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Assessment of physico-biochemical parameters of tomato (*Solanum lycopersicum* L.) genotypes using multivariate analysis

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ABSTRACT

The present study was conducted to assess the physico-biochemical variability in seventeen genotypes, including the check variety SolanLalima, using a Randomized Complete Block Design with three replications. The aim was to estimate variability, heritability, genetic advance, correlation, and path coefficient analysis for yield and other horticultural traits. The estimates of phenotypic and genotypic coefficients of variation (PCV and GCV) were high for titratable acidity (31.96% and 31.08%). High heritability and genetic gain were observed for titratable acidity (94.53% and 62.24%) and 100 seed weight (93.71% and 51.06%). Correlation studies at genotypic and phenotypic levels revealed significant positive correlations between fruit yield per plot and traits such as the number of clusters per plant, number of fruits per cluster, average fruit weight, fruit width, fruit length, pericarp thickness, number of seeds per fruit, 100 seed weight, harvest duration, plant height, total soluble solids, and ascorbic acid. Path coefficient analysis indicated that the number of clusters per plant (1.028) had the maximum positive direct effect on fruit yield per plot, followed by 100 seed weight (0.719), number of fruits per plant (0.741), average fruit weight (0.468), total soluble solids (0.416), fruit width (0.275), pericarp thickness (0.252), days to 50% flowering (0.227), number of locules per fruit (0.083), and harvest duration (0.013). Principal Component Analysis showed that the first four principal components captured most of the dataset variance, emphasizing traits like average fruit weight, fruit dimensions, plant height, and days to first flowering. This dimensionality reduction simplifies data analysis and highlights critical patterns, providing valuable insights for future crop improvement.

Keywords: *Correlation,Genetic gain, Heritability, Multivariate and Path analysis*

Introduction

Tomato (*Solanum lycopersicum*L.) is a solanaceous crop having a diploid chromosome number, 2n=24. It is one of the most widely grown, versatile and popular vegetable in the world and is originated in the Peru-Ecuador-Bolivia region of the Andes. The wild ancestor of tomato *Solanum lycopersicum* var. *cerasiforme*is still found in the Andean region and has small and yellow fruit. It is an annual to perennial and day-neutral herbaceous plant. The growth habit of the tomato plant is determinate, semi-determinate and indeterminate. The indeterminate type of plants terminates in a vegetative bud whereas in the determinate type of plants the main axis terminates in a flower bud. It is a warm-season crop which can tolerate heat and drought but cannot tolerate frost as well as waterlogged conditions.The ideal temperature for tomato cultivation is 20-24°C. The red color of tomato fruit is due to lycopene pigment and for lycopene production, the optimum temperature range is 21-24 °C. But if the temperature goes above 27°C then the production of lycopene pigment drops off rapidly [17]. The edible part of the plant is fruit and the shape of fruit is globular or ovoid. It can be bilocular or multilocular with numerous seeds present in the locular cavity. It is mainly a self-pollinated crop but some extent of cross-pollination also occurs [18]. Practically, it is grown in every country of world in greenhouses, open fields and net houses. Tomato is considered as “poor man's orange” in many countries due to its improved nutritional values. It has high yielding, wider adaptability and multipurpose uses in both fresh as well as processed form.

Tomato is at second position after potato in world vegetable production. India is the second largest producer of tomato in world and occupies an area of 852 thousand hectares with an annual production of 21,003 thousand metric tonnes[3]. In India, major tomato-growing states are Madhya Pradesh, Andhra Pradesh, Karnataka, Tamil Nadu, Orissa, Gujarat, West Bengal and Chhattisgarh. Tomato is a major cash-generating crop for farmers having low income and also provides opportunities of employment in the production and processed industry. In Himachal Pradesh, it is grown on an area of 13,714.8 hectares with an annual production of 4,74,338 metric tonnes[2]. It is widely grown as an off-season vegetable crop in the hilly regions of Himachal Pradesh [18]. The crop is becoming popular day by day among farmers due to its short duration, high market value and constant demand throughout the year on account of its popularity.

The present study was conducted to improve productivity per unit area and using tomato in future breeding programs, it is crucial to identify superior genotypes among the available germplasm.

