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Description of The Phenotypic Characteristics of Some Tomato Genotypes

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HIGHLIGHTS

- Tomato (*Solanum lycopersicum* L.), is one of the most economically valuable vegetable crops
- Phenotypic characterization studies are important for the appropriate assessment of many factors, such as plant genetic diversity and yield potential.

Abstract

This study was carried out in order to determine some morphological characteristics of 240 tomato genotypes at S2 level and to demonstrate the usability of these materials in breeding programs. Accordingly, the average fruit weight was between 553.11 g and 74.83 g. The mean pericarp thickness, carpel number, and soluble dry matter content of the genotypes were 7.38 mm, 3.6 pieces and 4.04% brix, respectively. While the fruit color of 165 genotypes was determined as red, the longitudinal section shape of the fruit was determined as slightly flattened in 106 genotypes. The flowering period of the genotypes was determined as medium flowering. The leaf posture of the genotypes was determined as attitude, and the leaf width was determined as medium and broad leaves. Based on these measurements and observations, tomato genotypes were also investigated using the Principal Component Analysis (PCA) methods. According to the PCA results, the first component explained 24.2% of the total variance, and the number of fruit carpels, average fruit weight, and fruit width were the most highly explained parameters. The second and third main components constituted 13.1% and 11.2% of the total. Based on the results of fruit characterization studies, genotypes 233, 447, 126, 22, 391, 118, 71, 100, 340, 102 were determined as superior. Overall, a high degree of phenotypic variation was detected among the characterized tomato genotypes.

Keywords: Principal Component Analysis; Morphological; Tomato

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1. Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most economically valuable vegetable crops. While 186 million tons of tomatoes are produced annually on 5 million hectares of land worldwide (FAO 2020), Türkiye ranks 4th with an annual production of 13 million tons on 181 thousand hectares (TURKSTAT 2022).

Tomato is a versatile vegetable that can be consumed both directly fresh and by processing in different ways, such as frozen, canned, paste, ketchup, pickled, sauce, dried, juice, pureed and chopped product (Günay 2005). As an important member of the *Solanaceae* family and a model plant, tomato is a widely studied species. The most essential element for improving tomato production and quality is for sure, high genetic performance. For this reason, tomato breeding studies are important for the sector and continuous breeding programs are carried out in order to develop new varieties. In addition to high yield and quality, stress resistance is often aimed to be establised in hybrid varieties (Kaloo 1988).

Detection of variation among parental genotypes is important in hybrid cultivar development for anticipating hybrid performance (Gözen 2008; Keskin 2014). In breeding studies, phenological characterization provide useful information in determining the desired traits. (Hernández-Villareal 2013). In this context, it is very important to determine the relationship between genotypes and to reveal the extent of genetic diversity (Oduor 2016). Phenotypic characterization is used to assess the diversity manifested by morphological traits (Bajracharya et al. 2006).

Fruit and plant characteristics come to the fore among tomato morphological characters (Altıntaş et al. 2016). When the relevant literature is examined, it is observed that research efforts continuously aim at improving the UPOV criteria in line with their aims (Kurt 2019). On the other hand, it is well known that the parameters examined in characterization studies are under the influence of many factors and features related to each other may require multiple factors to be considered.

Determination of phenotypic traits is time consuming and difficult due to the quantitative nature of the traits (Fiorani and Schurr 2013). Nevertheless, phenotypic characterization studies are required for appropriately assessing many factors such as plant genetic diversity and yield potential (Lopez et al. 1994; Dharmatti et al. 2001). In this context, multivariate analysis methods have been developed by examining more than one feature at the same time (Tahtalı 2005).

Principal component analysis is commonly performed in characterization studies (Karaağaç and Balkaya 2010). The aim of the present study was to reveal the diversity within a set of 240 S2 level tomato genotypes based on some morphological characters defined in UPOV criteria by clustering and principal component analysis.

2. Materials and Methods

In the study, 240 S2 level genotypes derived from Selko Arge company breeding gene pool were characterized. The seed sowing viols were filled homogeneously with 2 parts peat and 1 part perlite, and the seeds were sown in these viols. After the seedlings were grown according to the method, after the true leaves were formed on the seedlings, dilution was made in the viols. Seeds of the genotypes on July 22, 2019, under greenhouse conditions. Four weeks later, these seedlings were planted as double rows in 40x50x100 cm intervals, 18 of each genotype, in the greenhouse in Aksu district of Antalya province. During the fertilization period, 100 kg ha-1 N, 150 kg ha-1 P2O5 and 100 kg ha-1 K2O were applied in the experimental area in pure form. Weed control was carried out by hoeing, and diseases and pest management has been carried out by spraying regularly toprotect plant health and growth. 10 plants from each genotype were selected from the set of S2 level genotypes and the observations were taken according to some UPOV parameters (Tablo 1).

Growth type, number of flowers, inflorescence at first node, leaf attitude, leaf length, leaf width, presence of leaf blade, fruit width-length, cross-section, fruit shape in longitudinal section, fruit pericarp thickness, fruit locus amount, fruit presence of green neck, fruit maturity time, water soluble dry matter, fruit color were the observed characters. Measurements and observations were determined according to the upov criteria. In the study, leafing, leaf length and leaf width observations were determined by observations of plants in the whole plot relative to the seventh leaf. The number of flowers in the cluster was determined according to the 3rd brush. Average fruit weight, fruit length, fruit width, pericarp thickness, carpel number, fruit shape, fruit color, fruit longitudinal section and fruit cross-section shape were determined in the first 3 fruits in each brush.

Measurements and observations taken from 240 tomato genotypes were analyzed principal component analysis (PCA) using the JMP-14 software. Differences among genotypes were determined by examining the Score Plot graph created in line with the components obtained from the analysis.

Table 1. Measurements and observations made in tomato geno-types (UPOV 2011)

Features	Measurement and Observations
Plantgrowthtype	İndeterminate (2), Detarminate (1)
Leaf attitude	Semi-Erect (3), Horizontal (5), Semi-Dropping (7)
Leaf length	Short (3), Medium (5), Long (7)
Leaf width	Narrow (3), Medium (5), Broad (7)
İnflorescence at first node	Present (9), Absent (1)
Plant flowering time	Early (3), Medium (5), Late (7)
Fruit color	Light Pink (1), Pink (3), Light Red (5), Red (7), Dark Red (9)
Extent of green shoulder	Present (9), Absent (1)
Fruit shape	Flattened (1), SlightFlattened (2), Round (3), Ovate (6), Cordate (7),
Fruit diameter	Round (9), Nonround (1)
Fruit maturity time	VeryEarly (1), Early (3), Medium (5), Late (7), VeryLate (9)
Fruit weight (g)	
Fruit width (mm)	
Fruit length (mm)	
Number of locules	
Thickness of pericarp	
SÇKM	

3. Result and Discussion

3.1. *Morphological features*

Out of the 240 genotypes included in our study, 3 genotypes (1.2%) were determined as determinate and 237 (98.7%) were indeterminate. While flowering was observed in the first node in 7 genotypes (2.8%), it was not observed in 233 genotypes (86.2%). Small leaflets were detected in 207 genotypes (86.2%) and were absent in 33 genotypes (13.7%). Early flowering was detected in 39 of the genotypes (16.2%), flowering time was intermediate in 124 genotypes (51.6%), and late in 77 genotypes (32.2%). The number of flowers in a cluster was defined as 3-5 (44.1%) in 106 genotypes, 6-10 (44.1%) in 106 genotypes, and more than 10 (11.6%) in 28 genotypes. As a result of the observations made in the study, the leaf attitude of the genotypes was determined as semi-vertical (17%) in 41 genotypes, horizontal (53.3%) in 128 genotypes, and semi-drooping (29.5%) in 71 genotypes. According to leaf length observation values, 4 genotypes had short (1.6%), 62 genotypes had medium (25.8%) and 174 genotypes had long (72.5%) leaf structure. In terms of leaf width, 54 genotypes were narrow (22.5%), 100 genotypes were medium (41.6%) and 86 genotypes were determined as broad-leaved (35.8%) (Tablo 3).

