Morphological, biochemical and SSR marker based genetic diversity and identification of trait-specific accessions in exotic germplasm collection of tomato (Solanum lycopersicum L.)

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ABSTRACT

Characterization and evaluation of genetic base of exotic collections of germplasm hastens the process of crop breeding. Exotic collections of 25 tomato germplasm accessions along with a local check ‘Vaibhav’ were characterized at morphological, biochemical and DNA marker level in the University of Agricultural Sciences, Bangalore. Both morphometric and biochemical trait data divided the accessions into five clusters by model-based K-means cluster analysis. Accessions EC-620481 and EC-620554 were found highly diverse and promising to broaden the genetic base of breeding stocks in tomato. SSR marker based genetic parameter estimates inferred lower genetic differences at marker loci. However, UPGMA classification displayed similar kind of diversity as exhibited at morphometric level. Traits specific accessions identified have potential to accelerate trait specific breeding for economically important traits. This investigation resulted in the identification of such potential accessions for their use in commercial tomato breeding.

Introduction

Among the members of nightshade family Solanaceae, tomato is the major vegetable crop in the world (Rothanet al., 2019). The advanced plant breeding activities narrowed down the genetic base of available tomato breeding lines due to repeated selections (Miller and Tanksley, 1990). Introducing new variation into available breeding lines in tomato is need of the hour to broaden the genetic base. Inclusion of exotic variation into tomato breeding programs is necessary to introduce new gene combinations (Bergougnoux, 2014). Assessment of genetic diversity of such exotic germplasm accessions provides an insight about its value (Rick and Chetelat, 1995). Characterization based on morphological trait expression is most commonly employed for assessing genetic differences among individuals in a population (Anilkumar et al., 2017). In complement to it, the biochemical products produced during different stages of plant development also serve the purpose. Nevertheless, expression of these morphological and biochemical characters are highly influenced by environment and hinders the estimates of genetic diversity (Brunlop and Finckh, 2010). However, DNA markers are crop non-stage specific and environmentally neutral complement to the morphological characters in diversity study (Milevska et al., 2011). Supplementing morphological character based diversity with biochemical and DNA marker data assure breeders to strategically select appropriate genotype for breeding programs (Herraiz et al., 2015). The
objective of present investigation is to examine genetic diversity among exotic collection of tomato germplasm accessions at morphological, biochemical and SSR marker loci.

**Material and Methods**

The genetic material for the investigation consisted of 25 exotic germplasm collections obtained from National Bureau of Plant Genetic Resources (NBPGR), Regional station, Rajendranagar, Hyderabad, India and a local check variety ‘Vaibhav’ released by University of Agricultural Sciences, Bangalore (Table-1). The genotypes were evaluated at experimental plots of Department of Plant Biotechnology, University of Agricultural Sciences, Bangalore. The experiment was laid out in randomized complete block design with two replications. Four weeks old seedlings from nursery trays were transplanted to field maintaining a spacing of 75cm between rows and 45cm between plants. To ensure a healthy crop, the recommended tomato management practices like spacing and regular watering were followed.

Table 1: List of exotic collection of tomato accessions used in the study.

| Sl. No | Accessions     | Growth type | Flower color | Fruit color |
|--------|----------------|-------------|--------------|-------------|
| 1      | EC-620437      | Indet.      | Yellow       | Orange red  |
| 2      | EC-620438      | Indet.      | Yellow       | Deep red    |
| 3      | EC-620456      | Indet.      | Yellow       | Light yellow|
| 4      | EC-620460      | Indet.      | Yellow       | Deep red    |
| 5      | EC-620472      | Indet.      | Yellow       | Orange red  |
| 6      | EC-620474      | Indet.      | Yellow       | Deep red    |
| 7      | EC-620612      | Indet.      | Yellow       | Light yellow|
| 8      | EC-620614      | Indet.      | Yellow       | Orange red  |
| 9      | EC-620615      | Indet.      | Yellow       | Deep red    |
| 10     | EC-620616      | Indet.      | Yellow       | Light yellow|
| 11     | EC-620617      | Indet.      | Yellow       | Orange red  |
| 12     | EC-620618      | Indet.      | Yellow       | Deep red    |
| 13     | EC-620620      | Indet.      | Yellow       | Light yellow|
| 14     | EC-620621      | Indet.      | Yellow       | Orange red  |
| 15     | EC-620622      | Indet.      | Yellow       | Deep red    |
| 16     | EC-620623      | Indet.      | Yellow       | Light yellow|
| 17     | EC-620624      | Indet.      | Yellow       | Orange red  |

