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RESEARCH ARTICLE

Characterization of Exotic Tomato Germplasm from ICAR-NBPGR Gene Bank

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Abstract

The present study describes the characterization of 148 exotic tomato accessions from ICAR-NBPGR, New Delhi gene bank. The degree of variance for morphological features was high. Mean plant height of 72.36 cm, number of primary branches 2.7, days to 50% flowering 74.9, number of flower clusters per plant 5.91, number of flowers per cluster 3.91, number of locules per fruit 3.08, fruit weight 62.06 g, pericarp thickness 4.32 mm, fruit length 45.98 mm, fruit width 45.9 mm, total soluble solids 4.81° Brix and yield per plant 0.28 Kg were recorded. The first eight PCA extracted accounted for 89.23% of the total variation based on 12 phenotypic characters. A significant positive association was observed among the fruit characters. High PCV, GCV, heritability and GAM were recorded for most of the characters studied. The high variability especially for economically important fruit characters among the tomato germplasm like EC716696, EC715399, EC705451, EC705439, EC699717, EC695044, EC695038, EC695037, EC759285, EC759989 and EC759255 recorded higher TSS values and, germplasm like EC753226, EC716696, EC753220 and EC759989 recorded higher fruit yield per plant, makes this germplasm a potential resource for future tomato breeding programmes.

Keywords: Tomato, Diversity analysis, Genetic variation, Genetic advance, Correlation and Principal component analysis.

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Introduction

Plant genetic resources (PGR) form the basis of any crop improvement programme. India has a strong base of tomato research with both public and private sector institutions involved in tomato breeding. PGR exchange and their utilization in different crop improvement programmes is a continuous process. In order to fulfill future demands brought in by the introduction of new diseases, climate change, and increased demands for food and nutritional security, there is an ongoing quest for different new PGR (De Jonge, 2009). In India, for the management of PGR, National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi is the nodal organization under the aegis of the Indian Council of Agricultural Research (ICAR), New Delhi. The plant quarantine (Regulation of Import) into India, order 2003 specifies how any researcher or user in India must introduce or import germplasm if they need access to seeds or planting materials from other nations (Tyagi *et al.*, 2021).

Tomato (*Solanum lycopersicum* L.) is a globally important vegetable crop and is consumed both fresh and in the form of different processed products. It is a rich source of vitamins (A and C), minerals and antioxidants. In India, along with potato and onion, tomato is an important vegetable crop in respect of nutrition, consumption and price fluctuations. The Andean region, which today includes parts of Chile, Bolivia, Ecuador, Colombia, and Peru, is the center of the origin of tomato (Bai and Lindhout, 2007). Way back in 18th century, tomato was introduced in India and most of the present tomato introductions are bred varieties (Seshadri and Srivastava, 2002). Tomato was first among 25 different crops based on the number of requests for seed during 2014-19 received by ICAR-NBPGR, New Delhi (Tyagi *et al.*, 2021). In collaboration with other national organizations, ICAR-NBPGR also undertakes multiplication, characterization, evaluation, documentation and PGR conservation to promote sustainable use.

Understanding the genetic variation is the prerequisite for utilization of any PGR in improvement programmes. One of the intricate characteristics that can be ascribed to the numerous associated plant characteristics is yield. In addition to associations among different characters, the degree of heritability with genetic advancement is also crucial for crop development. Heritability and genetic advancement of different characters are the main considerations while making selections (Bhandari *et al.,* 2017). The main aim of the current study was to phenotypically characterize exotic germplasm for yield and related characters and to assess its breeding potential. This will facilitate understanding the potential of exotic tomato germplasm for proper utilization of the germplasm in future breeding programmes.

Materials and Method

The current study was carried out at ICAR-Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh, India (25°10′N latitude and 82°52′E longitude).

Plant Materials and Data Collection

A set of 148 exotic tomato accessions from National Gene Bank, ICAR-NBPGR, New Delhi was used in the study. Among them, 104 accessions were introduced from the World Vegetable Center in Taiwan, 40 from Jordan, and 4 from the SAARC - Agriculture Centre at the BARC Complex and Farm Gate in Dhaka (Table 1). All the exotic tomato accessions belong to *S. lycopersicum* L. that is cultivated tomato. The study also included five ICAR-Indian Institute of Vegetable Research (IIVR) released varieties (Kashi Amrit, Kashi Anupam, Kashi Aman, Kashi Hemant and Kashi Vishesh) as checks. Data was recorded for 12 agri-horticultural characters, namely, plant height (cm), number of primary branches, days to 50% flowering, number of flower clusters per plant, number of flowers per cluster, number of locules per fruit, average fruit weight (g), yield per plant (g), pericarp thickness (mm)**,** fruit length (cm)**,** fruit width (cm) and total soluble solids (TSS) in ^{0}Brix. Days to 50% flowering was recorded when 50% of the plants started flowering from the date of planting. All other parameters were the averages from five plants or fruits.

