



**REVIEW**

## Genetic Improvement of *Betula platyphylla* Suk. in China: A Review

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### ABSTRACT

Birch (*Betula platyphylla* Suk.), distributed in Eurasia, North America, and Australia, is a kind of cold-resistant, fast-growing, and vital pulpwood tree species. It is also one of the most important ecological restoration tree species with high values of economic benefits in Northeast China. To improve the genetic gain and expand the economic benefit of *B. platyphylla*, many genetic improvements have been carried out. In China, *B. platyphylla* is widely distributed and varied, and there are many varieties with excellent genetic characteristics. In this paper, the genetic improvement of *B. platyphylla* was reviewed, and the previous research results were discussed from two aspects: conventional breeding and molecular breeding. Some problems and corresponding solutions in the genetic improvement were put forward to provide ideas for *B. platyphylla* breeding in the future.

### KEYWORDS

*Betula platyphylla*; conventional breeding; molecular breeding; genetic improvement

## 1 Introduction

*Betula platyphylla* Suk., one of the most extensively distributed broadleaf trees in northern and southwestern forest areas of China [1], has a high reproduction ability of seeds and a strong adaptability of seedlings. It is an important component species of natural secondary forest and nearly one-third of mountain areas are covered by it in Northeast China [2,3]. Because of high wood quality and fast growth rate, birch is also an important commercial tree species for papermaking, furniture making, construction, plywood, and handicrafts production [4].

The genetic improvement of *B. platyphylla* had been investigated for more than 40 years, which included elite materials selection [5], physiological index evaluation [6], wood properties evaluation [7], stress resistance evaluation [8], population genetic structure [9], and transgenic breeding [10]. This review covered the recent research progresses in genetic improvement of *B. platyphylla* in China, specifically focused on conventional breeding and molecular breeding. Meanwhile, new research directions were devised with different breeding goals for further research.



## 2 Research Progress on Conventional Breeding of *B. Platyphylla*

### 2.1 Germplasm Resources of *B. Platyphylla*

In order to save, produce and utilize comprehensively the species, the germplasm resources of *B. platyphylla* have been investigated and collected by the Northeast Forestry University (NEFU) over the past two decades. More than 30 provenances and 400 full-sibling, half-sibling families and clones of birch were collected from China, Finland, Canada, Russia, Kazakhstan and Japan, including *B. pendula*, *B. kirghisorum*, *B. pendula* ‘Purple Rain’, *B. pendula* ‘Dalecarlica’, *B. populifolia* and Japanese birch. In addition, 13 germplasm conservation test forests have been established in Northeast and North China. Based on the materials, the mechanism of marginal cleavage in *B. pendula* ‘Dalecarlica’ [11,12] and the variation of leaf colour in *B. pendula* ‘Purple Rain’ [13–15] were studied.

### 2.2 Elite Provenances Selection of *B. Platyphylla*

Due to the wide distribution of birch and environmental differences caused by geographic area, there were great differences between and within varieties. The longitude distribution range of birch in China is 42°07'(Zhaosu)~130°01'(Wangqing), and latitude distribution range is 33°00'(Liupanshan)~52°10'(Moerdaoga), where are mainly temperate continental monsoon climates (Table 1 and Fig. 1). Exploration and evaluation of 16 provenances in *B. platyphylla* were based on multiple breeding traits, and then Wangqing and Liangshui were preliminarily considered the optimal provenances [16]. Provenance tests were established in three different sites (Caohekou in Jilin Province, Maoershan in Heilongjiang Province and Jinhe in Mongolia autonomous region) in Northeast China in 1997 (Fig. 1). After that, further studies of provenance were conducted based on the above materials. For example, the height of *B. platyphylla* from different provenances was negatively correlated with latitude and positively correlated with longitude when the trees were 4-year-old [17]. Three excellent provenances for cellulose timber (Dongfanghong, Maoershan and Wuyiling) were identified from fourteen provenances of 10-year-old *B. platyphylla* in the Maoershan test site [18]. Growth traits and wood properties of eighteen *B. platyphylla* provenances in three trial sites were also investigated and analyzed, which suggested that there existed significant differences among different sites and also in site × provenance interaction. Ultimately, twelve elite provenances were selected based on growth traits including 6 provenances for Maoershan site, 3 for Caohekou site and 3 for Jinhe site, respectively [19].

