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Chapter 3

Peach Breeding Studies in Turkey and the Evaluation of Peach and Nectarine Hybrids

Ayzin Baykam Kuden, Songul Comlekcioglu, Kadir Sarier, Burhanettin Imrak and Ali Kuden

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/intechopen.73440

Abstract

Peach (*Prunus persica* [L.] Batsch) is widely cultivated due to its easy adaptability to different ecological conditions, early fruit set and a long period of harvest. Peach cultivation extends along 30–45° North and South parallels of latitude. Around 21,638,953 tons of peaches are produced in an area of 1538,174 ha across the world. Turkey ranks sixth with a production of 637,573 tons/year in 29,092 ha area. Early fruiting habit and correlative characteristics of peaches encouraged fruit breeders to study on this fruit species. The main aims of the study are new cultivar or rootstock breeding, resistance to diseases, late ripening season, fruit quality improvement, fruit shape changes, new tree shapes, and low chilling cultivars. Breeding studies have been carried out at the Department of Horticulture at the University of Cukurova since 1990s. In these, peach and nectarine breeding programs with different aims such as late ripening, quality improvement, Sharka resistance, and low chilling cultivars were studied. In this chapter, some of the results on late ripening peach and nectarine breeding program have also been presented.

Keywords: molecular markers, embryo rescue, low and high chilling cultivars, Sharka resistance, fruit quality characteristics

1. Introduction

Iwata et al. [1] stated that in genomic analysis technologies, many new advancements promote the efficiency of plant breeding. They also determined that genome-wide association studies (GWAS) and genomic selection (GS) are very helpful, especially in various fruit tree breeding research programs. Breeding of fruit crops is not so easy, as it takes a very long time to get the quality fruits with good size of a tree, to overcome the juvenility period as well as to obtain

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desired fruits according to the aim of the breeding program [1]. Whole-genome sequences have been recently released for apple, peach, strawberry, Japanese apricot, and Chinese and European pear. After these developments, in breeding programs, marker-assisted selection has been used in wide genomics studies. These studies have caused to develop genome scale SNPs and SSR markers and to place reference linkage maps in Rosacea family to allow the identification of evolutionary relationships, which can be found in Genome Database in Rosaceae website. Yamamoto and Terakami [2] reviewed the recent advances in genomic studies and their practical applications for Rosaceae fruit trees, particularly in pear, apple, peach, and cherry.

Peach (*Prunus persica* [L.] Batsch) and nectarine (*P. persica* var. nectarine Maxim) belong to the *Rosaceae* family. Peach is widely cultivated due to its easy adaptability to different ecological conditions, early fruit set and a long period of harvest. Peach cultivation extends along 30–45° north and south parallels of latitude. At higher elevations, low winter temperatures and late spring frosts are limiting factors for peaches [3]. Around 21,638,953 tons of peaches are produced in an area of 1,538,174 ha across the world. Turkey ranks number 6, with a production of 637,573 tons/year in 29,092 ha area, following China (11,924,085 tons), Italy (1,401,795 tons), Spain (1,329,800 tons), the USA (964,890 tons), and Greece (666,200 tons) [4].

Fruit breeders preferred to work on peach breeding for its early fruiting habit and correlative characteristics [5]. In cultivar or rootstock breeding programs, disease tolerant genotypes, early or late ripening habit, improvement of fruit quality characteristics such as shape, aroma, flesh firmness, especially low chilling requirements and to improve tree shape were aimed [6]. Important characteristics on peach breeding have already been determined to be; white fruit flesh is dominant to yellow fruit flesh; pubescence to smooth skin; soft fruit flesh to firm and freestone to clingstone. In crossbreeding of peaches and nectarines, since pubescence characteristics are controlled by single gene, generally heterozygote variation of 3:1 is seen. In addition, several correlations between fruit flesh color and receptacle and the color of leaves are seen. These correlative characteristics reveal that early selection is available in peach breeding [7, 8].

