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Phenotypic Characterization and Association Analysis of Tomato (*Solanum lycopersicum* L.) Accessions.

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Abstract

In this study, 36 tomato accessions were subjected to variability and correlation analysis based on seventeen yield and quality traits. The traits *viz.*, plant height, number of clusters plant^{-1}, number of fruits plant^{-1}, ascorbic acid content and single fruit weight were exhibited a high level of variability, heritability and genetic advance as per cent of mean and these traits are positive and significantly associated with yield, which is clearly indicates that these traits are highly responsive and simple selection is very appropriate. Per cent fruit set negatively associated with earliness and its exhibited moderate level of variability shows the presence of non-additive gene action. Lycopene and β-carotene were not substantially linked with any of the traits but these are highly heritable in nature, to incorporate these two traits into any breeding programme, the parents must be excellent in these particular quality parameters.

Keywords:*Tomato; Variability; Correlation; Association analysis*

Introduction

Tomato (*Solanum lycopersicum*L.) is the most significant vegetable crop, produced all over the world for human consumption and numerous industrial purposes. It belongs to the family Solanaceae. It has tremendous genetic and genomic resources, making it more evolutionary (Foolad, 2007; Ranjan*et al.*, 2012), and it is helpful for genetic studies. Due to its adaptability to a diverse array of soil and climate conditions, it is grown across the world. The earliest domestication of highly autogamous tomato was in Mexico in the 15th century from *Solanum pimpinellifolium*and *Solanum cerasiforme*(Bai and Lindhout, 2007). Cultivated tomato has a lower level of genetic diversity than the wild species *Solanum pimpinellifolium*and *S. cerasiforme*, but it has a higher level of phenotypic variability than *Solanum pimpinellifolium*(Miller and Tanksley, 1990). Tomato morphology and genetic variation are the key factors for improving tomato productivity, disease resistance, earliness and fruit quality (Foolad, 2007; Singh *et al.*, 2015). Information on the genetic parameters, such as genotypic and phenotypic coefficient of variation, heritability and genetic advance is necessary to formulate appropriate breeding strategies and exploit the inherent variability of the original population. Degree of heritability with genetic advance is crucial for crop improvement, (Johnson *et al.*, 1955; Golani *et al.*, 2007 and Bhandari *et al.*, 2017) in addition to correlations (Kumari*et al.*, 2020). Besides the variability study, the correlation analysis explores the association of traits with each other, either direct or indirect proportion. Yield is one of the intricate traits which is attributed to the numerous associated plant parameters and these uneconomic traits are also linked among themselves (Evans, 1996). Therefore, the major objective of the current study was to phenotypically characterize the collected germplasm for yield and related traits and to evaluate its breeding potential. The results of this study will assist tomato breeders to know the full potential of the germplasm and to design a suitable breeding program for the development of high yielding cultivars.

Materials and methods

Thirty-six tomato accessions obtained from NBPGR and repository of the Department of Vegetable Science, TNAU, Coimbatore, India were utilized in this experiment conducted in the orchard of Horticulture College and Research Institute, Tamil Nadu Agricultural University, Coimbatore during the late *Rabi* in 2019. The trial was undertaken in randomized block design with three replications. Spacing adopted was 90×60 cm and the package of practices was as per TNAU Agritech Portal. The replicated values were used for statistical analysis. From each replication five plants were selected randomly to observe plant height (cm), number of primary branches, days to flowering, days to 50% flowering, number of flowers cluster^{-1}, number of fruits cluster^{-1}, number of cluster plant^{-1}, Per cent fruit set, pericarp thickness (cm), number of locules, T.S.S. (°Brix), ascorbic acid content (mg/100 g), lycopene content (mg/100g), β-carotene content (mg/100g), single fruit weight (g), number of fruits plant^{-1}, yield plant^{-1} (g).The variability and correlation analysis for these traits was worked out using R Studio software.