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The existence of genetic variability and knowledge of the genotypic and phenotypic connection of yield and yield-attributing components are pre-requisite for the implementation of an effective improvement programme. The measure of genetic diversity is the tendency for genotypes within a population to differ from one another, the available germplasm into separate clusters or groups on the basis of genetic diversity among their morphological attributes using agglomerative hierarchical clustering and principal component analysis. Having performed analysis, the desirable groups of genotypes could be crossed with confidence to develop either open pollinated or hybrid varieties on commercial scale.

Materials and methods

In the present study 17 lines of tomato (table1)were grown in randomized block design with three replications during the summer season, 2022 at Experimental Research Farm, Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur (H.P). Each genotype/line was sown in 2 rows of 1.5 m long spaced at 90 cm apart. There were 4 plants per row and were spaced at 30 cm apart. In this way, there were 8 plants per plot. All the recommended packages of practice were adopted for raising healthy crops. Observations were recorded from 5 randomly selected plants for plant height (cm), and dry.

Statistical analysis

Genotypic coefficient of variation (GCV), phenotypic coefficient variation (PCV) was and Heritability in the broad sense (h^2) and expected genetic advance (GA) were worked out according to Johnson *et al.* [9]A phenotypic and genotypic correlation was worked out as per Al-Jibouri*et al.* [1]. Mahalanobis [12].Furthermore, Principal ComponentsAnalysis (PCA) and the hierarchical cluster analysis by ,were applied. These analyses were carried out usingSAS Version 10.0 software.All experiments were evaluated in triplicate.

Results and Discussion

The estimates for various genetic parameters, including GCV, PCV, heritability, and genetic advance for multiple traits, are presented in table 2 and figure1. The highest values of GCV and PCV (>30%) were observed for titratable acidity (31.08% and 31.96%), while the lowest values (<15%) were recorded for fruit yield per plot (GCV 14.33%), total soluble solids (13.73% and 14.59%), fruit length (11.49% and 11.94%), days to 50% flowering (11.12% and 11.37%), fruit width (10.98% and 11.25%), number of fruits per plant (8.79% and 9.36%), and days to first picking (6.40% and 7.11%). Moderate GCV and PCV values were noted for 100 seed weight (25.60% and 26.45%), number of seeds per fruit (21.54% and 22.07%), number of fruits per cluster (19.90% and 20.10%), harvest duration (19.60% and 20.70%), pericarp thickness (19.52% and 21.69%), number of clusters per plant (18.73% and 19.00%), average fruit weight (17.76% and 17.91%), number of locules per fruit (17.72% and 18.13%), ascorbic acid content (15.74% and 16.09%), and plant height (15.18% and 17.32%). High heritability, coupled with high genetic advance as a percentage of the mean, was observed for titratable acidity (94.53% and 62.24%) and 100 seed weight (93.71% and 51.06%), indicating that heritability for these traits is primarily due to additive gene effects. Consequently, phenotypic selection for these traits is likely to lead to significant improvement. These results align with the findings of Mazzucato et al. [13] and Zhou et al. [20].

Heritability

High heritability combined with moderate genetic advance (table 2 and Figure 2) was observed for traits such as the number of clusters per plant (97.22% and 38.04%), number of fruits per cluster (98.02% and 40.59%), average fruit weight (98.43% and 36.31%), number of locules per fruit (95.54% and 35.68%), pericarp thickness (81.00% and 36.20%), number of seeds per fruit (95.19% and 43.28%), harvest duration (89.69% and 38.24%), total soluble solids (88.52% and 26.60%), ascorbic acid content (95.66% and 31.71%), and fruit yield per plot (85.67% and 27.31%), indicating both additive and non-additive gene effects. Traits such as days to 50% flowering (95.73% and 22.42%), days to first picking (81.01% and 11.86%), number of fruits per plant (88.27% and 17.02%), fruit width (95.29% and 22.08%), and fruit length (92.60% and 22.77%) exhibited high heritability with low genetic advance, suggesting non-additive gene action and limited improvement through selection. Additionally, moderate heritability and genetic advance were noted for plant height (76.84% and 27.41%). These results align with the findings of Rai et al[15], and Kumar et al [10].