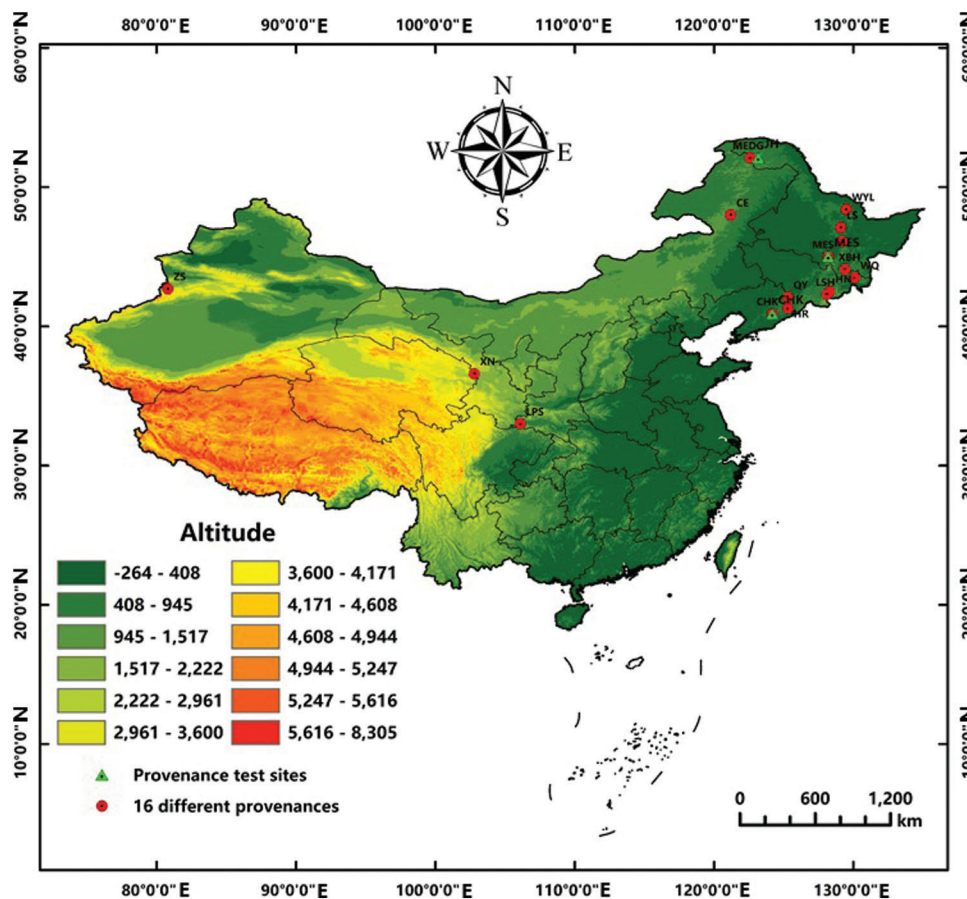
**Table 1:** The geographical and climatic factors of 16 representative provenances

Province	Site	Longitude (E) (°)	Latitude (N) (°)	Climate	Altitude (m.a.s.l.)	Annual average temperature (°C)	Annual precipitation (mm)	Relative humidity (%)	Duration of sunshine (h)	Frost-free season (d)
Ningxia	Liupanshan	33.0	106.1	Temperate monsoon climate	2928.0	4.5	571.0	60.0	2132.9	150.0
Qinghai	Xining	36.6	102.8	Semi-arid climate of continental Plateau	2261.0	5.5	369.3	64.0	2548.5	128.0
Xinjiang	Zhaosu	42.7	80.8	Semi-arid and semi-humid cold climate in continental temperate mountainous area	2250.0	2.9	511.8	72.0	2699.0	98.0

