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# The Collection, Conservation and Utilization of Wild Soybean (*Glycine soja*) and its Relatives in China

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**Abstract**: The global conservation priorities for wild crop relatives are one of the most important topics in worldwide. The wild crop relatives possess more genetic diversity which is useful for developing productivity, multi-resistance to diseases, and nutritious crop varieties. Here, we introduced the collection, conservation and utilization of the wild soybeans and its relatives in China. During the past 40 years, 8 518 wild soybean accessions on a large scale were collected in China for three times -the first time in 1978 – 1982, the second time in 1996 – 2000, and the third time in 2001 – 2010. These accessions were stored in the two tracks including the National Gene Bank in Beijing and the dry region of western China. Meantime, we investigated and utilized these wild soybean accessions in many ways on a large scale in China.

**Keywords**: Wild soybean (*Glycine soja*); Collection; Conservation; Utilization

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# 中国野生大豆和它的近缘的收集、保存和利用

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**摘　要**:野生作物近缘的保存是一个世界范围的重要的课题,野生的作物近缘拥有更多的遗传多样性对于育成高产、抗病和具有优良品质的作物品种意义重大。文章主要介绍了中国野生大豆及它的近缘的收集保存和利用情况,在过去的40多年中,中国先后进行了3次野生大豆种质资源收集工作,共收集资源8 518份,进行的时间分别为:第一次1978 – 1982年,第二次1996 – 2000年,第三次2001年 – 2010年。这些种质资源采用双轨制进行保存,分别保存在北京的国家基因库和中国的西部干燥区域。同时介绍了中国科研单位对野生大豆品种资源调查研究和利用的情况。

**关键词**:野生大豆资源; 收集; 保存; 利用

The world's food supply depends on a small number of crop species. Because the high-yielding cultivars dominate the production but are relatively few in numbers and are genetically similar, the genetic diversity in these crops is presumed to have declined to alarmingly low levels[1]. However, the wild relatives of domesticated crops possess abundant genetic diversity which is useful for developing more productivity, nutritious and resilient crop varieties[2]. Current evidence indicates that the cultivated soybean was domesticated from its wild relative *Glycine soja* Sieb. & Zucc in China[3], and the wild soybean has much more genetic biodiversity than that of the cultivated[4]. Although soybean genetic diversity has been eroded by human selection after domestication, it is notable that the diversity lost through the genetic bottlenecks of introduction and plant breeding was mostly due to the small number of Asian introductions and not the artificial selection subsequently imposed by selective breeding[5]. Therefore, it needs to broaden utilization of wild soybean and its relatives in soybean research.

## 1　Collection of wild soybean and relatives

During the past four decades, we collected 8 518 accessions of wild soybean (*Glycine soja* Sieb. et Zucc.) and its relatives on large scale for three times in China. The first time (1978 – 1982): The Institute of Crop Germplasm Resources of Chinese Academy of Agricultural Sciences organized collection of wild soybean and relatives in whole China and 5 939 wild soybean acces-

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sions were collected in whole China[6]. The wild soybean and relatives in the 823 counties from the 1 245 investigated counties, which accounted for 66.1% [7] were found, and the catalogue of wild soybean accessions in China[8] were published.

The protein content of collected wild soybean accessions was much higher than that of the cultivated soybean. High protein content is remarkable characteristic of wild soybean, it can be used in soybean breeding for increasing protein content of soybean cultivars. Especially, the Protein content ( >50% ) of collected wild soybean accessions accounted for 6.7% [9-10]. In the meantime, amounts of accessions with a lot of pods and long flower head were also collected. As one of the research teams in Heilongjiang Academy of Agricultural Sciences, we organized 24 scientists from different institutions to collect and investigate the wild soybean and relatives. In Heilongjiang province, we collected 547 accessions of wild soybean and relatives, and analyzed the protein content (Table 1).

**Table 1 The protein content of wild, semi-wild and cultivated soybean in China**[9-11]

| Protein content /% | Number of Cultivated soybean | Percentage /% | Number of semi-wild soybean | Percentage /% | Number of wild soybean | Percentage /% |
|---|---|---|---|---|---|---|
| 36.01 -40.00 | 2 | 28.5 | 1 | 2.6 | 1 | 0.9 |
| 40.01 -44.00 | 5 | 71.5 | 19 | 50.0 | 5 | 4.7 |
| 44.01 -48.00 | | | 18 | 47.4 | 51 | 48.1 |
| 48.01 -52.00 | | | | | 45 | 42.5 |
| >52.01 | | | | | 4 | 3.8 |

