



Gene-gene correlation, path coefficients and the genetic variability of tomato (*Solanum lycopersicum* L.) genotypes

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ABSTRACT

Indian tomatoes (*Solanum lycopersicum* L.) have produced stable yields since the last lustrum. An improvement is essential to enhance their production and productivity. Crop improvement in this solanaceous vegetable depends on the magnitude of genetic variability, heritability, and genetic advancement. Thus our study examined genetic variability, heritability, correlation, and path coefficients of 46 advanced tomato lines to determine the association between yield and morphological traits. Most of the traits studied under this experiment had higher phenotypic coefficient values than genotypic coefficient values, indicating the expression of environmental influences. Among nine different characters studied, the fruit number plant⁻¹ showed high variability, heritability, genetic advance, correlation and path coefficient values with the highest yield plant⁻¹. A greater dissimilarity coefficient value is associated with higher heterosis. In breeding programs, lines showing a higher dissimilarity coefficient value should be considered. Tomato genotypes BT-215-3-3-1 and BT-2 selected based on the fruit number plant⁻¹ may be used for the future hybridization program.

Keywords: Correlation, GCV, Heritability, PCV, *Solanum lycopersicum*

Tomato (*Solanum lycopersicum* L.) occupies a prime position among processed vegetables. Alam and Paul (2019) mentioned it's a good source of vitamins (A and C), minerals (Ca, P, and Fe) and antioxidant that helps to prevent cancer and cardiovascular diseases. As reported by Gopinath and Irene Vethamoni (2017); Kumari *et al.* (2020); and Akhter *et al.* (2021), red pigments in tomatoes, known as lycopene, are the "world's most powerful antioxidants" and Singh *et al.* (2018) recognized tomato as a "protective food". During this post-pandemic period, the tomato is in demand due to its high nutritive, therapeutic value and its wide consumption. Presently, India stands at second place in terms of production and area, with 19.01 million tonnes produced by an area of 0.7 million ha (FAOSTAT, 2021), but tenth in terms of productivity, with 24.34 t ha⁻¹ and remains unchanged since last lustrum, with a negligible increase from 24.20 t ha⁻¹ to 24.34 t ha⁻¹ (Anonymous, 2018). Odisha is one of the largest producers of commercially cultivated tomatoes, having an area of 0.095 million ha and average productivity of 15.29 t ha⁻¹ (Anonymous, 2020). However, the national and state tomato productivity is much lower than the global tomato productivity.

In order to meet the demands of the ever-growing population, it is important to bridge the productivity gap caused by the shrinkage of cultivable land and the unpredictable climatic conditions. It is only possible by the crop improvement programs of location-specific genotypes to develop an exceptional acclimatization ability to cultivate year-round. In India tomato is

predominantly cultivated during the *rabi* season. Among the strategies studied by Tripathy and Sahoo (2018), season-specific varieties, balanced nutrition, optimum water management and the use of plant protection measures in need-based situations are the key factors in improving productivity. So, evaluating off season genotypes will bring out possibly adequate information for the future breeding strategy. A large number of tomato germplasm are available for evaluation. Moreover, there is a tremendous variation among the maintained tomato genotypes. Selection of these genotypes with particular objectives is highly effective, at present, it is needed to investigate the inherent characteristic of these genotypes for the reduction of this productivity gap.

Assessment of genotypic and phenotypic coefficients of variation among the specific genotypes indicates the environmental influences upon the genotypes to be considered for the crop improvement program (Taiana *et al.*, 2015). Improving quality traits in tomato fruits is equally essential for the breeding strategy. Evaluation of quality-related traits such as fruits plant⁻¹, fruit shape, fruit size, fruit color, firmness of fruit, number of locules fruit⁻¹ and total soluble solids in fruit depicts wide genetic variation that could be utilized for crop improvement purposes. When a trait is highly heritable and genetically advanced among the genotypes evaluated, it indicates additive gene action and adequate selection conditions. Correlation studies between yield and yield attributing traits have significant contributions in designing a crop improvement program. Using path

analysis, the correlation coefficient can be separated into direct and indirect effects on yield and yield attributes. The analysis of path coefficients can also be utilized to determine the best breeding strategy for improving elite genotypes through selection in advanced generations (Gopinath and Irene Vethamoni, 2017). Our aim was to assess the attributes of 46 tomato genotypes during the off-season, in order to estimate the magnitude of variability, heritability, genetic advance, correlation, path coefficient analysis, and D² analysis for the breeding program in the future.

MATERIALS AND METHODS

An experiment was conducted at the Regional Research and Technology Transfer Station (OUAT), Semiliguda, India, located at 18°42'N latitude and 82°30'E longitude with an altitude of 884 m above mean sea level under the eastern ghat highlands of Odisha. During the experiment, soil pH was 5.6 and the soil texture was sandy loam, with N, P₂O₅ and K₂O available in quantities of 172, 16.8 and 145 kg ha⁻¹ respectively. The experiment was conducted in a subtropical climatic condition characterized by hot summer, cold winter and rainy season. The rainy season starts from mid-June and continues up to mid-October and during this period around 80% of the annual mean rainfall takes place due to the southwest monsoon. On average, the temperatures of this experimental site during the summer and winter ranged from 34 °C to 12 °C.

Forty-six tomato genotypes including thirty determinate, four semi-determinate and twelve indeterminate types with BT as the prefix, developed at All India Coordinated Research Project on Vegetable Crops operating at Odisha University of Agriculture and Technology (OUAT), Bhubaneswar, Odisha, India were collected and used as the experimental materials. An open field experiment was conducted under randomized block design (RBD) with the above said tomato genotypes and replicated twice.

To ensure healthy germination, the tomato seeds were treated with Bavistin @ 1g kg⁻¹ of seeds before being sown in seedbeds and covered with mulch. The mulching materials were removed soon after germination started. Later, a preventive spray of Carbendazim 12 % + Mancozeb 63 % WP @ 2g l⁻¹ of water was used to protect seedlings from fungal infections during the nursery stage. Simultaneously, the main field was thoroughly prepared to acquire the fine tilth. The recommended fertilizer doses were 125, 60, and 125 kg ha⁻¹ N, P₂O₅, and K₂O. Before planting, we applied complete decomposed farmyard manure at a rate of 10 t ha⁻¹, as well as a full dose of P₂O₅ and a half dose of N and K₂O. The remaining N and K₂O were applied in two equal parts 15 days and 30 days after planting. During the month of July, one-

month-old seedlings were treated with Carbendazim 12% + Mancozeb 63% WP @ 2g l⁻¹ solution and transplanted to the open field with a spacing of 75 x 60 cm on a sizeable raised bed of 13.5m². To ensure optimum plant survival under open field conditions, the seedlings were watered immediately after transplanting with a rosecane. A healthy tomato crop was raised by following all other cultural operations uniformly till harvest.

