

Progress on the Research of Peach Germplasm Resources and Breeding in China

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ABSTRACT

This paper reviews the progress on the research of peach germplasm resources and breeding in China in the last 20 years. Three national peach germplasm repositories were established in the late 1980s. About 1,300 accessions within China and from foreign countries were preserved *ex vitro*. In order to describe peach diversity, China made a “Peach Descriptors” in 1990 based on IBPGI Peach Descriptors in 1980. And a new peach descriptors system “Descriptors and Data Standard for Peach” was published in 2006. Evaluations were made based on these two descriptors, and evolutions and characterizations were also made through morphology, isozyme analysis, palynology and molecular markers. Breeding varieties with good taste, extension of ripening time, and increased fruit firmness for shipping are the main objectives of the breeding programs in China. Great progress was achieved in honey peach, flat peach and nectarine, especially in nectarine. We are also working on developing molecular markers, including RAPD, SSR and AFLP that are linked to specific characteristics.

Keywords: germplasm repository, descriptor, evaluation, molecular marker, new cultivar

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INTRODUCTION

Peach (*Prunus persica* (L.) Batsch.) is native to China where there are rich germplasm resources and a long cultivation history. According to the FAO, the world's peach production was 15.91 million tons from 1.41 million ha in 2005. China ranks first in both area harvested and production, with 0.60 million tons produced from 0.61 million ha in 2005. Much progress has been made in China in the last 20 years on research work of germplasm resources and breeding new varieties.

RESEARCH ON GERMPLASM RESOURCES

Germplasm repository

Three national peach germplasm repositories were established in the late 1980s. One was in Nanjing, and represents the southern part of China, one was in Zhengzhou, central China, and the other one was in Beijing, northern China. They contain a wide array of primitive and advanced germplasm. About 1,300 accessions were preserved in the field, among them 359 accessions from 14 foreign countries:

USA the most with 220 accessions, Japan second with 83 accessions. For most of the germplasm resources, two plants were planted for maintenance.

Descriptor system

Characterization plays an important role for people to know and identify fruit genetic resources. In order to describe peach diversity, China made a “Peach Descriptors” (Wang 1990) in 1990 based on IBPGI Peach Descriptors in 1980. This descriptor is made of two parts, one basic data with 36 items, another characteristic data with 117 items, altogether including 153 items.

A new peach descriptors system “Descriptors and Data Standard for Peach” (Wang *et al.* 2006) was published last year. This descriptor is made of 6 parts, first passport data, second botanic data, third fruit quality, fourth resistance to environmental stress, fifth resistance to disease and pest, last other characters. There are 151 total characteristics, with 35 primary characters, 99 optional characters, and 17 conditional characters. For characteristic data, in general, two reference cultivars were given, one US cultivar, the other which is widely planted or used in China.

Characterization and evaluation

Based on the Peach Descriptors in 1990, characterization and evaluation were made in the three national germplasm repositories. The results of characterization of 648 accessions were compiled in 1993 and 1998, most with fruit characters. This provides ground information to the research workers and helps them to decide how to use these varieties. Some varieties with excellent characters, like 'Fei Cheng Tao', 'Hua Yu Lu', 'Bai Hua', 'Jin Yu', 'Okubo', 'Mayfire', 'Early Red Two', among others were used successfully in commercial or breeding programs in China.

Based on the breeding program, the genotypes of some qualitative characters (pollen fertility, fruit shape, flesh color, flesh firmness, freestone or clingstone) of nearly 60 peach cultivars were evaluated (Yu *et al.* 1996). The apprehension of genotype would certainly have significant importance for exploration of peach germplasm for selecting desirable parents to increase the efficiency of peach breeding.

The chilling requirement of most peach varieties native to China was from 750~950h (Wang *et al.* 1997) while *P. davidiana*, *P. kansuensis*, *P. potanini* and *P. mira* have lower chilling requirement, from 250~550h. Ornamental peach has a higher chilling requirement, mostly higher than 900 h, the highest one is 'Ju Hua Tao' with 1250 h (Zhu *et al.* 2004).

Root-knot nematodes (*Meloidogyne* spp.) are serious pathogens in agriculture. *M. incognita* is the main species in central China (Zhu 1992). 'Shou Xing Tao 1' and 'Gan Su Tao 1' are immune to *M. incognita*.

Green aphid (*Myzus persicae*) is also an important pest in China. A study through field investigation and further inoculation (Wang *et al.* 2001) showed that the resistance of *P. davidiana* was strongest while that of *P. kansuensis* was weakest. 15 highly resistant varieties or clones were identified, including *P. davidiana*, dwarf and ornamental peach.

Gummosis is one of the main diseases in peach production, especially in southern China. There is no good method to control it until now. A field investigation (Zhao *et al.* 1996) showed that 'Tian Jin Shui Mi' (Wan), 'Bai Sha' and 'Da Hong Hua' were highly resistant to gummosis. 'Bai Hua', a local variety widely planted in southern China, exhibited high resistance to *Botryosphaeria dothidea* both in the field and under inoculation (Zhao *et al.* 1994).

