Plant Archives Vol. 25, No. 2, 2025 pp. 69-76 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.013

ASSESSMENT OF GENETIC ARCHITECTURE AND INTER-TRAIT DEPENDENCIES IN F_1 TOMATO HYBRIDS: A COMPARATIVE ANALYSIS OF VARIABILITY PARAMETERS, CHARACTER ASSOCIATION, PATH ANALYSIS, GENETIC DIVERSITY AND PRINCIPAL COMPONENT ANALYSIS

T. J. Solanki*, K. N. Prajapati, A. R. Donga, Aishwarya Deshpande, K. R. Prajapati and U. B. Jadav

Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar,
Dantiwada, Gujarat, India – 388506.
*Corresponding author E-mail: tanvi.solanki020@gmail.com

(Date of Receiving-30-05-2025; Date of Receiving-31-07-2025)

ABSTRACT

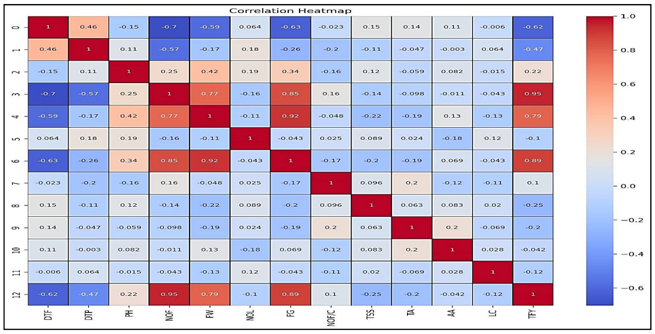
The current investigation was conducted using forty-five tomato genotypes during the *Rabi* – 2024-25 at Centre for vegetable research, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India. The study followed a Randomized Block Design with three replications and measurements were taken for thirteen traits which contributes for flowering, yield attributing, biochemical and fruit yield in tomato. The analysis demonstrated that all the traits exhibited significant variation across the germplasm. The traits like number of fruits per plant, lycopene content and titrable acidity were associated with higher phenotypic and genotypic coefficients of variation (PCV and GCV). A combination of high heritability with high genetic advance as per cent of mean were observed for total fruit yield, number of fruits per plant, total soluble solids, titratable acidity, lycopene content and ascorbic acid. The study showed positive and significant character association with total fruit yield per plant for the traits like number of fruits per plant, fruit weight and fruit girth. Path analysis revealed that the number of fruits per plant had the strongest positive direct effect on fruit yield per plant, followed by fruit girth, days to 50% flowering, and number of fruits per cluster. Also in the present investigation, forty-five diverse tomato genotypes were grouped into nine distinct clusters where the maximum number of genotypes was found in cluster 1 and the minimum number in cluster 6 and 9. The highest inter cluster D^2 value was observed between cluster 9 and 5. Genotypes from clusters 5, 8 and 9 possess distinct characteristics that could be useful in generating superior recombinants for future tomato breeding program. Out of 13, 5 components recorded eigenvalues (>1) considered as principal component which accounted for overall 72.01% of the variation observed among the forty-five tomato genotypes. The PC1, PC2, PC3, PC4 and PC5 involve characters *viz.*, plant height, number of fruits per plant, fruit weight, fruit girth, number of fruits per cluster and total fruit yield per plant. The results of the entire experiment showed that the presence of significant genetic variation among the tomato genotypes provides opportunities for selection and improvement of yield and quality traits through systematic breeding strategies.

***Key words*:** Variability parameters, Correlation, Path analysis, D^2 analysis, PCA, Tomato Hybrids, Tomato

Introduction

Tomato (*Solanum lycopersicum* L.) (2n=2x=24) is a popular vegetable in the *Solanaceae* family which commonly known as "Protective Food" and widely produced as annual plants all around the world (Rick, 1949). The tomato is one of the most commonly cultivated vegetable in households and the second most eaten vegetable worldwide after potato (*Solanum tuberosum* L.). The species is originated in South America, most likely Peru and Ecuador but it was first domesticated in Mexico (Benton, 2007). Tomato is beneficial supplement to a nutritious and well-balanced diet due to having low calories and high in vitamins A, C and minerals. It contains few amounts of vitamin B complex including thiamine, riboflavin and niacin (Sainju and Dris, 2006). Furthermore, tomato is also known as a "Functional Food" (Ranieri *et al.*, 2004) since it contains an extensive number of antioxidants like phenolic compounds, α-tocopherol (vitamin E) and carotenoids (lycopene, β-carotene).