We recorded morphological characteristics viz., plant height (cm), branch number plant⁻¹, flower number plant⁻¹, fruit number plant⁻¹ for ten randomly selected plants. However, ten randomly selected fruits from the produce of each genotype were measured for average fruit weight (g), fruit length (mm), fruit diameter (mm), number of locules fruit⁻¹ and TSS (°Brix). A digital slide caliper (Mitutoyo South Asia Pvt. Ltd.) was used to measure the diameter and length of selected fruits. The number of locules fruit⁻¹ was determined by counting the internal cavities in transverse sections of selected ripe fruits. The total soluble solid (°brix) was measured with a digital pocket refractometer (ATAGO and Co Ltd., Tokyo, Japan) using juice obtained from the selected fruits after crushing with a mortar and pestle. We recorded total fruit yield on a plot-by-plot basis and converted it to q ha⁻¹ at harvest.

The differences in tomato genotypes revealed by the measured parameters were compared using analysis of variance at the 1% and 5% probability levels. Statistical analyses like GCV, PCV, heritability in a broad sense (H²_{bs}), genetic advance (GA %), correlation studies and path coefficients analyses were conducted using the OPSTAT software developed by Sheoran *et al.* (1998). The mean data of 46 tomato genotypes were used for D² analysis developed by Mahalanobis (1936). According to Rao (1952), pivotal condensation was used to convert original measurements to uncorrelated standardized data. We used Tochers' method to group tomato genotypes and used Singh and Chaudhury's (1985) model to calculate the contribution of different characters to total divergence. Dissimilarity indexes were estimated using XLSTAT statistical software (XLSTAT Premium 2021.2.2, Addinosft, NY).

RESULTS AND DISCUSSION

Genetic variation within the crop is an essential component for the proper characterization, evaluation and improvement of that crop. Any crop's improvement is directly related to its genotypic variability. Considering the future threat of genetic erosion and the uncontrolled introduction of new varieties, thirty-six tomato advanced lines were evaluated against ten released varieties. All tomato genotypes showed significant magnitudes of variation for all the tested traits as expressed in Table 1.

Table 1: The performance of different tomato genotypes based on their growth characteristics and yield.

Sl.No.	Name of genotypes	Plant height (cm.)	Branch number plant ⁻¹	Flower number plant ⁻¹	Fruit number plant ⁻¹	Average fruit weight (g.)	Fruit length (mm.)	Fruit diameter (mm)	Locule number fruit ⁻¹	T.S.S (° brix)	Yield (q ha ⁻¹)
1	BT-442-2	65.50	5.10	15.70	15.35	29.30	33.60	39.50	3.90	4.20	145.45
2	BT-437-1-2	71.20	5.00	8.50	8.45	58.25	34.70	34.30	3.40	3.80	149.55
3	BT-429-2-2	90.70	5.50	13.95	13.95	32.80	35.70	33.70	2.80	5.00	156.65
4	BT-413-1-2	84.10	5.10	12.10	11.85	41.65	38.20	30.70	2.10	4.20	148.70
5	BT-429-1-1	92.00	5.40	9.40	9.30	39.30	27.00	36.50	4.50	5.00	129.95
6	BT-215-3-3-1	88.30	5.70	15.90	14.75	26.30	30.20	29.70	2.70	4.00	143.25
7	BT-22-4-1	75.70	5.80	14.10	11.35	45.70	43.70	46.70	5.80	4.30	127.15
8	BT-19-1-1-1	54.50	5.70	9.10	8.80	27.70	29.00	34.10	3.40	4.30	132.75
9	BT-12-2	64.50	6.40	12.30	12.10	24.90	28.30	28.50	3.00	4.40	146.95
10	BT-507-2-2	71.40	5.10	7.60	7.25	30.80	31.00	34.40	3.30	4.20	138.35
11	BT-506-1	68.00	5.90	14.80	14.50	31.90	23.70	25.40	2.70	5.40	140.15
12	BT-112-1	92.50	6.00	8.50	8.25	32.25	38.30	27.90	2.50	5.70	138.05
13	BT-508-1-1	88.40	6.50	18.80	18.35	31.95	28.20	31.60	3.10	4.70	182.55
14	BT-433-2-1	64.60	6.00	19.30	19.10	22.30	34.40	30.30	2.40	4.10	187.75
15	BT-21-2	94.60	6.00	12.70	12.65	24.45	28.70	34.60	4.70	4.50	161.25
16	BT-17-2	51.10	5.40	18.90	15.75	24.40	36.10	36.00	3.50	3.50	135.15
17	BT-19-1-1-1	66.30	5.40	14.90	14.85	25.45	26.70	31.00	3.30	4.20	161.80
18	BT-207-2	65.40	5.50	23.10	19.65	26.25	29.80	28.60	2.20	6.20	162.90
19	BT-433-3-2	75.00	6.50	13.15	13.15	31.95	33.90	38.60	4.00	5.10	163.45
20	BT-428-3	85.60	7.60	18.30	14.40	36.80	31.10	38.50	3.90	5.40	162.60
21	BT-306-1-2	68.90	6.00	15.80	15.35	24.05	30.00	35.40	3.60	3.90	158.50
22	BT-12-3-2	52.40	6.50	17.30	16.75	21.30	26.00	32.90	3.40	4.20	163.70
23	BT-224-3-1	71.20	5.30	20.00	16.70	30.55	30.10	40.30	5.40	4.50	135.45
24	BT-305-2-4-2	70.30	6.50	11.30	10.85	29.70	31.20	32.90	3.30	4.50	148.95
25	BT-3	55.10	5.60	18.30	17.15	28.35	29.00	37.80	4.30	4.20	159.95
26	BT-21	52.90	6.50	15.40	14.90	20.60	26.80	26.50	2.20	4.50	152.40
27	BT-101	70.00	6.10	24.90	14.10	36.45	29.20	32.10	3.60	4.90	145.75
28	BT-18	60.00	5.50	13.70	13.55	23.50	33.50	31.20	2.60	4.40	137.35
29	BT-17-2(5)	50.80	5.30	11.60	11.35	23.05	27.50	30.00	3.40	4.60	127.00
30	BT-317	59.70	5.10	17.00	16.85	23.05	28.10	30.80	3.00	4.90	136.10
31	BT-106	63.40	4.70	15.00	14.95	19.60	24.50	29.50	2.90	4.60	139.60
32	BT-17	59.30	5.10	17.00	16.65	20.10	26.60	30.80	3.10	4.40	148.50
33	BT-136	72.20	5.60	9.80	9.50	26.10	29.80	31.00	2.20	4.80	154.25
34	BT-218	49.40	5.00	10.70	10.35	24.80	28.30	30.80	2.30	4.30	150.15
35	BT-21	63.90	5.20	14.80	14.35	30.85	32.30	32.30	2.50	4.60	145.70
36	II/IOBW-3	76.00	5.00	13.00	13.00	32.55	42.40	38.10	3.10	5.20	128.70
37	BT-1	60.00	5.10	11.70	11.60	22.90	29.80	26.10	2.30	4.30	158.35
38	BT-2	49.00	5.10	15.80	15.70	21.60	29.90	25.70	2.10	4.40	144.45
39	BT-10	53.60	4.70	11.00	10.95	25.90	27.80	27.00	2.40	6.20	156.65
40	BT-12	66.40	5.30	22.50	19.75	25.65	44.60	33.40	2.00	5.00	137.75
41	BT-20-2-1	63.80	6.30	10.10	9.55	30.40	32.90	38.10	4.30	4.30	146.45
42	BT-II6-3-2	63.40	6.90	13.80	13.20	20.50	25.60	29.40	2.70	5.00	157.60
43	Arka Vikash	72.90	5.60	20.10	18.25	29.25	32.30	31.80	2.10	4.40	157.65
44	Megha Tomato	77.60	5.60	12.10	11.55	29.85	30.30	32.50	3.40	4.80	152.40
45	Pusa Ruby	74.10	6.20	8.50	8.30	28.55	28.00	32.80	3.10	5.40	151.10
46	IIVR Set-2	68.80	5.20	12.20	9.10	56.30	39.20	44.10	4.60	4.80	127.00