The second time (1996 -2000): 600 accessions of wild soybean and relatives were collected mainly from Inner Mongolia, Shandong, Jiangsu, Hubei, Henan, and Hebei provinces[12-13]. The academies of agricultural sciences of mentioned provinces attended the collection. The third time (2001 -2010): 1979 accessions of wild soybean and relatives were collected from 17 provinces of China, the academies of agricultural sciences of 17 provinces attended the collection. These accessions distributed in 318 counties and 930 towns in China[12-13]. Until 2005, 6 172 accessions were collected in the National Gene Bank, which were collected from different provinces and regions. According to Table 2, accessions of wild soybean and relatives were mainly concentrated in Northeastern provinces, Liaoning, Jilin, and Heilongjiang and Northern China-Shanxi, Shannxi, and Henan provinces. In southern China, the number of accessions was over 300 in Fujian province. In eastern China, the number of accessions was over 100 in Zhejiang, Jiansu, Anhui and Shandong provinces.

**Table 2 Number of wild soybean accessions documented and conserved in the National Gene Bank in each province** [6]

| Province | Number of accessions | Province | Number of accessions |
|---|---|---|---|
| Liaoning | 1248 | Guizhou | 86 |
| Jillin | 1220 | Sichuan | 83 |
| Heilongjiang | 789 | Hubei | 70 |
| Shanxi | 544 | Jiangxi | 64 |
| Shaanxi | 402 | Inner Mongolia | 58 |
| Fujian | 379 | Hunan | 56 |
| Henan | 305 | Hebei | 44 |
| Zhejiang | 166 | Ningxia | 24 |
| Jiangsu | 160 | Guangdong | 17 |
| Anhui | 129 | Beijing | 15 |
| Shandong | 120 | Tibet | 11 |
| Gansu | 90 | Yunnan | 2 |
| Guangxi | 90 | | |
| Total | 6172 | | |

## 2 Conservation of wild soybean and relatives

There are many ways for conservation accessions of wild soybean and relatives in China. Firstly, All accessions of wild soybean are conserved in the National Gene Bank, where located in Campus of Chinese Academy of Agricultural Sciences (CAAS, Beijing). Secondly, the other portion of these accessions of wild soybean and relatives are conserved in the western drought region of China. Thirdly, parts of accessions are also conserved in the mostly provincial academies of agricultural sciences and agricultural colleges and universities. In order to conserve vitality and sprout of wild soybean and relatives, our research staff in the Institute of Crop Science, CAAS and provincial academies and agricultural colleges will renew regularly these accessions of wild soybean and relatives. According to the statistics of research team of wild soybean of Crop Science Institute, Chinese Academy of Agricultural Sciences, in China 46 protection zones of wild soybean in 14 provinces during 2001 – 2011, including Heilongjiang -7 protection zones, Jilin- 4, Liaoning-3, Hebei-9, Shandong-1, Shanxi-1, Henan-4, Anhui-3, Hubei-3, Hunan-2, Jiangsu-1, Zhejian -1, Chongqing-3, Shangxi-1, and Gangsu-2. Central Government invested 41.8 million yuan RMB for to establish these protection zones.

## 3 Utilization of wild soybean and relatives

There are a lot of useful characters in the wild soybean and relatives, such as high protein content, more pods per plant, resistance to diseases and insects, resistance to drought and salt, and rich in linolenic acid, isoflavone and polysaccharide etc.

### 3.1 Utilization of wild and relatives for high protein content breeding

Three soybean cultivars with high protein were developed using wild soybean and relatives, such as Longdou 1, Longdou 3, and soybean line Ha-8807[13]. Yao et al[17] developed a soybean line Ha-8807 with protein content 48% by crossing wild with cultivated.

Wang et al[18] developed six soybean lines with protein content over 50% by crossing wild soybean with cultivated soybean and developed 7 lines with protein content over 45% by crossing semi-wild soybean with cultivated soybean. Wu et al[19] also developed a soybean line with protein content 48.34% by crossing wild soybean with cultivated, it is higher than Shennong 25104 for 3.69% of protein content.

Semi-wild soybean germplasm-Peking with highly resistant to cyst nematode was found in the evaluation research[14], which possessed the complementary action of three recessive genes (*rhg*1, *rhg*2, *and rhg*3)[15]. In 1970, US soybean field was damaged by soybean cyst nematode over 2.3 million acres in Ullinois, Missisipi, North Carolina, Arkansoy, and Louisanna states, the soybean yield decreased by 70 – 90%[16]. Soybean breeders used Peking, as one of the soybean parents to develop soybean cultivars Custer and Dyer with high resistance to cyst nematode[16]. Therefore, it is very important to utilize the wild and semi-wild soybean in soybean breeding.