Genotypic and phenotypic correlation

The genotypic and phenotypic correlation analysis (figure 3) revealed that fruit yield per plot had positive and significant correlations with several traits: number of clusters per plant (0.64 and 0.59), number of fruits per cluster (0.72 and 0.66), average fruit weight (0.82 and 0.76), fruit width (0.73 and 0.63), fruit length (0.61 and 0.54), pericarp thickness (0.58 and 0.46), number of seeds per fruit (0.48 and 0.43), 100-seed weight (0.70 and 0.66), harvest duration (0.88 and 0.75), plant height (0.85 and 0.70), total soluble solids (0.63 and 0.57), and ascorbic acid (0.38 and 0.33). Conversely, negative and significant correlations with fruit yield per plot were observed for days to 50% flowering (-0.71 and -0.64), days to first picking (-0.73 and -0.65), number of fruits per plant (-0.57 and -0.44), and number of locules per fruit (-0.39 and -0.36). These findings highlight key traits influencing tomato yield, providing a basis for targeted selection in breeding programs aimed at yield improvement. The identified positive and negative correlations offer insights for effective trait selection, corroborating the results of previous studies by Das et al. [5] and Kousar et al. [11].

Path coefficient analysis

Path coefficient analysis at the genotypic level (Table 3) indicated that positive direct effects on fruit yield per plot were exhibited by several traits: number of clusters per plant (1.028), 100-seed weight (0.719), number of fruits per plant (0.741), average fruit weight (0.468), total soluble solids (0.416), fruit width (0.275), pericarp thickness (0.252), days to 50% flowering (0.227), number of locules per fruit (0.083), and harvest duration (0.013). Conversely, negative direct effects were observed for traits such as fruit length (-0.773), days to first picking (-0.753), number of fruits per cluster (-0.404), ascorbic acid (-0.364), number of seeds per fruit (-0.347), titratable acidity (-0.296), and plant height (-0.190). These findings are consistent with previous studies by Golani et al. [6], Sharma and Singh [16], and Namdev and Dongre[14]. The study identifies key traits with positive and negative impacts on tomato yield, providing a basis for targeted selection in breeding programs to enhance yield. The correlation and path analysis results align with established research, reinforcing the validity of these findings.

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Cluster analysis

The dendrogram formed through cluster analysis based on 18 agro-morphological traits divided the 17 genotypes were divided into eight main clusters (I to VIII) (Figure 4). Each cluster was further divided into specific sub-clusters. Cluster I consisted of 4 genotypes and was further divided into two sub-clusters: IA and IB. Sub-cluster IA consisted of two genotypes (8 and 9), while sub-cluster IB included two genotypes (12 and 17). Cluster II comprised 3 genotypes and was divided into sub-clusters IIA and IIB. Sub-cluster IIA consisted of two genotypes (11 and 14), while sub-cluster IIB included one genotype (5). Cluster III consisted of 3 genotypes and was divided into sub-clusters IIIA and IIIB, with two genotypes (1 and 16) in sub-cluster IIIA and one genotype (3) in sub-cluster IIIB. Cluster IV included 2 genotypes (13 and 15) and was not further divided into sub-clusters. Cluster V had a single genotype (2), as did Cluster VII (7) and Cluster VIII (4). Cluster VI consisted of 2 genotypes (6 and 10) and was not further divided. This hierarchical clustering reveals the genetic relationships and groupings among the 17 genotypes, providing insights into their similarities and differences. The findings of the cluster analysis through agromorphological traits of tomato are in agreement with the results of Henareh et al.[7].

Principal Component Analysis (PCA)

The Principal Component Analysis (PCA) of our dataset reveals that the first four principal components (PCs) capture the majority of the variance, with eigenvalues and corresponding percentages of explained variance as follows: PC1 (10.05, 55.83%), PC2 (2.20, 12.22%), PC3 (1.76, 9.76%), and PC4 (1.01, 5.60%). Together, these components account for 83.41% of the total variance, indicating that they effectively summarize the dataset's variability. Subsequent components contribute progressively less, with PC5 to PC8 explaining between 4.27% and 2.04% each, and the remaining components (PC9 to PC16) each contributing less than 1.5% (Table 4 and figure 5). This significant drop in variance explained by higher-order components suggests that retaining the first four PCs is sufficient for capturing the essential information in the dataset, enabling effective dimensionality reduction while preserving critical data patterns.