Table 2: Genetic variability, heritability, and genetic advancement in tomato genotypes

Characters	Range		Mean	GCV	PCV	H ² _{bs} (%)	GA	GA (%)
	Minimum	Maximum						
Plant height (cm)	49.00	94.60	68.58	16.57	19.37	73.22	20.03	29.21
Branch number plant⁻¹	4.70	7.60	5.67	7.61	13.46	32.01	0.50	8.87
Flower number plant⁻¹	7.60	24.90	14.50	26.39	30.28	75.94	6.87	47.37
Fruit number plant⁻¹	7.25	19.75	13.44	22.35	26.70	70.02	5.18	38.52
Average fruit weight (g)	19.60	58.25	29.35	26.34	30.10	76.57	13.93	47.48
Fruit length (mm)	23.70	44.60	31.26	13.37	17.36	59.33	6.63	21.22
Fruit diameter (mm)	25.40	46.70	32.91	12.04	15.89	57.42	6.19	18.80
Locule number fruit⁻¹	2.10	5.80	3.19	25.52	29.94	72.61	1.43	44.79
TSS (° brix)	3.50	6.20	4.64	8.07	15.21	28.17	0.40	8.83
Yield (q ha⁻¹)	127.00	187.75	148.61	5.80	11.41	25.85	8.73	6.08

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H²_{bs} (%): Heritability in broad sense, GA: Genetic Advance, GA (%): Genetic Advance by percentage of means (%)

Morphological variability

The mean values of ten morphological traits studied for thirty-six advanced lines and ten checks are depicted in Table 1. The tomato genotype BT-21-2 reached an optimum height of 94.60 cm, whereas BT-2 the released variety recorded a minimum plant height of 49cm. Lowest branches plant⁻¹ (4.70) were noticed in the tomato genotype BT-106, on the other hand, the tomato genotype BT-428-3 produced the utmost branches plant⁻¹(7.60). In this study, tomato genotypes BT-507-2-2 recorded the least number of flowers plant⁻¹ (7.60) and minimum fruits plant⁻¹ (7.25) whereas, maximum flowers plant⁻¹ (24.90) was noticed in the tomato genotype BT-101 and maximum fruits plant⁻¹ (19.75) in genotype BT-12. Average fruit weight varied from 19.60g to 58.25g among the tested tomato genotypes. Tomato genotype BT-106 produced the lowest fruit weight (19.60g) and the least number of branches plant⁻¹ (4.70). whereas, genotype BT-437-1-2 produced the heaviest fruit weight (58.25g). Tomato genotype BT-506-1 recorded minimum fruit length (23.70 mm) and fruit diameter (25.40mm), while maximum fruit length (44.60mm) and maximum diameter (46.70mm) were recorded with the genotypes BT-12 and BT-22-4-1, respectively. The highest 6.20 °Brix of total soluble solid was recorded in the genotypes BT-207-2 and BT-10 indicating the extended keeping quality of the tomato fruits. The yield of tomato fruit varied from 127.00 – 187.75 q ha⁻¹ among the studied genotypes. Maximum fruit yield (187.75 q ha⁻¹) was recorded in the genotype BT-433-2-1. A minimum fruit yield of 127 q ha⁻¹ was noticed in the tomato genotypes BT-17-2(5) and IIVR SEL-2. The association of different traits for genetic variance expression should be considered a criterion for choosing parents during the crop improvement program in tomatoes (Singh *et al.*, 2018).

Coefficient of variation

In this study, the estimated range of PCV, GCV, heritability in the broad sense and genetic advance (GA) as a percentage of means are given in Table 2. The traits showing moderate PCV value (*i.e.* less than 20%) were yield (q ha⁻¹), TSS (°Brix), fruit diameter (mm), fruit length (mm), branches number plant⁻¹ and plant height. Similarly, traits such as the number of flowers plant⁻¹, number of fruits plant⁻¹, average fruit weight, number of locules fruit⁻¹ elicited high PCV value, *i.e.* more than 20 per cent (Panda *et al.*, 2016). A high PCV value for the above said traits indicated high degree of variation among the genotypes (Kumari *et al.*, 2020).

Similarly, the utmost GCV value was observed for the number of flowers plant⁻¹ (26.39 percent) followed by average fruit weight (26.34 per cent) and the lowest in yield q ha⁻¹ (5.80). Phenotypic coefficient values were higher than genotypic coefficient values for all most all the traits *viz.* plant height (PCV-19.36, GCV-16.57), number of branches plant⁻¹ (PCV-13.45, GCV-7.61), number of flowers plant⁻¹ (PCV-30.27, GCV-26.38), number of fruits plant⁻¹ (PCV-26.70, GCV-22.34), average fruit weight (PCV-30.10, GCV26.34), fruit length (PCV-17.36, GCV-13.37), fruit diameter (PCV-15.89, GCV-12.04), number of locules fruit⁻¹ (PCV-29.94, GCV-25.51), TSS (PCV-15.21, GCV-8.07), yield (PCV-11.41, GCV-5.80). This indicated that the environment influenced the expression of these characters (Hasan *et al.*, 2016; Pandey *et al.*, 2018; Saravanan *et al.*, 2019).