Experimental Design

Augmented randomized complete block design (ARCBD) was the experimental design to grow the accessions in the field. Checks were replicated in each block and treatments (germplasm accessions) were not replicated. 148 accessions were grown in 4 blocks with 37 accessions in each block. As 25 days old seedlings were transplanted in the main field at 60 × 45 cm spacing between rows and between the plants. Standard cultivation practices recommended for tomato crop has been followed to raise a good crop (ICAR, 2009).

Statistical Analysis

The R package 'augmented RCBD' was used to estimate adjusted averages for all the characters under consideration for all the genotypes (Aravind *et al.*, 2018). Genetic variability parameters, frequency distribution, and descriptive statistics were also estimated using the same R package. The following formulas were used to determine phenotypic variance, genotypic variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h2) (Lush, 1940), and genetic advance (GA) (Johnson *et al.*, 1955):

$$\text{Genotypic variance } (\sqrt[2]{\mathrm{g}} = \sqrt[2]{\mathrm{P}} - \sqrt[2]{\mathrm{e}})$$

Here,

$\sqrt[2]{P}$ = Phenotypic variance = Sum of squares of test treatments (genotypes)

$\sqrt[2]{e}$: = Error Variance = Sum of squares of residuals (error)

w

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{Phenotypic Variance}}{\sqrt{\text{mean}}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic Variance}}{\sqrt{\text{mean}}} \times 100$$

$$\text{Broad sense heritability } (\mathrm{h}^2) = \frac{\sqrt[2]{\mathrm{g}}}{\sqrt[2]{\mathrm{P}}}$$

$$\text{Genetic Advance (GA)} = k \times \sqrt{g} \times \frac{h^2}{100}$$

where, k = selection intensity and σg= genotypic standard deviation

Correlation analysis was performed using the R package 'metan' (Olivoto and Lúcio2020) and PCA using the R packages 'FactoMineR' (Le *et al.*, 2008).

Results and Discussion

Genetic Properties

Mean, range, variance, coefficient of variance, heritability and genetic advance.

Proper estimation and reporting of the genetic diversity within the germplasm is the foremost important activity for better utilization of any germplasm (Islam *et al.*, 2004). Since morphological features offer a straightforward, simple and less expensive method of quantifying genetic variation, they have been employed to estimate genetic diversity

