



Genetic Assessment of Diverse Tomato Species for Yield and Quality Traits under Polyhouse Conditions

Anuradha Sinha¹, Paramveer Singh¹, Ajay Bhardwaj¹, R.B. Verma¹

10.18805/ag.D-6108

ABSTRACT

Background: Climate change has an adverse impact on tomato yield and fruit quality, as elevated and fluctuating temperatures directly affects the flowering, fruit set and overall quality attributes. Furthermore, water stress disposes plants to pathogen attack and results in wilting or abscission of leaves, flowers and fruits. In this context, the present investigation was undertaken to evaluate wild and contemporary tomato genotypes in order to identify the most promising genotype for cultivation under polyhouse conditions.

Methods: Eleven genotypes of tomato were collected from different sources and the data were recorded from twenty-one yield contributing characters. The statistical analysis was followed to test the significant difference to compare among the means of significant traits. The correlations analysis, path analysis and PCA analysis were done using R studio software version 2023.03.1+446 and cluster analysis was done with the help of Star software version 2.0.1

Result: The highest phenotypic and genotypic coefficients of variation were observed for lycopene content (73.29% and 73.36%) and average fruit weight (77.92% and 78.00%). The top-most heritability was marked for number of fruits/plant (99.98%) with genetic advance 92.24%. PCA-Biplot and mean performance indicates that genotype 538408 has higher polar diameter, yield/plant, pericarp thickness and average fruit weight. Principal component analysis represents yield/plant, polar fruit diameter, pericarp thickness, average fruit weight, number of locules/fruit, equatorial fruit diameter, β -carotene and lycopene content reflected a positive contribution towards genetic divergence. Thus, this will be helpful for breeders to choose the desirable traits of tomato for future breeding program.

Key words: Genetic variability, Polyhouse conditions, Principal component analysis, Tomato.

INTRODUCTION

Tomato is second most consumed vegetable (FAO, 2016) and considered as protective fruit due to its nutritional content. A standard tomato consists of total protein 17.71 (g/100 g), ash 8.75%, moisture 91.18 (g/100 g), lipid 4.96 (g/100 g), total sugar 50.60 (g/100 g), acidity 0.48%, potassium 403.02 (mg/100 g), calcium 105.21 (mg/100 g), magnesium 172.58 (mg/100 g), vitamin C 36.16 (mg/100 g), vitamin K 98.28 (μ g/100 g) and vitamin A 614.44 (IU/100g) (Ali *et al.* 2021). Furthermore, processed products of tomato also had positive impact on human health (Gutierrez, 2018). Besides these, it is the delicious vegetable crops that give new flavour and appearance to dishes. It originates from Peru and its wild relatives are distributed in these regions. *Solanum lycopersicum* is the species of cultivated tomato while its closest relative is *Solanum pimpinellifolium* with a divergence of only 0.6% nucleotide base pairs (Sato *et al.*, 2012). Arrays of other wild tomato relatives are present in India viz., *Solanum chmiewelskii*, *Solanum chilense*, *Solanum lycopersicoides* etc.

Climate change factors such as water stress and extreme temperature have adversely impacted tomato yield and fruit quality, as temperature directly influences flowering, fruiting and quality parameters. For example, at temperatures between 26°C and 30°C, the total soluble solids (TSS) content increases, resulting in sweeter fruits (Beckles, 2012). The optimum temperature range for vegetative growth and fruit set has been reported as 18°C

¹Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural University, Sabour-813 210, Bhagalpur, Bihar, India.

Corresponding Author: Paramveer Singh, Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural University, Sabour-813 210, Bhagalpur, Bihar, India.

Email: shekhawatdeep@rediffmail.com

ORCID: 0000-0003-2996-8341

How to cite this article: Sinha, A., Singh, P., Bhardwaj, A. and Verma, R.B. (2025). Genetic Assessment of Diverse Tomato Species for Yield and Quality Traits under Polyhouse Conditions. *Agricultural Science Digest*. 1-10. doi: 10.18805/ag.D-6108.

Submitted: 01-07-2024 **Accepted:** 28-11-2025 **Online:** 15-01-2026

to 28°C and 14°C to 24°C, respectively (Jones, 2007) but the temperature above or lower than optimum directly or indirectly affect the crop production. In addition, water stress predisposes plants to pathogen infection and accelerates physiological disorders such as wilting and abscission of leaves, flowers and fruits. Thus, the present research work was conducted using wild to contemporaneous genotypes of tomato to find the best genotype for polyhouse conditions. Also, the wild tomatoes have high fruit quality related traits, as well as biotic and abiotic tolerance (Passam *et al.* 2007), thus have potential to withstand under changing climate.