According to the relevant literature, different scales of diversity are reported for the above-mentioned traits, as expected. For example, Özbay (2021) reported that flowering time varied between 12-30 days; Anisa et al. (2022) reported that the number of flowers in a cluster varied between 6 and 8. Salim et al. (2020) reported 59.09% of their observed genotypes as horizontal, 27.27% as semi-upright and 13.64% as semi-drooping. Kayak et al. (2022) determined that 43.6% of the genotypes they examined had semi-drooping, 47.8% had horizontal and 8.5% had semi-upright leaves. Kal et al. (2020) reported 43% short-leaved, 31% medium, and 26% long leaved genotypes within their observed pool of materials. The observed variation among different studies obviously sources from both the genetic make up of the characterized gene pools and the environment. Numbered lists can be added as follows:

While green neck character was not observed for 97.09% of the genotypes, it was observed in 2.9% of the genotypes. The ripening time was medium for 25%, late for 36.6%, very late for 34.1% and early for 4.1% of the genotypes. When mature fruit color was observed, 10.4% of the genotypes were pink, 4.5% were light pink, 8.7% were light red, 68.7% were red and 7.7% were dark red (Tablo 3).

Since tomato is rich in terms of color diversity, it is natural to have these differences within and among studies. According to the results of a similar study by Kayak et al. (2022), 1.06% of the genotypes were light pink, 39.36% were pink, 22.3% were light red, 35.1% were red, 2.1% were dark red. Jin et al. (2019) determined that 57.72% of their genotypes were red and 36.42% were pink. Altintas et al. (2016) detected 1.6% of their genotypes as orange, 25% as pink, 73.4% as red. In the work by Öztürk (2022), the limited number of genotypes included in the study were grouped according to maturity color as 1 yellow, 3 pink, 1 light red, 16 red, 2 dark red, 1 brown.

When the fruit shape in longitudinal section was examined in the present work, 32 flat (13.3%), 106 slightly flattened (44.1%), 66 round (27.3%), 31 heart-shaped (12.9%), 4 oval (1.6%), 1 rectangular (0.4%) genotypes were observed. Fruit cross-section shapes were determined as 43.3% round and 56.6% not round (Tablo 3).

In the relevant literature, Bota et al. (2014) identified their genotypes as 50% flattened, 31% round, and 19% heart, long and rectangular. According to the results reported by Bhattarai et al.(2018b), the genotypes were 60% flat, 6% slightly flattened, 1% very round, 8% round, 4% heart-shaped and 21% cylindrical. Kurt (2019) reported 43.5% of flattened, 31% of oval, 20.5% of round, and 5% of long genotypes in his study with 39 tomato genotypes. Salim et al. (2020) determined 50% round, 9% heart, 31% flattened, 4% elliptical genotypes. In the work of Öztürk (2022), 12 genotypes were observed as round, 1 genotype was observed as heart, 5 as flat, 5 as slightly flat and 1 genotype as cylindrical.

In our study, while the average fruit weight was determined as 204.28 grams, genotype 118 (553.11 g) had the highest and 108 (74.83 g) had the lowest fruit weights. In the study by Öztürk (2022), the fruit weight was ranged between 307.99 g and 16.63 g. Figàs et al. (2018), reported a fruit weight that ranged between 62.6 and 446.6 g. Thus, variation was observed for the fruit weight trait in all the above-mentioned studies. In the present work, while the average fruit width was measured as 59.82 mm, the highest and lowest values were measured for genotype 22 (99.50 mm) and genotype 108 (46.30 mm), respectively. The average fruit length of the genotypes was 66.09 mm. For genotype 391 (103.45 mm) was fruit length was the highest, and for genotype 199 (40.42 mm), fruit length was the lowest (Tablo 4).

According to Salim et al. (2020), fruit length varied between 3.91 and 6.57 cm, and fruit width varied between 3.63 and 8.15 cm. Kouam et al. (2018) reported that fruit length and fruit width were 3.74 to 5.34 and 3.64 to 5.71 cm, respectively. Figàs et al. (2015) reported the variation in fruit length as 1.88-9.57 cm and fruit width as 2.15-11.40 cm in their study.

According to our results, the mean pericarp thickness and carpel number of the genotypes were determined as 7.38 mm and 3.6 pieces, respectively (Tablo 4). As a result of the tomato characterization study by Singh and Aakansha (2015), it was reported that the number of carpels in fruits varied between 2 and 11. Figàs et al. (2015) reported a carpel number range from 2.00 to 18.33. In our study, the amount of soluble dry matter was determined as 4.04% brix. Singh and Aakansha (2015), Khushboo et al. (2015) and Vishwanath et al. (2014) reported values of 4.00%, 5.60%, 3.25-6.32%, 4.00% and 5.60%, respectively. The relevant literature displays wide differences in all above mentioned parameters, which would naturally be both genetic and under environmental influence.

3.2. Principal Component Analysis

The principal component (PC) axes, eigen values, variation and cumulative variation ratios obtained as a result of principal component analysis, and factor coefficients indicating the weight values of principal components on the basis of features are presented in detail in Table 2. It has been stated in studies that PCA analysis can be used effectively when the first two components explain more than 25% of the variance.

In their study, Seymen et al. (2019) determined that the three components represented approximately 48.39% in terms of 11 morphological features as a result of PCA. The eigen values of the first three components were found between 1.00-2.65. An eigen value greater than 1 indicates that the principal component weight values are reliable (Mohammadi and Prasanna, 2003). In the work of Mohammadi and Prasanna (2003), the first component explained 24.1% of the total variance, and the number of fruit carpels, fruit average weight, and fruit width were the highest explained parameters. The second and third main components constituted 13.06% and 11.16% of the total. In a study, they reported that it explained 63.35% of the total variation (Jin et al., 2019). Zhou et al. (2015) reported that they explained 78.54% of the total variation.

Kal et al. (2020) studied 77 cherry tomatoes, and the total variance was found to be 16.8% in PC1, 12.6% in PC2 and 10.2% in PC3. Figàs et al. (2015) reported that the total variation in the first and second components of PCA in tomato genotypes Cherry, Borseta, Cor, Penjar, Plana, Pruna, Redona and Valenciana was 22.6% and 11.8%, respectively. Bhattarai et al. (2016) obtained 5 principal component axes in 71 tomato genotypes and were reported to explain more than 92% of the total variation.