### 3.2 Utilization of wild soybean and relatives for high yielding breeding

The trait with more pods is one of the typical characters in wild soybean and relatives. For instance, a wild soybean line with over 3 000 pods per plant was collected in Yaoyang of Hunan province. Moreover, a wild soybean line with over 4 000 pods per plant was also collected in the Dali of Shanxi province[20-21]. Wu et al[22] also collected a semi-wild soybean with 2 900 pods per plant in the Kaiyuan County of Liaoning province.

Scientists of Jinzhou Agricultural Research Institute of Liaoning Province developed a new soybean line-5621 with high yielding and resistance to disease (semi-wild soybean, weight of 100 seeds, 6.0 g). A new soybean cultivar Tiefeng 18 was developed by crossing of cultivated line 45 – 15 with semi-wild line 5621 in Tieling Agricultural Research Institute of Liaoning Province in 1964. This cultivar was released in several provinces and won a First Prize of China National Invention in 1983[21]. Scientists of Liaoning province developed 33 soybean cultivars using line 5621, including seven cultivars during first cycle of crossing, such as Tiefeng 18, Tiefeng 19, Tiefeng 10, Kaiyu 9, Kaiyu 10, Liaodou 10 and Shennong 25104. These cultivars were planted in 4.34 million hectares in China during 1973 – 1990. From second cycle of crossing, they developed 26 cultivars[23-24]. We also developed several high yielding lines by using the crossing of Zhonghuang 13 with Tiefeng 18 or Zhonghuang 35 with Tiefeng 18, which named Zhongzuo 132, Zhongzuo133 and Zhongzuo 136, now these lines are in regional tests in different locations in China[25].

### 3.3 Utilization of wild and relatives for high resistance to insect

In 1979 – 1980, we analyzed the percentage of damage caused by soybean pod borer (*Leguminivora glycinivorella*-Mats.) in different types of soybean (Table 3) and concluded that it is possible to use the wild soybean and relatives with high resistance to insect for soybean breeding[9].

**Table 3 Percentage of damage caused by soybean pod borer (*Leguminivora glycinivorella*-Mats.) in different types of soybean**

| Type | Number of sample | Average damage ratio | Distribution of damage caused by pod borer types | | | | |
|---|---|---|---|---|---|---|---|
| | | | >10% | 5% – 10% | 1% – 4% | <1% | 0% |
| Wild | 175 | 0.4 | | | 13 | 81 | 81 |
| Semi-wild | 10 | 9.6 | 3 | 7 | | | |
| Cultivated | 6 | 17.0 | 6 | | | | |

### 3.4 Utilization of wild soybean and relatives for high resistance to disease

It is reported that soybean lines with high resistance to soybean cyst nematode was selected from the wild soybean accessions. For instance, U. S. scientists used Peking as one soybean parent and developed soybean cv. Custer and Dyer with high resistance to cyst nematode, which overcome the damage caused by cyst nematode in several states of USA[15].

During past 20 years we paid a lot of attention to the research on soybean cyst nematode. We found that there existed the dominant physiological race 4 of soybean cyst nematode in Beijing suburb[26]. We also developed several cultivars with high resistance to SCN using soybean semi-wild lines P. I. 437654, Huipizhiheidou, and Wuzaiheidou as parents to cross with cultivated soybean[27], such as Zhonghuang 26 (released in Beijing in 2003) and Zhonghuang 54 (released in Northern China and Northwestern China in 2012) with moderate resistance to SCN. The yield of cv. Zhonghuang 54 was 3 307 kg·ha$^{-1}$ in two years average.

### 3.5 Utilization of wild soybean and relatives with small seeds (about 8 – 12 g per 100 seeds)

This kind of cultivars can be used for fermentation of Natto, which is useful for human health. Natto is very popular soybean in Japan. Researchers from the Heilongjiang Academy of Agricultural Sciences developed several soybean cultivars with small seeds, such as Longxiaolidou 1[28] and Longxiaolidou 2 [29]. Soybean breeders from Jilin Academy of Agricultural Science and Northeastern Agricultural University also developed two cultivars with small seed named Jixiaolidou 1[30] and Dongnongxiaoli 1[13].

### 3.6 Fatty acid composition in wild soybean and relatives

Wang et al[10] analyzed the composition of fatty acids in the wild, semi-wild and cultivated soybean (Table 4). Characteristic of composition of fatty acids of wild soybean indicated: The content of linoleic acid of wild soybean much higher than cultivated soybean, the content of linoleic acid of wild soybean contain 18.69%, but the content of linoleic acid of cultivated soybean only 7.35%. The percentages of palmitic acid and linoleic acid are similar among three types of soybean[10]. Due to importance of flax seed oil in health care, the linolenic acid of oil of wild soybean and semi-wild soybean has useful prospect in health care.