The knowledge on the nature and amount of genetic variability for diverse traits would be helpful in selecting the desired parent for the development of a variety with a

desirable genotype. Therefore, it is important to assess the genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance of different traits, which helps the plant breeders to breed desired genotype. The yield is quantitative character and its expression depends on environmental conditions, genetic factor and their interaction on yield. Therefore, appraisal of inter-relationships among multiple traits is important for achieving genetic advancement in the desired direction. However, correlation analysis alone does not provide insights into the nature or magnitude of individual trait contributions to yield. Hence, evaluating trait inter-relationships is essential for targeted improvement, but additional analytical approaches are required to ascertain the extent of each trait's influence on yield. This is overcome by path analyses which partition the correlation into direct and indirect effects. Beside principal component analysis (PCA) was help to recognize important traits and curtail the traits that has negligible and non-significant role for larger number of observations to perform effective selection. This data helps in the selection of traits so that the improvement of the desired trait might be attain efficiently. Thus, it is an imperative need to evaluate potential tomato genotypes for important yield and its attributing traits for polyhouse conditions which is to be further utilizing in breeding programme.

MATERIALS AND METHODS

Experiment location

This research has been conducted from 2018 to 2019 in a naturally ventilated polyhouse at Polyhouse Complex, Deptt. of Horticulture (Veg. and Flori.), Bihar Agricultural University, Sabour, Bhagalpur. Based on the Global Positioning System (GPS), the research location was 25°15'40"N latitude and 87°2'42"E longitude. This place is characterized by a semi-arid and sub-tropical climate with dry summer, along with average precipitation and cold winter.

Genetic materials

Eleven genotype of tomato (Table 1) were collected from different sources and is sown in pro-tray using coco peat and vermi-compost as a composting material. Then 28 days old seedlings were transplanted inside naturally ventilated polyhouse (500 m²) at double row planting system (60 cm × 60 cm spacing). Before sowing, area inside the polyhouse was maintained to obtain good soil tilth. The standard packages of practices were followed to raise the good crop.

Experimental design and statistical analysis

All the genotype of tomato was shown in a randomized block design (RBD) with three replications. Data of twenty one yield contributing characters viz., days to first flower (DFF), number node to first flower (NNFF), days to fifty percent flowering (DFPF), number of flowers/truss (NFT), days to first fruiting (DTFF), number of fruits/truss (NFPT), plant height at 60 DAT (PH), days to first picking (DFP),

number of locules (NL), polar diameter (PD), equatorial diameter (ED), pericarp thickness (PT), total soluble solid (TSS), titratable acidity (TA), ascorbic acid (AA), β- carotene (BC), lycopene (LY), final plant height (FPH), average fruit weight (AFW), no. of fruits/plant (NFPP), yield/plant (YPP) were taken by following the tomato descriptors. The statistical analysis was followed to test the significant difference as suggested by Panse and Sukhatme (1967) to compare among the means of significant traits. The correlations analysis, path analysis and PCA analysis were done using R studio software version 2023.03.1+446 and cluster analysis was done with the help of Star software version 2.0.1.

Genetic parameter analysis

1. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was estimated as formula given by Comstock and Robinson (1952).

$$GCV \% = \frac{\sqrt{\text{Genotypic variance}}}{\bar{X}} \times 100$$

$$PCV \% = \frac{\sqrt{\text{Phenotypic variance}}}{\bar{X}} \times 100$$

$$\text{Relative difference (RD)} = \left(\frac{PVC - GCV}{PCV} \times 100 \right)$$

Where,

$\bar{X}$ = Grand mean

2. Broad sense heritability (h^2_b) was calculated as given by Lush (1940).

$$h^2_b = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

3= Genetic advance was estimated as suggested by Lush (1949) and Johnson *et al.* (1955).

$$GA = kxh^2\sqrt{(\sigma^2 p)}$$

Where,

k = Selection differential constant at 5%

$\sqrt{(\sigma^2 p)}$ = Phenotypic standard deviation

$$GA \text{ as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

RESULTS AND DISCUSSION

Mean Performance of diverse tomato species

Eleven genotypes were studied for higher yield and quality parameters (Table 2) and the relationship of average fruit weight (g) and number of fruits per plant with yield per plant (kg) is displayed in Fig 1. The genotype EC 538408 (1.79 kg) produced the maximum yield per plant followed by WIR 13700 (1.75 kg). In addition to this, EC 538408 was identified for maximum pericarp thickness (3.25 mm), polar diameter (3.22 cm), equatorial diameter (3.86 cm), lycopene

content (8.24 mg/100 g), beta carotene content (0.84 mg/100 g) and average fruit weight (18.53 g).