(Continued)

**Table 1 (continued)**

Province	Site	Longitude (E) (°)	Latitude (N) (°)	Climate	Altitude (m.a.s.l.)	Annual average temperature (°C)	Annual precipitation (mm)	Relative humidity (%)	Duration of sunshine (h)	Frost-free season (d)
Neimenggu	Chuoer	48.0	121.2	Temperate continental monsoon climate	900.0	-3.4	390.0	70.0	2647.5	100.0
	Modaergera	52.1	122.6	Cold temperate monsoon coniferous forest climate	940.0	-3.1	510.0	68.0	2467.8	92.0
Liaoning	Caohekou	40.9	124.2	Temperate continental monsoon climate	300.0	6.1	929.7	69.0	2393.9	132.9
	Huanren	41.3	125.3	Temperate continental monsoon humid climate	800.0	6.2	860.8	65.0	2419.2	228.6
	Qingyuan	42.1	125.3	Temperate continental monsoon climate	500.0	5.0	815.0	70.0	2406.6	234.3
Jilin	Wangqing	43.5	130.1	Temperate continental monsoon climate	750.0	3.8	263.7	68.0	2411.3	133.0
	Huinan	42.5	128.3	Northern temperate continental monsoon climate	520.0	3.4	750.0	68.0	2461.7	116.0
	Lushuihe	42.3	128.1	Temperate continental monsoon climate	800.0	3.4	743.0	66.0	2398.4	128.9
Heilongjiang	Xiaobeihu	44.1	129.4	Temperate continental monsoon humid climate	810.0	3.5	506.4	66.0	2655.5	136.7
	Dongfanghong	46.1	129.2	Temperate continental monsoon climate	150.0	2.8	566.0	70.0	2422.8	135.2
	Wuyiling	48.4	129.5	Temperate continental monsoon climate	350.0	-1.0	650.5	73.0	2235.1	104.9
	Liangshui	47.1	129.1	Temperate continental monsoon climate	400.0	0.4	630.8	70.0	2375.2	114.9
	Maershan	45.0	128.2	Temperate continental monsoon climate	400.0	2.3	666.1	73.0	2552.5	120.0



**Figure 1:** Distribution of 16 representative provenances of *B. platyphylla* in china and the provenance trial sites in Northeast China

Note: Red dots represent 16 representative provenance areas and the green triangles denote the provenance trial sites. LPS: Liupsan; XN: Xining; ZS: Zhaosu; CE: Chaoer; MEDG: Moerdaoga; CHK: Caohekou; HR: Huanren; QY: Qingyuan; WQ: Wangqing; HN: Huinan; LSH: Lushuihe; XBH: Xiaobeihu; DFH: Dongfanghong; WYL: Wuyiling; LS: Liangshui; MES: Maershan; JH: Jinhe.

### 2.3 Elite Family Selection of *B. Platyphylla*

Selective breeding is usually required for tree genetic improvement to obtain superior clones and families. Due to the low survival rate of cutting and grafting in *B. platyphylla*, families and clones were important materials in the breeding research. Researchers made studies on the selection of elite families, which included higher yield, wood characteristics, and stress resistance of forest trees [5,20–22]. For instance, tree height and ground diameter were investigated among 21 half-sib families of 2-year-old *B. platyphylla*, and 8 elite families with higher tree height and 7 families with wider ground diameter were selected [21]. Based on 11 growth characters, 17 half-sib families of *B. platyphylla* were evaluated, and two families were selected as excellent families [5]. Growth traits of 53 half-sibling families in *B. platyphylla* at three different sites were investigated, including the height, timber volume and diameter at breast height. Thereafter, based on the breeding values, 11 families (B34, B15, B28, B16, B51, B40, B42, B45, B48, B35 and B19) were rated as superior families, whose mean timber volumes were 8.29%, 9.80% and 13.60% higher than the average of all the families planted in Langxiang, Maershan and Jilin [22]. In addition, the growth traits of 37 *B. platyphylla* clones were evaluated; subsequently, seven superior clones were identified, whose mean height, ground diameter and number of lateral branches were 11.31%, 9.91% and 8.93% higher than the average of all the clones, respectively [23]. In another study,

five superior clones of *B. platyphylla* were selected according to plant height, ground diameter and volume after fertilization [24].