Table 2. Revealed eigenvalue, variation and principal component (PCA) axes of the properties examined as a result of PCA

Eigen value	2.6595	1.4363	1.2274
Variance %	24.177	13.057	11.158
Cumulative variance %	24.177	37.234	48.392
Traits	**PC1**	**PC2**	**PC3**
FWC	-0.17366	0.10916	-0.20372
FMT	0.16377	-0.00461	0.22267*
FC	-0.14824	0.44027*	0.46521*
FW	0.34171 *	0.41476	-0.39708*
FL	0.21458	-0.14225	0.60006*
SLS	-0.38755	0.05144*	-0.01321
FCS	-0.30346	0.03314	-0.08048
TP	0.05913	0.70866*	0.08749
CN	0.48645*	-0.25870*	-0.01390
SÇKM	-0.12980	-0.00752	0.39663*
AFW	0.50889*	0.17043	0.05417

FWC: Flower number of cluster, FMT: Fruit maturity time, FC: Fruit color, FW: Fruit widt, FL: Fruit lenght, SLS: Shape in longitudinal section, FCS: Fruit cross-section, TP: Thickness of pericarp, CN: Carpel number, SÇKM: Water soluble dry matter, AFW: Average fruit weight

When the results were examined, it was reported that it explained more than 48.3% of the first three components. The first component (PC1) explained 24.17% of the total variance and a high positive correlation was found between FW, AFW, and CN. The second component (PC2) explained 13.05% of the total variance and showed a high positive correlation between FC, TP nd while a strong negative relationship with CN. The third component (PC3) explains 11.15% of the total variance and shows a strong positive relationship between FMT, FL and while a strong negative relationship with FW. In another study with tomato breeding lines, it was reported that six principal component axes were independent from each other in terms of 17 traits, and these axes explained 63.35% of the total variation (Jin et al., 2019). To examine the interrelationships between features, a loading chart was created using principal component analysis. In the figure (Şekil 1), if <90° is a positive relationship, if >90° is a negative relationship, and if the angle is 90°, there is no significant relationship between vectors. When Figure 1 is examined, it is seen that there is a strong positive relationship between AFW, FW, FS and CN, while FLS and MT are explained with a strong negative relationship with them.

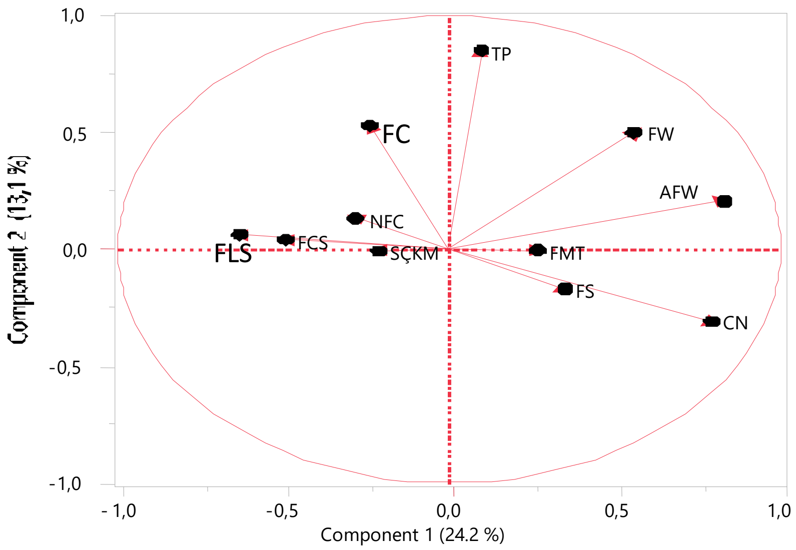

Figure 1. Loading plot graph obtained from PC1 and PC2 as a result of PCA made from fruit characteristics of tomato genotypes.

TP: Pericarp thickness, FW: Fruit width, AFW: Fruit average weight, FMT: Fruit maturity time, FS: Fruit size, CN: carpels number, FLS: Fruit longitudinal section, FCS: Fruit cross section, NFC: Number of flowers in cluster, FC: Fruit color, SÇKM: Water-Soluble Dry Matter (Brix)

A score graph was created for the evaluation of 240 tomato genotypes using PC1 and PC2 components (Figure 2). The fruit characteristics of the genotypes are located at the positive and negative intersection of both components. In terms of fruit characteristics, genotypes 233, 447, 126, 22, 391, 118, 71, 100, 340, 102 were determined as superior genotypes.