**Table 4 Fatty acid composition in the wild, semi-wild and cultivated soybean [10]**

| Type | Number of sample | Palmitic acid | Stearic acid | Oleic acid | Linoleic acid | Linolenic acid |
|---|---|---|---|---|---|---|
| Wild | 18 | 11.42 | little | 15.38 | 53.98 | 18.69 |
| Semi-wild | 4 | 12.46 | little | 18.80 | 55.00 | 13.69 |
| Cultivated | 2 | 11.50 | little | 28.86 | 52.07 | 7.35 |

The Criteria of healthy vegetable oils is as followed: In 1994, WHO and FAO suggested that the ratio of linoleic acid/linolenic acid was 5:1 – 10:1, and the dosage of vegetable oil per day is 25 g, in which the ADI of linolenic acid is not less than 1.0 g per day[31]. The content of linolenic acid (ω-3) of flaxseed oil is the highest than other crop oils, and the ratio of ω-6/ω-3 is ideal (Table 5), but the planting area of flax is limited. Moreover, the content of linolenic acid (ω-3) of soybean oil is 8%, and the ratio of ω-6/ω-3 is also ideal. The content of linolenic acid (ω-3) of wild soybean seed oil is about 18.69%. The content of linolenic acid (ω-3) of semi-wild soybean seed oil is about 13.69%. Therefore, it is possible to use wild soybean oil and semi-wild soybean seed oil for production of linolenic acid (ω-3) in the future.

**Table 5 The main fatty acid composition and ω-6/ω-3 ratio in various vegetable oils**[31]

| Oil type | Percentage of ω-9/% | Percentage of ω-6/% | Percentage of ω-3/% | ω-6/ω-3 ratio |
|---|---|---|---|---|
| Corn oil | 29 | 57 | 0.5 | 114:1 |
| Peanut oil | 48 | 33 | 1 | 33:1 |
| Soybean oil | 23 | 54 | 8 | 7:1 |
| Olive oil | 80 | 9 | 1 | 9:1 |
| Rice bran oil | 45 | 30 | 1 | 30:1 |
| Camellia seed oil | 74 | 11 | 1 | 11:1 |
| Blended oil | 30 – 35 | 30 – 50 | 1 – 3 | 15:1 |
| Flaxseed oil | 25 | 20 | 50 | 1:2.5 |

### 3.7 The use of wild soybean and relatives for feeding

Li et al[32] developed five feeding soybean lines by using the crosses between cultivated and wild soybean. Wang[33] developed some new soybean lines with luxuriant vegetation growth for green forage. In addition, using the intercropping model of wild soybean with feed sorghum, the yield and protein content of feed can be increased significantly[34]. Therefore, it is a good method by crossing between cultivated and wild soybean and relatives for breeding soybean as leguminous green-manuring crop. For instance, a novel soybean cultivar (Kengmo 1) was developed using a semi-wild soybean (Shuanghe Moshidou) as a parent in the Crop Science Institute of Heilongjiang Agricultural Reclamation Academy[35].

### 3.8 Sustainable utilization of genetic diversity in wild soybean and relatives

We characterized the genetic diversity using 72 SSR makers among 60 *Glycine soja* accessions collected in China and compared this diversity with 18 U.S. Ancestral soybean genotypes, 12 Chinese *Glycine max* plant introductions (Pls), and 47 elite soybean lines from the northern USA. The *Glycine soja* accessions were found to contain more alleles per locus (17.1) than the U.S. ancestral genotypes (5.8), the Chinese ancestral genotypes (5.5), and American soybean elite genotypes (4.5) (Table 6). Multivariate analyses were able to separate the *Glycine max* lines from the *Glycine soja* accessions and identify the most diverse subset of *Glycine soja* accessions. Multidimensional scaling separated the *Glycine soja* accessions from high and low latitudes, while Ward's clustering method separated the *Glycine soja* accessions into distinct clusters that tended to include accessions from similar geographical regions. These data will be useful to breeders selecting *G. soja* accessions as parents in a breeding program and for establishing a core collection of *G. soja* to be used in future research[4]. Therefore it needs to broaden the utilization of wild soybean and relatives in soybean research.