Results and discussion

The analysis of variance in the present study revealed that there were significant differences among the genotypes for all the characters studied, indicating the existence of variability. Therefore, the study is amenable to genetic analysis (Table 1). The high PCV and GCV were observed for twelve traits such as β-carotene content (48.66 and 48.55 %), number of fruits cluster^{-1} (39.37 and 33.48 %), number of cluster plant^{-1}(36.27 and 27.87 %), lycopene content (30.45 and 30.41 %), ascorbic acid content (27.68 and 27.55 %), single fruit weight (27.56 and 27.44 %), number of locule (27.34 and 27.30 %), number of fruits plant^{-1} (27.08 and 26.98 %), yield plant^{-1} (25.94 and 25.82 %), number of primary branches (24.61 and 24.52 %), pericarp thickness (21.99 and 21.84 %) and plant height (20.40 and 20.22 %) (Fig. 1). Ghosh *et al.*(2010); Dharminder*et al.* (2013); Shashikanth*et al.* (2010) reported the same. The relative magnitude of the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for most of the characters, indicating the magnitude of environmental influence on the individual trait. The GCV was recorded as high for these traits, which indicates that these traits are highly heritable in nature (Khan and Samadia, 2012; Singh and Singh, 2019). This offers the chance for exploitation of these characters for crop improvement. The genetic variability in terms of GCV alone is not sufficient for the determination of the amount of heritable variability. In addition to heritability, GAM is also needed to assess the extent of genetic gain expected for effective selection. Heritability estimates as per cent were found to be high for all the characters studied except number of cluster plant^{-1} (59.05 %) and per cent fruit set (28.40 %). Similar results are reported by Dhankhar*et al.* (2006); Sidhya*et al.* (2014). The trait, per cent fruit set (18.50 %) alone showed a moderate value, whereas all the other traits exhibited a high magnitude of GAM (Fig.2). Singh, 2005 reported almost identical results for all the characters studied. The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or hybridization followed by selection. High heritability coupled with high GAM for all the traits except number of cluster plant^{-1} and per cent fruit set. This indicated the preponderance of fixable additive gene action for these traits and thus, these traits would respond effectively to selection. Basavaraj*et al.* (2015) delineated high heritability and high estimates of genetic gain for fruits per cluster and fruits per plant. Moreover, Singh *et al.* (2015) and Rai *et al*., (2016) reported the same. Additionally, the traits *viz.*, plant height, number of clusters plant^{-1}, number of fruits plant^{-1}, ascorbic acid content and single fruit weight were highly associated with yield plant^{-1}(Fig.3) which clearly indicates that these traits are highly responsive to crop improvement programmes and transferring of these traits to advanced generations is extremely simple.

High PCV and moderate GCV was recorded for the traits, per cent fruit set (31.61 and 16.85 %) and number of flowers cluster^{-1}(22.33 and 17.33 %) (Fig. 1). Which clearly indicates these traits are highly influenced by the environment and expresses well only in a favorable environment. Comparable results were reported byAradhana and Singh (2003); Sidhya*et al.* (2014).Heritability in broad sense was found to be moderate for number of cluster plant^{-1} (59.05 %) which recorded high GAM (44.12%) whereas per cent fruit set exhibited low heritability and moderate GAM. Moderate heritability coupled with high or low genetic advance suggests the presence of non-additive gene action and therefore, these traits cannot be improved through simple selection. Both of these traits are indirectly related to yield via a significantly positive correlation with number of fruits plant^{-1} and number of fruits cluster^{-1}, both of which have a significant and positive relationship with yield. The per cent fruit set showed a significant negative correlation with days to 50% flowering and negative correlation with days to flowering. As a result, it is possible to consider that earliness is an indirect proposition to yield and most yield related characteristics.

Moderate PCV and GCV were found in three characters, *viz.*, days to flowering (11.57 and 11.26 %), TSS (11.56 and 11.26 %) and days to 50 % flowering (10.98 and 10.77 %) (Fig. 1). Patel *et al.* (2013) reported moderate phenotypic and genotypic coefficients of variation for total soluble solids similar to Basfore*et al.* (2020) who reported moderate phenotypic and genotypic coefficient of variation for total soluble solids and pericarp thickness. Low values of phenotypic and genotypic coefficient of variation were observed for days to 50 % flowering and days to marketable maturity. Comparably low PCV and GCV for harvest duration and days to 50 % flowering were reported by Reddy *et al.* (2013).These traits may have limited utility for selection in the improvement of the crop.