Heritability and genetic advance (GA)

As shown in Table 2, the characters such as average fruit weight, number of flowers plant⁻¹, plant height, number of locules fruit⁻¹, number of fruits plant⁻¹ showed

Table 3: Genotypic (above diagonal) and Phenotypic (below diagonal) correlations matrix of forty-six tomato genotypes

Characters	Plant height (cm.)	Branch number plant ⁻¹	Flower number plant ⁻¹	Fruit number plant ⁻¹	Average fruit weight (g.)	Fruit length (mm.)	Fruit diameter (mm)	Locule number fruit ⁻¹	T.S.S (° brix)	Yield (q ha ⁻¹)
Plant height (cm)	1.00	0.33**	-0.11	-0.15	0.47**	0.33**	0.29**	0.26*	0.32**	0.10
Branch number plant ⁻¹	0.22*	1.00	0.09	-0.01	-0.08	-0.08	0.26*	0.20	0.17	0.68**
Flower number plant ⁻¹	-0.09	0.15	1.00	0.92**	-0.20	0.12	0.12	-0.11	-0.19	0.31**
Fruit number plant ⁻¹	-0.18	0.09	0.89**	1.00	-0.40**	-0.02	-0.05	-0.26*	-0.22*	0.50**
Average fruit weight (g)	0.40**	-0.05	-0.22*	-0.42**	1.00	0.64**	0.66**	0.53**	0.12	-0.27**
Fruit length (mm)	0.23*	-0.19	-0.02	-0.08	0.39**	1.00	0.53**	0.19	0.14	-0.49**
Fruit diameter (mm)	0.21*	-0.01	-0.06	-0.19	0.49**	0.51**	1.00	1.12**	-0.13	-0.44**
Locule number fruit ⁻¹	0.20	0.15	-0.01	-0.14	0.34**	0.06	0.63**	1.00	-0.45**	-0.57**
TSS (° brix)	0.20	0.10	0.12	0.03	-0.02	-0.12	-0.23*	-0.07	1.00	0.00
Yield (q ha ⁻¹)	0.10	0.35**	0.28**	0.37**	-0.26*	-0.22*	-0.21*	-0.13	0.03	1.00

* and **: Significant at 1% and 5% probability level by F test, respectively.

a high degree of heritability, *i.e.* more than 70 per cent. Several traits with high heritability were reported by Saravanan *et al.* (2019). This suggested that selection based on phenotypic performance would be of great benefit. In general, estimating heritability alone cannot be relied upon to predict a selection effect. Genetic advancement combined with estimated heritability is more useful in predicting the effect of selecting the best genotype than heritability alone since it indicates additive effects (Johnson *et al.*, 1955). Genetic advances for ten studied characters are presented in Table 2, which ranges from 0.40 to 20.03 among the studied characters. Moderate genetic advances were witnessed for the plant height (20.03) and average fruit weight (13.93). Similarly, the low genetic advance was observed for TSS (0.40), number of branches plant⁻¹(0.50), number of locules fruit⁻¹(1.43), number of fruits plant⁻¹(5.18), fruit diameter (6.19), fruit length (6.63), number of flowers plant⁻¹ (6.87) and yield (8.73).

Correlation

The correlation coefficients between all possible pairs of ten quantitative characters are given in Fig. 1 and Table 3. Based on correlation analysis, it is possible to determine the component character on which selection can be based to improve yield. There were significant genotypic and phenotypic correlations but genotypic correlations (rg) were greater than phenotypic correlations (rp), indicating that genes were involved in the expression of each character indicating that the characters studied were inherently associated. Panda *et al.* (2016) expressed that there was a strong positive correlation between character combinations and fruit yield, possibly due to genetic linkage and increased phenotypic correlation between some character combinations, such as fruit yield, fruit length and fruit diameter, which could be explained by reduced environmental variance.

As shown in Table 3 and Fig. 1, the number of branches plant⁻¹ (0.68,0.35), the number of flowers plant⁻¹ (0.31,0.28), and the number of fruits plant⁻¹ (0.50,0.37) were positively correlated (genotypic and phenotypic) with the fruit yield. A similar observation was made by Souza *et al.* (2012). The higher magnitude of positive and significant association of the number of branches plant⁻¹, number of flowers plant⁻¹, number of fruits plant⁻¹ with fruit yield suggested their importance as principal yield components in influencing the yield of the plant. So, choosing plants with more branches plant⁻¹ and more fruits plant⁻¹ would necessarily result in a greater yield of that plant.

Path coefficient analysis

We performed genotypic and phenotypic path-coefficient analysis for ten selected traits using yield as the

Table 4: Genotypic and phenotypic path coefficients (direct and indirect effect) between yield and nine component traits in tomato genotypes

Characters	Plant height (cm)	Branch number plant ⁻¹	Flower number plant ⁻¹	Fruit number plant ⁻¹	Average fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Locule number fruit ⁻¹	T.S.S (° brix)	Yield (q ha ⁻¹)
Plant height (cm)	G -0.43	0.48	0.22	-0.44	0.95	-0.23	-0.19	-0.16	-0.12	0.10 ^{NS}
	P 0.21	0.06	0.02	-0.10	-0.03	-0.03	0.00	-0.02	-0.01	0.10 ^{NS}
Branche number plant ⁻¹	G -0.14	1.48	-0.19	-0.02	-0.16	0.06	-0.17	-0.12	-0.06	0.68**
	P 0.05	0.27	-0.03	0.05	0.00	0.03	-0.00	-0.02	-0.01	0.35**
Flower number plant ⁻¹	G 0.05	0.14	-2.07	2.62	-0.40	-0.08	-0.08	0.06	0.07	0.31**
	P -0.02	0.04	-0.23	0.48	0.01	0.00	-0.00	0.00	-0.01	0.28**
Fruit number plant ⁻¹	G 0.07	-0.01	-1.90	2.86	-0.81	0.02	0.03	0.15	0.08	0.50**
	P -0.04	0.02	-0.20	0.54	0.03	0.01	-0.00	0.02	-0.00	0.37**
Average fruit weight (g)	G -0.20	-0.11	0.41	-1.15	2.01	-0.44	-0.43	-0.31	-0.05	-0.27**
	P 0.09	-0.01	0.05	-0.23	-0.06	-0.06	0.00	-0.04	0.00	-0.26*
Fruit length (mm)	G -0.14	-0.12	-0.25	-0.07	1.29	-0.69	-0.34	-0.12	-0.05	-0.49**
	P 0.05	-0.05	0.00	-0.04	-0.02	-0.15	0.00	-0.01	0.01	-0.22*
Fruit diameter (mm)	G -0.13	0.38	-0.24	-0.15	1.33	-0.36	-0.65	-0.67	0.05	-0.44**
	P 0.04	-0.00	0.01	-0.10	-0.03	-0.08	0.00	-0.07	0.01	-0.21*
Locule number fruit ⁻¹	G -0.11	0.29	0.22	-0.74	1.06	-0.13	-0.73	-0.60	0.17	-0.57**
	P 0.04	0.04	0.00	-0.08	-0.02	-0.01	0.00	-0.19	0.00	-0.13 ^{NS}
TSS (° brix)	G -0.14	0.25	0.39	-0.63	0.25	-0.09	0.08	0.27	-0.37	0.00 ^{NS}
	P 0.04	0.03	-0.03	0.02	0.00	0.02	-0.00	0.01	-0.06	0.03 ^{NS}

Genotypic residual effect = 0.166, Phenotypic residual effect = 0.6, ^{NS}: Nonsignificant, * and **: Significant at 1% and 5% probability level by F test, respectively.

