhter et al. (2021) <sup>[1]</sup>. Similar results were also observed for characteristics like the number of clusters per plant (Raut et al., 2021)<sup>[13]</sup> and number of fruits per cluster (Rawat et al., 2020)<sup>[15]</sup>. High heritability and genetic advance as per cent of the mean was observed for the number of fruits per plant, average fruit weight and total yield per plant. Similar results were obtained by Raut *et al.* (2021)<sup>[13]</sup>. Quality parameters like TSS show higher heritability and lower genetic advance as per cent of mean and these results are corroborated with findings of Vinod et al., 2013<sup>[20]</sup>.

Table 1: Analysis of variance (ANOVA) for yield component and quality traits in FBT- 27 × Sankranti cross

Source of variation	DF		Mean Sum of Squares												
Source of variation		PHT	PB	NOFPC	NOCPP	FLO	DFF	D50F	FL	FD	AFW	NOF	YPP	PH	TSS
Block	4	4.53	0.24	0.09	$1.8^{*}$	0.09	0.74	1.74	0.0019	0.02	5.2	1.24	0.0011	0.01	$0.02^{*}$
Entries	226	139.3**	1.73**	1.34**	15.36**	$0.66^{**}$	9.85**	14.6**	0.84**	$0.74^{**}$	89.65**	575.46**	0.C92**	$0.08^{**}$	$0.07^{**}$
Checks	6	1286.03**	3.22**	2.31**	35.98**	$2.22^{**}$	35.56**	23.31**	1.11**	4.46**	143.1**	1168.66**	3.47**	$0.08^{**}$	$0.76^{**}$
Lines	219	108.44**	$1.68^{**}$	1.13**	14.44**	$0.61^{**}$	14.3**	10.55**	0.82**	0.64**	88.22**	556.61**	0.81**	$0.07^{**}$	$0.05^{**}$
Checks vs. Lines	1	16.56**	3.97**	42.19**	92.68**	2.36**	19.46**	$850.08^{**}$	4.28**	0.47**	80.38**	1145.8**	9.23**	$1.18^{**}$	0.24**
Error	24	2.11	0.2	0.12	0.62	0.11	1.71	0.95	0.03	0.06	2.15	2	0.00077	0.01	0.01

*Significant at 5% probability level	** Significant at 1% probability level	
PHT-Plant height (cm)	PB-Number of branches per plant	NOFPC-Number of fruits per cluster
NOCPP-Number of cluster per plant	FLO-Number of locules per fruit	DFF-Days to first flowering
D50F-Days to 50 percent flowering	FL-Fruit length (cm)	FD-Fruit diameter (cm)
AFW-Average fruit weight (g)	NOF-Number of fruits per plant	YPP-Total yield per plant (kg)
TSS: Total soluble solid		

Table 2: Genetic variability parameters for yield component and quality traits in FBT 27 × Sankranti cross

Trait	PCV (%)	GCV (%)	Heritability (%)	GAM (%)
PHT	12.89	12.76	98.05	26.07
PB	19.31	18.12	87.98	35.05
NOCPP	24.73	24.2	95.74	48.85
NOFPC	25.71	24.35	89.7	47.58
FLO	26.38	24	82.72	45.03
DFF	11.12	10.02	81.24	18.63
D50F	10.24	9.78	91.24	19.27
FL	20.83	20.42	96.07	41.29
FD	16.65	15.92	91.44	31.4
AFW	23.69	23.4	97.56	47.68
NOF	36.06	36	99.64	74.13
YPP	35.65	35.63	99.91	73.48
TSS	5.33	5.03	88.91	9.78
PH	6.47	6.08	88.45	11.8

PHT-Plant height (cm)	PB-Number of branches per plant	NOFPC-Number of fruits per cluster		
NOCPP-Number of cluster per plant	FLO-Number of locules per fruit	DFF-Days to first flowering		
D50F-Days to 50 percent flowering	FL-Fruit length (cm)	FD-Fruit diameter (cm)		
AFW-Average fruit weight (g)	NOF-Number of fruits per plant	YPP-Total yield per plant (kg)		
TSS: Total soluble solid				

#### Conclusion

Thus, the evaluation of 220 recombinant inbred lines of tomato indicated a wide range of variability for different yield and quality traits. From above study it can be concluded that number of fruits per plant, average fruit weight and fruit yield per plant are the most important traits for which straight selection may bring worthwhile improvement in identifying superior inbred lines of tomato which could be used in future breeding programme.

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