Table 1: List and source of the introduced tomato accessions in the study

S. No	Accession	Country
1	EC700930	Taiwan, Province of China
2	EC700931	Taiwan, Province of China
3	EC700933	Taiwan, Province of China
4	EC700936	Taiwan, Province of China
5	EC700938	Taiwan, Province of China
6	EC705436	Taiwan, Province of China
7	EC705437	Taiwan, Province of China
8	EC705438	Taiwan, Province of China
9	EC705439	Taiwan, Province of China
10	EC705440	Taiwan, Province of China
11	EC705442	Taiwan, Province of China
12	EC705443	Taiwan, Province of China
13	EC705444	Taiwan, Province of China
14	EC705445	Taiwan, Province of China
15	EC705446	Taiwan, Province of China
16	EC705447	Taiwan, Province of China
17	EC705449	Taiwan, Province of China
18	EC705450	Taiwan, Province of China
19	EC705451	Taiwan, Province of China
20	EC705452	Taiwan, Province of China
21	EC705453	Taiwan, Province of China
22	EC715376	Taiwan, Province of China
23	EC715377	Taiwan, Province of China
24	EC715380	Taiwan, Province of China
25	EC695037	Taiwan, Province of China
26	EC715382	Taiwan, Province of China
27	EC715383	Taiwan, Province of China
28	EC715384	Taiwan, Province of China
29	EC715385	Taiwan, Province of China
30	EC715386	Taiwan, Province of China
31	EC715387	Taiwan, Province of China
32	EC715388	Taiwan, Province of China
33	EC715389	Taiwan, Province of China
34	EC715391	Taiwan, Province of China
35	EC715393	Taiwan, Province of China
36	EC715394	Taiwan, Province of China
37	EC715396	Taiwan, Province of China
38	EC715397	Taiwan, Province of China
39	EC715398	Taiwan, Province of China
40	EC715399	Taiwan, Province of China
41	EC695036	Taiwan, Province of China
42	EC695037	Taiwan, Province of China
43	EC695038	Taiwan, Province of China
44	EC695039	Taiwan, Province of China
45	EC695040	Taiwan, Province of China
46	EC695041	Taiwan, Province of China
47	EC695042	Taiwan, Province of China
48	EC695043	Taiwan, Province of China
49	EC695044	Taiwan, Province of China
50	EC695045	Taiwan, Province of China
51	EC699710	Taiwan, Province of China
52	EC699714	Taiwan, Province of China
53	EC699715	Taiwan, Province of China
54	EC699716	Taiwan, Province of China
55	EC699717	Taiwan, Province of China
56	EC721954	Taiwan, Province of China
57	EC721955	Taiwan, Province of China
58	EC721957	Taiwan, Province of China
59	EC721958	Taiwan, Province of China
60	EC721959	Taiwan, Province of China
61	EC721961	Taiwan, Province of China
62	EC721963	Taiwan, Province of China
63	EC716696	Taiwan, Province of China
64	EC759989	Taiwan, Province of China
65	EC759991	Taiwan, Province of China
66	EC759992	Taiwan, Province of China
67	EC759993	Taiwan, Province of China
68	EC759997	Taiwan, Province of China
69	EC759998	Taiwan, Province of China
70	EC759999	Taiwan, Province of China
71	EC760002	Taiwan, Province of China
72	EC760003	Taiwan, Province of China
73	EC760004	Taiwan, Province of China
74	EC760005	Taiwan, Province of China
75	EC760006	Taiwan, Province of China
76	EC760007	Taiwan, Province of China
77	EC760008	Taiwan, Province of China
78	EC760009	Taiwan, Province of China
79	EC760011	Taiwan, Province of China
80	EC752609	Taiwan, Province of China
81	EC752610	Taiwan, Province of China
82	EC752612	Taiwan, Province of China
83	EC752613	Taiwan, Province of China
84	EC752614	Taiwan, Province of China
85	EC752615	Taiwan, Province of China
86	EC752616	Taiwan, Province of China
87	EC752617	Taiwan, Province of China
88	EC752618	Taiwan, Province of China
89	EC753216	Taiwan, Province of China
90	EC753218	Taiwan, Province of China
91	EC753219	Taiwan, Province of China
92	EC753220	Taiwan, Province of China
93	EC753221	Taiwan, Province of China
94	EC753223	Taiwan, Province of China

Table cont....

S. No	Accession	Country
95	EC753224	Taiwan, Province of China
96	EC753225	Taiwan, Province of China
97	EC753226	Taiwan, Province of China
98	EC753227	Taiwan, Province of China
99	EC753228	Taiwan, Province of China
100	EC753230	Taiwan, Province of China
101	EC753231	Taiwan, Province of China
102	EC753232	Taiwan, Province of China
103	EC753233	Taiwan, Province of China
104	EC738047	Dhaka, Bangladesh
105	EC738050	Dhaka, Bangladesh
106	EC738054	Dhaka, Bangladesh
107	EC738055	Dhaka, Bangladesh
108	EC739326	Taiwan, Province of China
109	EC759243	Amman, Jordan
110	EC759244	Amman, Jordan
111	EC759246	Amman, Jordan
112	EC759247	Amman, Jordan
113	EC759248	Amman, Jordan
114	EC759250	Amman, Jordan
115	EC759251	Amman, Jordan
116	EC759252	Amman, Jordan
117	EC759254	Amman, Jordan
118	EC759255	Amman, Jordan
119	EC759258	Amman, Jordan
120	EC759259	Amman, Jordan
121	EC759261	Amman, Jordan
122	EC759262	Amman, Jordan
123	EC759263	Amman, Jordan
124	EC759264	Amman, Jordan
125	EC759265	Amman, Jordan
126	EC759266	Amman, Jordan
127	EC759267	Amman, Jordan
128	EC759268	Amman, Jordan
129	EC759269	Amman, Jordan
130	EC759270	Amman, Jordan
131	EC759271	Amman, Jordan
132	EC759272	Amman, Jordan
133	EC759273	Amman, Jordan
134	EC759274	Amman, Jordan
135	EC759275	Amman, Jordan
136	EC759276	Amman, Jordan
137	EC759277	Amman, Jordan
138	EC759278	Amman, Jordan
139	EC759279	Amman, Jordan
140	EC759280	Amman, Jordan
141	EC759281	Amman, Jordan
142	EC759282	Amman, Jordan
143	EC759283	Amman, Jordan
144	EC759284	Amman, Jordan
145	EC759285	Amman, Jordan
146	EC759286	Amman, Jordan
147	EC759287	Amman, Jordan
148	EC759288	Amman, Jordan