Table 5: Clustering pattern of forty six tomato genotypes

Cluster No.	No. of genotypes	Name of the genotypes
I	3	BT-442-2 BT-317 BT-17
II	2	BT-19-1-1-1 BT-17-2(5)
III	2	BT-12-2 BT-116-3-2
IV	7	BT-437-1-2 BT-429-2-2 BT-413-2 BT-305-2-4-2
V	2	BT-1 BT-218
VI	2	BT-21 BT-2
VII	2	BT-1-1-1 BT-306-1-2
VIII	2	BT-18 BT-21
IX	2	BT-136 PUSARUBY
X	2	BT-433-2-1 ARKA VIKASH
XI	5	BT-22-4-1 BT-507-2-2 BT-20-2-1
XII	2	BT-12-3-2 BT-3
XIII	2	BT-207-2 BT-12
XIV	2	BT-508-1-1 BT-428-3
XV	3	BT-112-1 BT-21-2 11/TOBW-3
XVI	2	BT-17-2 BT-101
XVII	2	BT-106 BT-10
XVIII	1	IIVR SEL-2
XIX	1	BT 224-3-1
Total	46	

Table 6 : Cluster wise mean values of ten quantitative traits of forty six tomato genotypes

Cluster No.	Plant height (cm)	Branch number plant ⁻¹	Flower number plant ⁻¹	Fruit number plant ⁻¹	Average fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Locule number fruit ⁻¹	T.S.S (° brix)	Yield (q ha ⁻¹)
I	61.50	5.10	16.56	16.28	24.15	29.43	33.70	3.33	4.50	143.35
II	52.65	5.50	10.35	10.07	25.37	28.25	32.05	3.40	4.45	129.87
III	63.95	6.65	13.05	12.65	22.70	26.95	28.95	2.85	4.70	152.27
IV	82.02	5.54	12.20	11.52	36.83	32.47	32.90	3.17	4.47	147.06
V	54.70	5.05	11.20	10.97	23.85	29.05	28.45	2.30	4.30	154.25
VI	50.95*	5.80	15.60	15.30	21.10*	28.35	26.10	2.15	4.45	148.42
VII	67.60	5.70	15.35	15.10	24.75	28.35	33.20	3.45	4.05*	160.15
VIII	61.95	5.35	14.25	13.95	27.17	32.90	31.75	2.55	4.50	141.52
IX	73.15	5.90	9.15*	8.90*	27.32	28.90	31.90	2.65	5.10	152.67
X	68.75	5.80	19.70	18.67	25.77	33.35	31.05	2.25	4.25	172.70**
XI	70.78	5.92	12.04	11.16	34.15	33.04	36.64	4.02	4.66	143.11
XII	53.75	6.05	17.80	16.95	24.82	27.50	35.35	3.85	4.20	161.82
XIII	65.90	5.40	22.80**	19.70**	25.95	37.20	31.00	2.10*	5.60**	150.32
XIV	87.00**	7.05**	18.55	16.37	34.37	29.65	35.05	3.50	5.05	172.57
XV	87.70**	5.66	11.40	11.30	29.75	36.47	33.53	3.43	5.13	142.66
XVI	60.55	5.75	21.90	14.92	30.42	32.65	34.05	3.55	4.20	140.45
XVII	58.50	4.70*	13.00	12.95	22.75	26.15*	28.25*	2.65	5.40	148.12
XVIII	68.80	5.20	12.20	9.10	56.30**	39.20**	44.10**	4.60	4.80	127.00*
XIX	71.20	5.30	20.00	16.70	30.55	30.10	40.30	5.40**	4.50	135.45
Mean	66.39	5.65	15.11	13.82	28.85	31.05	33.07	3.22	4.65	148.62

* and ** indicate lowest and highest values respectively.

Table 7: Intra (diagonal) and inter cluster distances (D^2) corresponding D (D^2) values (in Parentheses) among groups

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	3.97 (15.78)	5.63 (31.75)	5.71 (32.60)	7.07 (50.04)	6.88 (47.34)	6.02 (36.24)	3.33 (11.14)	4.25 (18.08)	7.14 (50.99)	5.33 (28.41)	7.24 (52.41)	4.23 (18.44)	7.26 (52.67)	6.66 (44.35)	7.81 (61.01)	8.36 (69.82)	6.86 (47.03)	10.84 (117.2)	7.13 (50.91)
II		2.15 (4.62)	3.65 (13.35)	7.72 (59.65)	4.26 (18.13)	4.91 (24.16)	5.11 (26.17)	4.50 (20.28)	4.71 (22.21)	7.82 (61.27)	7.24 (52.36)	5.96 (35.53)	9.50 (90.19)	8.96 (80.27)	8.15 (66.51)	9.54 (90.95)	5.61 (31.52)	11.50 (132.16)	10.10 (101.93)
III			2.33 (5.44)	7.28 (53.01)	3.96 (15.65)	3.80 (14.41)	4.66 (21.70)	3.93 (15.46)	3.71 (13.77)	6.34 (40.21)	7.63 (58.25)	6.22 (38.70)	8.46 (71.66)	7.77 (60.37)	7.56 (57.62)	9.67 (93.61)	5.45 (29.77)	12.55 (157.39)	10.86 (118.01)
IV				6.87 (47.30)	8.31 (69.07)	8.43 (71.08)	6.45 (41.56)	6.20 (38.47)	7.10 (50.40)	7.29 (53.18)	7.49 (56.06)	8.01 (64.29)	8.94 (79.96)	6.80 (46.13)	7.05 (49.67)	10.65 (113.43)	8.52 (72.55)	9.76 (95.33)	9.79 (95.84)
V				2.60 (6.79)	2.60	3.50	6.18	4.65	4.53	7.11	8.97	7.60	9.04	9.83	9.01	10.22	5.00	13.38	12.51
VI						2.66	5.66	3.93	5.85	5.64	9.08	6.70	7.39	9.10	9.17	9.05	5.60	13.49	11.72
VII							(7.05)	(32.00)	(34.28)	(31.77)	(82.41)	(45.00)	(54.67)	(82.82)	(84.02)	(81.98)	(31.43)	(182.05)	(137.33)
VIII								(7.13)	(38.11)	(24.60)	(46.33)	(15.21)	(60.66)	(35.59)	(53.83)	(71.36)	(42.60)	(120.13)	(55.25)
IX									5.11	4.41	6.93	5.46	6.18	6.76	6.90	8.37	5.62	10.66	9.40
X										(19.43)	(48.06)	(29.87)	(38.15)	(45.77)	(47.61)	(70.00)	(41.64)	(113.74)	(88.41)
XI									3.09	7.81	7.78	8.04	9.64	8.38	7.10	11.44	5.53	12.27	12.08
XII									(9.58)	(60.93)	(60.57)	(64.69)	(92.86)	(70.29)	(50.44)	(130.85)	(30.63)	(150.67)	(146.10)
XIII											7.92	7.36	9.90	7.49	7.87	10.47	9.14	8.90	9.51
XIV										(10.68)	(73.29)	(37.14)	(24.99)	(38.01)	(69.63)	(64.55)	(61.22)	(136.85)	(90.40)
XV												4.24	8.22	6.81	9.07	7.97	7.96	10.44	8.86
XVI												(17.97)	(67.57)	(46.39)	(82.27)	(63.54)	(63.33)	(108.95)	(45.91)
XVII													5.43	7.87	9.48	8.08	9.33	11.82	10.42
XVIII														(29.45)	(89.87)	(65.29)	(87.09)	(139.76)	(108.55)
XIX															5.48	9.69	9.68	9.38	7.95
															(30.05)	(56.97)	(93.95)	(93.67)	(88.12)
																7.91	11.71	8.92	10.76
																	(62.65)	(137.18)	(79.63)
																		6.73	11.26
																		(45.30)	(126.89)
																			7.69
																			13.34
																			12.05
																			(59.16)
																			(145.21)
																			9.38
																			(87.92)
																			0.00
																			(0.00)