Tomato stands out as a vegetable that has consistently drawn the attention of breeders around the world. The success of crop improvement largely relies on the extent of genetic variability in economically important traits. Therefore, assessing and effectively utilizing this variability in the desired direction is crucial for any yield enhancement programme (Allard, 1960). The degree of genetic variation in a breeding population is determined by both the genetic makeup of the included genotypes and the nature of its past selection processes. Therefore, to enhance breeding efficiency, it is important to explore the extent of usable genetic variability and the nature of correlations among diverse plant traits. Phenotypic traits in plants results from the interaction between their genetic background and the environmental conditions under which they are cultivated. The genetic variance associated with quantitative traits arises from both additive and non-additive components, including dominance and epistatic (non-allelic) interactions. To evaluate the potential for genetic improvement, it is crucial to break down the total phenotypic variability into its heritable and non-heritable components using parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance. The magnitude of genetic advance serves as a critical parameter for assessing the success of selection strategies. To make selection more effective, it is important to evaluate the relative contribution of different traits to yield. The path coefficient analysis is a useful tool for quantifying the direct and indirect effects of various traits on yield, based on their overall correlation (Kumar *et al.*, 2014). The use of Mahalanobis D^2 statistics and principal component analysis provide valuable insights into the extent of genetic diversity and the component-wise variation within a population. Several studies have been carried out using a diverse genetic pool comprising cultivars, elite lines, accessions and landraces of tomato (Rai *et al.*, 2016; Zannat *et al.*, 2023). However, limited studies have focused on assessing hybrids or first filial generations that exhibit distinct and pronounced heterotic effects. Based on these approaches, the present study was conducted to assess variability, heritability, genetic advance, character association, path analysis, D^2 analysis and PCA in forty-five tomato hybrids which is developed from half diallel mating design.



	DTF	DTP	PH	NOF	FW	NOL	FG	NOF/C	TSS	TA	AA	LC	TFY
0	1	0.46	-0.15	-0.7	-0.59	0.064	-0.63	-0.023	0.15	0.14	0.11	-0.006	-0.62
1	0.46	1	0.11	-0.57	-0.17	0.18	-0.26	-0.2	-0.11	-0.047	-0.003	0.064	-0.47
2	-0.15	0.11	1	0.25	0.42	0.19	0.34	-0.16	0.12	-0.059	0.082	-0.015	0.22
3	-0.7	-0.57	0.25	1	0.77	-0.16	0.85	0.16	-0.14	-0.098	-0.011	-0.043	0.95
4	-0.59	-0.17	0.42	0.77	1	-0.11	0.92	-0.048	-0.22	-0.19	0.13	-0.13	0.79
5	0.064	0.18	0.19	-0.16	-0.11	1	-0.043	0.025	0.089	0.024	-0.18	0.12	-0.1
6	-0.63	-0.26	0.34	0.85	0.92	-0.043	1	-0.17	-0.2	-0.19	0.069	-0.043	0.89
7	-0.023	-0.2	-0.16	0.16	-0.048	0.025	-0.17	1	0.096	0.2	-0.12	-0.11	0.1
8	0.15	-0.11	0.12	-0.14	-0.22	0.089	-0.2	0.096	1	0.063	0.083	0.02	-0.25
9	0.14	-0.047	-0.059	-0.098	-0.19	0.024	-0.19	0.2	0.063	1	0.2	-0.069	-0.2
10	0.11	-0.003	0.082	-0.011	0.13	-0.18	0.069	-0.12	0.083	0.2	1	0.028	-0.042
11	-0.006	0.064	-0.015	-0.043	-0.13	0.12	-0.043	-0.11	0.02	-0.069	0.028	1	-0.12
12	-0.62	-0.47	0.22	0.95	0.79	-0.1	0.89	0.1	-0.25	-0.2	-0.042	-0.12	1

Fig. 1: Correlogram illustrating the interrelationship between yield and its contributing traits.

Materials and Methods

The present study utilized forty-five genetically diverse tomato genotypes were developed from 10 parental lines of tomato at Centre for vegetable research, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India during *Rabi* 2023-24. The seeds of hybrids were sown in a Randomized Block Design (RBD) with three replications in *Rabi* 2024-25. The crop was grown at a spacing of 90 cm × 45 cm and all recommended agronomic practices and plant protection measures were followed in a timely manner to ensure successful crop cultivation. Data were recorded from five randomly selected plants per replication for each genotype, focusing on thirteen quantitative traits, *viz.*, days to 50% flowering, days to first picking, plant height (cm), number of fruits per plant, fruit weight (gm), numbers of locules per fruit, fruit girth (cm), numbers of fruits per cluster, total fruit yield per plant (kg), total soluble solids (°Brix), titrable acidity (%), ascorbic acid (mg/100g) and lycopene content (mg/100g). Statistical analysis was performed on the mean performance of each genotype across all recorded traits. Genetic variability parameters, including heritability and genetic advance, were calculated as per the methodology outlined by Johnson *et al.*, (1955). Correlation studies are conducted as per Panse and Sukhatame (1978). The construction of path coefficient analysis was carried out as per the procedure outlined by Dewey and Lu (1959).

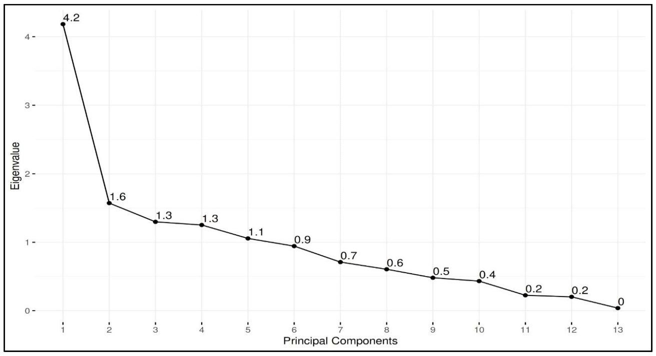


Fig. 2: Scree plot presenting eigen values and percentage of cumulative variability.

Table 1: Estimates of GCV (%), PCV (%), broad-sense heritability, and genetic advance as percent of mean for 13 traits across forty-five genotypes of tomato.