Genetic variations in tomato genotypes

The results on genotypic and phenotypic covariance, variability, relative differences (RD), heritability and genetic advance as a percent were unveiled in Table 3. The results manifested that the genotypic variance (σ^2_g) varied from 0.04 (beta-carotene) to 12156 (number of fruits per plant). In similar fashion, beta- carotene represents the least (0.05), whereas number of fruits per plant (12159.38) reported the highest phenotypic variance. Also, the phenotypic variance is a little higher than the respective genotypic variance for all the traits, hence the expression of these traits is affected by the environment. Further, the PCV and GCV were categorised as low (<10%), medium (10% to 20%) and high (>20%) as suggested by Sivasubramanian and Madhava (1973).

Based on these criteria, our results indicate that both GCV and PCV were higher for almost all the traits except for number of nodes to first flowering (15.53, 16.75), total soluble solids (16.01, 16.45) and days to first picking (8.19, 8.65), which shows moderate to low genetic variability. The significance of genetic variability is the necessity of any breeding population, not only for selection, but also provides imperative facts about the selection of parents for utilization in hybridization (Upadhyay *et al.*, 2019). The high genetic variability might be helpful for effective selection for the improvement of the traits. Analogous results were also observed by Khuntia *et al.* (2019), Sinha *et al.* (2020), Venkadeswaran *et al.* (2020) and Golani *et al.* (2023).

The relative difference (RD) is an estimation of the ratio of GCV to PCV. The estimated RD values varied from 0.00% (number of fruits per plant) to 7.28% for number of node to first flowering indicating minimum relative

Table 1: List of genotypes.

Genotypes	Image	Characteristics
<i>Solanum chilense</i>		<i>Solanum chilense</i> boost resistance to Tomato Mosaic Virus Y and <i>Verticilium dahlia</i> in commercial tomato.
EC 538408		Resistance against Varanasi strain (tomato leaf curl Gujarat virus).
EC 520076		Tolerance at 100 mM NaCl conc.
EC 520060		Highly resistant to tomato leaf curl virus
WIR 13700		Round with uniform red color fruit
<i>Solanum peruvianum</i>		Fruit has a sweet tomato-like flavor; grow under drought and soil salinity.
EC 520075		Round with uniform reddish pink color fruit
<i>Solanum cheesmanii</i>		Very sweet and cherry-like fruits; enhance salinity tolerance.
<i>Solanum pimpinellifolium</i>		Source of Pto gene which resistance to bacterial speck disease; high salinity tolerance.
NTH 1831		Oblong fruit shape with uniform green shoulder color; Good Firmness; Sour taste.
Akshaya		High yielder; resistance to bacterial wilt; appropriate for rain shelter farming.

difference. So, the variation exists amongst the traits is due to genetic effect, which has a better response for direct selection.

The heritability of the traits ranged between 86.06% (number of node to first flowering) to 99.98% (number of fruits per plant). Generally high heritability ($h^2_b \geq 60\%$) was marked for all the traits under study and genetic advance as a % of mean (GA %) varied from 15.96 (days to first fruit picking) to 160.30% (average fruit weight). Genetic advance was high ($GA \leq 20\%$) for all traits except days to first fruit picking which indicate ($10\% \leq GA \leq 20\%$) moderate genetic advance. Rasheed *et al.* (2023) noted high genetic advance (%) coupled with higher h^2_b % for yield per plant and the

number of fruits per cluster. Anyaoha *et al.* (2023) recorded high heritability along with high genetic advance (%) for carotene content.

Apparently, in this work, all the traits had high heritability along with high GA (%) except days to first fruit picking which had high heritability along side with moderate GA (%). Traits manifested high heritability with high GA (%) indicates prevalence of additive gene effect, thus direct selection is effective. Therefore, it is meaningful to favour traits with high GCV, PCV, heritability and genetic advance (Sabri *et al.* 2020). The powerful selection can be attained when additive genes effects are stronger than the environmental effects (Usman *et al.*, 2014).

Table 2: Mean performance of different tomato species.