Significant associations among various traits give an insight into the scope of simultaneous improvement of traits and their direct and indirect effects will lead to simultaneous improvement of yield and quality. The number of fruits plant^{-1}, number of cluster plant^{-1}, plant height, single fruit weight and ascorbic acid content have a significantly positive association with yield whereas days to flowering, days to 50% flowering, number of locules and lycopene content were negatively and non-significantly associated with yield plant^{-1}. Lycopene and β-carotene, which are quality indicators, were not substantially linked with any of the traits. To incorporate these two traits into any breeding programme, the parents must be exceptional in these quality parameters. The magnitude of GCV, PCV, h^2 and GAM were high (Fig.1&2) for both, indicating their highly heritable nature. Breeding to improve ascorbic acid content can increase the number of fruits cluster^{-1}, flowers cluster^{-1} and TSS as it is obvious from their strong positive correlation with ascorbic acid content. The findings were identical to those of Hussain *et al.* (2016); De-Souza *et al*. (2016); Singh *et al.* (2018).

Conclusion

About twelve traits exhibit a high amount of variation and are highly heritable. Most of the yield related traits are highly associated with yield, either directly or indirectly. One of the important quality characteristics, carotene was not associated with any of these traits studied and is highly heritable in nature. Ascorbic acid content is highly associated with many of the yield oriented traits and it is strongly positively associated with TSS. Earliness and per cent fruit set exhibited negative significant relations.

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Ethics statement

No specific permits were required for the described field studies because no human or animal subjects were involved in this research.

Originality and plagiarism

Authors should ensure that they have written and submitted only entirely original works, and if they have used the work and/or words of others, that this has been appropriately cited. Plagiarism in all its forms constitutes unethical publishing behavior and is unacceptable.

Consent for publication

All the authors agreed to publish the content.

Competing interests

There were no conflict of interest in the publication of this content

Data availability

All the data of this manuscript are included in the MS. No separate external data source is required. If anything is required from the MS, certainly, this will be extended by communicating with the corresponding author through corresponding official mail; purushothj14@gmail.com

Author contributions

Research grant- JP, TS, Idea conceptualization- JP, TS, Experiments- JP, TS, TK, Guidance- TS, TK, RS, MK, BA, Writing original draft- JP, TS, Writing- reviewing & editing- JP, TS, TK, BA

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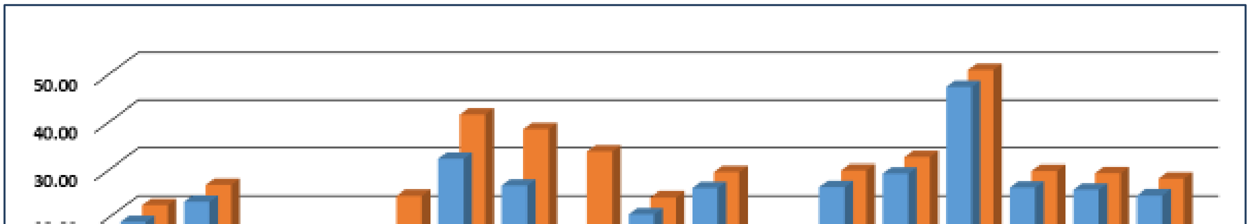

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Figure 1. Graphical representation of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV)