Sr. No.	Characters	GCV (%)	PCV (%)	$h^2_{(b.s)}$ (%)	GA	GA as % of Mean
1	Days to 50% flowering	7.86	8.47	86.25	8.16	15.04
2	Days to first picking	6.48	7.31	78.57	13.30	11.82
3	Plant height	16.21	19.66	68.00	34.42	27.54
4	Number of fruits per plant	37.16	38.70	92.20	14.90	73.50
5	Fruit weight	17.93	20.54	76.17	14.32	32.24
6	Numbers of locules per fruit	24.04	24.76	94.23	1.46	48.07
7	Fruit girth	8.25	12.11	46.39	1.51	11.58
8	Numbers of fruits per cluster	18.39	20.21	82.79	1.17	34.47
9	Total soluble solids	24.29	24.34	99.63	1.62	49.95
10	Titrable acidity	26.23	26.37	98.92	0.54	53.74
11	Ascorbic acid	17.05	17.44	95.62	5.44	34.35
12	Lycopene content	32.00	32.18	98.89	12.21	65.55
13	Total fruit yield per plant	38.88	40.36	92.81	0.72	77.17

Diversity analysis was conducted following the procedure outlined by Rao (1952). The multivariate analysis divergence using Mahalonabis's D^2 statics. Genotypic clustering was carried out using Tocher's method.

Analysis of genetic variability, heritability, genetic advance, correlation, path analysis and PCA using AGRI ANALYZE computer software and D^2 analysis using TNAU STAT computer software.

Table 2: Genotypic and phenotypic correlation coefficients among thirteen different traits in tomato.

		DTF	DTP	PH	NOF	FW	NOL	FG	NOFC	TSS	TA	AA	LC	TFY
DTF	r_g	1	0.455**	-0.149	-0.704**	-0.590**	0.064	-0.630**	-0.024	0.154	0.138	0.106	-0.006	-0.621**
	r_p	1	0.393**	-0.125	-0.613**	-0.462**	0.053	-0.403**	0.002	0.142	0.128	0.089	-0.002	-0.554**
DTP	r_g		1	0.111	-0.572**	-0.173	0.184	-0.260	-0.198	-0.112	-0.047	-0.003	0.064	-0.465**
	r_p		1	0.102	-0.487**	-0.154	0.149	-0.216*	-0.148	-0.093	-0.043	-0.014	0.055	-0.389**
PH	r_g			1	0.247	0.416**	0.194	0.338*	-0.157	0.122	-0.059	0.082	-0.015	0.221
	r_p			1	0.187*	0.323**	0.175*	0.214*	-0.097	0.107	-0.047	0.072	-0.006	0.161
NOF	r_g				1	0.771**	-0.163	0.847**	0.156	-0.137	-0.098	-0.011	-0.043	0.951**
	r_p				1	0.632**	-0.151	0.550**	0.116	-0.132	-0.096	0.0003	-0.044	0.899**
FW	r_g					1	-0.112	0.915**	-0.048	-0.218	-0.190	0.134	-0.126	0.785**
	r_p					1	-0.092	0.552**	-0.077	-0.193*	-0.158	0.115	-0.111	0.665**
NOL	r_g						1	-0.043	0.025	0.089	0.024	-0.182	0.117	-0.102
	r_p						1	0.014	0.040	0.084	0.025	-0.173*	0.115	-0.084
FG	r_g							1	-0.171	-0.200	-0.193	0.070	-0.043	0.885**
	r_p							1	-0.103	-0.135	-0.122	0.045	-0.031	0.584**
NOFC	r_g								1	0.096	0.205	-0.121	-0.106	0.103
	r_p								1	0.086	0.186*	-0.115	-0.093	0.081
TSS	r_g									1	0.062	0.083	0.020	-0.252
	r_p									1	0.062	0.083	0.021	-0.241**
TA	r_g										1	0.202	-0.069	-0.205
	r_p										1	0.201*	-0.069	-0.200*
AA	r_g											1	0.028	-0.042
	r_p											1	0.023	-0.033
LC	r_g												1	-0.121
	r_p												1	-0.120
TFY	r_g													1
	r_p													1

*, ** significant at 5% and 1% level of significance, respectively.

DTF= Days to 50% flowering, DTP = Days to first picking, PH = Plant height, NOF = Number of fruits per plant, FW = Fruit weight, NOL = Numbers of locules per fruit, FG = Fruit girth, NOFC = Numbers of fruits per cluster, TFY = Total fruit yield per plant, TSS= Total soluble solids (°Brix), TA = Titrable acidity, AA = Ascorbic acid and LC = Lycopene content

Table 3: Direct and indirect effects of yield component on total fruit yield in tomato.