Classical plant breeding depends on the phenotypic selection of superior genotypes obtained as a result of crossbreeding. However, genotype × environment interaction causes time consumption and is quite difficult. Moreover, phenotypic selection is expensive and most of the time is not feasible for some characteristics like tolerance to abiotic stress conditions. Marker-assisted selection is an approach developed as an alternative to these problems faced in classical plant breeding [9]. Usually, fruit demand of the consumers in peach is large weight and big-sized fruits, which are quantitative characters (QTLs) affected by several genes and various environmental conditions. Linge et al. [10] carried out an experiment on these characteristics and determined a genetic map of an F2 progeny with 117 individuals of PI91459 ('NJ Weeping') 9 'Bounty' with SNP markers. The fruit quality characters such as fruit weight, height, width, and depth of the progeny and parents were determined in 2011 and in 2012 and were compared with SNP markers. They found a positive correlation between characteristics of fruit weight and characteristics of fruit size. They also constructed a SNP map obtained from 1148 markers distributed across more than eight linkage groups. With this study, they identified 28 QTLs for these characters in which 11 of them were stable in both2011 and 2012 [10].

Various regions of Turkey are suitable to grow peaches under different ecological conditions. The Marmara region can grow high chilling requiring peaches, but the ripening time of the latest peach cultivars is about mid-September. A peach breeding study was carried out by Eroglu [11] in this important peach growing area. In this project, five foreign cultivars (Rio Oso Gem, Fortuna, Monroe, Jungerman and Vivian) and four local types (Bayramiç Tüysüzü, Alyanak Hulu, Sarı Papa and Takunyacı I) were hybridized to obtain fresh market peaches and two foreign and one local type peaches were hybridized for processing peaches. Eroglu et al. [12] stated the fruit quality performances of 121 peach genotypes for fresh market and 35 genotypes for processing. Adana province in Cukurova plain at the Mediterranean region has a subtropical climate. It is located very close to the Mediterranean Sea, thus this condition is suitable to grow only low or midseason chilling requiring peach cultivars. Within 1 h distance to this area, in Taurus Mountains (1100 m elevation) region, high chilling requiring cultivars could be grown efficiently [5].

a. The first peach breeding study in Turkey was conducted by Tanriver and Kuden [13] on 'Ustun', a very late ripening (in mid-October) peach cultivar from the beginning of the 1990s. This study was carried out for [1] breeding of early cultivars for subtropical regions and [2] breeding of late ripening cultivars for cold regions, during 1995–1999. In the breeding experiments, carried out in Adana for early peach cultivars, Springtime, Suncrest, Flavorcrest and Redcap peach cultivars were used. Embryo rescue method was used with the combinations, where Springtime was used as a mother parent. As a result, embryo size was found to be important for the success of embryo rescue, and early cultivars should be used as pollinators. In the breeding studies to obtain late ripening peach cultivars, 'Monroe', 'Rio-Oso-Gem' and 'Ustun' were crossed reciprocally, while 'J.H. Hale' (pollen sterile) was used only as a mother plant at Pozantı Agricultural Research Center of Cukurova University. Seeds from crosses were grown in the orchards, of the Horticultural Department in Adana, under subtropical conditions. Morphological, pomological and isozyme analysis were also carried out in Adana [14].

Among the peach hybrids, especially Rio-Oso-Gem × Ustun combination yielded very good results, and six hybrids of this combination were placed among 20 promising candidate cultivars. As a result of this study, several high-quality, very late ripening hybrids were identified [15]. The best results for late ripening, yield and fruit quality characteristics were obtained from the hybrids of Rio-Oso-Gem × Ustun combination, Nos. 24 and 19. These were followed by Ustun × Monroe 14, J.H. Hale × Rio-Oso-Gem 14, Rio-Oso-Gem × Ustun 21, and Independence open pollinated hybrid No. 8. The promising genotypes were planted at the orchards of Pozanti Agricultural Research and Application Center to see the real performances of these high chilling requiring peach and nectarine genotypes. According to the observations among the hybrids, some of them were found to be resistant to *Taphrina deformans*. The band profiles of 12 enzyme systems of parent cultivars were investigated and polymorphism obtained in 7 enzyme systems (MDH, PRX, ADH, AMY, IDH, PEP and ACP). In 31 hybrids, polymorphism in enzyme systems was found to be suitable to Mendel Segregation rates. As a result of this experiment, two very late ripening peach cultivars from Rio Oso Gem × Ustun combination and two peach cultivars from J.H. Hale open pollination were registered and patented. All these new cultivars are of good quality and high chilling requiring cultivars.