Table 8: Contribution of different characters to genetic divergence in tomato genotypes

Name of characters	Number of times ranked 1 st	Percent contribution
Plant height (cm)	145	14.009
Branch number plant ⁻¹	19	1.835
Flower number plant ⁻¹	92	8.888
Fruit number plant ⁻¹	32	3.091
Average fruit weight (g)	90	8.695
Fruit length (mm)	58	5.603
Fruit diameter (mm)	28	2.705
Locule number fruit ⁻¹	207	20.000
TSS (° brix)	87	8.405
Yield (q ha ⁻¹)	277	26.763
Total	1035	100

dependent variable as shown in Table 4 and Fig. 2. The analysis of path coefficients showed that traits such as the number of fruits plant⁻¹ (2.86), average fruit weight (2.01) and the number of branches plant⁻¹ (1.47) had a positive direct influence on yield, which indicates that they have a direct influence on yield. Interestingly, Islam *et al.* (2010) showed that the number of fruits plant⁻¹ had a direct effect on fruit yield, whereas, flower number, plant height at first flowering, branch number and fruit length indirectly influenced tomato fruit production. There is a positive correlation between the number of flowers plant⁻¹ and the yield plant⁻¹ in part due to the indirect positive effect of plant height, branches, number of branches plant⁻¹, number of fruits plant⁻¹, locule counts and of the TSS (° brix), despite the negative effect of the direct relationship between the number of flowers and yield plant⁻¹.

By assessing the residual effect, we can evaluate which causal factors best account for the variability of the dependent factor, in this case, the yield plant⁻¹. Among the nine traits evaluated in this study, the residual effect was 0.16, which means only 84 per cent of the variance in yield plant⁻¹ can be explained by the nine traits. This is because the correlation between some traits and yield is very low and insignificant. Furthermore, Hasan *et al.* (2016) mentioned that some other factors, which haven't been included, also need to be considered to fully understand the variation in yield observed.

Cluster analysis

On the basis of Mahalanobis D^2 analysis, forty-six tomato genotypes were clustered into nineteen clusters and depicted in Table 5. The largest group (Cluster IV) included 7 genotypes followed by cluster XI comprising 5 genotypes. Cluster I and XV - 3 genotypes in each cluster, cluster II, III, V, VI, VII, VIII, IX, X, XII, XIII, XIV, XVI and XVII with 2 genotypes in each cluster whereas, clusters like XVIII and XIX has only one genotype in an individual cluster.

In crop improvement programs, the basic objective is to enhance yield and its related traits. Therefore, the cluster means and their major contributing components for fruit yield in a single plant must be carefully considered in order to select the right parents. Table 6 summarizes the means for the ten quantitative characters for groups of tomato genotypes. Cluster X comprising 2 genotypes namely BT-433-2-1 and Arka Vikash showed the highest value in yield (172.70). Cluster XIII contains 2 genotypes that expressed the highest values for the number of flowers plant⁻¹ (22.80), number of fruits plant⁻¹ (19.70) and total soluble solids (5.60), whereas the lowest value in the number of locules fruit⁻¹ (2.10). Cluster XIV which contains 2 genotypes showed values for plant height (87.00) and the number of branches plant⁻¹ (7.05). Cluster XV contains 3 tomato genotypes that exhibited the utmost value in plant height (87.00). Plant height the most commonly observed character showed the highest value (87.00) in both the clusters. Cluster XVIII contains only one genotype (IIVR Sel-2) recorded the highest values in respect of average fruit weight (56.30), fruit length (39.20) and fruit diameter (44.10), whereas the lowest value for yield (127.00). Cluster XIX containing one genotype BT-224-3-1 revealed the maximum value for the number of locules fruit⁻¹ (5.40).

The intra and inter-cluster distances among the groups are reported in Table 7. It is clear from Table 7 that minimum intracluster distance (4.62) and maximum intracluster distance (182.05) were observed in cluster II and cluster XVIII, respectively.

Following Tocher's method of clustering, 46 genotypes were grouped (on the basis of genetic affinity) into 19 clusters represented in table 5. Cluster IV retained the highest number of 7 genotypes followed by cluster XI - 5 numbers; whereas cluster XVIII and XIX are monogenotypic clusters.

The results showed that genotypes obtained from the same source also showed different grouping patterns.