Sr.	Traits	DTF	DTP	PH	NOF	FW	NOL	FG	NOFC	TSS	TA	AA	LC	TFY
1	**DTF**	**0.119**	-0.004	0.0002	-0.503	0.155	0.002	-0.355	-0.003	-0.019	-0.016	0.0002	0.001	-0.621**
2	**DTP**	0.054	**-0.007**	-0.0001	-0.408	0.045	0.005	-0.146	-0.020	0.014	0.005	-0.00001	-0.006	-0.465**
3	**PH**	-0.018	-0.001	**-0.001**	0.176	-0.110	0.005	0.190	-0.016	-0.015	0.007	0.0002	0.002	0.221
4	**NOF**	-0.084	0.004	-0.0003	**0.712**	-0.202	-0.004	0.476	0.016	0.017	0.011	-0.00002	0.004	0.951**
5	**FW**	-0.070	0.001	-0.0004	0.550	**-0.263**	-0.003	0.513	-0.003	0.026	0.022	0.0003	0.012	0.785**
6	**NOL**	0.008	-0.001	-0.0002	-0.116	0.029	**0.026**	-0.024	0.003	-0.011	-0.003	-0.0004	-0.011	-0.102
7	**FG**	-0.075	0.002	-0.0004	0.605	-0.240	-0.001	**0.562**	-0.017	0.024	0.022	0.0001	0.004	0.885**
8	**NOFC**	-0.003	0.001	0.0002	0.111	0.013	0.001	-0.096	**0.101**	-0.012	-0.024	-0.0002	0.010	0.103
9	**TSS**	0.018	0.001	-0.0001	-0.098	0.057	0.002	-0.113	0.010	**-0.121**	-0.007	0.0002	-0.002	-0.252
10	**TA**	0.016	0.0003	0.0001	-0.070	0.050	0.001	-0.109	0.021	-0.008	**-0.114**	0.0004	0.007	-0.205
11	**AA**	0.012	0.00002	-0.0001	-0.008	-0.035	-0.005	0.039	-0.012	-0.010	-0.023	**0.002**	-0.003	-0.042
12	**LC**	-0.001	-0.0005	0.00001	-0.031	0.031	0.003	-0.024	-0.011	-0.003	0.008	0.0001	**-0.096**	-0.121

*, ** significant at 5% and 1% level of significance, respectively. (Residual effect = 0.267)
DTF= Days to 50% flowering, DTP = Days to first picking, PH = Plant height, NOF = Number of fruits per plant, FW = Fruit weight, NOL = Numbers of locules per fruit, FG = Fruit girth, NOFC = Numbers of fruits per cluster, TFY = Total fruit yield per plant (Genotypic correlation with TFY), TSS= Total soluble solids (°Brix), TA = Titrable acidity, AA = Ascorbic acid and LC = Lycopene content

Results and Discussion

Genetic variability within the germplasm is a prerequisite for any meaningful progress in plant breeding efforts. The analysis of variance revealed that the differences among genotypes were statistically significant for all the traits evaluated.

Genotypic and Phenotypic coefficient of variation (GCV and PCV)

The maximum genotypic and phenotypic coefficient of variances were observed for total fruit yield per plant, followed by traits such as number of fruits per plant, lycopene content and titrable acidity (Table 1). Similar findings were also reported by Kumar (2013) and Mohamed *et al.*, (2012).

Heritability and Genetic Advance as percent mean

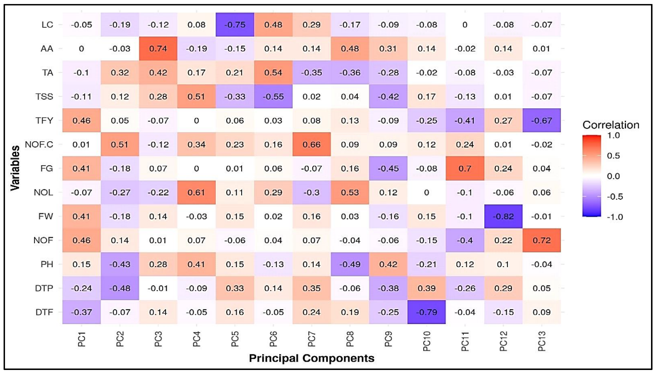
Heritability is a critical parameter in predicting the potential genetic gain achievable through selection. (Burton and De Vane 1953; Johnson *et al.*, 1955). Traits such as total fruit yield, number of fruits per plant, total soluble solids, titratable acidity, lycopene and ascorbic acid showed high heritability with high genetic advance (Table 1). This finding indicates that the traits followed simple inheritance patterns, controlled by major genes or additive effects. This is in conformity with the findings of Hasan *et al.*, (2016), Meitei *et al.*, (2014) and Mohamed *et al.*, (2012).

Correlation analysis (Genotypic and Phenotypic)

Correlation studies reveal the degree and direction of trait relationships with total fruit yield per plant, which helps in identifying elite genotypes from the population. Table 2 represents the genotypic and phenotypic correlation coefficients between total fruit yield per plant and its associated traits. The present study found that the genotypic correlations values were higher than phenotypic correlations value for all the traits which suggesting the minimal environmental influence on the expression of the traits. Number of fruits per plant, fruit weight and fruit girth showed positive and significant association with total fruit yield per plant which is similar to the findings of Meitei *et al.*, (2014), Saleem *et al.*, (2013), Mohamed *et al.*, (2012) and Rani and Anitha (2011).