Ten randomly tagged plants were considered for recording observations on 11 morphometric traits. The traits recorded were days to flowering, days to flowering to fruit set, plant height at 65 days, number of branches, fruits per cluster, fruits per plant, fruit length, fruit width, fruit weight, number of locules and plant yield. Apart from these, qualitative trait data were also recorded on flower color, fruit color and growth habit of experimental material (Table 2 and Figure 1). The data on biochemical parameters viz., lycopene content (Ranganna, 1976); total soluble solids (TSS) and ascorbic acid content (Johnson, 1948) were recorded. TSS was recorded from five randomly selected fruits from all accessions by squeezing the juice on Erma hand refractometer (0-32° Brix) at room temperature and mean was worked out.

The genomic DNA of 26 genotypes was extracted from young and healthy leaves using CTAB method (Doyle and Doyle, 1987). A total of 42 SSR markers (Table 3) were used to differentiate 26 genotypes at SSR marker loci. The size variations of amplicons produced at SSR priming regions in the genomic DNA were scored as different alleles at each SSR loci and subjected to analysis.

**Table 2: Qualitative characters in different tomato accessions.**

| No | Accessions     | Growth type | Flower color | Fruit color |
|----|----------------|-------------|--------------|-------------|
| 1  | EC-620437      | Indet.      | Yellow       | Orange red  |
| 2  | EC-620438      | Indet.      | Yellow       | Deep red    |
| 3  | EC-620456      | Indet.      | Yellow       | Light yellow|
| 4  | EC-620460      | Indet.      | Yellow       | Deep red    |
| 5  | EC-620472      | Indet.      | Yellow       | Orange red  |
| 6  | EC-620474      | Indet.      | Yellow       | Deep red    |
| 7  | EC-620481      | Indet.      | Yellow       | Deep red    |
| 8  | EC-620521      | Indet.      | Yellow       | Light yellow|
| 9  | EC-620643      | Determinate | Yellow       | Orange red  |
| 10 | EC-620644      | Indet.      | Yellow       | Deep red    |
| 11 | EC-620545      | Indet.      | Yellow       | Light yellow|
| 12 | EC-620546      | Indet.      | Yellow       | Orange red  |
| 13 | EC-620550      | Indet.      | Yellow       | Deep red    |
| 14 | EC-620553      | Determinate | Yellow       | Light yellow|
| 15 | EC-620554      | Determinate | Yellow       | Deep red    |
| 16 | EC-620557      | Determinate | Yellow       | Orange red  |
| 17 | EC-620560      | Indet.      | Yellow       | Light yellow|
| 18 | EC-620563      | Indet.      | Yellow       | Orange red  |
| 19 | EC-620567      | Determinate | Yellow       | Orange red  |
| 20 | EC-620568      | Indet.      | Yellow       | Deep red    |
| 21 | EC-614997      | Determinate | Yellow       | Light yellow|
| 22 | EC-614998      | Indet.      | Yellow       | Light yellow|
| 23 | EC-620343      | Indet.      | Yellow       | Orange red  |
| 24 | EC-620394      | Determinate | Yellow       | Orange red  |
| 25 | EC-632946      | Indet.      | Yellow       | Light yellow|
| 26 | Vaibhav (Check)| Indet.      | Yellow       | Deep red    |

Statistical analysis

The mean data on 11 morphological characters recorded over two years was subjected to Levene’s
test (Levene, 1960) of variance using SPSS V.16 software. The test results assured pooling of data from two years as their variances did not differ significantly. The pooled data was subjected to K-means cluster analysis using RStudio version 1.2.133 (RStudio team, 2019). Trait specific accessions were identified for each morphological traits based on comparative performance of accessions with check. Among the 42 SSR markers used, 23 were found polymorphic across the germplasm collection. Powermarker V3.25 (Liu and Muse, 2005) was used for estimation of various population genetic parameters such as polymorphic information content (PIC), major allele frequency and gene diversity. The same data was also subjected to UPGMA classification using DARwin 6 software to classify the accessions.