The Principal Component Analysis (PCA) conducted on our dataset elucidates the underlying structure by revealing key variables that contribute most to the observed variance (Table). The first principal component (PC1), explaining 55.83% of the total variance, is strongly associated with variables such as average weight (0.30), fruit width (0.30), fruit length (0.28), 100 seed weight (0.27), and plant height (0.26). The second principal component (PC2), accounting for 12.22% of the variance, is characterized by high loadings on days to first flowering (0.37), total soluble solids (TSS) (0.37), ascorbic acid (0.36), and cluster per plant (0.18). PC3, which explains 9.76% of the variance, is primarily influenced by fruits per cluster (0.62) and locules per fruit (-0.46). Lastly, PC4, capturing 5.60% of the variance, shows significant contributions from seeds per fruit (0.54), cluster per plant (0.39), and average weight (0.22). These results highlight that PC1 and PC2 capture the bulk of the variability in our dataset, emphasizing fruit characteristics and plant growth parameters as critical factors.

which are in agreement with the findings of Bhattarai et al. [4],Hu et al. [8,]Mazzucato et al. [13] and Zou et al. [20] who characterized tomato genotypes in different regions round the globe, using molecular and phenotypic traits.

Consequently, retaining the first four principal components is sufficient for effectively summarizing the dataset's variability, thereby facilitating dimensionality reduction and enhancing the interpretability of the data. Further analysis of these components can offer deeper insights into the complex relationships among the variables.

Conclusion

The study revealed significant genotypic and phenotypic variations among tomato genotypes. High heritability and genetic gain in traits like titratable acidity and 100-seed weight suggest strong additive gene action, enabling efficient selection. Positive correlations with fruit yield were found for traits such as clusters per plant, fruits per cluster, average fruit weight, fruit dimensions, pericarp thickness, seeds per fruit, 100-seed weight, harvest duration, plant height, total soluble solids, and ascorbic acid. Path coefficient analysis identified positive direct effects on yield through several key traits, confirming their importance for targeted selection. Principal Component Analysis showed that the first four principal components captured most of the dataset variance, emphasizing traits like average fruit weight, fruit dimensions, plant height, and days to first flowering. This dimensionality reduction simplifies data analysis and highlights critical patterns.

Furute scope: The study provides valuable insights for future crop improvement and agricultural practices. Hence, direct selection for these traits would be more effective for improvement of yield in tomatoes.

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Conflict of interesrest: The authors declare that there is no conflict of interest pertaining to
this study.

Figure 1: Graphical presentation of Genotypic and Phenotypic coefficients of different genotypes

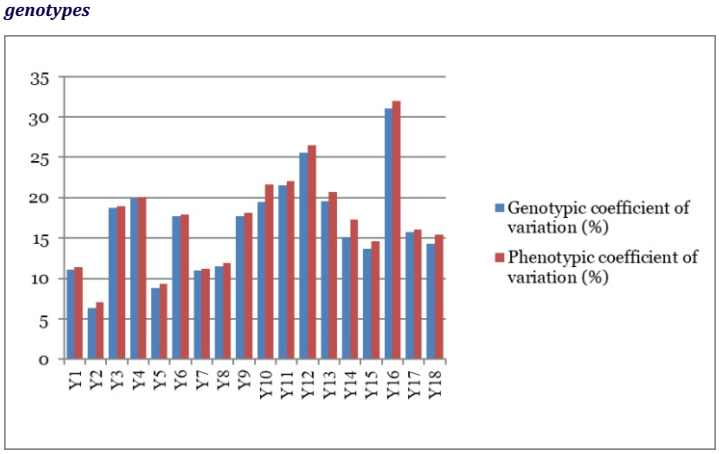

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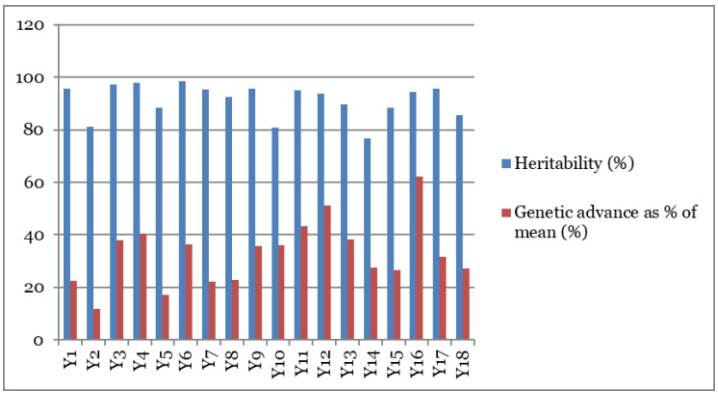
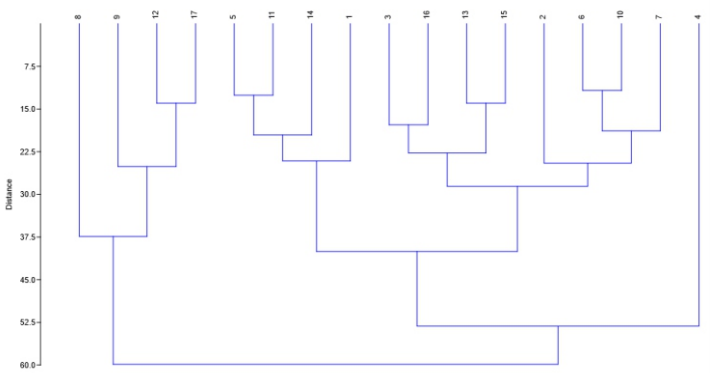
Figure 2: Graphical presentation of heritability (%) and genetic advance as % of different genotypes