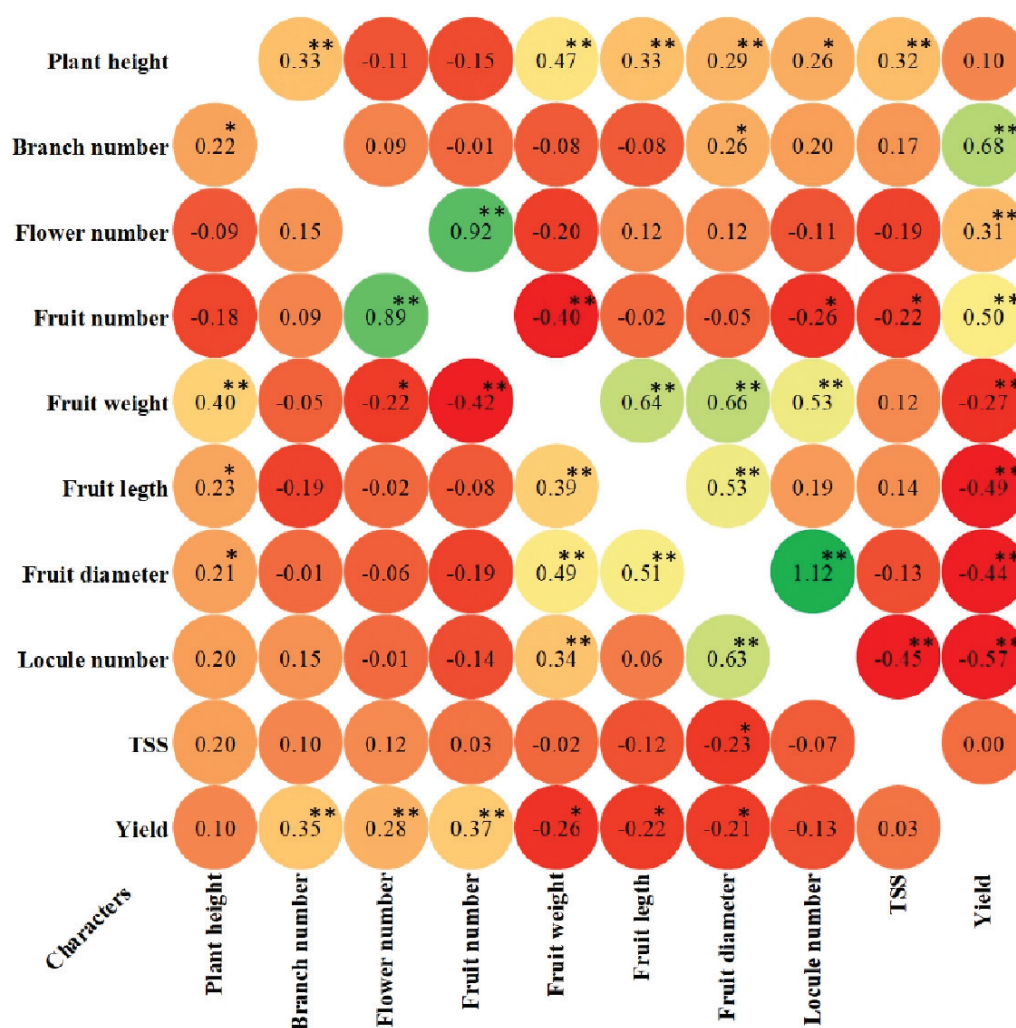


Fig. 1: Genotypic (above diagonal) and Phenotypic (below diagonal) correlations between yield and yield attributing traits of forty-six tomato genotypes.

(* and ** indicates $p \leq 0.05$ and $p \leq 0.01$, respectively.)

Genotypic distribution in clusters indicated there was no association between genetic divergence and geographical differentiation and clusters varied by geographical origin. The tendency for clustering to occur irrespective of geographical boundaries reveals that the factor contributing to natural population diversity is not just geographic isolation, but also genetic differences, spontaneous mutation, natural selection and artificial selection. Environmental genetic divergence is a process by which selection causes genetic barriers to form populations that are adapted to different environments, which can be a precursor of speciation. Those four modules fit almost perfectly with the habitat features suggesting that genetic variation is remarkable for its modular structure. Deschepper *et al.* (2017) found that populations developed genetic structures within small spatial units as a result of small-scale landscape changes.

From the above results, it could be suggested that crosses involving genotypes from divergent clusters (XVII and VI, XVIII and V, XVIII and XVII, XIX and XVII) are likely to produce desirable hybrids. Likhita Kiran *et al.* (2017) reported crossing parents selected from cluster III (BT-12-2, BT-507-2-2, BT-506-1, BT-112-1, BT-508-1-1, Megha tomato and BT-21-2) with parents from cluster VI (BT-17-2 (5) and Utkal Deepti can result in superior hybrids. The selection of tomato parents using cluster distance could be useful for developing an integrated strategy to improve the quality of hybrids or segregants. The results also indicated that genotypes from IIVR had higher genetic distances than other genotypes. The degree of intra-cluster distance ranged between 2.15 (cluster II) and 7.92 (cluster XI) suggesting heterogeneous and homogeneous strains within and between clusters.

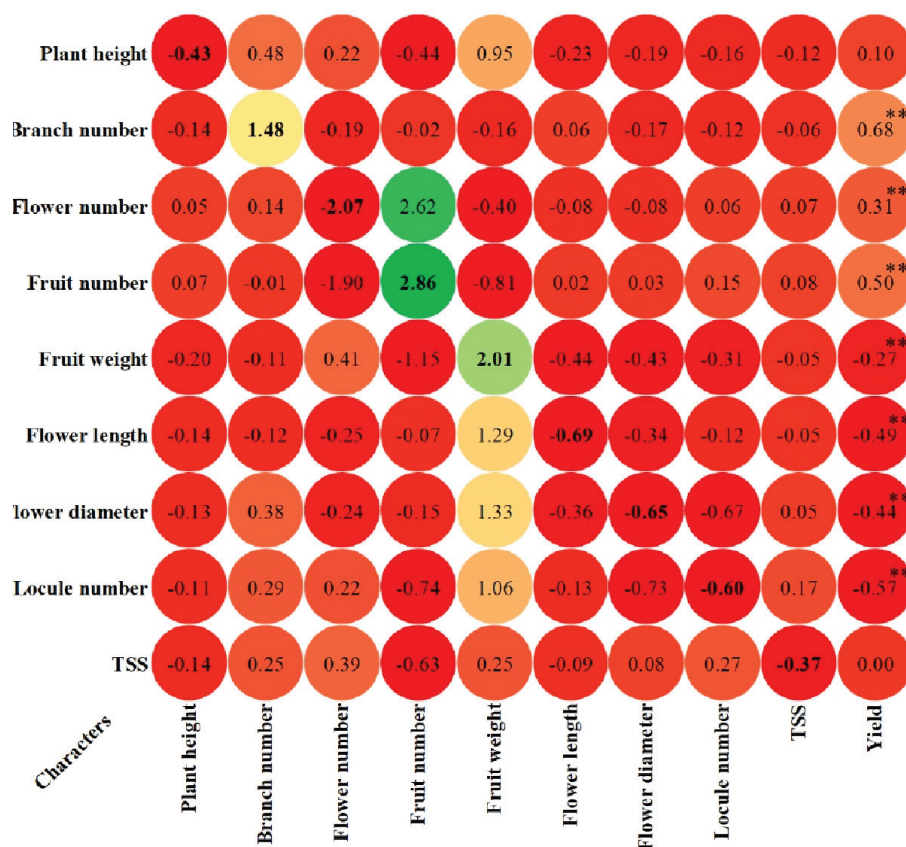


Fig. 2: Genotypic path coefficients between yield and nine component traits in tomato genotypes. (** indicates $p \leq 0.01$.)

Ten quantitative traits were examined in table 8 by averaging individual characters over 1035 paired combinations in order to determine their relative contribution to genetic divergence among the forty-six tomato genotypes. The highest contribution to divergence came from yield (26.763) followed by the number of locules fruit⁻¹ (20.000) and plant height (14.009).