**Results and Discussion**

The highest plant height was recorded in EC-620563 and EC-620546 (126.25 and 124.25 cm). The number of branches per plant were higher in EC-614998 (63.50) followed by EC-620546 (62.00). Among twenty five tomato accessions studied, seventeen were indeterminate type and eight accessions were determinate type. There was no significant difference in the number of days taken for flowering and it ranged from 31.00 to 36.00. There was significant variation among the accessions for the individual fruit weight. The higher fruit weight was recorded in EC-620998 (104g) and the lower fruit weight was recorded in EC-620554 (33g). Three accessions recorded higher number of fruits per plant viz EC-620546, EC-620568, and EC-614997 (70.00 to 72.25 fruits/plant) whereas the check variety Vaibhav recorded around 46.75 fruits/plant which was on par with the average mean. The number of fruits per cluster varied from 4.50 to 12.50, the higher number was recorded in EC-620557 and EC-620568 followed by EC-620553 as compared to Vaibhav with 5.50 fruits per cluster. The total fruit yield per plant varied from 1.43kg to 6.30kg/plant. The higheeryields were obtained in EC-614997 (6.30kg) followed by EC-620560 (6.14kg). However the average mean yield per plant was 3.59kg. Similar type of variability with respect to yield parameters was reported by Pradeep Kumar et al. (2001); Kaushik et al. (2011) and Reddy et al. (2013). The growth type of determinate (17) and indeterminate (8) were observed in the accessions. Flower color in all the accessions was yellow. Fruit color varied from deep red to light yellow. Study conducted by Hussain et al. (2021) also indicated that the PCV and GCV were found to be higher for number of fruits plant-1, average fruit weight (g), fruit yield hectare-1 (q), and pericarp thickness (mm), indicating greater phenotypic and genotypic variability among the accessions. Significantly higher lycopene content was observed in two accessions viz., EC620521 (5.47mg/100g) and EC-620550 (5.21mg/100g). Higher TSS was observed in EC-632946 (6.95°Brix) followed by EC-620557 and EC-620550 (6.15°Brix and 6.05°Brix). The ascorbic acid levels were very high in some of the accessions. It varied from 8.76mg/100g to 55mg/100g. Similar reports on the variations in the lycopene content, TSS and ascorbic acid content are reported by Bose et al. (2002); Collins and Veazie (2006) and Panthee et al. (2012). Hussain et al. (2021) reported that the PCV and GCV for total Soluble Solids (°Brix) ranged from 6.86 to 48.78 for reducing sugar (%). The pooled mean values of 11 morphological characters subjected to K-means clustering divided 26 accessions into five different clusters. Among five clusters, cluster four was included highest number of accessions and cluster two was found solitary with only accession EC-620481 inferring its distinctness from other accessions (Fig. 2). The heat map of Euclidian genetic distance among 26 accessions clearly depicted the differences among themselves (Fig.3). The estimate of genetic distance for accession EC-620554 (15) and EC-620481 (7) were higher from any other accessions under the study inferring the genetic worth of these accessions. Genotypes with higher genetic distances can be best utilized for developing heterotic hybrids in practical plant breeding schemes (Anilkumar and Lohithaswa, 2018). Based on three biochemical traits, genotypes were grouped into five clusters (Fig. 4), while the composition of these clusters differed with those based on morphometric traits. However, the results from biochemical data paved the path for selection of genotypes in breeding programs targeted to improve quality. Observed gene diversity and Polymorphic information content (PIC) value
Table 3: List of SSR markers used in the study.