Traits	1	2	3	4	5	6	7	8	9	10	11
DFF	28.80	40.47	30.53	35.00	34.00	22.07	34.20	23.13	29.40	59.87	61.60
NNFF	9.93	10.00	9.73	12.73	10.07	8.00	10.47	11.67	9.47	7.93	7.60
DFFP	33.20	45.20	35.47	35.87	39.20	25.07	34.80	26.53	34.00	68.80	67.47
NFT	12.53	7.93	14.80	14.33	7.20	9.47	5.87	9.93	10.47	11.87	12.93
DTFF	46.80	54.33	49.27	51.13	53.93	36.13	49.87	41.07	44.93	72.53	73.00
DFPPr	54.13	61.20	57.20	59.33	62.00	40.93	56.67	47.33	50.67	85.73	84.53
NFTT	9.67	6.47	5.00	6.20	3.20	3.20	3.53	5.00	4.13	9.93	10.47
PH	144.9	94.40	152.7	128.4	139.6	80.27	145.6	112.8	103.6	93.33	80.73
DFP	116.0	116.6	106.3	110.6	124.4	100.8	123.2	108.8	121.6	126.8	133.1
NL	2.00	3.00	2.00	2.00	2.13	2.00	3.53	2.00	2.53	2.00	2.00
PT	1.32	3.25	0.83	1.00	1.67	1.54	1.38	1.25	1.54	1.70	1.19
ED	1.80	3.86	1.36	1.27	2.39	2.26	2.56	1.88	1.86	1.62	1.40
DP	1.72	3.22	1.34	1.19	2.13	2.34	2.25	1.65	1.63	2.29	2.03
TSS	7.52	5.25	7.66	7.29	6.43	6.37	6.10	6.66	7.20	9.00	8.98
AA	25.46	19.76	38.80	25.08	39.56	16.24	60.00	27.26	23.64	41.47	22.57
TA	0.71	0.69	0.90	0.73	0.77	1.02	0.90	1.26	0.70	0.52	0.44
LY	2.14	8.24	0.50	7.33	4.14	3.26	2.14	2.05	6.19	1.42	1.59
BC	0.31	0.84	0.08	0.54	0.45	0.51	0.31	0.39	0.56	0.14	0.24
FPH	358.2	273.8	359.8	356.0	370.0	306.3	398.1	397.6	385.6	233.0	164.4
AFW	3.00	18.53	1.27	1.13	9.13	5.53	13.47	3.40	13.07	6.87	4.47
NFPF	329.7	96.50	385.9	432.0	191.9	231.3	123.9	321.2	127.6	233.5	234.3
YPP	0.99	1.79	0.49	0.49	1.75	1.28	1.67	1.09	1.67	1.60	1.05

Legend: 1- *S. chilense*, 2- EC 538408, 3- EC 520076, 4- EC 520060, 5- WIR 13700, 6- *S. peruvianum*, 7- EC 520075, 8- *S. cheesmanii*, 9- *S. pimpinellifolium*, 10- NTH 1831, 11- Akshaya.

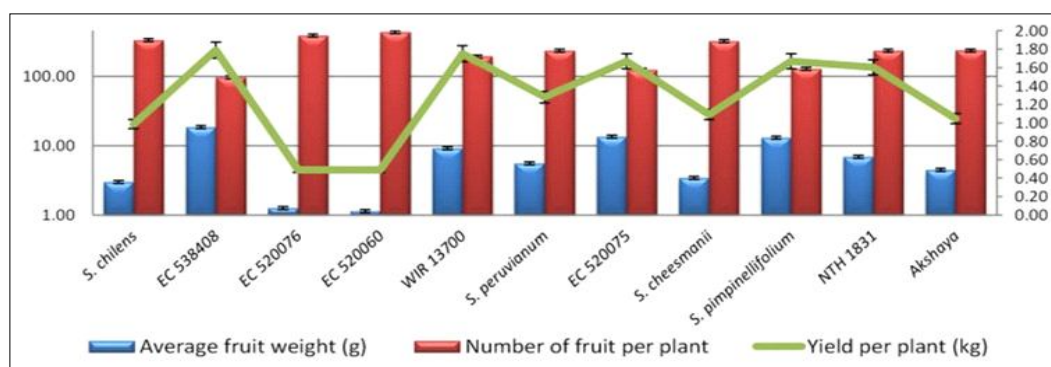


Fig 1: Graphical presentation of relationship between average fruit weight (g) and number of fruits per plant with yield per plant (kg).

Correlation and path analysis

Association among twenty-two traits based on Pearson's correlation analysis given in Fig 2. Non-significant correlation was found for days to first flowering, number node to first flower, days to fifty percent flowering, days to first fruiting, number of fruits/truss, plant height at 60 DAT, titratable

acidity, ascorbic acid, lycopene content and final plant height along with yield. β -Carotene had significant weak and positive association with yield ($r=0.38$; $p\leq0.05$). Pericarp thickness ($r=0.68$; $p\leq0.001$), days to first picking ($r=0.45$; $p\leq0.01$), polar diameter ($r=0.74$; $p\leq0.001$), equatorial diameter (0.68 , $p\leq0.001$) and number of locules ($r=0.56$;

Table 3: Estimation of genetic variability in tomato.