**Table 6　Number of alleles per simple sequence repeat maker locus in each *Glycine max* (L.) Merr. or *Glycine soja* Sieb. & Zucc. germplasm group and total as calculated by the FSTAT program. Data from University of Illinois crossing block material (UIUC CXB) were from a previously collected data set [4]**

| Marker | Linkage group | *G. soja* collection | U. S. *G. max* | Chinese *G. max* | Total | UIUC CXB | Marker | Linkage group | *G. soja* collection | U. S. *G. max* | Chinese *G. max* | Total | UIUC CXB |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Satt196 | K | 18 | 5 | 5 | 18 | 5 | Satt259 | C2 | 14 | 8 | 5 | 14 | 4 |
| Satt002 | D2 | 18 | 6 | 4 | 19 | 2 | Satt453 | D1a + Q | 19 | 8 | 8 | 20 | 7 |
| Satt141 | D1b + W | 10 | 5 | 6 | 15 | 7 | Satt354 | C1 | 25 | 7 | 7 | 25 | – |
| Satt236 | A1 | 12 | 4 | 5 | 12 | 4 | Satt414 | I | 19 | 6 | 6 | 21 | 5 |
| Satt143 | L | 17 | 5 | 4 | 18 | 6 | Satt588 | K | 18 | 5 | 8 | 20 | 4 |
| Satt253 | H | 16 | 4 | 5 | 17 | 1 | Satt534 | O | 23 | 8 | 9 | 28 | 8 |
| Satt175 | A1 | 14 | 9 | 7 | 18 | 6 | Satt300 | B1 | 16 | 6 | 3 | 16 | 5 |
| Satt180 | C1 | 13 | 5 | 4 | 16 | 4 | Satt411 | I | 9 | 3 | 5 | 12 | 4 |
| Satt294 | C1 | 15 | 6 | 4 | 17 | 6 | Satt179 | J | 20 | 5 | 4 | 21 | 5 |
| Satt038 | E | 12 | 6 | 7 | 13 | 5 | Satt415 | K | 14 | 6 | 5 | 14 | 5 |
| Satt114 | D2 | 11 | 5 | 6 | 13 | 5 | Satt022 | B2 | 17 | 6 | 6 | 17 | 4 |
| Satt009 | G | 22 | 8 | 7 | 26 | 7 | Satt186 | A1 | 13 | 5 | 4 | 14 | 4 |
| Satt173 | F | 23 | 9 | 7 | 27 | 6 | SAtt419 | E | 19 | 5 | 6 | 19 | 3 |
| Satt184 | N | 19 | 6 | 8 | 20 | 3 | Satt156 | D1a + Q | 18 | 5 | 3 | 18 | 2 |
| Satt243 | O | 18 | 5 | 5 | 21 | 4 | Sarr268 | B1 | 18 | 5 | 6 | 21 | 4 |
| Satt281 | D1a + W | 28 | 10 | 6 | 29 | 4 | Ssatt157 | N | 33 | 110 | 8 | 35 | 7 |
| Satt276 | O | 29 | 14 | 11 | 41 | 7 | Satt329 | D2 | 17 | 7 | 6 | 18 | 4 |
| Satt358 | C2 | 22 | 5 | 6 | 22 | 4 | Satt554 | I | 28 | 4 | 6 | 30 | 2 |
| Satt353 | A1 | 13 | 6 | 5 | 14 | 4 | Satt424 | L | 11 | 6 | 4 | 15 | 5 |
| Satt324 | O | 13 | 5 | 3 | 13 | 4 | Satt271 | N | 7 | 3 | 4 | 7 | 2 |
| Satt373 | H | 17 | 10 | 4 | 21 | 5 | Satt292 | E | 14 | 7 | 6 | 16 | 4 |
| Satt172 | G | 8 | 4 | 3 | 9 | 5 | Satt665 | D1b + W | 18 | 6 | 5 | 18 | 4 |
| Satt168 | L | 17 | 4 | 4 | 17 | 5 | Satt199 | A2 | 14 | 4 | 4 | 14 | 3 |
| Satt146 | D1b + W | 16 | 6 | 6 | 17 | 6 | Satt565 | F | 15 | 3 | 4 | 15 | 4 |
| Satt308 | B2 | 20 | 7 | 6 | 20 | 6 | Satt590 | A2 | 32 | 10 | 10 | 33 | 7 |
| Satt197 | F | 20 | 6 | 7 | 20 | 5 | Satt592 | D1b + W | 12 | 3 | 8 | 14 | 3 |
| Satt249 | M | 11 | 4 | 4 | 14 | 3 | Satt440 | I | 16 | 4 | 3 | 16 | 5 |
| Satt441 | B1 | 23 | 10 | 8 | 24 | 7 | Satt242 | B1 | 16 | 6 | 6 | 20 | 5 |
| Satt409 | J | 23 | 7 | 6 | 26 | 5 | Satt177 | G | 15 | 4 | 5 | 15 | 3 |
| Satt307 | K | 14 | 5 | 4 | 15 | 4 | Satt339 | M | 19 | 5 | 6 | 19 | 5 |
| Satt577 | A2 | 15 | 6 | 4 | 15 | 5 | Satt192 | C1 | 23 | 4 | 4 | 23 | 3 |
| Satt434 | C2 | 25 | 4 | 6 | 25 | 4 | SAtt510 | O | 14 | 5 | 3 | 15 | 6 |
| Satt431 | B2 | 17 | 5 | 6 | 18 | 5 | Satt385 | H | 18 | 5 | 6 | 19 | 5 |
| Satt191 | H | 15 | 6 | 6 | 16 | 4 | Satt226 | F | 5 | 2 | 2 | 5 | – |
| Satt357 | J | 18 | 3 | 3 | 19 | 2 | Satt194 | A1 | 6 | 7 | 8 | 14 | 3 |
| Satt147 | G | 15 | 7 | 6 | 17 | 4 | Average |  | 17.1 | 5.8 | 5.5 | 18.6 | 4.5 |