***Where**, Y1= Days to 50% flowering (days), Y2= Days to first picking,Y3= Number of clusters per plant , Y4= Number of fruits per cluster, Y5= Number of fruits per plant, Y6= Average fruit weight(g), Y7= Fruit Width (cm), Y8= Fruit length(cm), Y9= Number of locules per fruit, Y10= Pericarp thickness (mm), Y11= Number of seeds per fruit, Y12= 100 seed weight (g),Y13= Harvest duration, Y14= Plant height(cm), Y15= TSS(°Brix), Y16= Titratable acidity(%), Y17= Ascorbic acid(mg/100g) and GCCTYP= Genotypic correlation coefficient with fruit yield per plot.*

Figure 3: Genotypic and phenotypic coefficients of correlation among different horticultural traits in tomato

Figure 4: Dendrogram showing the genetic diversity within 17 tomato accessions through agro-morphological traits

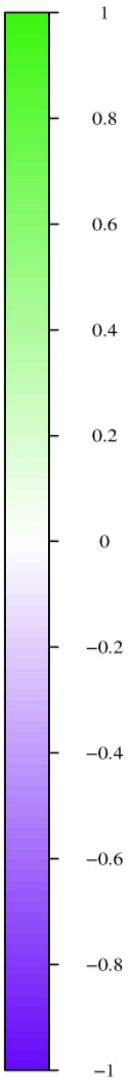


***Where**, Y1= Days to 50% flowering (days), Y2= Days to first picking,Y3= Number of clusters per plant , Y4= Number of fruits per cluster, Y5= Number of fruits per plant, Y6= Average fruit weight(g), Y7= Fruit Width (cm), Y8= Fruit length(cm), Y9= Number of locules per fruit, Y10= Pericarp thickness (mm), Y11= Number of seeds per fruit, Y12= 100 seed weight (g),Y13= Harvest duration, Y14= Plant height(cm), Y15= TSS(°Brix), Y16= Titratable acidity(%), Y17= Ascorbic acid(mg/100g) and GCCTYP= Genotypic correlation coefficient with fruit yield per plot.*