Traits	Range	Grand mean	(σ^2_g)	(σ^2_p)	GCV (%)	PCV (%)	RD (%)	h^2_b %	GA %
DFF	20.80-61.60	36.28	171.0	179.1	36.05	36.89	2.28	95.47	72.56
NNFF	7.40-14.2	9.78	2.31	2.68	15.53	16.75	7.28	86.06	29.69
DFFP	24.40-71.60	40.51	213.4	221.0	36.07	36.70	1.72	96.56	73.01
NFT	5.87-15.80	10.67	8.40	8.74	27.17	27.72	1.98	96.06	54.86
DTFF	33.80-73.20	52.09	132.4	135.0	22.09	22.31	0.99	98.07	45.06
DFFP _r	39.60-89.60	59.98	190.6	199.2	23.02	23.53	2.17	95.69	46.38
NFPT	3.00-10.80	6.07	7.59	7.72	45.35	45.77	0.92	98.21	92.58
PH	78.4-154.20	116.05	738.6	755.2	23.42	23.68	1.10	97.81	47.71
DFP	100.0-133.8	117.15	91.99	102.7	8.19	8.65	5.32	89.60	15.96
NL	2.00-3.80	2.29	0.27	0.28	22.53	23.26	3.14	93.85	44.96
PT	0.82-3.49	1.51	0.40	0.41	41.89	42.23	0.81	98.41	85.61
ED	1.21-3.86	2.02	0.55	0.56	36.49	36.94	1.22	97.59	74.27
PD	1.16-3.42	1.98	0.32	0.33	28.45	28.74	1.01	98.02	58.03
TSS	5.00-9.04	7.14	1.30	1.38	16.01	16.45	2.67	94.66	32.08
AA	15.57-61.0	30.89	163.0	164.1	41.33	41.47	0.34	99.31	84.84
TA	0.43-1.28	0.79	0.05	0.05	29.13	29.33	0.68	98.68	59.61
LY	0.41-8.26	3.55	6.75	6.76	73.29	73.36	0.10	99.82	150.84
BC	0.07-0.86	0.40	0.04	0.05	54.18	54.30	0.22	99.57	111.38
FPH	164.20-401	327.57	5669	5683	22.99	23.01	0.09	99.76	47.29
AFW	1.00-18.8	7.26	32.00	32.07	77.92	78.00	0.10	99.78	160.33
NFPP	96.30-432.9	246.19	12156	12159	44.78	44.78	0.00	99.98	92.24
YPP	0.43-1.81	1.26	0.22	0.23	37.98	38.36	0.99	98.03	77.47

Legend: σ^2_g : Genotypic variance, σ^2_p : Phenotypic variance; h^2_b : Heritability in broad sense; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; RD: Relative difference; GA: Genetic advance.

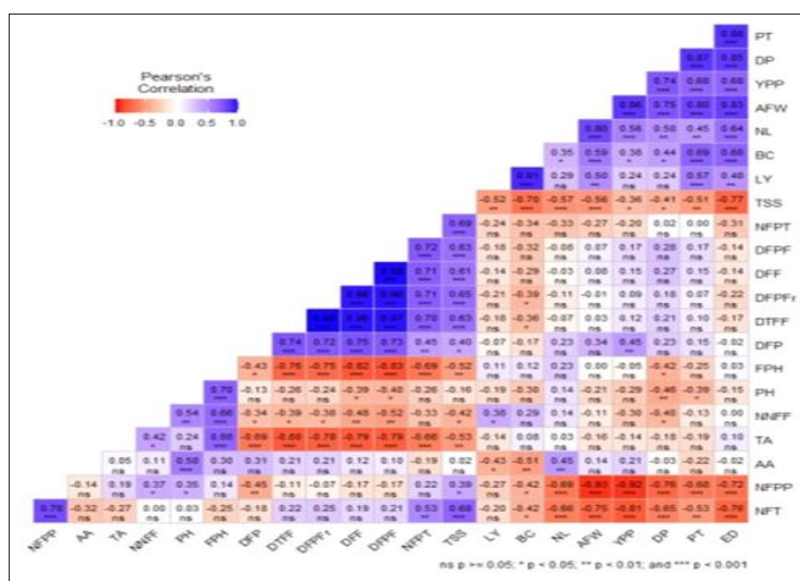


Fig 2: Correlation analysis of twenty-two traits in tomato.

$p \leq 0.01$) had highly significant positive and moderate ($0.25 \leq r < 0.75$) correlation with yield and average fruit weight ($r = 0.86$; $p \leq 0.001$) had highly significant positive and strong correlation with yield. The positive correlation between average fruit weight, pericarp thickness, days to first picking, polar diameter, equatorial diameter, number of locules with fruit yield may suggest that these traits share some common gene. Number of flowers per truss ($r = -0.81$; $p \leq 0.001$) and number of fruits per plant ($r = -0.92$, $p \leq 0.001$) had highly significant negative and strong ($0.75 \leq r < 1.00$) relation with yield. Moreover, TSS had significant weak ($0.0 \leq r < 0.25$) and negative association with yield ($r = -0.36$; $p \leq 0.05$). Lower number of flowers per truss and number of fruits per plant may increase fruit weight leads to enhance the yield of tomato. Adebisi *et al.* (2004) confirmed that reflection of correlation values amongst the variables is crucial for the selection of superior genotypes. Therefore, emphasis given on selection of higher fruit weight, pericarp thickness, polar diameter, equatorial diameter, lower number of flowers per truss and lower number of fruits per plant during the selection could be helpful for genetic improvement of tomato. Our results are in the same tune of Sharma *et al.* (2019), Arya *et al.* (2023), Meena *et al.* 2023 and Reddy *et al.* (2023).