Wood is one of the most dominant renewable resources for human beings [25], and its properties could be roughly divided into five categories: (1) Mechanical properties (e.g., longitudinal growth strain, modulus of elasticity, strength), (2) Technological characteristics (e.g., splitting index), (3) Physical properties (e.g., wood density, shrinkage), (4) Anatomical properties (e.g., fiber length, fiber thickness, coarseness), (5) Chemical properties (e.g., cellulose and lignin content, lignin composition) [26]. The estimated values for some wood properties of *B. platyphylla* are shown in Table 2 [7,27–29]. Wood properties (chemical properties of wood, fiber length and width, content of lignin, cellulose, and holocellulose) among 31 seed trees of tetraploid *B. platyphylla* were measured, which suggested that 19 tetraploid individuals with excellent wood properties can be used as the preferred variety of pulpwood [29]. In addition, other properties of wood such as the wood moisture content, air-dry density, oven-dry density, flexural strength, elastic modulus, shear strength, compressive strength parallel to the grain, and compressive strength stripes of *B. platyphylla* were also investigated, and 6 elite half-sib families in northeast China were deemed superior based on wood properties [7]. Regarding growth and wood properties, tree height, diameter at breast height, fiber aspect ratio, and hemicellulose content of 36 half-sib *B. platyphylla* families were researched, and the results indicated that 13 excellent families were identified [30].

**Table 2:** Estimated values for some wood traits

Wood properties	Approximation	Reference
Fiber length	800 $\mu\text{m}$	Wang et al. 2007 [27]
Fiber width	15 $\mu\text{m}$	
Wood density	0.5642 $\text{g}/\text{m}^3$	Guo et al. 1999 [28]
Cellulose content	48.75%	Liu et al. 2017 [29]
Holocellulose content	69.32%	
Lignin content	11.75%	
Wood moisture content	9.21%	
Air-dry density	0.450 $\text{g}/\text{cm}^3$	Liang et al. 2018 [7]
Oven-dry density	0.429 $\text{g}/\text{cm}^3$	
Flexural strength	58.38 Mpa	
Elastic modulus	7251.92 Mpa	
Shear strength	7.27 Mpa	
Compressive strength parallel to the grain	29.98 Mpa	
Compressive strength stripes	6.95 Mpa	

#### 2.4 Resistance Breeding of *B. Platyphylla*

Forest trees are vulnerable to natural and unnatural factors due to the complex climate, soil types, and complicated geographical environments. It is necessary to strengthen resistance breeding [31], including cold resistance, drought resistance, and saline-alkali resistance. Temperature is an essential environmental factor that seriously affects the growth, development, and geographical distribution of plants [32]. The enzyme recovery system of *B. platyphylla* was affected by low temperature; for example, some birches from warm climates in Europe were introduced and planted in higher latitudes/colder areas in China, and the growth and physiological characters were slightly lower than those of native *B. platyphylla* [33].

Promoted lignification and enhanced cold resistance of the seedlings were observed when the leaves of *B. platyphylla* were sprayed with potassium chloride, potassium dihydrogen phosphate, borax, and boric acid [34]. Drought is another important abiotic stress during tree growth and development [35]. The drought tolerance of forest species has been investigated earlier. In 1973, Hsiao studied plants' adaptation mechanisms to drought stress and put forward a specific standard for the water stress gradient in mesophytes. For *B. platyphylla* seedlings, the accumulation of malondialdehyde (MDA) decreased and the soluble sugar content significantly increased with the deepening of drought stress [36]. The leaves of 2-year-old *B. platyphylla* were sprayed with different concentrations of paclobutrazol (a kind of plant growth retardant), and then the drought resistances were evaluated by the membership function method. It was found that the drought resistance of seedlings treated with paclobutrazol was improved when the solution concentration was  $750 \text{ mg L}^{-1}$  [37].