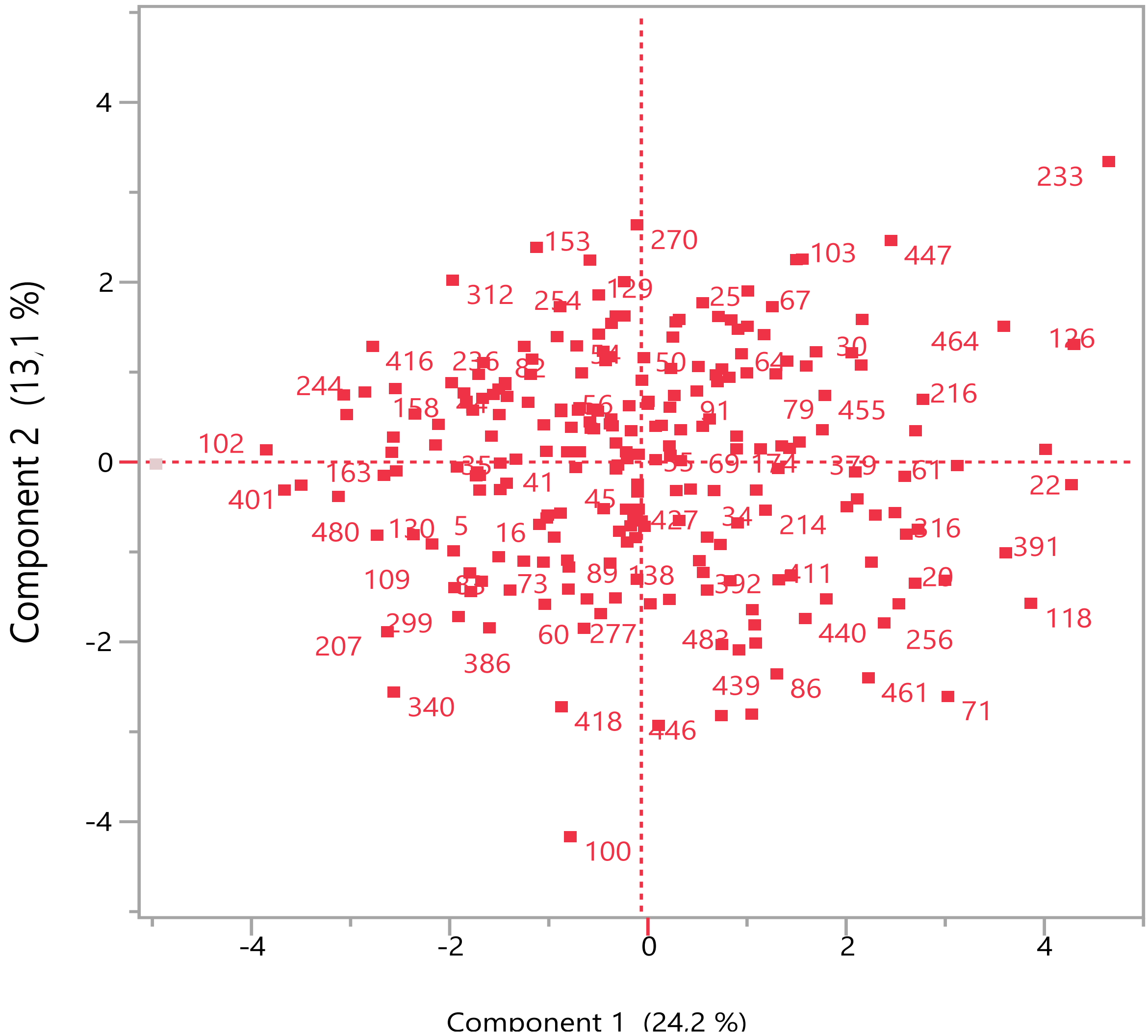

Figure 2. Score plot graph obtained from PCA result PC1 and PC2

4. Conclusions

In this study, some fruit and plant characteristics of 240 tomato genotypes in S2 stage were determined and the relationships between these characteristics were interpreted. As a result of the study, it was observed that there is a wide degree of variation between genotypes. As a result of the measurements, fruit weight differed between 553 and 74.83 grams. Fruit length varied between 103.45 and 40.42 mm and fruit width varied between 99.5 and 46.30 mm. It was determined that pericarp thickness ranged between 4.12 and 7.38 mm. The number of carpels in fruits varied between 2 and 7.

Based on morphological measurements and observations, 240 tomato genotypes were evaluated using Principal Component Analysis (PCA) method. As a result of the Principal Component Analysis (PCA), in terms of 11 morphological features, the three components represented approximately 48.39. The eigen values of the first three components were found between 1.00 and 2.65. As a result of PCA analysis, genotypes 233, 447, 126, 22, 391, 118, 71, 100, 340, 102 were determined as superior genotypes in terms of fruit characteristics. Overall, according to the data collected in the course of the present work it was determined that the variation between genotypes is high and, in this context, the evaluated gene pool qualifies as a potential core collection for future breeding programs.

5. Appendices

Table 3. Leaf and fruit characteristics of tomato genotypes

Genotype number	PGT	LA	LL	LW	IFN	FT	NFC	FC	PGN	GND	NS	FCS	FLS	MT
2	2	5	7	5	9	5	3	3	1	-	-	2	9	5
5	2	7	7	5	1	3	5	5	1	-	-	3	9	7
10	2	7	7	5	1	5	3	7	1	-	-	2	9	5
14	2	5	7	7	9	3	3	7	1	-	-	2	1	5
16	2	7	5	5	9	7	3	7	1	-	-	3	9	9
19	2	7	7	7	1	5	7	7	1	-	-	2	1	7
20	2	7	7	7	1	3	5	3	1	-	-	2	1	7
22	2	5	7	5	1	5	3	3	1	-	-	2	1	7
25	2	3	7	5	1	5	5	7	1	-	-	2	9	7
27	2	3	7	7	1	5	5	5	1	-	-	2	9	5
30	2	5	7	5	9	3	3	7	9	3	3	2	1	5
34	2	3	7	3	9	5	5	5	1	-	-	2	1	5
35	2	5	7	5	9	5	5	1	1	-	-	2	9	5
36	2	3	5	5	9	3	5	5	1	-	-	2	9	7
37	2	5	7	7	9	5	5	7	1	-	-	2	1	7
41	2	5	5	3	1	5	7	7	1	-	-	2	9	7
43	2	5	5	5	1	7	5	7	1	-	-	7	9	5
44	2	3	5	5	9	7	7	7	1	-	-	3	9	7
45	2	3	5	3	1	5	5	3	1	-	-	2	9	5
50	2	7	7	3	9	3	5	9	1	-	-	2	1	5
52	2	7	7	5	1	5	5	9	1	-	-	3	9	3
54	2	5	5	3	9	5	3	9	1	-	-	7	9	9
55	2	3	7	5	9	5	3	9	1	-	-	1	1	5
56	2	7	3	3	9	5	3	7	1	-	-	3	9	7
60	2	3	5	3	9	5	5	7	1	-	-	3	9	9
61	2	5	7	5	9	5	3	7	1	-	-	1	1	9
64	2	5	5	5	9	5	5	7	1	-	-	2	9	9
66	2	3	7	7	9	7	3	7	1	-	-	2	9	9
67	2	5	5	5	9	7	3	7	1	-	-	2	1	9
69	2	3	5	3	9	5	3	7	1	-	-	2	9	7
70	2	5	7	7	9	3	3	5	1	-	-	1	9	7
71	2	5	5	7	9	5	3	1	9	3	3	1	1	7
72	2	7	7	7	1	7	7	5	1	-	-	**3**	**9**	7
73	2	5	7	5	9	3	5	1	1	-	-	3	9	5
74	2	5	7	5	9	3	3	7	1	-	-	2	1	7
76	2	3	5	3	9	7	3	7	9	3	5	2	9	5
78	2	7	7	7	9	5	3	7	1	-	-	7	1	9
79	2	5	5	7	9	5	5	7	1	-	-	2	1	9
82	2	3	7	3	9	3	5	7	1	-	-	6	1	5
83	2	3	7	3	9	3	5	5	1	-	-	3	9	7
85	2	7	5	3	9	5	3	3	1	-	-	3	9	5
86	2	7	7	5	9	5	7	1	1	-	-	1	1	5
88	2	5	7	5	9	7	3	5	1	-	-	2	1	7
89	2	5	7	5	9	7	3	7	9	5	5	**2**	**9**	5
90	2	5	7	5	9	5	3	3	1	-	-	3	9	9
91	2	5	7	5	9	3	3	7	1	-	-	**2**	**9**	5
93	2	7	7	7	9	3	5	1	1	-	-	**3**	**9**	5
96	2	3	7	5	9	7	3	7	1	-	-	2	9	9
98	2	3	5	7	9	7	3	7	1	-	-	3	9	7