b. The aim of the second peach breeding program was to improve some quality characteristics of Ustun peach to obtain high chilling, late ripening, good quality and good yielding peach, as well as nectarine cultivars. In this study, the pollen of Ustun cultivar was crossed with Venus and Stark Red Gold nectarines [16]. By crossing Venus and Stark Red Gold nectarines, with Ustun peach cultivar, 61 genotypes from VxU combination and 115 genotypes from SRGxU combination were obtained. A total of 176 genotypes were investigated for their morphological as well as phenological characteristics and were analyzed pomologically. Also, some pomological characters were compared by BPPCT009, MA014, MA040, and STS-OPAG8 SSR primer pairs to investigate the effectiveness of the marker-assisted selection in F_1 genotypes.

In the weighted ranking method, VxU-55, VxU-41, VxU-34, VxU-14, VxU-1, VxU-13, VxU-24, VxU-26 peach genotypes and VxU-31, VxU-42, VxU-53, VxU-15 nectarine genotypes in VxU combination gave the highest points. In SRGxU combination, SRGxU-101, SRGxU-28, SRGxU-88, SRGxU-84, SRGxU-36, SRGxU-57, SRGxU-23, SRGxU-92, SRGxU-93 peach, and SRGxU-5 nectarine genotypes gave the highest points for the same scaling method.

No gene amplification was obtained from the PCR reactions among VxU and SRGxU populations analyzed by MA040 and STS-OPAG8 SSR primer pairs. BPPCT009 and MA014SSR primer pairs were also insufficient to determine fruit shape and free stone characteristics for VxU and SRGxU populations. These selected genotypes will eventually be taken under registration very soon.

Detailed information on this research is given below.

c. Another peach and apricot breeding program resistant to Sharka has been completed with a cooperative research between BETA Private Research Center, Malatya Fruit Research Institute and Cukurova University. This study aimed to obtain peach, nectarine, and apricot genotypes resistant to "Sharka" with crossbreeding method. Plum pox virus (PPV) causing Sharka disease is the most important viral agent for stone fruits. This disease is most harmful to apricot, plum, and peach trees. In Valencian Institute of Agricultural Research (IVIA), peach breeding program on apricot and on peach was started in 1993 and 1997, respectively. The aim of the study on apricot was to adapt to Southern Europe and to obtain high-quality cultivars resistant to the Sharka disease. Sharka or PPV is the most important limiting factor in the production of apricot. It was first described in Spain in 1984, causing serious loss of fruit and destruction of more than 1.5 million trees. The disease resistance breeding program is based on the transfer of resistance from local cultivars of Sharka disease to other cultivars by crossbreeding experiments. With 15 genotypes selected in accordance with the program's objectives, they were worked on apricot production areas in Spain. The aim of the peach breeding program was to obtain new cultivars of peach and nectarine that ripen early and provide good quality cultivars found in the market. The main market in Spain is the European countries, just as the big world producers are in the countries. In some parts of Valencia, Murcia, and Andulacia, climatic conditions allow the production of early cultivars that mature so as not to conflict with other European countries. In this study, 15 apricot genotypes and 12 peach genotypes selected for the purposes of the peach breeding program have been defined as resistant to the Sharka disease [17].