Source: for accessions from serial number 1 to 103 and 108 World Vegetable Centre, P.O.Box 42, Shanhua Tainan-74199; for accessions from serial number 104 to 107 SAARC, Agriculture Centre ,BARC Complex, Farm Gate Dhaka-1215; for accessions from serial number 109 to 148 225 5th Floor Office # 504 P O Box 830917, Amman.

and cultivar development (Fufa *et al*., 2005). In the present study, a significant range of variance was seen among the tomato accessions for the twelve characters. ANOVA analysis showed that variance for all the characters was highly significant, indicating inherent genetic differences. All the characters show wide range (Table 2). The coefficient of variation (CV %) varied from 3.47 for number of days to 50% flowering to 17.96 for yield per plant. In the past many studies used molecular markers in tomatoes to study the diversity (Hu *et al*., 2012; Cebolla-Cornejo *et al*., 2013; Corrado *et al.,* 2013; Zhou *et al.,* 2015), but in this study we used only morphological characters for diversity study. Morphological characterization is not only simple, less expensive but also informative for breeding programs and also high levels of diversity based on morphological characters are associated with tomato lines that have a low level of genetic diversity with molecular markers (Mazzucato *et al*., 2008; Cebolla-Cornejo *et al*., 2013). Morphological characters have been utilized for diversity studies in the past in tomatoes (Henareh *et al*., 2015; Bhattarai *et al*., 2016).

For all the characters, phenotypic variance was higher than genotypic variance, indicating the environmental influence on all these characters (data not presented). Except for days to 50% flowering and TSS, the remaining characters found to have high PCV and GCV. The heritability in broad sense was higher for all the characters under study. A good measure of the progress that may be anticipated as a result of applying selection in a population is genetic advancement (GA). Heritability along with genetic advances, would provide a more accurate estimate of selection value (Johnson *et al.,* 1955). GA as a percent mean was recorded as high for all the characters except for days to 50% flowering (10.91). Days to 50% flowering recorded low GCV and PCV in the germplasm studied, indicating low variation for the

Table 2: Genetic variability parameters of the tomato germplasm

Trait	*Mean*	*Range*	*CV (%)*	*GCV*	*GCV category*	*PCV*	*PCV category*	*ECV*	*hBS (h^2) (%)*	*hBS category*	*GA*	*GAM (%)*	*GAM category*
PH	72.36	38.25–114.22	4.97	20.97	High	21.54	High	4.93	94.77	High	30.47	42.1	High
PB	2.74	0.91–8.04	13.17	37.24	High	39.52	High	13.21	88.83	High	1.99	72.42	High
DFF	74.9	58.48–83.84	3.47	6.09	Low	7.01	Low	3.47	75.44	High	8.17	10.91	Medium
NC	5.91	2.27–35.12	7.04	87.47	High	87.74	High	6.9	99.38	High	10.62	179.89	High
NFPC	3.91	1.72–7.96	6.09	31.3	High	31.88	High	6.06	96.38	High	2.48	63.39	High
LN	3.08	1.93–7.03	5.6	30.37	High	30.88	High	5.6	96.72	High	1.9	61.61	High
FW	62.06	8.99–158.75	6.05	50.73	High	51.12	High	6.27	98.49	High	64.46	103.87	High
PT	4.32	0.93–7.35	7.66	36.9	High	37.73	High	7.87	95.65	High	3.21	74.44	High
L	45.98	2.24–67.85	4.08	23.48	High	23.84	High	4.09	97.06	High	21.95	47.73	High
W	45.9	3.6–77.8	4.59	22.41	High	22.88	High	4.61	95.94	High	20.79	45.29	High
TSS	4.81	2.21–7.31	4.58	16.85	Medium	17.46	Medium	4.56	93.18	High	1.61	33.57	High
YPP	0.28	0.01–2.4	17.96		High	128.38	High	18.62	97.9	High	0.74	259.28	High