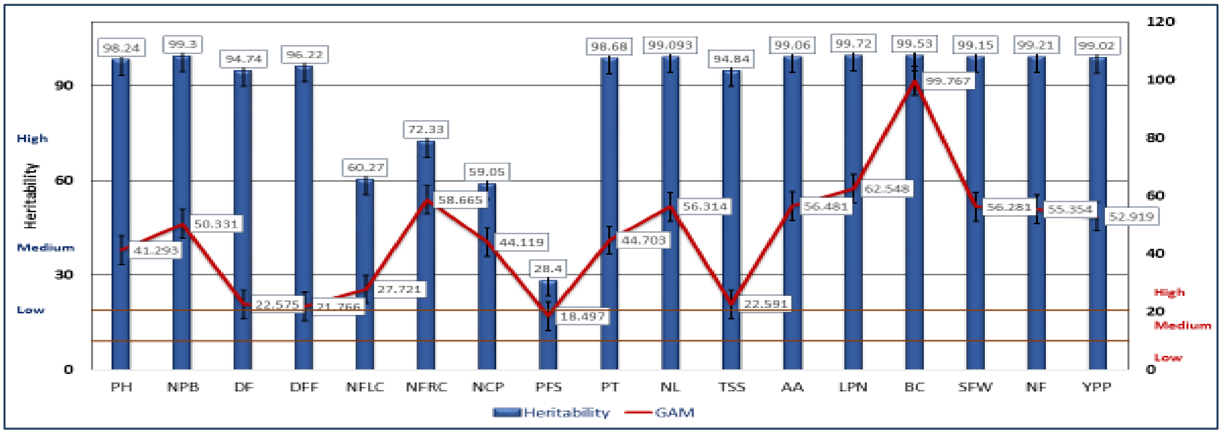
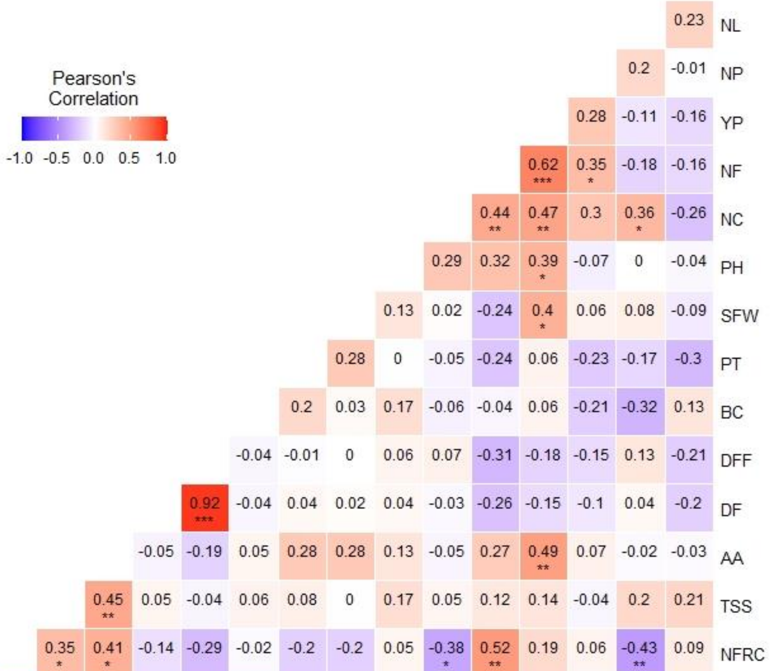


Figure 2. Graphical representation of heritability (h^2) and genetic advance (GAM)



PH - Plant height; **NP -** Number of primary branches; **DF -** Days to flowering; **DFF -** Days to fifty per cent flowering; **NFLC -** Number of flowers cluster^{-1}; **NFRC -** Number of fruits cluster^{-1}; **NCP -** Number of cluster plant^{-1}; **PFS -** Per cent fruit set; **PT -** Pericarp thickness; **NL -** Number of locules; **TSS** – Total soluble solids; **AA -** ascorbic acid content; **LPN -**Lycopene content; **BC -** β-carotene content; **SFW** – Single fruit weight; **NF -** Number of fruits plant^{-1}; **YPP -** yield plant^{-1}

Figure 3. Pearson's correlation coefficients among yield and yield attributes of tomato genotypes

Table 1: Analysis of variance for different characters in tomato genotypes

Source of variation	Replication	Genotypes	Error	SEM	CD 5%	CD 1%
DF	2	35				
PH	9.580	1129.750	6.700	1.494	4.215	5.596
NP	0.001	19.219	0.045	0.123	0.346	0.459
DF	0.176	21.221	0.385	0.358	1.011	1.342
DFF	0.272	24.221	0.313	0.323	0.911	1.209
NFLC	0.898	2.977	0.536	0.423	1.193	1.583
NFRC	0.037	3.781	0.428	0.378	1.065	1.414
NCP	27.382	191.081	35.875	3.458	9.754	12.949
PFS	42.080	389.840	177.990	7.703	21.726	28.844
PT	0.001	0.045	0.001	0.009	0.024	0.032
NL	0.001	3.391	0.001	0.001	0.001	0.001
TSS	0.029	0.785	0.014	0.068	0.193	0.256

AA	0.630	160.276	0.504	0.410	1.156	1.534
LPN	0.013	10.389	0.010	0.057	0.160	0.212
BC	0.042	18.411	0.029	0.099	0.279	0.370
SFW	0.250	816.140	2.330	0.880	2.483	3.297
NF	0.060	813.690	2.140	0.845	2.384	3.165
YPP	1721.000	773964.000	2532.000	29.053	81.945	108.794