The Sharka disease is a race such as PPV-D, PPV-M, and PPV-Rec, and new breeds can be taken out from a combination of these races. PPV-T is a combination of PPV-M and PPV-D races, and it was found to be a race belonging to Turkey. In this study, local apricot cultivars Hacıhaliloglu and Kabaası were crossed with foreign apricot cultivars such as Stark Early Orange, Rojo Pasion, Murciana, and P 1908 (peach clone from *Prunus davidiana*), which are known to be resistant to PPV. For peaches, commercial peach cultivars such as Flored and Carolina were crossed with PPV resistant Stark Early Orange (apricot) and P 1908 peach clone. In the hybridization studies, embryo rescue was performed with the combinations in which Flored peach variety was used as a mother parent, and in other combinations, the seeds were folded. Murashige & Skoog (MS) and Woody Plant Medium (WPM) nutrient media were used for embryo rescue combinations. Molecular studies were used to determine early resistance to Sharka disease in the hybridized individuals. Studies of the PGS1.21, PGS1.24, and ZP002 markers in hybrid subjects revealed the presence of resistance, tolerance, and susceptibility alleles. A total of 365 genotypes from crossing among 12 combinations of apricot and peach were tested with SSR markers (P GS1.21, PGS1.24, and ZP002). Approximately, 138 genotypes were found to be candidates for PPV resistance in future studies [18]. Individuals with endurance allele at the next stage of the study will be protected for other tests and observations to be made by grafting on the clone rootstock.

d. Current peach breeding work is focused on breeding of low chilling, good quality genotypes, and to obtain flat and nonacid peaches (*Prunus persica* var. platycarpa). For this aim, Venus, Maycrest, Early Silver, and Gransun peach and nectarine cultivars and four flat and nonacid local peach genotypes, which were obtained by a selection study (Flat peach genotype 1, Flat peach genotype 2, Flat peach genotype 4, and Flat peach genotype 5), were used as parents. Phenological observations (blistering, green tip, pink tip, balloon, full bloom, and fall of petals) and pomological analyses (fruit weight, fruit height, fruit length, fruit width, total acid, pH, firmness, fruit top color, ground color, fruit pulp color, freestone state, fruit shape, and pubesence) were also studied. Wang et al. [19] stated that the nonacid peaches are preferred in the market, and this trait is usually selected in the commercial breeding programs. A major gene (D/d) located on chromosome 5 of peach has been described for this character, where the nonacid character is determined by the dominant D allele. Flavor analysis in fruit juice samples taken from genotypes will be carried out using the HS-GCMS technique, while sugar and organic acids will be carried out by the HPLC technique. Thus, the aroma, sugar, and organic acid levels of each individual will be determined.

In this chapter, brief information on the results of the second (b) peach breeding experiment at Cukurova University is provided.

2. Material and method

In this breeding study, Ustun peach cultivar was used as a father parent, and Venus and Stark Red Gold nectarine cultivars were used as mother parent. In the trial, 61 F_1 hybrids obtained

from Venus × Ustun crossbreeding and 115 F_1 hybrids obtained from Stark Red Gold × Ustun crossbreeding, and a total of 176 F_1 hybrids were used as plant material.

Ustun peach cultivar has been emerged as a result of bud mutation from peach cultivar of J.H.H. It matures between the first week and the third week of October (1400–1500 altitude). Fruit peel is fairly hairy, red cheek on yellow ground, fruit stalk is short, flesh is hard and yellow color and it has a very good aroma (**Figure 1**).

Venus and Stark Red Gold are kinds of nectarine with a yellow flesh. They have quite good properties in terms of fruit weight, color, and taste. Venus matures 10 days later than the Stark Red Gold.

2.1. Phenological, morphological, and pomological analyses

A total of 176 F_1 hybrids, that is, 61 from Venus × Ustun crosses and 115 from Stark Red Gold × Ustun crosses were compared for their correlative, phenological (pink tip, balloon, first bloom, full bloom, harvest date), morphological (plant length and trunk diameter, tree form, flower property, flower color), and pomological (fruit weight, fruit height, fruit length, fruit width, seed weight, Brix, % acidity, pH, pulp/seed rate, fruit shape, fruit tip, rupture state of the fruit, pubesence, fruit top color, fruit ground color, red blush in flesh, fruit attractiveness, firmness, taste, freestone, and fruit flesh color) characteristics in this experiment [20, 21]. Also, the marker-assisted selection effectiveness of F_1 peach hybrids was determined by two SSR markers.

2.2. Molecular analysis (SSR)

High molecular weight genomic DNA was extracted from the leaf samples of each F_1 hybrids for SSR analysis. SSR analysis was performed in accordance with Aka-Kacar et al. [22]. Two primer pairs (BPPCT009/b, MA014a) were used to generate the SSR genotyping. DNA profiles of parents and F1 hybrids were recorded, and their allelic profiles were compared. Results obtained from the SSR analysis were evaluated with the pomological features of genotypes.