99	2	5	7	5	1	3	5	7	9	7	7	**3**	**9**	5
100	2	3	7	3	9	7	3	1	1	-	-	3	9	7
101	2	7	7	7	9	3	3	9	1	-	-	3	9	7
102	2	5	7	7	9	7	5	9	1	-	-	7	9	5
103	2	7	5	7	1	3	3	9	1	-	-	2	1	5
108	2	5	5	5	9	3	7	9	1	-	-	6	9	3
109	2	5	7	5	9	7	5	1	1	-	-	3	9	5
110	2	3	7	3	9	7	3	7	1	-	-	7	9	9
112	2	7	7	5	9	5	3	7	1	-	-	3	9	7
114	2	5	7	5	9	7	3	7	1	-	-	1	1	9
116	2	5	7	5	9	3	7	5	1	-	-	2	1	7
117	2	5	7	5	9	7	3	7	1	-	-	3	9	7
118	2	7	7	7	9	5	5	1	1	-	-	2	1	5
119	2	5	7	7	9	3	7	7	1	-	-	**2**	**9**	7
120	2	5	7	3	9	3	7	7	1	-	-	6	1	5
121	2	5	7	5	9	7	5	7	1	-	-	2	1	5
122	2	5	5	3	1	5	5	9	1	-	-	2	9	7
126	2	7	7	7	9	3	3	7	1	-	-	2	1	9
128	2	5	7	7	9	3	7	7	1	3	3	2	1	5
129	2	5	5	3	9	3	7	7	9	3	5	2	9	3
130	2	5	7	5	1	5	5	7	1	-	-	3	9	7
131	2	5	7	5	9	3	3	7	1	-	-	2	9	5
132	2	5	7	3	9	7	3	7	1	-	-	2	9	7
134	2	7	7	3	9	5	3	7	1	-	-	6	1	9
136	2	5	7	5	1	3	5	9	1	-	-	3	9	5
138	2	5	7	3	9	7	5		1	-	-	2	1	5
139	2	5	5	3	9	7	3	7	1	-	-	2	9	3
140	2	7	7	7	9	5	3	3	1	-	-	1	1	9
143	2	7	7	7	9	5	3	3	1	-	-	7	9	5
145	2	7	7	7	9	5	5	3	1	-	-	2	1	5
146	2	7	5	7	9	5	5	7	1	-	-	7	9	3
147	2	7	7	5	9	5	5	7	1	-	-	3	9	7
149	2	7	7	5	9	5	5	3	1	-	-	2	1	5
150	2	5	7	3	9	7	5	7	1	-	-	7	9	5
151	2	7	7	7	9	3	5	3	1	-	-	2	1	7
152	2	5	7	5	1	5	5	7	1	-	-	2	9	7
153	2	7	7	7	9	7	3	9	1	-	-	3	9	7
155	2	7	7	7	9	5	3	7	1	-	-	2	9	5
158	2	7	7	7	9	5	3	7	1	-	-	3	9	5
159	2	3	7	5	9	5	5	7	1	-	-	2	1	5
160	2	5	7	7	9	3	5	7	1	-	-	2	9	7
161	2	7	7	7	9	5	5	7	1	-	-	2	9	3
163	2	5	7	7	9	5	3	7	1	-	-	7	9	7
164	2	5	5	5	9	5	5	7	1	-	-	3	9	5
Genotype number	**PGT**	**LA**	**LL**	**LW**	**IFN**	**FT**	**NFC**	**FC**	**PGN**	**GND**	**NS**	**FCS**	**FLS**	**MT**
165	2	5	7	5	9	5	5	7	1	-	-	1	1	7
166	2	5	7	7	9	5	5	3	1			2	1	9
167	2	5	5	7	9	3	7	7	1	-	-	2	1	3
169	2	7	7	7	9	5	5	5	1	-	-	7	1	9
171	2	5	7	7	9	3	7	7	1	-	-	3	9	5
172	2	7	7	7	9	5	3	7	1	-	-	2	9	9
173	2	7	7	7	9	5	7	3	1	-	-	3	9	7
174	2	7	7	7	9	5	5	7	1	-	-	2	9	7
180	2	5	5	3	9	5	5	7	1	-	-	7	9	5
181	2	7	5	7	9	7	5	7	1	-	-	7	9	7
182	2	7	7	7	9	7	3	7	1	-	-	7	9	5
183	2	5	7	7	9	5	5	7	1	-	-	2	1	7
184	2	5	7	7	9	5	5	7	1	-	-	3	9	7
185	2	5	7	7	9	7	3	7	1	-	-	1	1	7

186	2	7	7	7	9	5	7	7	1	-	-	7	1	7
188	2	5	7	7	9	3	3	7	1	-	-	3	1	7
193	2	5	7	5	9	3	5	7	1	-	-	2	9	9
194	2	5	7	7	9	7	3	1	1	-	-	2	9	7
196	2	7	7	7	9	3	5	7	1	-	-	2	9	7
197	2	5	7	5	9	7	5	7	1	-	-	3	9	7
198	2	5	7	7	9	7	7	7	1	-	-	2	9	7
199	2	7	7	7	1	5	5	7	1	-	-	1	1	7
200	2	7	7	5	9	7	3	3	1	-	-	2	1	9
201	2	7	7	5	9	5	5	3	1	-	-	3	9	9
205	2	7	7	5	9	3	5	7	1	-	-	7	1	7
206	2	7	7	5	9	5	3	7	1	-	-	1	1	9
207	2	3	7	5	9	7	3	7	1	-	-	3	9	5
209	2	5	7	3	1	3	3	3	1	-	-	2	9	7
210	2	5	5	3	9	5	3	7	1	-	-	2	9	5
213	2	5	7	7	9	5	7	7	1	-	-	3	9	7
214	2	7	7	7	9	7	3	7	1	-	-	2	1	7
215	2	7	7	7	9	7	3	7	1	-	-	2	9	9
216	2	5	5	5	9	5	3	7	1	-	-	1	1	9
217	2	5	7	3	9	7	3	7	1	-	-	2	9	9
218	2	5	7	3	9	7	3	7	1	-	-	1	1	7
220	2	5	7	7	9	5	5	7	1	-	-	2	9	9
221	2	3	7	5	9	5	5	7	1	-	-	7	1	9
222	2	7	7	5	9	3	3	7	1	-	-	2	9	7
223	2	7	7	3	1	5	5	7	1	-	-	3	9	5
224	2	5	7	3	9	5	5	7	1	-	-	3	9	7
233	2	7	7	7	9	7	3	9	1	-	-	1	1	7
234	2	7	7	5	9	7	3	7	1	-	-	3	9	9
235	2	5	7	3	9	3	5	7	1	-	-	2	1	9
236	2	7	7	5	9	5	5	7	1	-	-	7	9	9
238	2	5	5	5	9	5	5	7	1	-	-	3	9	9
239	2	3	5	3	9	7	3	7	1	-	-	2	1	9
240	2	7	7	5	9	3	5	9	1	-	-	2	1	9
242	2	7	7	7	9	5	5	7	1	-	-	7	1	9
243	2	7	7	5	1	5	5	7	1	-	-	2	1	7
244	2	7	7	7	9	5	5	7	1	-	-	7	9	7
245	2	5	7	5	9	5	5	7	1	-	-	2	9	9
248	2	7	7	5	9	5	5	5	1	-	-	1	1	9
249	2	7	7	5	9	5	3	7	1	-	-	3	9	9
252	2	7	7	7	9	5	3	7	1	-	-	1	1	9
254	2	5	5	5	9	5	5	7	1	-	-	2	9	5
255	2	3	7	3	9	5	5	7	1	-	-	2	1	7
256	2	5	5	3	9	5	5	3	1	-	-	2	1	5
260	2	7	7	7	9	5	3	7	1	-	-	2	1	7
263	2	7	7	7	9	5	3	7	1	-	-	3	9	9
264	2	7	7	5	9	5	5	7	1	-	-	3	9	7
270	2	7	7	7	9	7	5	7	1	-	-	2	1	7
271	2	5	5	5	9	5	5	7	1	-	-	2	9	9
Genotype number	**PGT**	**LA**	**LL**	**LW**	**IFN**	**FT**	**NFC**	**FC**	**PGN**	**GND**	**NS**	**FCS**	**FLS**	**MT**
273	2	7	5	3	9	5	5	7	1	-	-	1	1	7
277	2	5	7	3	9	7	3	3	1	-	-	2	9	7
278	2	5	7	7	1	5	5	7	1			3	9	7
280	2	7	5	7	9	7	7	7	1	-	-	3	9	7
281	2	5	5	5	9	7	3	7	1	-	-	2	9	9
283	2	5	7	7	9	5	5	7	1	-	-	2	9	9
284	2	5	7	7	1	5	5	7	1	-	-	3	9	9
286	2	7	5	5	9	7	5	7	1	-	-	7	1	9
287	2	5	7	5	9	5	5	7	1	-	-	3	9	7
288	2	7	7	7	9	5	7	7	1	-	-	3	9	7