Genetic divergence

In the present study, forty-five genotypes of tomato were divided into nine clusters using Tocher's approach which is shown in Table 4. The results reported that cluster 1 had the highest number of diversified genotypes (12 genotypes), followed by nine genotypes in cluster 3, seven genotypes in cluster 7 and five genotypes in cluster 2. These observations align with the work of Kumar *et al.*, (2017), Islam *et al.*, (2016) and Ullah *et al.*, (2015). Table 5 provides the estimates of intra- and inter-cluster distances. The table showed that inter-cluster distances were greater than intra-cluster distances which indicates greater genetic divergence among tomato genotypes of different clusters compared to those within the same



Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
LC	-0.05	-0.19	-0.12	0.08	-0.75	0.48	0.29	-0.17	-0.09	-0.08	0	-0.08	-0.07
AA	0	-0.03	0.74	-0.19	-0.15	0.14	0.14	0.48	0.31	0.14	-0.02	0.14	0.01
TA	-0.1	0.32	0.42	0.17	0.21	0.54	-0.35	-0.36	-0.28	-0.02	-0.08	-0.03	-0.07
TSS	-0.11	0.12	0.28	0.51	-0.33	-0.55	0.02	0.04	-0.42	0.17	-0.13	0.01	-0.07
TFY	0.46	0.05	-0.07	0	0.06	0.03	0.08	0.13	-0.09	-0.25	-0.41	0.27	-0.67
NOF.C	0.01	0.51	-0.12	0.34	0.23	0.16	0.66	0.09	0.09	0.12	0.24	0.01	-0.02
FG	0.41	-0.18	0.07	0	0.01	0.06	-0.07	0.16	-0.45	-0.08	0.7	0.24	0.04
NOL	-0.07	-0.27	-0.22	0.61	0.11	0.29	-0.3	0.53	0.12	0	-0.1	-0.06	0.06
FW	0.41	-0.18	0.14	-0.03	0.15	0.02	0.16	0.03	-0.16	0.15	-0.1	-0.82	-0.01
NOF	0.46	0.14	0.01	0.07	-0.06	0.04	0.07	-0.04	-0.06	-0.15	-0.4	0.22	0.72
PH	0.15	-0.43	0.28	0.41	0.15	-0.13	0.14	-0.49	0.42	-0.21	0.12	0.1	-0.04
DTP	-0.24	-0.48	-0.01	-0.09	0.33	0.14	0.35	-0.06	-0.38	0.39	-0.26	0.29	0.05
DTF	-0.37	-0.07	0.14	-0.05	0.16	-0.05	0.24	0.19	-0.25	-0.79	-0.04	-0.15	0.09

Fig. 3: Correlogram of principal component analysis.

Table 4: Cluster distribution of different tomato genotypes that have been assessed for total fruit yield.

Cluster	Number of Genotypes	Name of genotypes
Cluster 1	12	Kashi Adarsh × SKT-06, Kashi Adarsh × Kashi Anupam, SKT-06 × SKT-08, JT- AV-2019-3× Kashi Anupam, ATL-21-01× JT- AV-2019-3, SKT-06× Kashi Anupam, ATL-21-01× JT-AV-2019-1, Kashi Adarsh × ATL-21-01, SKT-07× ATL-21-01, SKT-08× ATL-21-01, SKT-06 × ATL-21-01, Kashi Adarsh × SKT-07
Cluster 2	5	Kashi Adarsh × Kashi Chayan, JT- AV-2019-1× Kashi AnupamSKT-06 × Kashi Amrut, Kashi Adarsh × SKT-08, Kashi Chayan × Kashi Anupam
Cluster 3	9	Kashi Adarsh × Kashi Amrut, Kashi Chayan × Kashi Amrut, SKT-08× JT-AV-2019-1, Kashi Adarsh × JT- AV-2019-3, Kashi Amrut × JT- AV-2019-3, SKT-06 × JT- AV-2019-3, SKT-07× Kashi Anupam, SKT-08× Kashi Anupam, SKT-07× JT- AV-2019-3
Cluster 4	3	Kashi Adarsh × JT-AV-2019-1, Kashi Chayan × JT-AV-2019-1, Kashi Chayan × SKT-07
Cluster 5	3	SKT-06× Kashi Chayan, Kashi Amrut × Kashi Anupam, SKT-06 × SKT-07
Cluster 6	1	SKT-06 × JT-AV-2019-1
Cluster 7	7	Kashi Chayan × SKT-08, SKT-08× JT- AV-2019-3, Kashi Amrut × SKT-08, Kashi Amrut × ATL-21-01, Kashi Amrut × JT-AV-2019-1, Kashi Chayan × JT- AV-2019-3, Kashi Amrut × SKT-07
Cluster 8	4	Kashi Chayan × ATL-21-01, ATL-21-01× Kashi Anupam, JT- AV-2019-3× JT-AV-2019-1, SKT-07× JT-AV-2019-1
Cluster 9	1	SKT-07× SKT-08

cluster. These findings were confirmed by Islam *et al.*, 2016, Evgenidis *et al.*, (2011) and Basavaraj *et al.*, (2010). The maximum inter-cluster D² value was recorded between cluster 9 and 5 (4218.21) and followed by cluster 9 and 1 (3358.07) and the lowest between 6 and 1 (563.98) (Table 5).

In the current research, high mean values by cluster 6 (137.66) and (4.00) for plant height and number of fruits per cluster, respectively. Cluster 2, cluster 5 and cluster 8 had highest mean value for lycopene content (24.10) and titrable acidity (1.37) and days to 50% flowering, respectively. The highest average value for days to first picking (118.50) and number of locules per fruit (3.86) represented by cluster 4 in Table 6. Cluster 9 had maximum mean value for number of fruits per plant (35.07), fruit weight (53.49), fruit girth (14.87), total fruit yield (1.44), total soluble solids (5.00) and ascorbic acid (22.10). Inter-mating the genotypes grouped in these clusters could effectively introduce desirable variability which useful to the strategic enhancement of fruit yield in tomato. The present findings also recorded by Roy and Sharma (1966) and Kumar *et al.*, (2013).