PH = plant height (cm), PB = number of primary branches, DFF = days to fifty percent flowering, NC = number of flower clusters per plant, NFPC = number of flowers per cluster, LN = number of locules per fruit, FW = average fruit weight (g), PT = pericarp thickness (mm), L = fruit length (mm), W = fruit width (mm), TSS = total soluble solids (TSS) in ^{O}Brix , YPP = yield per plant (Kg), CV% = Coefficient of variation and GAM = genetic advance as 5 % of mean

character. This gave rise to medium GA as a percent mean for the character even though it recorded high for heritability in a broad sense parameter. In all the remaining characters, both GCV and heritability in the broad sense were high leading to high GA as a percent mean (Table 2). The variation in genotypes for the characters under study may be due to genetic diversity and differences in adaptability (Hassan *et al.,* 2021). Variability and genetic diversity among the genotypes and higher heritability offer higher genetic gains in breeding programmes (Olakojo and Adetula 2014; Bhattarai *et al.,* 2016).

Frequency Distribution of Yield and TSS

Genotypes EC705450 (1380 g), EC759989 (1680 g), EC753220 (2112 g), EC716696 (2226 g) and EC753226 (2400 g) gave fruit yield of more than one kilogram per plant. TSS has special significance in breeding aspects of tomatoes for the processing industry. TSS in the germplasm ranged from 2.21 to 7.31 with around 39% the genotypes recording TSS greater than 5 ^{0}Brix. Eleven genotypes namely, EC759255 (6.00), EC759989 (6.01), EC759285 (6.1), EC695037 (6.21), EC695038 (6.21), EC695044 (6.21), EC699717 (6.21), EC705439 (6.24), EC705451 (6.24), EC715399 (6.41) and EC716696 (7.31) recorded ≥ 6.00 TSS. From the breeding point of view, TSS has been reported to have a negative correlation with fruit size and yield. There are few reports where TSS was improved without much effect on yield (Eshed and Zamir, 1995; Yousef and Juvik, 2001). Increased TSS increases the turnover of processed goods like paste and lowers the cost of tomato processing (Beckles, 2012; Reddy *et al.,* 2020).

Correlation

Correlation analyses is an important component of any breeding program as associated characters influence the selection and genetic gain of complex characters like yield. Pearson correlation coefficients were calculated to assess character correlations (Figure 1). Yield per plant has a significant positive correlation with number of flower clusters per plant (r = 0.39, *p*<0.001), number of primary branches (r = 0.33, *p*<0.001) and number of flowers per cluster (r = 0.28, *p*<0.001). Tiwari and Upadhyay (2011) reported a positive and highly significant association between fruit yield and number of branches per plant. Yield

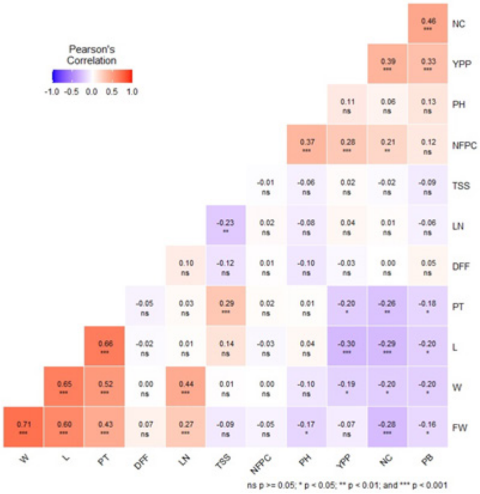

Figure 1: Graphical depiction of correlation among the quantitative characters in the tomato germplasm.

was negatively correlated with fruit length (r = -0.3, p<0.001), pericarp thickness (r=-0.2, p<0.05) and fruit width (r=-0.19, p<0.05). TSS was positively correlated with pericarp thickness (r = 0.29, p<0.001) and negatively correlated with number of locules per fruit (r = -0.23, p<0.01). The number of locules per fruit was positively correlated with fruit width (r = 0.44, p<0.001) and fruit weight (r = 0.27, p<0.001). Fruit characters ie fruit length, fruit width, fruit weight and pericarp thickness, were positively correlated among them and were negatively correlated with the number of primary branches and number of flower clusters per plant. Mishra and Nandi (2018) reported that fruit weight positively correlated with fruit width, length, number of locules per fruit and pericarp thickness. The number of flowers per cluster was positively correlated with plant height and number of flower clusters per plant. Similar observations were also reported by Kumar *et al.,* (2013) and Singh *et al.,* (2018).