Linkage group names and the assignment of markers to linkage groups are according to the integrated soybean genetic linkage map of Cregan et al. (1999)[36]

### 3.9 Isozyme variation in four populations of *Glycine soja*

We analyzed isozyme variation in four populations of wild soybean (*Glycine soja*). Genetic variation was estimated by starch gel electrophoretic resolution of 14 putative isozyme loci in four populations of *Glycine soja* from the various regions in China. The results indicated the presence of obvious high variance. The results also showed that there were nine polymorphic loci. The average number of alleles per locus, percent of polymorphic loci and expected heterozygosity in the total population were 1.77, 0.692, and 0.133, respectively[37-38]. This amount of variation was close to the average of genetic variation in South Korea ($A = 1.4$, $P = 0.37$, $He = 0.134$)[39]. These results indicated that the level of genetic diversity and variation in China and South Korea was higher than the level of population from suburbs of Mishima in Japan ($A = 1.14$, $P = 0.14$, $He = 0.046$)[40].

### 3.10 The use of male sterility of wild soybean in soybean breeding

Sun et al[41] developed a male-sterile line using the wild soybean and released a hybrid soybean cultivar. Zhao et al[42] also developed a cytoplasmic male sterile line (NJCMS3A) in Nanjing of China.

## 4 Conclusion

It needs to broaden the collection of wild soybean and relatives in new area, where had never been investigated and collected for wild soybean and relatives. Owing to the investigation and distribution area of wild soybean is decreasing[6], we suggest to enhance and expand the protection zone of wild soybean and relatives in different ecotype zones in order to conserve the novel wild soybean and relatives accessions in China.

As we known that it can often produce the intermediate types of soybean using the cross between cultivated and wild soybean. These intermediate types possess the valuable characters, such as high yielding, more pods per plant, resistance to disease and insect, high protein, high isoflavone, high content of linolenic acid, resistance to drought, resistance to salt. Therefore, we can utilize these ideal traits to develop a series of soybean cultivars needed in soybean production.

## 参考文献

[1] Esquinas-Alcázar J. Science and society: Protecting crop genetic diversity for food security: Political, ethical and technical challenges[J]. Nature Reviews Genetics, 2005, 6(12):946-953.

[2] Castañedaálvarez N P, Khoury C K, Achicanoy H A, et al. Global conservation priorities for crop wild relatives[J]. Nature Plants, 2016, 2(4):16022.

[3] Boerma H R, Specht J E. Soybeans: Improvement, production, and uses. 3rd ed[M]. Madison: American Society of Agronomy, 2004: 303-416.

[4] Nichols D M, Wang L Z, Pei Y L, et al. Variability among Chinese *Glycine soja* and Chinese and North American soybean genotypes[J]. Crop Science, 2007, 47(3):1289-1298.

[5] Hyten D L, Song Q, Zhu Y, et al. Impacts of genetic bottlenecks on soybean genome diversity[J]. Proceedings of National Academy of Sciences of the United States of America, 2006, 103(45): 16666-16671.

[6] 李向华, 王克晶, 李福山. 中国部分地区一年生野生大豆资源考察、收集及分布现状分析[J]. 中国遗传资源学报, 2005, 6(3):319-322. (Li X H, Wang K J, Li F S. Analysis on the current status of annual wild soybean distributed in part of China [J]. Journal of Plant Genetic Resources, 2005, 6(3): 319-322.)

[7] 王连铮,郭庆元. 现在中国大豆[M]. 北京:金盾出版社:2007. (Wang L Z, Guo Q Y. Soybean in modern China[M]. Beijing: Jindun Publishing House, 2007.)

[8] 李福山. 中国野生大豆资源研究进展[M]. 北京:中国农业出版社,1990. (Li F S. The catalogue of wild soybean germplasm accessions in China [M]. Beijing: China Agriculture Press, 1990.)