Principal component analysis

Principal Component Analysis (PCA) define as an effective method for summarizing the variability of numerous traits by condensing them into principal components, where the first few components capture the majority of the total variation. As PCA based on a correlation matrix does not rely on the assumption of normal population distribution, it serves as an ideal method for identifying the most significant components (Chaudhary *et al.*, 2015; Sharma *et al.*, 2020). Components exhibiting high eigenvalues and strong factor loadings were interpreted as the most representative of the overall set of traits. Hence, Principal Component Analysis (PCA) was employed in the present study to examine yield and its contributing traits in tomato. Among the thirteen, five main components have more than one eigenvalue.

Table 5: Average intra (bold) and inter cluster (D^2) value for various genotypes of Tomato.

Cluster	1	2	3	4	5	6	7	8	9
1	**306.30**	1064.94	696.56	1128.18	718.80	563.98	1539.48	2583.68	3358.07
2		**666.91**	1120.77	1863.49	1491.88	857.21	1536.06	3378.38	3291.02
3			**359.94**	935.71	1050.77	967.45	642.33	1477.06	1797.83
4				**404.65**	2180.13	937.15	1145.93	970.98	1927.87
5					**682.89**	1616.26	2034.56	3511.57	4218.21
6						**0.00**	1542.42	2609.11	2913.96
7							**527.58**	1096.15	963.43
8								**390.24**	983.47
9									**0.00**

Table 6: Cluster mean for 13 different characters in various genotypes of tomato.

Trait	DTF	DTP	PH	NOF	FW	NOL	FG	NOFC	TFY	TSS	TA	AA	LC
Cluster 1	55.02	111.89	120.06	21.27	45.89	2.67	13.33	3.47	1.05	2.56	1.09	15.75	15.32
Cluster 2	52.86	116.40	133.39	21.11	51.54	3.31	13.60	2.83	0.99	2.69	0.54	15.24	24.10
Cluster 3	53.40	108.80	119.38	22.24	41.76	3.22	12.96	3.86	0.93	3.32	1.09	15.20	21.39
Cluster 4	55.91	118.50	129.89	16.96	45.87	3.86	12.68	3.25	0.93	3.54	0.89	15.15	8.19
Cluster 5	51.67	117.78	129.21	18.89	45.19	3.33	13.41	2.73	0.90	2.44	1.37	18.36	22.90
Cluster 6	47.33	108.00	137.66	24.73	46.75	2.07	13.48	4.00	1.28	2.73	0.62	15.51	10.79
Cluster 7	54.50	110.50	125.48	19.01	40.88	2.97	12.50	3.55	0.87	3.97	0.94	16.21	23.55
Cluster 8	58.08	116.75	134.05	12.65	38.69	3.23	12.21	3.27	0.49	4.62	1.16	14.79	13.37
Cluster 9	51.36	103.00	113.61	35.07	53.49	2.13	14.87	3.00	1.44	5.00	0.94	22.10	19.40

The greatest proportion of total variability was captured by the first five PCs, with PC1 alone explaining 32.18 % of the total variation. This was followed by PC2 (12.08%), PC3 (9.98%), PC4 (9.63%) and PC5 (1.02%) as shown in Table 7. The plant height, number of fruits per plant, fruit weight, fruit girth, number of fruits per cluster, total fruit yield per plant and ascorbic acid showed as the main contributors to the variance depicted in the first principal component. Number of fruits per plant, number of fruits per cluster, total fruit yield, total soluble solids and titrable acidity are the main contributors to variances for the second principal component traits. Whereas, days to 50% flowering, plant height, number of fruits pe plant, fruit weight, fruit girth, total soluble solids, titrable acidity and ascorbic acid had key significant contributors to variances for the third principal component traits. Plant height, number of fruits pe plant, number of locules per fruit, fruit girth, number of fruits per cluster, total fruit yield, total soluble solids, titrable acidity and lycopene content found as the main contributors to the variance depicted in the fourth principal component. While 5th principal component had major significant contributors like days to 50% flowering, days to first picking, plant height, fruit weight, number of locules per fruit, fruit girth, number of fruits per cluster, total fruit yield and titrable acidity (Table 8).

Table 7: Eigenvalues and percent variance explained in various PCs for thirteen traits of tomato.

Component	Total	% Variance	% Cumulative
1	2.046	32.185	32.185
2	1.254	12.089	44.274
3	1.139	9.983	54.257
4	1.120	9.629	63.886
5	1.027	8.12	72.006
6	0.971	7.257	79.263
7	0.843	5.463	84.726
8	0.778	4.656	89.381
9	0.694	3.703	93.085
10	0.658	3.328	96.413
11	0.475	1.734	98.147
12	0.450	1.56	99.707
13	0.195	0.293	100

The scree plot represents the cumulative proportion of total variation accounted for by successive principal components, based on their respective eigenvalues. Figure 1 clearly depicts a substantial difference in variation between component 1 and 2, in which component 1 showed significantly higher proportion of total variability as indicated in Table 7. The results estimated that the importance of specific traits associated with each PC in distinguishing among tomato genotypes. Principal Component Analysis (PCA) plays a vital role in handling large datasets by identifying key traits contributing to variability while discarding repetitive or overlapping ones. This not only simplifies the selection process but also minimizes manual effort and increases the reliability of genotype selection.