Principal Component Analysis

Principal component analysis (PCA) was used to assess diversity on multivariate scales. The PCA simplifies the interrelationship among a large set of characters into a small

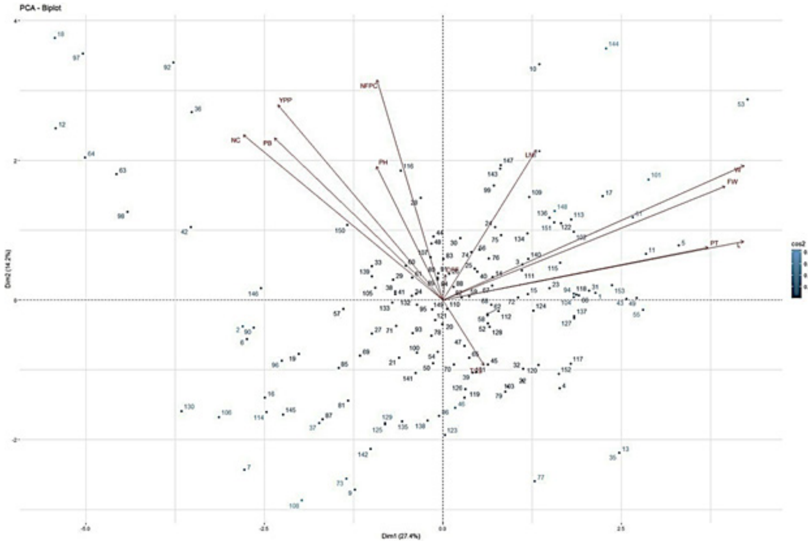

Figure 2: Two dimensional graphical representations of component patterns along with different variables based on PC1 and PC2

Table 3: Eigen values, proportion of the total variance represented by first eight principal components, cumulative percent variance and component loading of different characters in tomato

	PC1	*PC2*	*PC3*	*PC4*	*PC5*	*PC6*	*PC7*	*PC8*
Eigen value	3.28	1.71	1.52	1.13	0.96	0.85	0.68	0.58
%variance Expressed	27.35	14.24	12.66	9.40	8.00	7.07	5.66	4.84
Cumulative variance Expressed	27.35	41.60	54.26	63.66	71.66	78.73	84.39	89.23
PH	-0.035	0.223	-0.033	0.935	-0.070	0.046	0.024	-0.024
PB	-0.065	-0.155	-0.104	0.213	0.091	0.835	0.235	-0.103
DFF	-0.007	0.024	-0.054	-0.064	0.990	0.021	-0.023	0.050
NC	-0.249	0.325	0.051	-0.160	-0.070	0.803	0.061	0.093
NFPC	0.022	0.910	-0.019	0.243	0.032	0.067	0.161	-0.008
LN	0.123	-0.006	-0.122	-0.017	0.056	-0.008	0.045	0.964
FW	0.827	-0.053	-0.229	-0.189	0.063	-0.164	0.192	0.136
PT	0.755	0.015	0.369	0.106	-0.018	-0.077	-0.144	-0.032
L	0.877	-0.007	0.081	0.080	-0.012	-0.088	-0.200	-0.107
W	0.813	0.042	-0.026	-0.099	-0.038	-0.072	-0.076	0.412
TSS	0.069	-0.016	0.952	-0.043	-0.055	-0.037	0.050	-0.118
YPP	-0.155	0.177	0.048	0.028	-0.030	0.240	0.911	0.042

PH = plant height (cm), PB = number of primary branches, DFF = days to fifty percent flowering, NC = number of flower clusters per plant, NFPC = number of flowers per cluster, LN = number of locules per fruit, FW = average fruit weight (g), PT = pericarp thickness (mm), L = fruit length, W = fruit width (mm), TSS = total soluble solids (TSS) in ^{0}Brix and YPP = yield per plant (Kg) set of components without losing any essential information of the original data set. Thus PCA gives information of important characters that have a greater impact on the total variation and the degree of contribution (Sanni *et al.,* 2008). In the present study, the major portion of variance (63.65%) among the tomato genotypes is explained by the first four components with eigenvalue >1.0 (Table 3). The first component (PC1) accounted for 27.35% of variation largely through fruit characters like, average fruit weight, pericarp thickness, fruit length**,** fruit width; PC2 accounted for 14.24% of variation contributed through number of flowers per cluster, number of flowers clusters per plant and plant height, PC3 contributed for 12.66% of variation through total soluble solids and pericarp thickness and PC4 contributed for 9.4% of variation mainly through plant height, number of flowers per cluster and a number of primary branches. Two-dimensional graphical representations of component patterns along with different variables based on PC1 and PC2 is shown in Figure 2. The first two PCs contributed to 41.59% to the total variation with eigenvalues 3.28 and 1.71, respectively. These two PCs indicated that the main discriminatory characters were average fruit weight, fruit length, fruit width, number of flowers per cluster, number of flower clusters per plant, yield per plant, and number of primary branches. In similar studies, Mazzucato *et al*., (2008) and Hu *et al*., (2012) fruit characters contributed greatly to variation among tomato germplasm. In another study by Cebolla-Cornejo *et al.,* (2013) performed a diversity analysis of tomato germplasm, mainly including landraces from Spain. In their study, the first PC was also associated with fruit-size characters. Bhattarai *et al.,* (2016) studied the genetic diversity of 71 tomato genotypes based on its horticultural characteristics. In their study, five principal components explained more than 92% of the total phenotypic variation and fruit characters like fruit size, shape, and category were included in PCA1.