Figure 1. Ustun local peach cultivar.

http://dx.doi.org/10.5772/intechopen.73440

3. Results and discussion

3.1. The morphological, phenological, and pomological analyses

If we consider the trunk diameter measurements on F_1 hybrids, following results were obtained; In VxU combination, the highest value (87.65 mm) was obtained from VxU-18 genotype, whereas the lowest one (33.54 mm) was obtained from VxU-56 genotype. In SRGxU combination, the highest trunk diameter value (99.44 mm) was determined in SRGxU-9 genotype, while the lowest one (21.92 mm) was determined in SRGxU-100 genotype. The genotypes reached full bloom phase on March 11, the earliest and on April 6, the latest. The hybrids showed the characteristics of rosaceae and campanula flower [16].

To get faster growth and earlier fruit set, F_1 seeds of the genotypes were sown and grown under the subtropical conditions of Adana at the Cukurova University (50 m elevation). The genotypes could not show their best performances in Adana, but they gave us early selection opportunities. Although to the low chilling and sea-level conditions in Adana, some genotypes showed very late ripening habit such as, September 3–18. If we consider Ustun late peach cultivar is ripening at the end of September in Pozanti, some of these genotypes could be ripen later than the parents under Pozanti conditions.

The highest mean fruit weights in VxU combination were obtained from VxU-58 (137.30 g) and VxU-55 (136.95 g) genotypes. In SRGxU combination, the highest fruit weights were obtained from SRGxU-32 (154.30 g) and SRGxU-82 (150.90 g) genotypes.

Brix values among all hybrids (**Table 1**) were the highest in VxU-4 (14.40), SRGxU-110 (13.0), and SRGxU-111 (13.0) genotypes. These results are in accordance with the results of Tanriver and Kuden [13] and Monet [7, 20, 23] who stated that the hybrids showed their best performances (fruit weight, color, Brix value, and especially for their harvesting dates) in the areas convenient for their chilling requirements. Harvesting dates and fruit characteristics of the selected genotypes are given in **Tables 2** and **3**.

The data obtained from the observations and analyzes were weighed out in the individuals in both combinations. According to results, VxU-55, VxU-41, VxU-34, VxU-14, VxU-1, Vx-13, VxU-24, and VxU-26 genotypes gave the best results among the peach genotypes in VxU combination. In the same combination, VxU-31, VxU-42, VxU-53, and VxU-15 were found to be the best nectarine genotypes. In the other combination (SRGxU), the performances were obtained from SRGxU-101, SRGxU-28, SRGxU-88, SRGxU-84, SRGxU-36, SRGxU-57, SRGxU-23, SRGxU-92, and SRGxU-93 peach genotypes and SRGxU-5 nectarine genotype (**Table 1**).

Harvest date	20	Fruit shape	7
Fruit weight	20	Fruit ground color	7
Brix	13	Fruit tip state	5
Attractiveness	12	Red color under skin	3
Freestone state	10	Red color around seed	3

Table 1. Weighted grading types and scores.

Genotypes	Harvest date	Fruit weight (g)	TSS (%)	Acidity
VxU-55	08/14–27	136.95	12	0.73
VxU-41	08/27	173.20	12	0.68
VxU-34	08/26	163.10	15	0.64
VxU-14	08/26	171.28	12	0.68
VxU-1	07/12–21	108.60	12.9	0.75
VxU-13	08/20–27	120.12	13.15	0.82
VxU-24	08/1–13	142.25	11	0.54
VxU-26	08/14–09/18	129.15	12.9	0.66
VxU-31	09/03	79.8	13	0.77
VxU-42	08/02–09/03	108.23	11.5	0.51
VxU-53	06/28	131.74	10	1.03
VxU-15	06/10–29	87.42	10	0.60
SRGxU-101	08/14	161.75	12	0.53
SRGxU-28	07/24	109.8	12	0.50
SRGxU-88	08/14–27	136.95	12	0.48
SRGxU-84	07/04	164.21	12	0.67
SRGxU-36	08/12	152.89	10	0.38
SRGxU-57	07/27	106.6	10.5	0.66
SRGxU-23	07/23–08/27	118.37	11	0.69
SRGxU-92	07/12	110.64	10	0.58
SRGxU-93	07/08	209.17	12	0.46
SRGxU-5	08/24	108.09	11.5	0.49

Table 2. Harvesting dates and the fruit characteristics of the selected genotypes.