Conclusion

The present study confirms the existence of considerable genetic diversity and trait variability among genotypes which indicates the strong potential for selection-based improvement in tomato. High heritability estimates combined with high genetic advance were estimated for total fruit yield, number of fruits per plant, total soluble solids, titratable acidity, lycopene and ascorbic acid suggests that the inheritance of these traits is predominantly controlled by additive gene action, and therefore, direct selection could prove more efficient in achieving the desired genetic improvement.

Correlation between total fruit yield per plant and number of fruits per plant, fruit weight and fruit girth were estimated as positive and significant which indicates that direct selection for these traits could effectively contribute to advancement in yield performance in tomato.

Path coefficient analysis revealed that certain traits like number of fruits per plant followed by fruit girth, days to 50% flowering and number of fruits per cluster resulted highest direct positive effect towards the fruit yield per plant and each trait should be carefully

Table 8: The compound matrix computed in the PCs of tomato genotypes.

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
DTF	-0.369	-0.071	0.138	-0.050	0.157	-0.051	0.241	0.189	-0.246	-0.789	-0.036	-0.154	0.091
DTP	-0.237	-0.482	-0.007	-0.085	0.334	0.136	0.350	-0.057	-0.380	0.388	-0.256	0.293	0.054
PH	0.147	-0.427	0.281	0.412	0.154	-0.126	0.139	-0.489	0.424	-0.206	0.123	0.104	-0.042
NOF	0.458	0.135	0.006	0.066	-0.061	0.042	0.067	-0.036	-0.062	-0.155	-0.397	0.220	0.723
FW	0.414	-0.185	0.143	-0.030	0.148	0.017	0.160	0.035	-0.158	0.147	-0.097	-0.817	-0.014
NOL	-0.069	-0.270	-0.221	0.608	0.106	0.292	-0.304	0.532	0.121	0.001	-0.097	-0.059	0.063
FG	0.408	-0.180	0.070	0.002	0.015	0.064	-0.073	0.161	-0.447	-0.083	0.702	0.244	0.042
NOFC	0.008	0.514	-0.117	0.343	0.234	0.162	0.660	0.088	0.095	0.122	0.238	0.010	-0.016
TFY	0.456	0.052	-0.068	0.001	0.061	0.032	0.082	0.128	-0.089	-0.248	-0.411	0.273	-0.666
TSS	-0.112	0.116	0.279	0.507	-0.329	-0.552	0.017	0.039	-0.417	0.170	-0.129	0.009	-0.068
TA	-0.102	0.322	0.422	0.174	0.209	0.537	-0.354	-0.356	-0.285	-0.015	-0.077	-0.030	-0.075
AA	0.004	-0.030	0.735	-0.186	-0.154	0.143	0.143	0.477	0.305	0.139	-0.023	0.136	0.005
LC	-0.050	-0.195	-0.115	0.081	-0.754	0.480	0.292	-0.173	-0.088	-0.084	-0.003	-0.078	-0.068

considered while selecting superior genotypes.

Utilization of cluster analysis aids in strategic parent selection and in identifying the most promising crosses to generate improved genotypes for targeted traits. Intercrossing the genetically distant genotypes from clusters 5, 8 and 9 can help create extensive genetic variation and facilitate the selection of transgressive segregants with enhanced fruit production in tomato. Intercrossing genotypes from these clusters would be advantageous for enhancing diversity in the associated traits and systematically improving fruit yield in tomato.

PCA enables the identification and evaluation of genetic variability within a given set of genotypes. Since no single method is perfect for analysing and classifying genetic data, a comparison of all methods was done to select the best-performing genotypes according to their important quantitative traits like plant height, number of fruits per plant, fruit weight, fruit girth, number of fruits per cluster and total fruit yield per plant.

Acknowledgment

The Authors extend their profound appreciation to Centre for Vegetable Research, Department of Genetics and Plant Breeding, C.P.C.A., S.D.A.U., Sardarkrushinagar and Director of Research & Dean PG studies for providing research materials, vital laboratory facilities and technical support during this research program.

References

Allard, R.W. (1960). In Principles of Plant Breeding. John Wiley and Sons, Inc. New York, 485.

Basavaraj, S., Patil B.C., Salimath P.M., Hosamani R.M. and Krishnaraj P.U. (2010). Genetic divergence in tomato (*Solanum Lycopersicon* L.). *Karnataka J. Agric. Sci*.,, **23(3)**, 538-539.

Benton, J., Jr. (2007). Tomato plant culture: In the field, greenhouse, and home garden. CRC Press, London. 1-420

Burton, G.W. and De Vane D.E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material.

Chaudhary, S., Sagar P., Hooda B.K. and Arya R.K. (2015). Multivariate analysis of pearl millet data to delineate genetic variation. *Forage Res*. **40**, 201-208.

Dewey, D.R., Lu K. (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy journal*. **51(9)**, 515-518.

Evgenidis, G., Traka-Mavrona E. and Koutsika-Sotiriou M. (2011) Principal component and clusters analysis as a tool in the assessment of tomato hybrids and cultivars. *Internat. J. Agron*. 1-7.