Conclusion

These diversified exotic germplasm are a reservoir of important genes/alleles for yield and fruit characters. Genotypes like EC753226, EC716696, EC753220 and EC759989 for yield per plant and, genotypes like EC716696, EC715399, EC705451, EC705439, EC699717, EC695044, EC695038, EC695037, EC759285, EC759989 and EC759255 for TSS can be used as principal foundation material in different breeding programmes for the development of new improved tomato varieties.

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References

Aravind, J., Sankar, M. S., Dhammaprakash, P. W.,&Kaur, V. (2018). augmentedRCBD: Analysis of Augmented Randomized Complete Block Designs. R package version 0.1.0, *https://aravind-j.github.io/augmentedRCBD/.*

Beckles, D. M., (2012). Factors affecting the postharvest sugars and total soluble solids in tomato (*Solanum lycopersicum* L.) fruits. *Postharvest Biol. Technol.* **63:** 129–140.

Bai, Y.,&Lindhout, P. (2007). Domestication and breeding of tomatoes: what have we gained and what can we gain in the future? *Ann. Bot.* **100(5):** 1085-94. *doi: 10.1093/aob/mcm150.*

Bhandari, H. R., Srivastava, K., & Eswar Reddy, G. (2017). Genetic variability, heritability and genetic advance for yield traits in tomato (*Solanum lycopersicum* L.). *Int J Curr Microbiol Appl Sci,* **6(7):** 4131–8.

Bhattarai, K., Louws, F. J., Williamson, J. D., & Panthee, D. R. (2016). Diversity analysis of tomato genotypes based on morphological traits with commercial breeding significance for fresh market production in eastern USA. *Aust. J. Crop Sci.* **10(8):** 1098–103.

Cebolla-Cornejo, J., Rosello, S., &Nuez, F. (2013). Phenotypic andgenetic diversity of Spanish tomato landraces. *Sci. Hortic.* **162:** 150-164.

Corrado, G., Piffanelli, P., Caramante, M., Coppola, M., & Rao, R. (2013). SNP genotyping reveals genetic diversity between cultivated landraces and contemporary varieties of tomato. *BMC Genom.* **14:** *DOI: 10.1186/1471-2164-14-835.*

DeJonge, (2009) Plants, Genes and Justice: An enquiry into fair and equitable benefit-sharing. Unpublished Ph D dissertation, Wageningen: Wageningen University. *http://www.fao.org/ agriculture/crops/thematic-sitemap/theme/seeds-pgr/conservation/en/).*

Eshed, Y., & Zamir, D. (1995). An introgression line population of *Lycopersicon pennellii*in the cultivated tomato enables the identification and fine mapping of yield-associated Qtl. *Genetics,* **141:** 1147-1162.

Fufa, H., Baenziger, P. S., Beecher, B. S., Dweikat, I., Graybosch, R. A., & Eskridge, K. M. (2005). Comparison of phenotypic and 1103 molecular marker-based classifications of hard red winter wheat cultivars. *Euphytica,* **145:** 133-146.

Hassan, Z., Ul-Allah, S., Khan, A. A., Shahzad, U., Khurshid, M., Bakhsh, A., *et al.* (2021). Phenotypic characterization of exotic tomato germplasm: An excellent breeding resource. *PLoS ONE,* **16(6):** e0253557

Henareh, M., Dursun, A., & Mandoulakani, B. A. (2015). Genetic diversity in tomato landraces collected from Turkey and Iran revealed by morphological characters. *Acta Sci. Pol.. Hortorum Cultus.* **14:** 87-96.