3.2. The molecular analysis

A total of 176 F_1 hybrids were examined by using two different SSR primer pairs for early marker-assisted selection. The fruit characteristics of some F_1 hybrids are found to be different as compared to their parents, while some of them were almost found to be the same.

Among the molecular data determined from MA014a primer pair, with pomological analysis of hybrids, more correct results were obtained from MA014a primer pair in the genotypes of SRGxU combination (42.02%) and in the genotypes of VxU combination (85.29%). Also, BPPCT009/b primer pair was used to determine freestone characteristics of the hybrids. SRGxU combination gave 38.35% of correct results, and VxU combination gave 30.50% of

Genotypes	Firmness (kg/cm²)	Freestone	Fruit shape	Pulp color	Pubescence
VxU-55	2.92	Semi freestone	Oval	Yellow	Medium
VxU-41	2.67	Semi freestone	Round	Yellow	Medium
VxU-34	2.19	Cling stone	Round	Yellow	Medium
VxU-14	2.06	Cling stone	Round	Yellow	Medium
VxU-1	3.12	Freestone	Oval	Yellow	Medium
VxU-13	1.88	Cling stone	Oval	Yellow	Medium
VxU-24	2.68	Freestone	Oval	Yellow	Medium
VxU-26	2.9	Semi freestone	Oval	Yellow	Medium
VxU-31	1.5	Freestone	Oval	Yellow	Nectarine
VxU-42	3.10	Cling stone	Oval	Yellow	Nectarine
VxU-53	3.06	Cling stone	Oval	White-Red	Nectarine
VxU-15	2.28	Semi freestone	Round	White-Red	Nectarine
SRGxU-101	2.07	Freestone	Oval	Yellow	Medium
SRGxU-28	3.26	Freestone	Round	Yellow	Medium
SRGxU-88	2.92	Semi freestone	Oval	Yellow	Medium
SRGxU-84	2.65	Cling stone	Oval	Yellow	Medium
SRGxU-36	1.86	Freestone	Round	Yellow	Medium
SRGxU-57	2.75	Freestone	Round	Yellow	Medium
SRGxU-23	2.45	Freestone	Round	Yellow	Medium
SRGxU-92	2.34	Semi freestone	Oval	Yellow	Medium
SRGxU-93	3.47	Cling stone	Round	Yellow	Medium
SRGxU-5	2.75	Freestone	Round	Yellow	Nectarine

Table 3. The fruit characteristics of the selected genotypes.

correct results. As a conclusion, for early selection criteria, SSR primer pairs are good molecular markers to be used for this aim. However, in this research, we could not obtain a very good relationship among our hybrids.

Dirlewanger et al. [24] stated that MA014a SSR primer pair is associated with fruit shape and flat fruit. In our experiments, we found that MA014a primer pair was more suitable to VxU population, but not for SRGxU population. For freestone character, BPPCT009/b SSR primer pair was used (**Figure 2**) to determine the freestone character. This primer was not compatible for SRGxU and VxU F_1 populations. Freestone characters of hybrids and allelic profiles did not match each other properly. The photos of some of the selected genotypes are shown in **Figures 3–16**.