Residual effect = 0.04234

Diagonal figures represent the direct effect

	DFF	DIF	NCPP	NFPC	NFPP	AFW	FW	FL	locules	PT	NSPF	TSW	HD	PH	Tss	TA	AA	yield
DFF	1	0.91	−0.27	−0.08	0.57	−0.75	−0.74	−0.67	0.42	−0.6	−0.21	−0.83	−0.66	−0.66	−0.29	−0.19	−0.22	−0.7
DIF	0.91	1	−0.28	0.05	0.46	−0.75	−0.77	−0.62	0.34	−0.55	−0.48	−0.78	−0.62	−0.57	−0.34	−0.12	−0.32	−0.73
NCPP	−0.27	−0.28	1	0.17	−0.73	0.73	0.63	0.57	−0.43	0.41	0.48	0.37	0.6	0.51	0.68	−0.27	0.36	0.62
NFPC	−0.08	0.05	0.17	1	−0.21	0.13	0.15	0.25	−0.45	0.42	−0.03	−0.06	0.13	0.03	0.21	−0.09	−0.19	0.05
NFPP	0.57	0.46	−0.73	−0.21	1	−0.77	−0.81	−0.68	0.55	−0.62	−0.38	−0.62	−0.62	−0.54	−0.7	0.18	−0.32	−0.57
AFW	−0.75	−0.75	0.73	0.13	−0.77	1	0.9	0.84	−0.52	0.68	0.58	0.8	0.8	0.71	0.63	−0.09	0.47	0.83
FW	−0.74	−0.77	0.63	0.15	−0.81	0.9	1	0.85	−0.55	0.73	0.58	0.81	0.76	0.67	0.72	−0.24	0.54	0.74
FL	−0.67	−0.62	0.57	0.25	−0.68	0.84	0.85	1	−0.44	0.67	0.4	0.79	0.82	0.67	0.63	−0.19	0.52	0.67
locules	0.42	0.34	−0.43	−0.45	0.55	−0.52	−0.55	−0.44	1	−0.86	−0.06	−0.42	−0.37	−0.46	−0.41	0.03	−0.21	−0.39
PT	−0.6	−0.55	0.41	0.42	−0.62	0.68	0.73	0.67	−0.86	1	0.24	0.64	0.59	0.56	0.56	−0.12	0.33	0.61
NSPF	−0.21	−0.48	0.48	−0.03	−0.38	0.58	0.58	0.4	−0.06	0.24	1	0.35	0.4	0.19	0.57	−0.34	0.52	0.52
TSW	−0.83	−0.78	0.37	−0.06	−0.62	0.8	0.81	0.79	−0.42	0.64	0.35	1	0.86	0.75	0.46	−0.05	0.5	0.72
HD	−0.66	−0.62	0.6	0.13	−0.62	0.8	0.76	0.82	−0.37	0.59	0.4	0.86	1	0.81	0.67	−0.29	0.47	0.86
PH	−0.66	−0.57	0.51	0.03	−0.54	0.71	0.67	0.67	−0.46	0.56	0.19	0.75	0.81	1	0.65	−0.38	0.49	0.79
Tss	−0.29	−0.34	0.68	0.21	−0.7	0.63	0.72	0.63	−0.41	0.56	0.57	0.46	0.67	0.65	1	−0.75	0.62	0.68
TA	−0.19	−0.12	−0.27	−0.09	0.18	−0.09	−0.24	−0.19	0.03	−0.12	−0.34	−0.05	−0.29	−0.38	−0.75	1	−0.65	−0.28
AA	−0.22	−0.32	0.36	−0.19	−0.32	0.47	0.54	0.52	−0.21	0.33	0.52	0.5	0.47	0.49	0.62	−0.65	1	0.44
yield	−0.7	−0.73	0.62	0.05	−0.57	0.83	0.74	0.67	−0.39	0.61	0.52	0.72	0.86	0.79	0.68	−0.28	0.44	1



***Where**, DFF= Days to 50% flowering (days), DIF= Days to first picking, NCPP= Number of clusters per plant , NFPC= Number of fruits per cluster, NFPP= Number of fruits per plant, AFW= Average fruit weight(g), FW= Fruit Width (cm), FL= Fruit length(cm), locules= Number of locules per fruit, PT= Pericarp thickness (mm), NSPF= Number of seeds per fruit, TSW= 100 seed weight (g),HD= Harvest duration, PH= Plant height(cm), Tss= TSS(°Brix), TA= Titratable acidity(%), AA= Ascorbic acid(mg/100g) and FYPP= Fruit yield per plot.*

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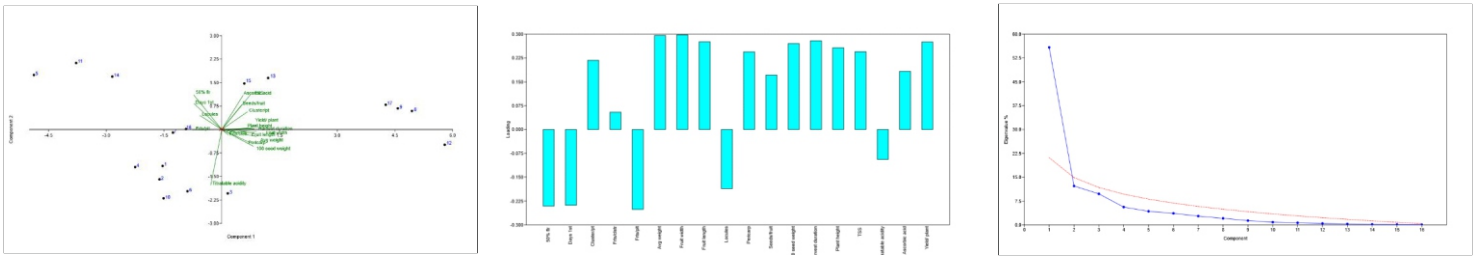