| Marker | Sequence | Expected product size (bp) |
|--------|----------|---------------------------|
| SSR111 | F: TTCTTCCCTTCCATCGTTCT  
        | R: TTGTTGCTATATCTGCTGACA  | 190 |
| SSR134 | F: CCCTCTTGCTAAACATCCA  
        | R: CGTTGCAAATTCAGATATGG  | 175 |
| SSR146 | F: TATGCGCTAGGCTGAACC  
        | R: CGAACGCCACACTACACT  | 220 |
| SSR248 | F: GCATTCGCTGCTGCTGTT  
        | R: GGGAGCTTCATCATAGTAACG  | 270 |
| SSR310 | F: GCGATGAGGATGACATGG  
        | R: TTTACAGGCTGTCGCACT  | 175 |
| SSR318 | F: GCAGAGGATATGGCATCGC  
        | R: CAAAACGAACCATCAAGG  | 180 |
| TOM49  | F: AAGAAACTTTTTTGAAATGG  
        | R: ATACAATTTAGAGGATCAAGG  | 190 |
| TOM144 | F: CTGGTTACCTCAAGAGGGCTG  
        | R: ACTTTACCTTATATTGCGACG  | 180 |
| TOM152 | F: ATTCAGGAACCTTTTGACTCC  
        | R: TGCCATTAGGCTGCTGTAATA  | 190 |
| TOM184 | F: CAACCCCTCCTCTCTCTCT  
        | R: CTGCTTTGTCCAGATTTGAA  | 180 |
| TOM210 | F: GTTGGATTACTGAGAGGGTTTA  
        | R: ACAAAAATTCACCCCCATCG  | 205 |
| TOM236 | F: GTTTTTTCACATCAAGAGCT  
        | R: GGATGTTTTGCTGCTGTAACT  | 200 |
| TGS0385| F: ATGCCAAAAAGTGATACGGG  
        | R: GGGACAAAAGCTGTAACACACA  | 163 |
| TGS2259| F: AGCGAAGCTGAAGCCATAAT  
        | R: GTCCTCCGCTGCTGACTG  | 205 |
| Eaat001| F: GATGGACACCCCTGCAATTATAGGT  
        | R: TCCACGTATACGGCACCAGC  | 136 |
| LEaat002| F: GCCAAGAGATGATCTTACAGCATAG  
        | R: CTTCTCCCATGACGTCTTCTCTCT  | 106 |
| LEaat003| F: CTGGTTGCGAAAATATGACAC  
        | R: AAGGCAGGTGATGTGATGAG  | 189 |
| LEaat006| F: GCCACGTATCTGATATACATAG  
        | R: GCCTCGGACAAATGATTG  | 174 |
| LEaat007| F: CAACAGCATAGTGAGGAGG  
        | R: TACATTTTCTTCTTCTCCATAG  | 100 |
| LEaat008| F: GAGTCGAGGAGAGCATAGTGGGAGG  
        | R: CGTGCAGATTCTCAAGGCAGC  | 178 |
| LEat006| F: CATAATCACAAGGCTCTCTTGCCA  
        | R: CATATGCGCTGTTATGTAAT  | 166 |
| LEat012| F: CGGAAAGGGAGGACTGGAATTG  
        | R: GTCGCGGAGTGAACCTTACGGA  | 110 |
| LEat013| F: ATCAACAGCTTCTTCGCCCACA  
        | R: ACCCATATCGCTCGGTTCC  | 163 |
| LEat018| F: CCCGCTATACGGCTGCTGTTG  
        | R: GCCGACCTCTCTTTGTTGTAA  | 120 |
| LEat020| F: ACTGCGCTCTCTCCTAAAGATAAAGG  
        | R: ACGGAAAATGCTCTACAAGAGTGG  | 212 |
| LEga003| F: TCGGGTTATCTTCGCCAACC  
        | R: GCCCTGAGATGTTTCTGCCA  | 241 |
| LEga005| F: TTTGCCCTAATCTCTTTGTCAT  
        | R: AACATAGTGCAAGTCTTATAAGGG  | 314 |
| LEga006| F: CCGTCCAGAAAGACGATGTAA  
        | R: CAAAGTCTTGCCCAAAATCC  | 248 |
| Marker      | Sequence               | Expected product size (bp) |
|------------|------------------------|---------------------------|
| LEga007    | F: CCTTGCACTGGAGGTGAATT  | 193                       |
|            | R: TCAAGCCTACATCAATCA   |                           |
| LEgata002  | F: TTGGTAATTATGTAGCGTGA| 344                       |
|            | R: TTGAGCGAGTATTTAAGTTT |                           |
| LEta002    | F: GCCCTCCACAAATCATCTATACA| 190                      |
|            | R: TCTCTGCATTTGACATCTTTTT |                      |
| LEta003    | F: GCTCTGTCTCTAAATGATACCTCC | 111                     |
|            | R: CAATGCTGGGACAGAGATTATAG |                     |
| LEta006    | F: CCTCTTCCTAACACATCC   | 167                       |
|            | R: TCTACTCGCTGGCAATTTCAG |                       |
| LEta007    | F: GCCGTGCTTGTTGGATTAG  | 291                       |
|            | R: CCTCTTTCGTCATTGTC     |                           |
| LEta015    | F: ATATGCAATGGACAATCTGAGGG | 107                     |
|            | R: TCTGCGATCAAATTAATATCAG |                     |
| LEta016    | F: AGTGTTGAAAAAGACTAAATCAGG | 174                     |
|            | R: CAACCAACATGTCACTTAAGAC |                     |
| LEta020    | F: AACGTTGAAAACATTGGTTA  | 275                       |
|            | R: CACCACAAACCCATCGTC    |                           |
| LEtaa002   | F: TGAGGAGAGTCAACCAACTCC | 133                       |
|            | R: ACTACTCTCTACTCTATATCC |                           |
| LEtca001   | F: TGATGCGCAAATTAAGTC    | 176                       |
|            | R: CTTGATGCACTTCATTG     |                           |
| SSR45      | F: TGTATCCTGTGGACAAATG   | 260                       |
|            | R: TCCAAGATACAGGCCACACCA |                           |
| SSR96      | F: GGGTTATCAATGATGCAATAG | 210                       |
|            | R: CCTTATGCTCGCCGTTT     |                           |
| SSR104     | F: TCCATATGGATATTCACCACCC| 220                      |
|            | R: CCCACTGCACATCACTGAC   |                           |