Genetic evolution

Isozyme analysis, palynology, karyotypes and molecular markers were used to evaluate the peach genetic evolution. Isozyme analysis (Wang *et al.* 1990) indicated that the isozyme patterns of petioles and anthers are significantly correlated with the flesh texture and pollen fertility, respectively. This proposed that the evolution of peach varieties follows the order wild peach to crisp peach to mitao peach to honey peach. The patterns of water-soluble proteins from sepal tubes and petals by isoelectric focusing can distinguish the yellow peach from the white peach, and the patterns of petals can differentiate between showy and non-showy peach flowers (Lu *et al.* 1990). Flavonoid compound analysis in peach leaves by HPLC was performed by Zhou *et al.* (1996) to study the origin and evolution of peach germplasm within China and from foreign countries. Pollen morphology of 103 peach cultivars (Wang *et al.* 1990) showed that *P. davidiana*, *P. persica* and *P. ferganensis* have a close relationship, and that all of them originated from *P. kansuensis*. SDS electrophoresis analysis of pollen proteins showed that the evolution follows *P. mira* to *P. kansuensis* to *P. davidiana* to *P. potanini* to *P. ferganensis* to *P. persica* (Zong *et al.* 1995). *P. kansuensis* and *P. davidiana*, *P. persica* and *P. ferganensis* had similar chromosome karyotypes and close relationships (Guo *et al.* 1996). *P. kansuensis* had the strongest original nature (this means *P. davidiana*, *P. ferganensis* and *P. persica* are ori-

ginated from *P. kansuensis*), follows *P. davidiana*, then *P. ferganensis* and *P. persica*.

Molecular marker analysis

Molecular marker analysis has been used in peach research work in recent years.

Cheng *et al.* (2003a) studied the genetic difference in groups of *P. persica* by RAPD with 203 accessions. The results indicated that the dwarf, weeping, red-leaf, and ornamental peach groups were the most original, while the crisp peach, mitao, honey peach, flat peach, nectarine and yellow peach groups were more evolutionary. The genetic diversity in different groups was: yellow peach > mitao > flat peach > red-leaf peach > crisp peach > ornamental peach > honey peach > nectarine > dwarf peach > weeping peach (Cheng *et al.* 2004). RAPD analysis showed that *P. ferganensis* was classified into *P. persica* and that it may have originated from *P. persica* (Yang *et al.* 2001, 2002), or that it should be a variant of *P. persica* and named as *P. persica* var. *ferganensis* (Cheng *et al.* 2001). A similar result was obtained through SSR (Yu *et al.* 2004). SSR analysis showed that the evolution follows *P. mira* to *P. kansuensis* to *P. potanini* to *P. persica* and *P. ferganensis* (Yu *et al.* 2004). This was basically identical with the results of morphology, isozyme and karyotypes analyses.

RAPD markers have also been used for peach cultivar identification (Cao *et al.* 2003; Zong *et al.* 2005a) and their mutation (Jin *et al.* 1998; Ran *et al.* 2004). Seven honey peach cultivars 'Okayamahaku', 'Springtime', 'Robin', 'Hakuho', 'Xiahui 2', 'Zhaoyan', 'Fenghuayulu' (Cheng 2004); six nectarine cultivars 'Shuguang', 'Ruiguang 2', 'Mayfire', 'Aimila', 'Hongliguang', 'Armking' (Cheng *et al.* 2002); four mitao cultivars 'Qiumi', 'Taiyuanshuimi', 'Shenzhouhongmi', 'Wenzhoushuimi' (Cheng 2003); six crisp peach cultivars 'Dahongpao', 'Wuyuexian', 'Qinglingdongtao', 'Yixianhong', 'Yangquanroutao', 'Datiantao'; two yellow peach cultivars 'Fertini Moretini', 'Elberta' (Cheng *et al.* 2003c); five flat peach cultivars 'Yulupantao', 'Wuyuexianpantao', 'Sulianpantao', 'Jiaqingpantao'; 124 pantao cultivars (Cheng *et al.* 2003d) were the key germplasm to preserve. 'Hunchuntao' is a preferential germplasm to preserve, and not the hybrid of *P. persica* × *P. davidiana*, but rather *P. persica* according to clustering analysis and genetic distance (Zong *et al.* 2005b).

Molecular marker and genetic map

Molecular markers linked to white/yellow, peach/nectarine, non-acid/acid, pollen fertility/sterility were identified in China. RAPD marker OPP20-2200 and OPU03-850 was linked to peach/nectarine and white/yellow with a distance of 5.0 cM and 9.6 cM respectively (Yang *et al.* 2000), and converted into SCAR markers SCP20-2258 and SCU03-900 (Jiang *et al.* 2005a, 2005b). The linkage distance is 7.8 cM between SCP20-2258 and the peach/nectarine character, and 21 cM between SCU03-900 and flesh color. SSR marker UDP96-018 (300 bp) was linked to peach gene with a distance of 4.5 cM, and UDP98-407 (680 bp) linked to white flesh gene with a distance of 2.2 cM (Yu *et al.* 2006). Marker NNJ-I (600 bp) and NNJ-I (900 bp) were amplified by primers which were designed according to male sterility sequence of *Arabidopsis thaliana* and were tightly linked to the male sterility gene with a distance of 0 cM (Yu *et al.* 2006). Two AFLP markers AF_{TA-CTC}, AF_{AT-CTA} were found linked to the fruit non-acid/acid trait (Wu *et al.* 2004a, 2004b). The linkage distances were 1.47 cM and 2.99 cM respectively. The D/d gene linkage groups was established, and AF_{TA-CTC}, and AF_{AT-CTA} were located in two sides of the D/d locus.