The remaining characters contributing to divergence in descending order were the number of flowers in a plant (8.888), average fruit weight (8.695), total soluble solids (8.405), fruit length (5.603), number of fruits in a plant (3.091), fruit diameter (2.705) and number of branches in a plant (1.835).

Among the 19 clusters studied for cluster mean (Table – 6), cluster XIV, XV for plant height, cluster XIV for the number of branches plant⁻¹, XIII for number of flowers plant⁻¹, XIII for the number of fruits plant⁻¹, XVIII for average fruit weight, XVIII for fruit length, XVIII for fruit breadth, XIX for the number of locules fruit⁻¹, XIII for TSS with IX for yield (q ha⁻¹) showed superiority with respect to respective traits.

No cluster came out on top for all important characters when measuring the mean performance of different

clusters. However, cluster XIII showed superiority for some of the important economic traits such as the number of flowers plant⁻¹, average fruit weight and TSS due to linkage and pleiotropic effect of genes. Aiming at idiotypic plant types. Genotypes of cluster XIII (BT – 207-2, BT-12) may be taken for the future breeding program.

Table 8 illustrates the relative importance of ten traits to the genetic divergence of 46 genotypes for deciding on the cluster that exhibited the most divergence and subsequently selecting the parents for hybridization.

Among the important economic traits, the maximum contribution towards divergence was made by yield (26.76) followed by the number of locules per fruit (20.00), plant height (14.00) and the rest of the characters contributing to the divergence in order were number of flowers per plant (8.88), average fruit weight (8.69), TSS (8.40), fruit length (5.60), number of fruits per plant (3.09), fruit diameter (2.70), number of branches per plant (1.83).

Hierarchical clustering was performed based on the yield and yield attributes among the studied tomato genotypes. In the study, the dissimilarity coefficients among

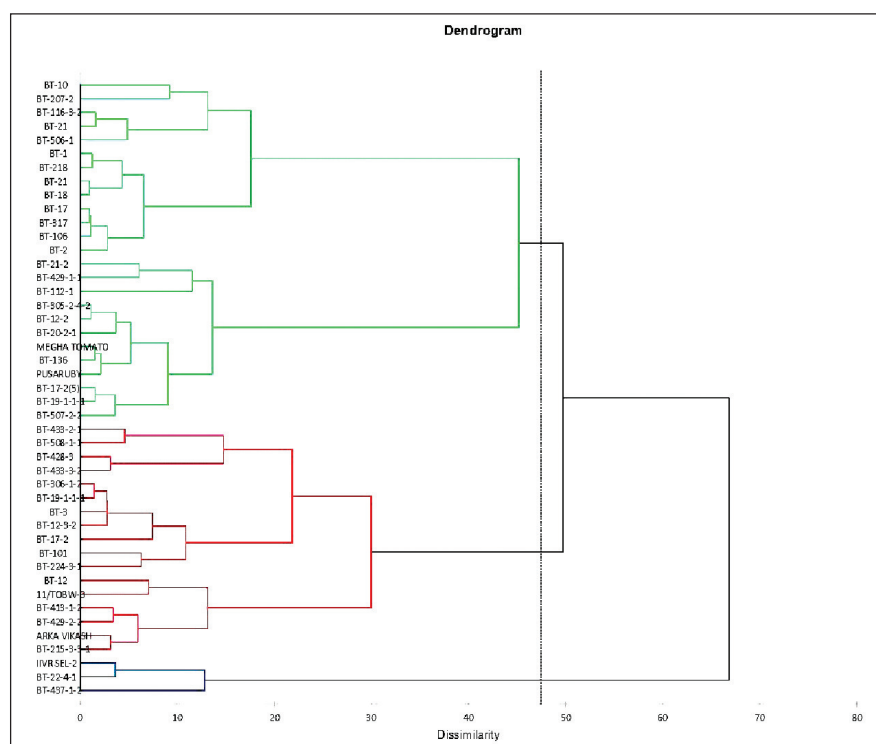


Fig. 3: Hierarchical clustering of 46 tomato genotypes for yield and yield attributed traits

the 43 parents ranged from 67% to 2%, and the similarity coefficients ranged from 33% to 98%. A cluster dendrogram was created by using these coefficients as part of the UPGMA method. Fig. 3 shows two main clusters in the dendrograms. The first smaller cluster was composed of parental lines such as BT-437-1-2, BT-22-41 and IIVR selection 2. IIVR selection 2 and BT-22-41 were less dissimilar, more similar. The second cluster consisted of many subclusters. In second cluster the lines such as BT-116-9, Bt-21, BT-1 and BT-218, Bt-21 and BT-18, BT-17 and BT-317, BT-305-2-4-2 and BT-12-2, BT-306-1-2 and BT-19-1-1-1 showed less dissimilarity i.e. more similarity coefficient value suggesting origin from a similar progenitor. More the diversity, more the heterosity. The lines showing more dissimilarity coefficient value be considered in breeding programs.

Genotypes for the traits studied showed a wide range of variation. The traits such as number of flowers plant⁻¹ (PCV = 30.28, GCV= 26.39), average fruit weight (PCV= 30.10, GCV=26.34), number of locules fruit⁻¹ (PCV= 29.94, GCV=25.52) exhibited a high amount of variability raising hopes of the future breeding program. Similarly, the traits such as average fruit weight ($H^2_{bs} = 76.57$, GA = 47.48), number of flowers plant⁻¹ ($H^2_{bs} = 75.94$, GA = 47.37), number of locules fruit⁻¹ ($H^2_{bs} = 72.61$, GA = 44.79) showed superior heritability along with genetic progress representing an improvement through simple selection. The traits such as plant height

with high heritability ($H^2_{bs} = 73.22$, GA = 29.21) and moderate genetic advance can be upgraded with hybridization followed by progeny selection.

The correlation analysis showed that selecting the traits such as the number of branches plant⁻¹, number of flowers plant⁻¹ and number of fruits plant⁻¹ with the lowest average fruit weight, fruit length, fruit diameter and the number of locules fruit⁻¹ would produce higher fruit yield plant⁻¹. Based on the mean value, the genotypes such as BT-215-3-3-1 and BT-21 may be selected for a future breeding program as these two genotypes possessed the above-discussed characters. By analyzing the path coefficient analysis, we found that a high correlation coefficient and a high positive direct effect were demonstrated by the number of branches plant⁻¹ and the number of fruits plant⁻¹. Following the D² analysis, the 46 tomato genotypes were grouped into 19 clusters with no direct correlation between geographical origin and genetic divergence. Further, crosses involving genotypes from divergent clusters may produce desirable hybrids.

Among the nine different characters studied in tomato, the number of fruits plant⁻¹ showed high variability, heritability, genetic advance besides high correlation and path coefficient values with yield plant⁻¹. Hence, this trait should be given due importance during the selection process for the development of superior genotypes.

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