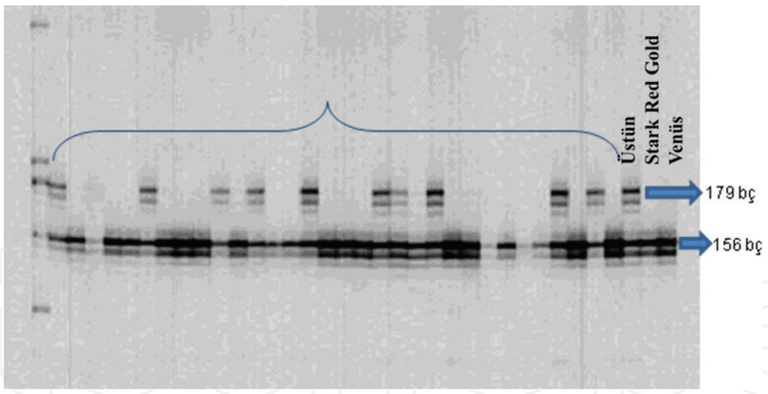


Figure 2. Polyacrylamide gel image of SSR bands of BPPCT009 primer pair with SRGxU population.



Figure 3. Fruits of VxU-55 genotype.



Figure 4. Fruits of VxU-41genotype.



Figure 5. Fruits of VxU-14 genotype.

http://dx.doi.org/10.5772/intechopen.73440



Figure 6. Fruits of VxU-1 genotype.



Figure 7. Fruits of VxU-13 genotype.



Figure 8. Fruits of VxU-24 genotype.



Figure 9. Fruits of VxU-26 genotype.



Figure 10. Fruits of SRGxU-101 genotype.



Figure 11. Fruits of SRGxU-28 genotype.



Figure 12. Fruits of SRGxU-88 genotype.



Figure 13. Fruits of SRGxU-84 genotype.

http://dx.doi.org/10.5772/intechopen.73440



Figure 14. Fruits of VxU-53 genotype.



Figure 15. Fruits of VxU-15 genotype.



Figure 16. Fruits of SRGxU-5 genotype.

4. Conclusion

This peach breeding study was carried out to obtain late ripening, high chilling, good quality peaches, and nectarines suitable for more continental climates. As a result of the experiment, some genotypes were found to be later fruit ripening producers than their parents (September 3–18) under Adana subtropical climatic conditions (23 m elevation). The results showed that these late genotypes could ripen later under the continental climatic conditions. This means that these genotypes could have better performances at Taurus Mountains in Pozanti under higher elevation conditions (1100 m).

One of the parents of these genotypes was Ustun, late peach cultivar, which ripened at the end of September in Pozanti. This observation lead us to think that some of these genotypes ripen on 3rd-18th September. Under Adana subtropical climatic conditions, they could ripen later than their parents in Pozantı (may be at the end of September or at the beginning of October). Thus, this will be a very good opportunity to get very high market prices with these very late season peaches and nectarines.

Considering the fruit quality characteristics of the genotypes, among F1 hybrids, VxU-18 and SRGxU-9 genotypes gave better trunk development than the others. For the fruit weight characteristics, SRGxU-32, SRGxU-82, VxU-58, and VxU-55 gave the biggest fruits among all the genotypes. The highest brix values were obtained from VxU-4, SRGxU-110, and SRGxU-111 genotypes.

In conclusion, the genotypes of VxU-55, VxU-41, VxU-34, VxU-14, VxU-1, Vx-13, VxU-24, VxU-26, SRGxU-101, SRGxU-28, SRGxU-88, SRGxU-84, SRGxU-36, SRGxU-57, SRGxU-23, SRGxU-92 and SRGxU-93 peaches and VxU-31, VxU-42, VxU-53, VxU-15 and SRGxU-5 nectarines were found to be promising ones.

The selected genotypes which were grafted onto GF-677 rootstock were taken to Pozanti Agricultural Research and Application Center at the Taurus Mountains in Pozanti to compare their performances at high chilling area under second selection. Also in the future studies, more locus specific molecular marker systems such as SSRs or SNPs could be used to find out better characterization of the hybrid populations.

Author details

Ayzin Baykam Kuden[1]*, Songul Comlekcioglu[1], Kadir Sarier[2], Burhanettin Imrak[2] and Ali Kuden[1]

*Address all correspondence to: abkuden@gmail.com

1 Department of Horticulture, University of Cukurova, Faculty of Agriculture, Saricam, Adana, Turkey

2 Pozanti Agricultural Research and Application Center, University of Cukurova, Saricam, Adana, Turkey

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