[9] 王连铮,吴和礼,姚振纯,等. 黑龙江省野生半野生大豆资源的观察研究[J]. 中国油料,1980(3):48-53. (Wang L Z, Wu H L, Yao Z C, et al. Observation and research of wild and semi-wild soybean in Heilongjiang province[J]. Chinese Journal of Oil Crop Sciences, 1980(3):48-53.)

[10] 王连铮,吴和礼,姚振纯,等. 黑龙江省野生大豆的考察和研究[J]. 植物研究,1983, 3(3):116-130. (Wang L Z, Wu H L, Yao Z C, et al. Investigation and research of the wild soybean in Heilongjiang Province[J]. Bulletin of Botanical Research, 1983, 3(3):116-130.)

[11] Wittwer S, Yu Y Y, Sun H, et al. Feeding a billion[M]. East Lansing: Michigan State University Press, 1987:183-199.

[12] Wang K J, Li X H. Exploration and studies of wild soybean germplasm resources in the China Gene bank during recent decade[J]. Plant Genetic Resources,2012, 13(4):507-514.

[13] 来永才. 中国寒地野生大豆资源图鉴[M]. 北京:中国农业出版社, 2015. (Lai Y C. Illustrated handbook of wild soybean growth in the cold region of China[M]. Beijing: China Agriculture Press, 2015.)

[14] 姚振纯,林红. 大豆优异种间杂交新种质选育新进展[J]. 大豆科学,1993, 12(3):196. (Yao Z C, Lin H. Research advance of elite novel resources by the soybean interspecies crossing[J]. Soybean Science, 1993, 12(3):196.)

[15] 王金陵,孟庆喜,杨庆凯,等. 回交对克服栽培大豆与野生和半野生大豆杂交后代蔓生倒伏性的效应[J]. 大豆科学,1986, 5(3):181-187. (Wang J L, Meng Q X, Yang Q K, et al. Effect of backcrossing on overcoming viny and lodging habit of cultivated

× wild and cultivated × semi-wild crosses[J]. Soybean Science, 1986, 5(3):181-187.)

[16] 吴冈梵,张仁双,付连舜.野生大豆整理、归并和分类问题的商讨[J].中国油料,1983(4):27-28.(Wu G F, Zhang R S, Fu L S. A discussion on interspaces crossing[J]. Chinese Journal of Oil Crop Sciences, 1983(4):27-28.)

[17] Ross J P, Brim C A. Resistance of soybean to the soybean cyst nematode as determined by a double-row method[J]. Plant Disease Reporter, 1957, 41(11):923-924.

[18] Norman A G. The soybean[M]. New York and London: Academic Press, 1963.

[19] Caldwell B E. Soybean: Improvement, production, and uses [M]. Madison: American Society of Agronomy, 1973.

[20] 王连铮,王彬如,吴和礼,等.大豆高产品种选育的研究[J].黑龙江农业科学, 1980(1):13-17.(Wang L Z, Wang B R, Wu H L, et al. Study on soybean breeding for high yield[J]. Heilongjiang Agricultural Sciences, 1980(1):13-17.)

[21] 王连铮,王金陵.大豆遗传育种[M].北京:科学出版社,1992.(Wang L Z, Wang J L. Soybean genetics and breeding[M]. Beijing: Science Press,1992.)

[22] 吴冈梵,付连舜.辽宁省野生大豆的管理与分类[J].大豆科学, 1985, 4(3):235-237.(Wu G F, Fu L S. Arrangement and Classification of wild soybean in Liaoning Province[J]. Soybean Science, 1985, 4(3):235-237.)

[23] 董钻,单维奎,宋书宏.辽宁大豆研究60年[M].北京:中国农业出版社,2010: 195-207.(Dong Z, Shan W K, Song S H. Soybean research for 60 years in Liaoning Province[M]. Beijing: China Agriculture Press, 2010: 195-207.)

[24] 孙贵荒,宋书宏,孙恩玉,等.大豆种质5621对所衍生品种的遗传贡献[J].中国油料作物学报,2002, 24(1):38-41.(Sun G H, Song S H, Sun E Y, et al. Genetic contribution of soybean germplasm 5621 to the released soybean cultivars in Liaoning province[J]. Chinese Journal of Oil Crop Sciences, 2002, 24(1): 38-41.)

[25] Lemes E, Castro L, Assis R. Diseases, genetic improvement and management of soybean [M]. Campinas: Millennium Editora, 2015.

[26] 颜清上,陈品三,王连铮.北京地区大豆孢囊线虫4号生理小种的验证[J].大豆科学,1995, 14(4):355-359.(Yan Q S, Chen P S, Wang L Z. The verification of race 4 of soybean cyst nematode in suburban Beijing[J]. Soybean Science,1995, 14(4):355-359.)