The path coefficient analyses (Table 4) give clear idea about the nature of association between the different traits for forming proficient selection approach. The results revealed that the number of flowers/truss, days to first picking, polar diameter and TSS had positive direct effect on yield. However, highest positive direct effect on yield was exhibited by polar diameter. It is stated above that the correlation between the polar diameter and yield is positive and statistically significant ($r = 0.74$; $p \leq 0.01$). This implies that higher polar diameter leads to increased fruit yield. Hence, selection based on polar diameter would be

effective. Number of fruits per plant showed negative direct effect on fruit yield per plant (-1.92) similar to its correlation with yield (-0.92), implying that true relation exists between these traits. However, number of fruits per plant has high indirect effect on yield per plant through polar diameter (1.47). In the same way, number of locules, pericarp thickness and average fruit weight had positive indirect effect on yield through number of flowers per truss. Moreover, highest significant association between number of fruits per plant and yield ($r = -0.92$; $p \leq 0.001$) were observed, that may be due to the indirect effect of number of fruits per plant on polar fruit diameter. Thus, we advocated that selection based on polar diameter is made deliberately. Similar observations were also reported by Sehgal *et al.* (2018), Ritonga *et al.* (2018) and Sharma *et al.* (2019).

Cluster analysis

The dendrogram for cluster analysis is displayed in Table 5 and Fig 3 using "Star Software". Cluster analysis help in selection of genotype based on nature and degree of genetic divergence. The result revealed that the genotypes were grouped into 3 major clusters. Cluster II comprised the highest proportion of genotypes (45.46%), including *Solanum chilense*, EC 520076, EC 520060, *Solanum peruvianum* and *Solanum cheesmanii*. In contrast, Cluster III contained the lowest proportion (18.18%) with genotypes NTH 1831 and Akshaya, while Cluster I accounted for 36.36% of the total population, consisting of four genotypes viz., EC 538408, WIR 13700, EC 520075 and *Solanum pimpinellifolium*.

The genotype chosen from different cluster for hybridisation may results in isolation of transgressive segregants. The random distribution of genotypes of different origin in a single cluster designated that the diversity might be due to genetic architecture, heterogeneity or homogeneity of traits

Table 4: Direct and indirect effect of twenty-two traits of tomato.

Traits	NFT	DFP	NL	PT	ED	PD	TSS	BC	AFW	NFPP	r YPP
NFT	0.57	-0.01	0.43	0.17	0.04	-0.84	0.02	0.06	0.56	-1.50	-0.81***
DFP	-0.10	0.07	-0.15	-0.05	0.00	0.30	0.01	0.02	-0.26	0.88	0.45**
NL	-0.38	0.02	-0.65	-0.15	-0.04	0.65	-0.02	-0.05	-0.60	1.33	0.56**
PT	-0.30	0.01	-0.30	-0.32	-0.05	1.13	-0.02	-0.10	-0.61	1.31	0.68**
ED	-0.43	0.00	-0.42	-0.28	-0.06	1.10	-0.03	-0.10	-0.63	1.38	0.69**
PD	-0.37	0.02	-0.32	-0.27	-0.05	1.30	-0.01	-0.06	-0.57	1.47	0.74**
TSS	0.39	0.03	0.37	0.16	0.04	-0.54	0.03	0.10	0.42	-0.75	-0.36*
BC	-0.24	-0.01	-0.23	-0.22	-0.04	0.57	-0.02	-0.14	-0.45	0.80	0.37*
AFW	-0.43	0.02	-0.52	-0.25	-0.05	0.97	-0.02	-0.08	-0.76	1.78	0.86***
NFPP	0.44	-0.03	0.45	0.22	0.04	-0.99	0.01	0.06	0.70	-1.92	-0.92***

Legends: ***= $p \leq 0.001$, **= $p \leq 0.01$, *= $p \leq 0.05$.

Table 5: Cluster analysis of tomato genotypes.

Cluster	Genotype number	Genotypes
Cluster I	4	EC 538408, WIR 13700, EC 520075, <i>Solanum pimpinellifolium</i>
Cluster II	5	<i>Solanum chilense</i> , EC 520076, EC 520060, <i>Solanum peruvianum</i> , <i>Solanum cheesmanii</i>
Cluster III	2	NTH 1831, Akshaya

and history of selection. Different clustering patterns confirmed by Sinha *et al.* (2021), Vargas *et al.* (2020) and Naveen *et al.* (2018).