Figure 1: Variation in number of locules as high as 10 (EC-620481) to as low as 2 (EC-620456).

Figure 2: Grouping of genotypes using K-means cluster analysis based on 11 morphological characters.

Figure 3: Heat map representing Euclidian genetic distance between germplasm accessions based on 11 morphological characters.

Figure 4: Clustering of genotypes based on data recorded on three important biochemical parameters.
Figure 5: Tree diagram depicting SSR marker based UPGMA classification of germplasm accessions.

Table 4: List of 23 polymorphic markers and their major allele frequency, gene diversity, polymorphic information and content (PIC).

| Marker name | Major Allele Frequency | Allele No. | Gene Diversity | PIC  |
|-------------|------------------------|------------|----------------|------|
| SSR111      | 0.81                   | 2.00       | 0.30           | 0.26 |
| SSR134      | 0.94                   | 1.50       | 0.10           | 0.09 |
| SSR146      | 1.00                   | 1.00       | 0.00           | 0.00 |
| SSR318      | 1.00                   | 1.00       | 0.00           | 0.00 |
| TOM49       | 0.96                   | 1.50       | 0.07           | 0.07 |
| TOM144      | 0.92                   | 1.50       | 0.13           | 0.11 |
| TOM152      | 1.00                   | 1.00       | 0.00           | 0.00 |
| TOM184      | 0.81                   | 2.00       | 0.28           | 0.23 |
| TGS0385     | 0.85                   | 1.50       | 0.21           | 0.17 |
| Eaat001     | 0.98                   | 1.50       | 0.04           | 0.04 |
| LEaat002    | 1.00                   | 1.00       | 0.00           | 0.00 |
| LEat013     | 0.96                   | 1.50       | 0.07           | 0.07 |
| LEat020     | 1.00                   | 1.00       | 0.00           | 0.00 |
| LEga003     | 0.85                   | 1.50       | 0.21           | 0.17 |
| LEga005     | 0.94                   | 1.50       | 0.10           | 0.09 |
| LEta006     | 0.75                   | 2.00       | 0.34           | 0.27 |
| LEta015     | 0.75                   | 1.50       | 0.25           | 0.19 |
| LEta016     | 1.00                   | 1.00       | 0.00           | 0.00 |
| LEta020     | 0.87                   | 1.50       | 0.20           | 0.16 |
| SSR45       | 0.85                   | 1.50       | 0.21           | 0.17 |
| SSR96       | 0.65                   | 2.00       | 0.45           | 0.35 |
| SSR104      | 0.75                   | 2.00       | 0.36           | 0.29 |
| LEaat007    | 0.81                   | 2.00       | 0.31           | 0.26 |
### Table 5: Promising trait specific accessions in exotic collection of tomato germplasm.