290	2	5	7	7	1	5	3	7	1	-	-	1	1	7
291	2	5	7	5	9	7	5	7	1	-	-	3	9	9
293	2	5	7	3	9	5	3	7	1	-	-	3	9	9
299	2	5	7	7	9	5	3	7	1	-	-	7	9	9
302	2	3	5	7	9	5	5	7	1	-	-	3	9	9
304	2	5	7	3	9	5	7	7	1	-	-	7	9	9
306	2	5	7	3	9	7	5	7	1	-	-	3	9	7
312	2	5	5	5	9	5	3	7	1	-	-	7	9	5
315	2	5	7	7	9	7	3	7	1	-	-	1	1	9
316	2	5	5	7	9	5	3	7	1	-	-	1	1	7
319	2	5	7	7	9	3	7	7	1	-	-	3	9	9
320	2	3	5	7	9	7	7	7	1	-	-	3	9	9
322	2	7	7	7	9	5	3	3	1	-	-	2	1	9
323	2	5	5	5	9	7	7	7	1	-	-	2	1	9
325	2	5	7	5	9	7	3	9	1	-	-	1	1	9
326	2	7	5	5	9	7	3	3	1	-	-	7	1	9
327	2	5	7	5	9	5	5	3	1	-	-	2	1	9
328	2	7	7	5	9	5	5	7	1	-	-	2	1	9
331	2	3	7	3	9	5	5	7	1	-	-	7	1	5
334	1	5	7	5	9	7	5	7	1	-	-	2	1	9
337	2	5	7	5	9	7	5	7	1	-	-	3	9	5
340	2	5	3	3	9	5	5	7	1	-	-	7	9	5
345	2	5	7	5	9	5	3	7	1	-	-	2	9	3
350	2	3	5	3	9	5	3	7	1	-	-	3	9	5
351	2	5	7	5	9	5	3	7	1	-	-	1	1	7
361	2	7	5	3	9	5	3	7	1	-	-	3	9	5
362	2	5	7	7	9	5	3	7	1	-	-	3	9	7
371	1	3	3	5	1	5	3	7	1	-	-	3	9	9
377	2	5	7	5	9	5	7	9	1	-	-	1	1	7
379	2	5	7	5	9	5	5	7	1	-	-	2	1	9
383	2	3	5	5	9	7	3	7	1	-	-	2	9	9
384	2	5	5	5	1	7	3	7	1	-	-	2	1	9
386	2	3	5	5	1	7	3	9	1	-	-	2	9	7
391	2	5	7	5	9	5	5	1	1	-	-	1	1	7
392	2	5	7	5	9	5	5	5	1	-	-	1	1	7
393	2	5	7	7	9	5	5	9	1	-	-	2	1	9
395	2	3	5	3	9	7	3	5	9	5		3	9	5
396	2	5	5	3	9	5	5	1	1	-	-	3	9	7
398	2	3	7	5	9	5	5	7	1	-	-	3	1	7
399	2	5	7	5	9	7	5	7	1	-	-	3	9	9
401	2	5	7	7	9	5	7	9	1	-	-	4	1	5
407	2	3	5	3	9	7	3	7	1	-	-	1	1	9
408	2	5	7	5	9	7	3	7	1	-	-	3	9	9
409	2	3	7	5	9	7	3	7	1	-	-	7	9	9
411	2	3	5	5	9	7	3	7	1	-	-	1	1	9
413	2	5	7	5	9	7	3	5	1	-	-	2	9	9
416	2	5	5	3	9	5	7	9	1	-	-	3	9	3
418	2	5	7	5	9	5	5	3	1	-	-	3	9	5
422	2	5	5	7	9	5	5	7	1	-	-	2	1	9
423	2	5	7	3	1	7	5	7	1	-	-	2	1	3
424	2	5	5	5	9	5	7	9	1	-	-	1	1	5
427	2	5	5	5	9	7	5	5	1	-	-	2	1	9
Genotype number	**PGT**	**LA**	**LL**	**LW**	**IFN**	**FT**	**NFC**	**FC**	**PGN**	**GND**	**NS**	**FCS**	**FLS**	**MT**
430	2	5	7	7	9	5	3	3	1	-	-	**2**	**1**	9
433	2	5	7	5	9	5	5	7	1	-	-	2	1	9
437	2	7	7	7	9	3	3	3	1	-	-	2	9	5
439	2	5	5	5	9	5	3	5	1	-	-	2	1	7
440	2	5	5	3	9	7	3	5	1	-	-	2	1	7
441	2	7	7	7	1	5	3	5	1	-	-	3	9	9

442	2	5	5	5	1	7	5	7	1	-	-	7	9	7
446	1	3	5	5	9	7	3	7	1	-	-	1	1	7
447	2	3	3	3	9	7	3	5	1	-	-	2	1	9
450	2	7	7	7	9	5	5	7	1	-	-	3	9	9
453	2	5	7	7	9	5	5	3	1	-	-	2	1	7
455	2	5	7	3	9	7	5	7	1	-	-	2	1	7
461	2	3	7	3	9	5	3	7	1	-	-	1	1	9
462	2	3	7	5	9	5	5	7	1	-	-	7	1	7
463	2	5	5	7	9	7	3	7	1	-	-	3	9	7
464	2	3	5	3	9	7	3	7	1	-	-	1	1	7
465	2	3	7	3	9	7	7	7	1	-	-	2	1	5
466	2	5	7	7	9	7	3	7	1	-	-	2	1	9
467	2	5	5	3	9	7	3	7	1	-	-	2	9	9
469	2	5	7	5	9	5	5	7	1	-	-	7	9	7
471	2	5	7	7	9	7	5	7	1	-	-	2	1	9
480	2	5	7	7	9	7	5	7	1	-	-	7	9	5
483	2	5	7	7	9	7	5	7	1	-	-	1	1	5

PGT: Plant growth type: LA: Leaf attitude LL: Leaf length LW: Leaf width IFN: İnflorescence at first node FT: Flowering time NFC: Number of flowers per cluster FC: Fruit color PGN: Presence of green neck GND: Green neck density GNS: Green neck size FCS: Fruit cross section FLS: Fruit longitudinal section MT: Maturity time