Establishing a genetic map has just begun in China. The genetic linkage map of Beijing '2-7' was elaborated with a total of 19 loci by using Mapmaker. Seven linkage groups covering 221.7 cM of the peach genome were found. The genetic linkage map of 'Baihuashanbitao' was elaborated

with a total of 103 loci by using Mapmaker. 12 linkage groups covering 1238.8 cM of the peach genome were found (Qiao *et al.* 2006). With AFLP, a total of 144 markers were assigned to 11 linkage groups (LOD 3.0), and the total length of the linkage map was 1167.6 cM covering 97.3% of the peach genome. The average length of 11 groups and the average interval between markers was 106.15 cM and 12.04 cM, respectively (Xin *et al.* 2006).

BREEDING PROGRAM

Breeding early-ripening cultivars for the fresh market was the main objective in the 1960s and 1970s. In 1970s and 1980s, breeding cultivars for canning was also a main objective then. Later, nectarine and flat peach cultivars was gradually emphasized in the 1980s and 1990s. According to the available literature, about 167 cultivars have been introduced since 1986. Among them, cultivars for fresh consumption peaches represent the greatest part of the new cultivars (87; 53.1%), followed by nectarine (39; 23.3%), then the canning clingstone peaches (21; 12.6%), and flat peach (20; 12.0%). It should be mentioned that most of the nectarine cultivars were published since 1998, and that great progress have been made in this field. In the early 1980s, several varieties such as 'Mayfire', 'Armking', 'NJN76' and 'Fantasia' from the USA were planted in China, but within a small acreage due to their acidity. There was a nectarine boom in the late 1990s, especially in northern China with the release of 'Shuguang' (Zong *et al.* 1999), 'Ruiguang' (Jiang *et al.* 1998), 'Zao Hongzhu' (Wang *et al.* 1995) and others. Now most of the nectarine varieties commercially planted are Chinese varieties.

According to their genetic origin, 67.1% of the cultivars have been obtained through cross-pollination (50.1% peaches, 80.9% canning clingstone, 92.3% nectarine, 75% flat peach), 12.0% by open pollination (14.9% peaches, 19.0% canning clingstone, 2.5% nectarine, 10% flat peach), 9.6% by mutation (14.9% peaches, 0% canning clingstone, 5.12% nectarine, 5% flat peach), 11.3% unknown (19.5% peaches, 0% canning clingstone, 0% nectarine, 10% flat peach). 26 cultivars were obtained from embryo culture (Wang *et al.* 1995, 2003; Yang *et al.* 2004; Wang *et al.* 2005; Ye *et al.* 2005).

The ripening calendar shows the amount of work done in breeding early ripening peach cultivars, 56.3% of the cultivars are early ripening (fruit development period, FDP <90 d), 23% mid-season (FDP: 91~120 d), 20.7% late ripening (FDP >121 d). Nectarines have a similar distribution, 64.1% of the cultivars are early ripening, 28.2% mid-season. Only 7.7% are late ripening. The canning clingstone peach cultivars are 33.3% early ripening, 52.4% mid-season, and 14.3% late ripening. The flat peach cultivars are 40% early ripening, 45% mid-season, and 15% late ripening. The shortest FDP is a flat peach, with only 45 d, while the longest FDP is peach, with 210 d (Lv *et al.* 2000).

As for the flesh color, 74.8% of the cultivars are white fleshed (95.4% fresh consumption peaches, 59% nectarine, 90.4% flat peach) while all the canning clingstone peaches are yellow fleshed. 19 peaches, 2 canning peach and 1 flat peach are pollen-sterile, while all the others are pollen fertile. 95.8% of the cultivars are clingstone, with only 16 being freestone (12 peach, 2 nectarine, 2 flat peach).

CONCLUDING REMARKS

As a peach native country, China has made great progress in the last 20 years. But compared to USA, Japan, and some other countries, we still have much work to do. First of all, wild or semi-wild, local germplasm needs to be explored, preserved and utilized. Biotechnology also needs to be emphasized to evaluate germplasm. It is important to work together in molecular marker and genetic mapping, like the European working group, so that we can work more efficiently. Even though much progress has been made in the breeding program, fruit firmness, fruit shape, and soluble

solid content (SSC) need to be improved further. As for flesh color, among the 87 fresh consumption peach cultivars, only four are yellow in flesh. This situation needs to be changed, and more yellow fleshed peaches should be introduced. Large fruits, good flavor, high SSC, and increased fruit firmness for shipping are the main objectives of the breeding program at present.

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