Hu, X. R., Wang, H., Chen, J., & Yang, W. C. (2012). Genetic diversity of Argentina tomato varieties revealed by morphological traits, simple sequence repeat, and single nucleotide polymorphism markers. *Pak. J. Bot.* **44:** 485-492.

ICAR, (2009). Handbook of Horticulture. New Delhi: Indian Council of Agricultural Research, pp. 464–470.

Islam, F. M. A., Beebe, S., Munoz, M., Tohme, J., Redden, R. J., & Basford, K. E. (2004). Using molecular markers to assess the effect of introgression on quantitative attributes of common bean in the Andean gene pool. *Theor. Appl. Genet.* **108:** 243-252.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *J. Agron.* **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., & Kumar, P. (2013). Genetic Variability, Correlation and Path Coefficient Analysis in Tomato. *Int. J. Veg. Sci.* **19(4):** 313-323.

Le, S., Josse, J., & Husson, F. (2008), FactoMineR: An R Package for Multivariate Analysis. *J. Stat. Softw.* **5(1):** 1-17.

Lush, J. L. (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *Proceeding of American Society of Animal Nutrition,* **1940:** 293–301.

Mazzucato, A., Papa, R., Bitocchi, E., Mosconi, P., Nanni, L., Negri, V., Picarella, M. E., Siligato, F., Soressi, G. P., Tiranti, B., & Veronesi, F. (2008). Genetic diversity, structure and marker-trait associations in a collection of Italian tomato (*Solanum lycopersicum* L.) landraces. *Theor. Appl. Genet.* **116:** 657-669.

Mishra, A., & Nandi, A. (2018). Correlation and path coefficient analysis for quality traits in tomato (*Solanum lycopersicon* L.). *J. pharmacogn. phytochem.* **7(1):** 1733–1738.

Olakojo, S. A., & Adetula, O. A. (2014). Comparison of qualitative and quantitative traits of some advanced breeding lines of tomato (*Lycopersicon esculentum* L.). *Afr. J. Plant Sci.* **8(10):** 457–61.

Olivoto, T., & Lúcio, A. D. (2020). metan: An Rpackage for multi-environment trial analysis. *Methods Ecol. Evol.* **11:** 783–789. *https:// doi.org/10.1111/2041-210X.13384*

Reddy, B. R., Singh, A. K., Pal, A. K., Reddy, Y. S., & Eswara Reddy, G. (2020). Combining ability and heterosis studies in tomato (*Solanum lycopersicum* L.) for quality traits and yield. *Int. J. Chem. Stud.* **8(2):** 2788-2792.

Sanni, K. A. I., Fawole, R. G., Guei, D. K., Ojo., & Somado, E. A. (2008). Geographical patterns of phenotypic diversity in *Oryza sativa* landraces of Côte d'Ivoire. *Euphytica,* **60:** 389-400.

Seshadri, V. S., & Srivastava, U. (2002). Genetic Resources and Improvements (Vegetable crops), p. 41–62. In: V.S. Seshadri and U. Srivastava (eds.). Evaluation of vegetable genetic resources with special reference to value addition. International conference on vegetables: Vegetables for sustainable food and nutritional security in the new millennium, organized by Dr. PremNath, Agricultural Science Foundation, Bangalore, Indian Society of Vegetable Science, New Delhi and Indian Institute of Horticultural Research, Bangalore, India.

Singh, A. K., Solankey, S. S., Akhtar, S., Kumari, P., & Chaurasiya, J. (2018). Correlation and Path Coefficient Analysis in Tomato (*Solanum lycopersicum* L.). *Int J Curr Microbiol Appl Sci,* **7:** 4278-4285.

Tiwari, J. K., & Upadhyay, D. (2011). Correlation and path-coefficient studies in tomato *Lycopersicon esculentum* Mill.). *Res. J. Agric. Sci.* **2(1):** 63–68.

Tyagi, V., Brahmi, P., Yadav, S. K., Pragya, Singh S. P., Singh, S., & Singh, K. (2021). Germplasm Access from ICAR-NBPGR and Use within India. *Indian J. Plant Genetic Resources,* **34(2):** 216–220.

Yousef, G. G., & Juvik, J. A. (2001). Evaluation of breeding utility of a chromosomal segment from *Lycopersicon chmielewskii* that enhances cultivated tomato soluble solids. *Theor. Appl. Genet.* **103:** 1022-1027.

Zhou, R., Wu, Z., Cao, X., & Jiang, F. L. (2015). Genetic diversity of cultivated and wild tomatoes revealed by morphological traits and SSR markers. *Genet. Mol. Res.* **14:** 13868-13879.