Table 4. Fruit characteristics of tomato genotypes

Genotype number	FW	FS	PT	CN	SÇKM	AFW
2	71.88	55.77	6.30	3	4.20	198.33
5	61.60	53.20	7.64	3	3.88	125.00
10	57.78	62.84	6.49	4	4.09	153.70
14	82.15	62.09	8.59	4	4.46	239.57
16	68.85	57.01	6.00	3	4.05	148.00
19	62.54	50.59	6.75	3	4.17	123.33
20	82.39	60.07	5.62	6	3.73	298.33
22	99.50	64.29	6.97	6	3.92	338.83
25	83.71	68.04	8.30	3	4.15	269.00
27	77.92	55.44	6.05	4	3.33	177.20
30	84.47	63.50	8.27	5	4.04	276.00
34	75.94	56.90	6.46	5	4.00	207.71
35	60.79	51.26	9.25	2	4.30	138.50
36	73.65	57.02	8.42	4	5.05	205.00
37	64.44	68.45	7.33	3	4.15	194.00
41	69.87	52.98	6.53	4	3.13	166.67
43	62.49	66.38	7.73	2	4.90	160.40
44	67.86	58.83	7.62	3	4.26	140.17
45	72.32	55.09	7.79	4	4.15	204.50
50	75.13	60.64	7.59	4	3.75	194.33
52	64.09	71.27	7.84	3	3.61	186.86
54	64.02	78.21	9.50	4	3.55	225.00
55	56.73	78.86	8.58	4	4.97	199.67
56	71.98	66.94	7.67	3	4.63	209.17
60	62.09	65.03	5.48	5	4.70	172.75
61	85.88	55.26	6.28	6	3.97	239.00
64	81.83	62.25	8.36	4	3.22	243.50
66	76.53	60.41	7.63	3	2.15	196.00
67	81.77	62.33	8.79	3	4.20	244.00
69	66.65	67.40	8.36	6	3.73	231.71
Genotype number	FW	FS	PT	CN	SÇKM	AFW
70	58.24	92.05	7.34	6	3.65	262.25
71	65.40	89.86	6.52	6	4.10	288.75
72	69.93	60.31	7.70	4	3.20	204.44
73	65.54	56.30	7.05	3	4.25	138.00

74	77.36	70.38	8.38	4	4.28	271.20
76	73.70	66.34	9.49	4	4.41	229.11
78	64.40	60.05	4.91	2	4.05	153.33
79	69.14	74.04	8.72	4	3.87	258.30
82	68.31	64.55	8.42	3	3.72	174.00
83	59.04	67.62	5.68	2	3.90	159.50
85	64.29	56.35	6.32	3	2.95	138.33
86	56.32	81.19	7.34	6	3.50	197.00
88	62.83	50.40	6.50	4	3.97	148.00
89	62.16	64.02	6.85	5	3.61	180.25
90	63.27	61.69	5.96	3	3.83	164.93
91	79.85	74.71	8.29	5	7.69	297.11
93	64.71	68.67	5.21	5	3.63	198.00
96	67.32	69.31	7.50	4	4.20	218.80
98	71.67	56.93	5.10	4	5.10	175.50
99	70.80	64.79	8.92	3	3.68	185.11
100	54.05	67.06	4.17	4	3.13	124.40
101	67.27	67.89	7.93	2	4.00	194.00
102	60.95	54.25	6.36	2	4.90	118.66
103	80.12	72.24	9.38	4	3.82	272.00
108	46.30	55.91	7.23	2	5.07	74.83
109	61.40	53.57	7.93	2	4.63	120.00
110	78.76	61.04	8.28	3	3.50	250.83
112	72.18	64.92	7.51	3	4.03	184.33
114	66.08	101.48	8.12	7	4.12	396.20
116	77.00	58.37	7.54	3	4.27	223.33
117	67.52	62.33	7.28	3	3.87	179.33
118	70.40	60.50	5.46	5	3.73	553.11
119	70.80	64.79	9.45	3	3.68	248.00
120	56.11	59.90	8.58	2	4.53	111.75
121	74.73	63.18	8.91	3	3.75	222.25
122	73.57	61.82	9.29	3	4.13	200.85
126	90.76	68.06	7.80	6	3.33	400.71
128	66.70	70.04	8.18	5	3.92	229.29
129	78.37	64.66	8.63	3	4.00	242.50
130	58.63	62.61	5.97	2	4.78	145.40
131	74.80	61.04	6.80	4	3.89	209.25
132	80.58	71.16	9.87	4	4.20	306.38
134	66.74	72.87	6.42	3	3.42	180.20
136	58.34	63.80	8.46	3	3.48	163.90
138	77.35	54.27	4.86	5	4.16	193.20
139	69.22	62.29	7.11	3	3.41	192.83
140	83,39	63,09	7.14	4	3.85	225.00
143	71.97	60.73	8.14	3	3.93	185.33
145	73.99	67.78	7.74	4	3.81	233.86
146	69.44	64.81	7.50	2	3.92	185.19
147	69.46	74.77	6.78	5	4.17	247.33
149	78.63	73.27	6.56	7	3.68	295.33
150	66.98	61.70	6.97	3	3.67	176.67
151	85.28	60.01	6.38	5	3.42	294.27
152	66.74	69.19	7.59	3	3.79	199.88
153	66.77	65.86	10.06	2	3.75	185.00
155	74.23	59.24	7.87	4	4.14	206.97
158	65.33	61.31	8.31	2	4.73	155.00
159	57.55	70.24	6.96	3	4.77	168.67
160	82.22	63.45	8.88	4	3.63	273.00
161	74.00	67.55	7.68	4	3.59	232.00
Genotype number	FW	FS	PT	CN	SÇKM	AFW
163	65.69	57.37	7.22	2	4.25	148.71

164	65.18	67.37	8.04	4	3.98	190.60
165	65.49	96.82	8.27	5	3.98	360.00
166	90.40	63.77	7.32	6	4.40	293.89
167	55.91	78.22	5.70	5	4.67	190.00
169	66.30	76.92	6.39	2	3.85	222.00
171	66.65	55.98	8.20	3	3.80	130.50
172	67.60	53.71	7.25	5	4.50	156.17
173	61.57	61.22	6.72	2	3.95	146.00
174	79.86	64.53	6.54	5	4.55	262.50
180	69.53	65.53	6.36	3	3.77	191.22
181	62.71	68.89	5.89	5	4.15	194.50
182	73.97	66.36	7.37	3	3.95	225.18
183	60.70	76.65	8.59	4	3.81	223.18
184	69.16	59.40	8.05	4	3.87	171.50
185	59.12	84.31	8.28	4	3.49	242.86
186	71.67	61.11	8.08	3	4.28	161.06
188	61.72	51.15	5.61	2	3.55	115.00
193	68.98	63.20	5.78	5	4.01	244.11
194	67.08	61.70	8.36	3	4.06	160.33
196	77.65	57.75	6.90	4	3.60	208.50
197	56.65	75.98	6.85	5	4.60	164.00
198	65.43	69.33	7.88	4	3.83	213.44
199	60.55	40.42	6.07	4	4.00	260.00
200	68.47	77.66	8.39	5	3.97	263.67
201	67.80	71.14	7.52	4	3.95	156.75
205	61.94	62.41	6.88	2	4.77	134.67
206	64.97	89.54	7.59	4	4.23	306.50
207	57.16	46.68	4.87	3	4.30	84.50
209	90.63	66.51	6.21	6	3.20	115.19
210	81.34	60.28	8.11	5	4.09	244.11
213	67.96	65.77	7.84	4	3.73	191.56
214	70.68	66.95	6.76	5	3.92	208.00
215	73.94	84.44	8.92	5	4.05	322.17
216	81.85	71.20	7.68	5	4.40	303.67
217	61.62	78.08	5.31	6	3.95	230.50
218	74.88	56.05	8.73	4	4.44	180.67
220	68.90	57.82	7.64	3	3.73	188.50
221	74.77	63.45	8.45	3	3.76	212.20
222	72.19	67.66	7.83	5	3.83	229.71
223	65.71	62.06	7.43	2	4.72	156.54
224	66.50	58.66	7.88	3	4.30	147.86
233	98.43	75.27	9.41	5	3.50	455.00
234	73.33	57.71	8.58	3	4.61	198.11
235	69.01	55.77	9.17	2	3.32	171.40
236	73.77	62.68	8.20	3	3.87	206.33
238	58,67	50,03	4.65	3	3.50	121.67
239	70.04	64.82	5.83	4	4.28	201.00
240	62.45	72.88	7.37	4	4.09	193.33
242	69.91	62.44	7.70	2	3.95	178.75
243	72.37	63.94	7.71	3	3.98	217.36
244	66.26	56.76	7.75	2	4.43	145.92
245	74.17	56.17	8.11	4	4.03	186.64
248	72.77	54.06	7.93	3	3.95	170.00
249	66.97	59.15	8.16	4	4.47	162.67
252	54.03	70.96	7.35	3	4.63	175.25
254	72.50	58.09	9.31	3	4.20	181.25
255	86.81	64.23	8.39	5	4,3	292.33
256	92.37	53.29	4.93	7	4.47	246.67
260	78.97	60.52	8.08	3	3.95	241.91