Principal component analysis (PCA)

It is used to sort the traits based on contribution to the total variation at each axis of differentiation. In the current research, PCA divide their 100% diversity into ten components in which four principal components *i.e.*, PC1 (8.10), PC2 (7.38), PC3 (2.77) and PC4 (1.59) had more than 1 eigen value with 90.18% of cumulative variability (Table 6 and Fig 4). The PCs with less than 1 eigen value

were considered non-significant and display lesser variability between the genotypes. Thus, it is inferred that data correspond to the first four PCs had higher variability. Therefore, the selection from these PCs will be valuable. Iqbal *et al.* (2014) reported 3 PCs with more than 1 eigen-value

The factor loading of traits is represented in Table 7 and Fig 5A revealed that the PC1 allowed maximum loading of traits like days to first flower, days to fifty percent flowering, days to first fruiting, days to fifty percent fruiting and TSS. In PC2, average fruit weight and no. of fruits/plant, in PC3, ascorbic acid and β -carotene and in PC4, lycopene and

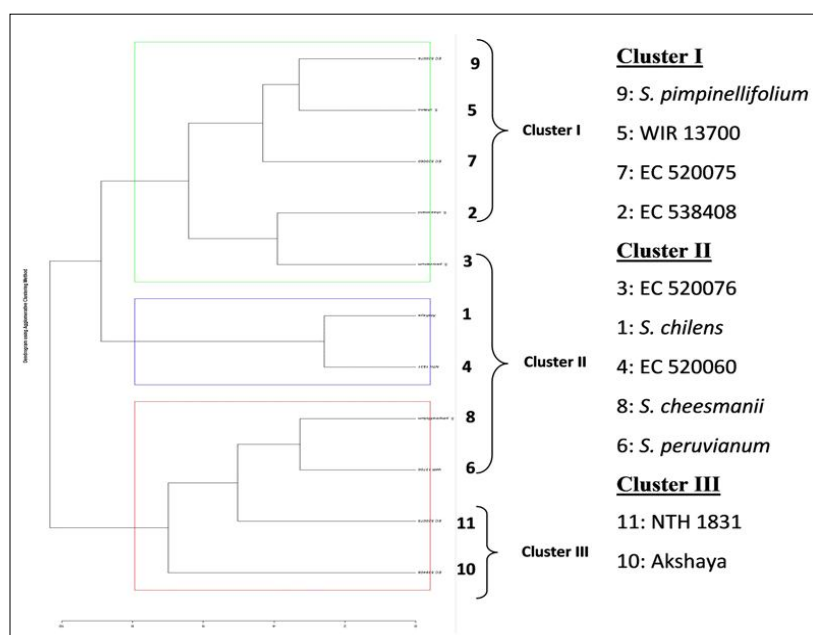


Fig 3: Dendrogram using agglomerative clustering method of eleven tomato genotypes.

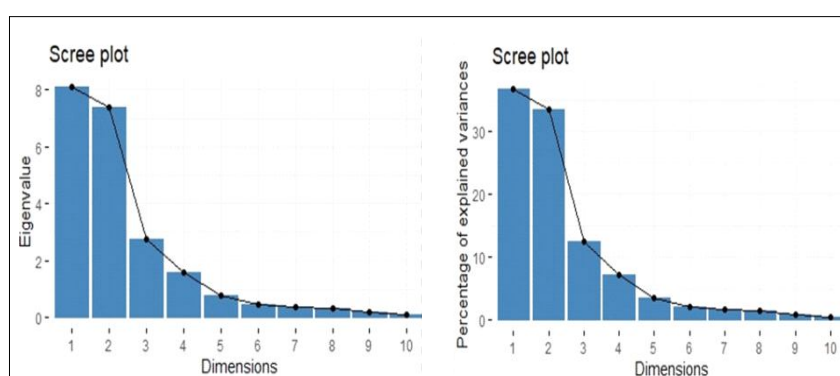


Fig 4: Scree plot showing the eigen value (Left) and percent proportion of variance (Right).

Table 6: Eigen values, proportion of variance (%) and cumulative variation % in tomato.