Hasan, M.M., Bari M.A. and Hossain M.A. (2016). Genetic variability and traits association analysis of tomato (*Lycopersicon esculentum* L.) genotypes for yield and quality attributes. *Universal Journal of Plant Science*. **4(3)**, 23-34.

Islam, S., Hossain M.K., Hasan R., Bashar A., Huque AKM M. and Alam N. (2016). Quantification of Genetic Diversity Analysis for the Improvement of Cultivated Tomato Genotypes. *Bangladesh J. Bot*. **45(3)**, 485-491.

Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soyabean. *Agronomy Journal*. **47**, 314-318.

Kumar, D., Kumar R., Kumar S., Bhardwaj M.L., Thakur M.C., Kumar R., Thakur K.S., Dogra B.S., Vikram A., Thakur A. and Kumar P. (2013). Genetic variability, correlation and path coefficient analysis in tomato. *International Journal of Vegetable Science*. **19(4)**, 313-323.

Kumar, M., Buckseth T., Thakur M.S. and Thakur K.S. (2013). Genetic divergence and cluster analysis in tomato (*Solanum lycopersicum*). *Progr. Agric*. **13(1)**, 114-117, 2013.

Kumar, N., Bhardwaj M.L., Sharma A. and Kumar N. (2017). Assessment of Genetic Divergence in Tomato (*Solanum lycopersicum* L.) through Clustering and Principal

Component Analysis under Mid Hills Conditions of Himachal Pradesh, India. *Int. J. Curr. Microbiol. App. Sci.* **6(5)**, 1811-1819.

Kumar, R., Ram C.N., Yadav G.C., Deo C., Vimal S.C. and Bhartiya H.D. (2014). *Plant Archives*. **14(1)**, 443-447.

Meena, O.P. and Bahadur V. (2015). Genetic Associations analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicum* L.) germplasm under open field condition. *Journal of Agricultural Science*. **7(1)**, 18-27.

Meena, R.K., Kumar S., Meena M.L. and Kumar A. (2018). Correlation and Characters association studies in tomato (*Solanum lycopersicum* L.). *International Journal of Pure & Applied Bioscience*. **6(1)**, 1291-1295.

Meitei K.M., Bora G., Singh S.J. and Sinha A.K. (2014). Morphology based genetic variability analysis and identification of important characters for tomato (*Solanum lycopersicum* L.) crop improvement. *American-Eurasian Journal of Agricultural and Environmental Sciences*. **14(10)**, 1105-1111.

Mohamed, S.M., Ali E.E. and Mohamed T.Y. (2012). Study of heritability and genetic variability among different plant and fruit characters of tomato (*Solanum lycopersicon* L.). *International journal of scientific & technology research*. **1(2)**, 55-58.

Mahalonobis, P.C. (1936). On the generalized distance in statistics. In: *Proceedings of the National Academy of Sciences* (India). **12**, 49-55.

Panse and Sukhatme (1978). Statistical method for Agricultural workers. Indian council of Agricultural Research, New Delhi. 381.

Rao, C.R. (1952). Advance Statistical Method in biometrical Research, John Wiley and sons publishers, New York. 224-252.

Rai, A.K., Vikram A. and Pandav A. (2016). Genetic variability studies in tomato (*Solanum lycopersicum* L.) for yield and quality traits. International Journal of Agriculture, Environment and Biotechnology. **9(5)**, 739-744.

Rani, K.R. and Anitha V. (2011). Studies on variability, heritability and genetic advance in tomato (*Lycopersicon esculentum* Miil.). *Intl. J. Bioresour Stress Manag*. **2(4)**, 382-385.

Ranieri, A., Giuntini D., Lercari B. and Soldatini G.F. (2004). Light influence on antioxidant properties of tomato fruits. *Progress in Nutrition*. **6**, 44-49.

Rick, C.M. (1949). Rate of natural cross pollination of tomatoes in various localities in California as measured by the fruits and seed set on male sterile plants. *Proceedings American Society for Horticultural Science*. **54**, 237-252.

Roy, A. and Sharma R.N. (1996). Multivariate analysis in chilli (*Capsicum annum* L.). *Ann. Agric. Res*. **17(1)**, 30-32.

Sainju, U.M. and Dris R. (2006). Sustainable production of tomato. In: R. Dris (ed.), Crops: Quality, growth, and biotechnology. WFL Publisher, Helsinki, Finland. 190-216.

Saleem, M.Y., Iqbal Q. and Asghar M. (2013). Genetic variability, heritability, character association and path analysis in F1 hybrids of tomato. *Pak J Agric Sci*. **50(4)**, 649-653.

Sharma, B., Chugh L., Singh V.K., Shekhar C. and Tanwar N. (2020). Characterization of rancidity indicators in selected pearl millet genotypes by multivariate analysis. *Plant Arch*. **20**, 229-235.

Ullah, M.Z., Hassan L., Singha T. and A.K. (2015). Patwary. Genetic divergence in tomato lines (*Solanum lycopersicum* L.). *J. Bangladesh Agril. Univ*. **13(1)**, 61-64.

Zannat, A., Hussain M.A., Abdullah A.H.M., Hossain M.I., Saifullah M., Safhi F.A. and Hossain M.S. (2023). Exploring genotypic variability and interrelationships among growth, yield, and quality characteristics in diverse tomato genotypes. *Heliyon*. **9(8)**.