[27] 颜清上,王连铮,常汝镇.大豆孢囊线虫病抗源筛选和利用研究概述[J].大豆科学, 1997, 16(2):162-167.(Yan Q S, Wang L Z, Chang R Z. Screening and utilization of soybean sources resistant to *Heterodera glycines*[J]. Soybean Science, 1997, 16(2):162-167.)

[28] 林红,来永才,齐宁,等.大豆种间杂交新品种龙小粒豆一号的选育[J].中国油料作物学报, 2003, 25(4):46-48.(Lin H, Lai Y C, Qi N, et al. Breeding of Longxiaolidou No. 1, a new soybean variety from inter-specific crossing[J]. Chinese Journal of Oil Crop Sciences, 2003, 25(4):46-48.)

[29] 刘广阳,齐宁,林红,等.高可溶性糖含量大豆新品种龙小粒豆2号的选育[J].大豆科技,2008(5):46-47. (Liu G Y, Qi N, Lin H, et al. Development and selection of Longxiaolidou-No. 2 with high content of soluble sugars[J]. Soybean Science & Technology. 2008(5):46-47.)

[30] 杨光宇.东北地区野生、半野生大豆在大豆育种中利用研究进展[J].大豆科学,1997, 16(3):259-263.(Yang G Y. Advance of study on usage of wild and semi-wild soybean in soybean breeding in the Northeast of China[J]. Soybean Science, 1997, 16(3):259-263.)

[31] Wang W Y. Therapy of Dr´s. Johhanna Budwig[M]. Beijing: China Culture Publishing House, 2015: 60-61.

[32] 李莹,卫保国,任建华.大豆种间杂交产量性状的遗传变异[J].华北农学报,1986, 1(3):10-17.(Li Y, Wei B G, Ren J H. Genetic variance of yield characters between different species of soybean[J]. Acta Agriculturae Boreali-Sinica, 1986, 1(3): 10-17.)

[33] 王金陵,许忠仁,杨庆凯.东北地区野生大豆种质资源的扩充与改良[J].哈尔滨:黑龙江科技出版社,1994.(Wang J L, Xu R Z, Yang Q K. Broaden use and improvement of Soybean germplasm resources in Northeast of China[M]. Harbin: Heilongjiang Science and Technology Press, 1994.)

[34] 李川东.一年生野生大豆和饲用高粱间作及其混合青贮的研究[D].南京:南京农业大学,2008.(Li C D. Study on intercropping of annual wild soybean with feed sorghum and mixture feed for silage [D]. Nanjing: Nanjing Agriculture University, 2008.)

[35] 胡明祥,田佩占.中国大豆品种志(1978-1992)[M].北京:中国农业出版社,1993:73.(Hu M X, Tian P Z. China soybean cultivars(1978-1992)[M]. Beijing: China Agriculture Press, 1993:73.)

[36] Cregan P B, Jarvik T, Bush A L, et al. An integrated genetic linkage map of the soybean genome[J]. Crop Science, 1999, 39: 1464-1490.

[37] 裴颜龙,王岚,葛颂,等.野生大豆遗传多样性研究Ⅰ4个天然居群等位酶水平的分析[J].大豆科学, 1996, 15(4): 302-309.(Pei Y L, Wang L, Ge S, Wang L Z. Studies on genetic diversity of *Glycine soja* isozyme variation in four populations[J]. Soybean Science, 1996, 15(4): 302-309.)

[38] Pei Y L, Wang L Z. Isozyme variation in Chinese natural population of wild soybean[C]. Abstracts of International Symposium on Floristic Characteristic and Diversity of East Asian Plants. Kunming, July25-27, 1996: 253-254.

[39] Yu H, Kiang Y T. Genetic variation in South Korea natural populations of wild soybean (*Glycine soja*)[J]. Euphytica, 1993, 68, 213-221.

[40] Bult C J, Kiang Y T. Electrophoretic and morphological variation within and among natural populations of wild soybean (*Glycine soja* Sieb. & Zucc.). [J]. Botanical Bulletin of Academia Sinica, 1992, 33:111-122.

[41] 孙寰,赵丽梅,黄梅.大豆质核互作不育系研究[J].科学通报,1994, 39(2):175-176.(Sun H, Zhao L M, Huang M. Study on cytoplasmic-nucleic male sterile soybean[J]. Chinese Science Bulletin, 1994, 39(2):175-176.)

[42] Zhao T J, Gai J Y. Discovery of new male-sterile cytoplasm sources and development of a new cytoplasmic-nuclear male sterile line NJCMS3A in soybean[J]. Euphytica, 2006, 152:387-396.