263	66.74	57.00	6.32	2	4.35	155.50
Genotype number	FW	FS	PT	CN	SÇKM	AFW
264	75.82	63.98	8.00	3	3.89	218.88
270	72.97	66.64	10.66	2	4.10	196.50
271	66.25	89.92	7.04	6	3.88	319.17
273	73.96	56.57	8.26	4	3.50	183.60
277	63.11	61.00	6.99	4	3.91	150.62
278	64.03	45.56	6.54	3	3.83	130.00
280	67.08	73.04	7.57	2	3.88	196.25
281	72.23	58.00	7.18	3	4.22	206.80
283	81.09	63.40	8.66	4	4.28	240.00
284	70.96	60.36	8.18	3	3.72	183.33
286	57.39	58.39	6.09	2	4.20	103.00
287	70.25	59.91	7.53	3	3.56	183.63
288	68.74	59.88	7.25	2	3.95	167.25
290	80.82	59.95	7.86	3	2.85	230.50
291	65.54	56.30	7.05	3	4.25	138.00
293	69.30	57.48	7.14	4	3.90	171.00
299	54.66	66.31	6.13	4	4.30	147.00
302	63.97	55.84	8.59	3	4.12	131.00
304	55.25	57.76	6.69	2	4.37	108.33
306	78.23	70.45	7.79	3	4.18	247.75
312	72.31	61.30	9.50	2	4.33	196.22
315	70.99	64.85	8.53	3	4.31	213.43
316	76.95	63.26	6.30	7	4.40	256.00
319	73.71	60.14	9.05	4	3.48	194.75
320	74.41	88.22	6.83	5	4.08	340.00
322	85.69	60.78	6.47	5	3.43	264.00
323	72.02	73.57	7.14	5	4.18	265.50
325	74.90	66.83	8.30	3	4.47	228.71
326	77.11	65.26	7.15	3	3.75	231.00
327	62.90	61.24	6.33	3	3.35	162.17
328	74.65	55.09	8.51	4	3.60	164.50
331	61.83	62.06	7.17	2	4.53	144.33
334	76.69	64.01	8.78	3	3.38	219.00
337	60.41	67.62	7.20	2	3.87	160.33
340	53.54	60.75	4.18	4	3.93	134.25
345	59.17	84.55	8.45	4	4.77	241.33
350	55.19	58.34	7.71	2	4.65	109.40
351	58.24	92.05	7.34	6	3.65	262.25
361	65.51	64.01	7.47	2	4.00	165.00
362	70.80	81.32	5.63	4	4.20	283.00
371	51.84	62.97	6.38	3	3.45	113.00
377	56.73	70.14	6.40	4	3.10	174.50
379	73.44	69.98	7.57	5	4.11	270.11
383	59.76	71.42	7.12	4	3.65	186.00
384	63.80	69.52	7.44	4	3.92	191.67
386	60.60	74.15	6.06	3	4.67	76.80
391	70.68	103.45	8.01	5	3.95	377.00
392	72.71	49.90	5.62	5	4.03	154.33
393	64.78	92.18	8.66	4	4.54	334.80
395	72.94	54.55	8.34	4	4.67	196.38
396	65.74	61.08	7.32	5	4.55	214.50
398	62.44	62.70	8.15	3	5.00	159.50
399	64.12	61.13	7.95	2	4.90	177.30
401	51.87	47.93	6.33	2	5.47	110.86
407	53.39	81.24	6.57	5	4.18	204.00
408	66.70	68.47	6.66	4	4.04	197,2
409	69.19	60.05	7.31	4	3.50	173.33

411	56.34	86.80	6.92	5	4.60	223.50
413	66.26	65.78	8.54	4	4.20	191.60
416	58.90	54.13	8.20	2	3.33	148.25
418	68.14	60.00	4.11	4	4.33	174.33
Genotype number	FW	FS	PT	CN	SÇKM	AFW
422	60.05	70.27	7.69	3	4.08	172.00
423	75.27	54.07	6.71	4	3.90	179.29
424	53.15	76.45	6.11	3	4.55	190.25
427	67.71	59.62	6.59	3	3.62	162.00
430	63.19	66.99	6.85	6	4.03	283.10
433	70.21	72.25	7.72	5	4.26	233.71
437	64.66	73.72	7.60	5	4.75	226.13
439	56.73	80.30	6.25	5	4.37	211.67
440	53.52	84.46	7.46	6	3.55	220.00
441	62.34	74.48	6.26	3	4.15	153.00
442	70.03	76.46	7.68	4	4.79	250.13
446	47.62	77.21	5.43	6	3.95	174.50
447	79.62	62.95	11.09	4	3.60	300.00
450	68.47	55.18	7.62	2	4.30	164.75
455	85.87	65.22	7.87	6	3.85	188.67
453	62.73	62.61	5.23	6	3.92	190.00
461	57.32	81.54	4.95	6	4.10	289.00
462	59.37	69.86	7.28	3	4.50	176.60
463	61.05	73.25	9.94	3	3.97	186.67
464	93.33	64.04	8.30	6	3.80	317.00
465	79.12	55.94	8.93	5	3.53	135.20
466	68.58	69.18	5.68	5	3.75	224.00
467	58.71	67.44	6.62	3	4.23	159.00
469	64.57	53.37	7.77	3	3.30	138.67
471	68.49	59.09	7.60	3	4.82	171.33
480	66.22	62.70	5.94	2	4.40	134.50
483	59.82	65.39	5.29	5	3.80	250.00
Average	68.74	66.09	7.38	3.6	4.04	204.28

FW: Average fruit width (mm); FS: Average fruit size (mm); PT: Average Pericarp Thickness (mm); CN: Average Number of Carpels (pcs:); SÇKM Average Water-Soluble Dry Matter (Brix); FW: Average fruit weight (g)

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