| Traits                          | Selection criteria | Range          | Vaibhav (Check) | Accessions                                                                 |
|--------------------------------|--------------------|----------------|-----------------|---------------------------------------------------------------------------|
| **Days to flowering**           | Earliness          | 62-73          | 69              | EC-620474, EC-620546, EC-614997, EC-620472, EC-620544, EC-620550, EC-620553, EC-620481, EC-620521, EC-620545, EC-620546, EC-614998, EC-620438 and EC-620394 |
| **Flowering to fruit set**      | Earliness          | 6-12           | 10              | All the accessions except EC-614998 and EC-620554                            |
| **Plant height at 65 days**     | High               | 124-252 cm     | 185 cm          | EC-620563, EC-620546, EC-620544, EC-620474, EC-632946, EC-620560, EC-620543, EC-620550, EC-620557, EC-620437, EC-620567, EC-614998, EC-620553 and EC-620343 |
| **Number of branches**          | Medium             | 42-125         | 46              | EC-620456, EC-620460 and EC-620472                                          |
| **Fruits per cluster**          | High               | 9-12.5         | 11              | EC-614998, EC-620438, EC-620474, EC-620521, EC-620437, EC-620550, EC-620545, EC-620546, EC-620567, EC-614997, EC-620343, EC-632946, EC-620460, EC-620544, EC-620481, EC-620472, EC-620543, EC-620563, EC-620553, EC-620557 and EC-620568 |
| **Fruits per plant**            | High               | 32-170         | 94              | EC-620554, EC-620546, EC-620568, EC-614997, EC-620543, EC-620521, EC-620560, EC-620557, EC-620550, EC-620567, EC-620343 and EC-620568 |
| **Fruit length**                | High               | 8.24 – 13.82 cm| 10.48 cm        | EC-620543, EC-614997, EC-620472, EC-614998, EC-620544, EC-620545, EC-620553, EC-620550, EC-620568, EC-620557, EC-620456, EC-620437, EC-620546, EC-620460, EC-620438, EC-620394, EC-632946, EC-620474 and EC-620560 |
| **Fruit width**                 | High               | 8.52-12.90 cm  | 9.82 cm         | EC-620481, EC-620550, EC-614997, EC-620546, EC-620553, EC-620545, EC-620544, EC-620472, EC-620474, EC-620568, EC-620343, EC-620456, EC-620437, EC-620567, EC-620560, EC-620557, EC-632946, EC-620394 and EC-620438 |
| **Fruit weight**                | High               | 66-208 g       | 144.20 g        | EC-614998, EC-614997, EC-620553, EC-620563, EC-620394, EC-620545, EC-620481, EC-620474, EC-620460, EC-620456, EC-620437, EC-620546, EC-620438 and EC-620521 |
| **Number of locules**           | Fewer              | 2-10           | 7               | EC-620456, EC-620472, EC-620543, EC-620460, EC-620394, EC-620554, EC-620567, EC-620438, EC-620544, EC-620560, EC-620563, EC-620568, EC-614998, EC-620521, EC-620550 and EC-620557 |
| **Plant yield**                 | High               | 2.88-12.61 Kg  | 6.58 kg         | EC-614997, EC-620546, EC-620545, EC-620553, EC-620568, EC-620550, EC-620545, EC-620521, EC-614998, EC-620567, EC-620554 and EC-620481 |
inferred the lower differences between accessions at SSR marker loci (Table 4). However, tree constructed based on SSR amplicon data using UPGMA approach provided the visibility of diversity among accessions (Fig. 5). The accessions EC-620481 (7) and EC-620472 (5) formed solitary branches away from other accessions, proving its distinctness from other accessions. However, accession EC-620472 (5) was in cluster four under morphometric cluster analysis. This might be due to differences at genomic regions that amplified at SSR loci. These results indicated the significant differences at genetic level which can be exploited by strategic breeding programs. Brake et al. (2021) in their study, among the genotypes screened for variability using ISSR markers observed the lowest genetic similarity value (0.46) was found between landraces Jo964 and Jo955, while the highest (0.94) was obtained between landraces Jo983 and 29. The accessions were compared with check variety to identify some accessions which are superior to check variety with respect to 11 morphological traits (Table 5). Such accessions which surpassed local check variety for given trait were considered as trait-specific accessions. The germplasm accessions identified for specific traits can be potentially used for trait specific breeding activity without further evaluation, saving breeder’s time and resources.

Conclusion
It is concluded that this investigation resulted in the identification of specific traits which are economically important, and are having potential to be utilised in commercial tomato breeding.

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Conflict of interest
The authors declare that they have no conflict of interest.

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