Figure.5 *PCA of the tomato genotypes for different traits illustrated by* ***(a)*** *factor loadings* ***(b)*** *scatter with bi-plot* ***(c)*** *scree plot. viz. days to 50% flowering, days to first picking, number of clusters per plant , number of fruits per cluster, number of fruits per plant, average fruit weight(g), fruit width (cm), fruit length(cm), number of locules per fruit, pericarp thickness (mm), number of seeds per fruit, 100 seed weight (g), harvest duration, plant height(cm), tss(°brix), titratable acidity(%),ascorbic acid* ***(****mg/100g****)*** *and fruit yield per plot.*

Table 1. List of tomato genotypes studied along with their sources

Genotypes	Source
EC-635529, EC-687604, EC-631415, EC-631438, EC-635526, EC-692336	NBPGR, New Delhi
TOM-COHF-NERI-1, TOM-COHF-NERI-2, TOM-COHF-NERI-3, TOM-COHF-NERI-4, TOM-COHF-NERI-5, TOM-COHF-NERI-6, TOM-COHF-NERI-7 TOM-COHF-NERI-8, TOM-COHF-NERI-9 , TOM-COHF-NERI-10	Department of Vegetable Science, COH&F, Neri, Hamirpur Dr. Y.S Parmar University of HorticultureandForestry,Nauni,Solan(H.P)
Solan Lalima	Dr. Y.S Parmar University of HorticultureandForestry,Nauni,Solan(H.P)

Table2: Estimates of different genetic parameters for various traits in tomato (Solanum lycopersicum L.)

Characters	Mean	Range		Coefficient of variation (%)		Heritability (%)	Genetic gain (%)
		Minimum	Maximum	Genotypic	Phenotypic		
Days to 50% flowering (days)	37.18	31.33	46.67	11.12	11.37	95.73	22.42
Days to first picking (days)	74.94	66.33	82.33	6.40	7.11	81.01	11.86
Number of clusters per plant	11.21	7.27	14.65	18.73	19.00	97.22	38.04
Number of fruits per cluster	3.50	2.32	4.93	19.90	20.10	98.02	40.59
Number of fruits per plant	20.49	17.89	24.71	8.79	9.36	88.27	17.02
Average fruit weight (g)	47.00	36.17	65.11	17.76	17.91	98.43	36.31
Fruit width (mm)	50.79	42.19	60.81	10.98	11.25	95.29	22.08
Fruit length (mm)	51.14	40.31	61.11	11.49	11.94	92.60	22.77
Number of locules	3.56	2.53	4.47	17.72	18.13	95.54	35.68
Pericarp thickness (mm)	4.17	3.1	5.57	19.52	21.69	81.00	36.20
Number of seeds per fruit	101.98	70.99	138.12	21.54	22.07	95.19	43.28
100 seed weight (g)	0.27	0.14	0.39	25.60	26.45	93.71	51.06
Harvest duration (days)	31.17	22.37	40.07	19.60	20.70	89.69	38.24
Plant height (cm)	96.71	69.50	122.10	15.18	17.32	76.84	27.41
TSS (°Brix)	3.80	3.11	4.70	13.73	14.59	88.52	26.60
Titratable Acidity (%)	0.37	0.23	0.59	31.08	31.96	94.53	62.24
Ascorbic Acid (mg/100g)	30.73	22.14	38.14	15.74	16.09	95.66	31.71
Fruit yield per plot (Kg)	7.11	5.42	9.01	14.33	15.48	85.67	27.31

Table 3: Genotypic path coefficient analysis for direct and indirect effects of component characters on yield per plot in tomato