Principal components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigen value	8.10	7.38	2.77	1.59	0.77	0.45	0.38	0.30	0.18	0.09
Proportion of variance (%)	36.83	33.55	12.58	7.23	3.52	2.03	1.72	1.35	0.81	0.39
Cumulative variation (%)	36.83	70.38	82.96	90.18	93.70	95.73	97.45	98.80	99.61	100.00

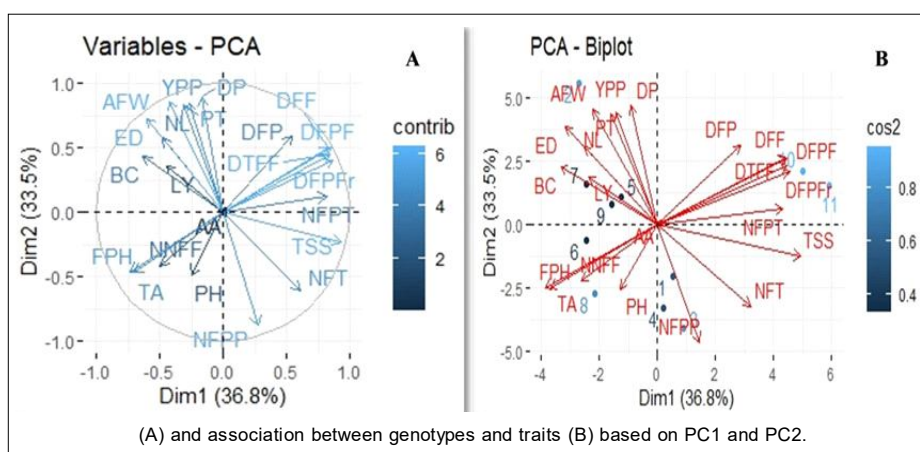


Fig 5: Graphical representation of distribution of traits.

Table 7: Principal loading factor of different traits in four principal factors.

Traits	PC1	PC2	PC3	PC4
DFF	8.63	3.38	0.11	1.15
NNFF	3.08	2.37	0.18	28.42
DFPF	8.91	3.38	0.05	0.39
NFT	4.61	5.05	4.54	2.20
DTFF	8.84	2.64	0.69	2.40
DFPF _r	9.24	2.19	0.73	2.17
NFPT	8.28	0.20	1.56	1.30
PH	0.75	3.20	13.87	9.44
DFP	3.68	4.70	5.17	3.02
NL	2.83	4.51	7.17	2.38
PT	1.18	9.37	3.13	0.39
ED	4.46	7.17	0.13	0.00
PD	0.37	10.71	0.33	3.47
TSS	10.86	0.75	0.04	0.33
AA	0.01	0.02	33.60	0.32
TA	6.04	3.01	0.26	7.69
LY	2.51	1.71	9.05	22.22
BC	4.94	2.52	10.73	5.84
FPH	6.71	2.97	4.92	2.07
AFW	2.24	10.03	0.60	0.53
NFFP	0.94	10.53	1.23	2.22
YPP	0.92	9.58	1.92	2.02

number node to first flower showed maximum positive loading. By considering these traits it showed that these PCs regulate the total variation for all yield contributing traits. Positive factor loading indicated significant variation in yield and quality trait so it plays important role for selection on the basis of yield and quality of tomato. Sehgal *et al.* (2018) and Sinha *et al.* (2021) observed that number fruits per plant, lycopene, ascorbic acid, titratable acidity contributed positively to PC. Kumar *et al.* (2017) reported that average fruit weight, TSS and fruit yield per plant give positive contribution to PC. Thus, trait-based selection might be helpful to formulate a valuable selection approach for further tomato improvement programs.

The biplot diagram (Fig 5B) shows the association among the traits and between genotype $\times$ traits. The vector length gives a picture of the contribution of traits to total variance, the longer the vector length, the higher the contribution of those traits. The trait yield/plant, polar diameter, pericarp thickness and average fruit weight showed the highest vector length representing its involvement to the entire diversity. The genotypes close to the vector trait are probably the best performing for particular traits. The genotype EC 538408 performs better for the polar diameter, yield/plant, pericarp thickness and average fruit weight; however NTH 1831 associated with days to first flower, days to fifty percent flowering and days to first fruiting.

CONCLUSION

It is noticeable from the current research that except days to first fruit picking all the traits have higher heritability and genetic advance indicating strong influence of additive gene action hence simple selection might be effective. Correlation and path analysis indicated that the higher polar diameter and lower number of fruits per plant leads to increased fruit yield. Consequently, selection based on these traits is made deliberately. PCA-Biplot and mean performance indicates that genotype 538408 has higher polar diameter, yield/plant, pericarp thickness and average fruit weight. 90.18% of variability present in first four PCs thus, the traits from these PCs contributes more to variability and have an affinity to stay interrelated. Thus, trait-based selection might be helpful to formulate a valuable selection approach for further tomato improvement programs.

ACKNOWLEDGEMENT

The authors express their sincere gratitude to Bihar Agricultural University for providing financial assistance and research facilities to conduct this study.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are

responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

Not applicable. This study did not involve human participants or animals.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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