	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	Y14	Y15	Y16	Y17	GCCFYPP
Y1	**0.227**	-0.717	-0.280	0.171	0.432	-0.354	-0.193	0.525	0.036	-0.156	0.073	-0.607	-0.009	0.133	-0.127	0.053	0.083	-0.712**
Y2	0.216	**-0.753**	-0.289	0.208	0.362	-0.368	-0.201	0.511	0.029	-0.152	0.173	-0.584	-0.009	0.118	-0.155	0.034	0.127	-0.734**
Y3	-0.062	0.212	**1.028**	-0.362	-0.554	0.345	0.171	-0.446	-0.036	0.109	-0.166	0.257	0.008	-0.101	0.291	0.083	-0.133	0.644**
Y4	-0.096	0.388	0.921	**-0.404**	-0.570	0.395	0.212	-0.517	-0.052	0.164	-0.219	0.390	0.009	-0.119	0.313	0.072	-0.161	0.724**
Y5	0.132	-0.367	-0.769	0.311	**0.741**	-0.368	-0.217	0.546	0.048	-0.166	0.137	-0.455	-0.008	0.111	-0.306	-0.054	0.120	-0.566**
Y6	-0.171	0.592	0.758	-0.341	-0.583	**0.468**	0.243	-0.654	-0.043	0.179	-0.203	0.581	0.010	-0.142	0.268	0.032	-0.172	0.822**
Y7	-0.159	0.550	0.639	-0.311	-0.585	0.413	**0.275**	-0.694	-0.038	0.169	-0.189	0.581	0.011	-0.146	0.320	0.096	-0.198	0.733**
Y8	-0.154	0.497	0.593	-0.270	-0.523	0.396	0.247	**-0.773**	-0.038	0.180	-0.137	0.575	0.011	-0.136	0.269	0.062	-0.194	0.606**
Y9	0.097	-0.260	-0.448	0.250	0.424	-0.244	-0.125	0.351	**0.083**	-0.228	0.022	-0.293	-0.005	0.093	-0.171	-0.014	0.078	-0.391**
Y10	-0.140	0.454	0.446	-0.262	-0.487	0.332	0.184	-0.553	-0.075	**0.252**	-0.092	0.471	0.008	-0.112	0.246	0.038	-0.129	0.580**
Y11	-0.048	0.374	0.492	-0.254	-0.293	0.274	0.150	-0.306	-0.005	0.067	**-0.347**	0.249	0.005	-0.037	0.247	0.103	-0.195	0.476**
Y12	-0.191	0.611	0.368	-0.219	-0.469	0.378	0.222	-0.618	-0.034	0.165	-0.120	**0.719**	0.011	-0.150	0.196	0.019	-0.185	0.704**

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Y13	-0.154	0.516	0.635	-0.271	-0.474	0.382	0.231	-0.659	-0.032	0.157	-0.146	0.638	**0.013**	-0.163	0.290	0.095	-0.174	0.884**
Y14	-0.159	0.468	0.550	-0.254	-0.432	0.349	0.211	-0.553	-0.041	0.149	-0.068	0.571	0.011	**-0.190**	0.307	0.123	-0.190	0.852**
Y15	-0.069	0.281	0.718	-0.303	-0.545	0.301	0.211	-0.500	-0.034	0.149	-0.206	0.338	0.009	-0.140	**0.416**	0.230	-0.231	0.626**
Y16	-0.040	0.087	-0.288	0.098	0.136	-0.050	-0.089	0.163	0.004	-0.032	0.121	-0.046	-0.004	0.078	-0.324	**-0.296**	0.246	-0.238
Y17	-0.052	0.262	0.376	-0.179	-0.243	0.221	0.149	-0.412	-0.018	0.089	-0.186	0.365	0.006	-0.099	0.264	0.200	**-0.364**	0.379**

Table 4: Eigenvectors for four significant principal components of different traits in tomato genotypes.

Traits	PC 1	PC 2	PC 3	PC 4
Eigenvalue	10.05	2.20	1.76	1.01
% variance	55.83	12.22	9.76	5.60
50% flr	-0.24	0.37	0.15	0.09
Days 1st	-0.24	0.27	0.27	-0.07
Cluster/pt	0.22	0.18	0.15	0.39
Frts/clstr	0.05	-0.06	0.62	0.05
Frts/plt	-0.25	0.00	-0.17	-0.25
Avg weight	0.30	-0.07	-0.04	0.22
Fruit width	0.30	-0.02	-0.01	0.13
Fruit length	0.28	-0.04	0.02	-0.02
Locules	-0.19	0.15	-0.46	0.14
Pericarp	0.24	-0.14	0.31	-0.16
Seeds/fruit	0.17	0.26	-0.20	0.54
100 seed weight	0.27	-0.18	-0.20	-0.18
Harvest duration	0.28	0.00	-0.08	-0.14
Plant height	0.26	0.02	-0.07	-0.41
TSS	0.25	0.37	0.13	-0.02
Titratable acidity	-0.09	-0.58	-0.05	0.31
Ascorbic acid	0.18	0.36	-0.20	-0.23
Yield/ plant	0.28	0.01	-0.12	-0.02

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