Salt stress could inhibit plant growth and affect plant photosynthesis, protein synthesis, energy and fat metabolism [38]. There have been increasing studies on salt resistance of trees in recent years. Compared with other broadleaf species (such as *Vlmus pumila*, *Fraxinus mandshurica* and *Tilia amurensis*), the salt resistance of *B. platyphylla* is relatively weak by evaluating the plasma membrane permeabilities, which is an ideal indicator for studying salt resistance [39]. Introducing plants is also a good way to resistance breeding, and the salt-resistance of one-year seedlings of *B. kirghisorum*, *B. pendula* and *B. pubescens* brought from Kazakhstan, and the local *B. platyphylla*, were studied. The results showed that *B. kirghisorum* had the strongest resistance to neutral salt and *B. kirghisorum* and *B. pubescens* had more resistance to alkaline salt at high concentrations [40]. Moreover, growth traits and physiological characters from diverse *B. platyphylla* families showed significantly differences under salt stress, and the nine families with elite salt resistance were selected [41].

### 2.5 Ploidy Breeding of *B. Platyphylla*

Polyploidy is a ubiquitous phenomenon in higher plants [42,43]. The increase in chromosomes could result in increased gene dosages and cell volumes [44]. Therefore, polyploid plants usually have larger leaves, greater height and diameter, and increased ability to adapt to environment [45]. In order to obtain various ploidy materials, seeds of *B. platyphylla* were soaked in 0.1% colchicine, and 101 tetraploid individuals in total were obtained in the year of 2004 and 2009. Compared with diploids, these tetraploids showed larger leaf areas but shorter tree height during the seedling stages. Triploids were obtained by hybridization between diploid and tetraploid in *B. platyphylla*, and germination rate of the hybrid seeds were 3.33–45.33%; growth traits (tree height, leaf area and photosynthetic rate) of triploids were superior to those on diploids in current-year seedlings [46]. However, the growth traits (including tree height, diameter at breast height and volume) of 21 three-year-old *B. platyphylla* families from different ploidy level were investigated, which suggested that most diploid families were better than tetraploid and triploid families [47].

## 3 Research Progress on Molecular Breeding of *B. Platyphylla*

With the rapid development of modern molecular biotechnology and information technology, multiple breakthroughs have been made in plant genetic engineering and molecular breeding. Advanced breeding technologies have been increasingly implemented to improve critical commercial characteristics of plants (yield and resistance) [48]. Plant breeding in the world has gradually entered the molecular level, and the studies of genetics, genomics, molecular biology, and bioinformatics have been widely implemented. The conventional breeding methods are gradually transforming to molecular breeding methods. Molecular breeding represented by genetic engineering and molecular markers is gradually playing an essential role in plant breeding [49–51].

### 3.1 Genome Sequencing

The Human Genome Project (HGP) [52] promoted the development of genome sequencing technology, which plays a crucial role in the field of modern genetic research. In 2000, the whole genome sequencing of *Arabidopsis thaliana* was accomplished by using the first generation of sequencing technology [53], which opened the door to the whole genome of plants. Afterward, the draft genome of *Populus trichocarpa* had been reported, which was the first woody plant to have its genome fully sequenced. There were important guiding significance for exploring the origin and evolution of woody plants, mapping and cloning of essential functional genes, and molecular marker-assisted selection. Until now, the whole genome sequencing has been completed on more than 40 woody plant species [54]. A whole-genome reference sequence for the diploid species *B. nana* (dwarf birch) was generated, which is the keystone woody species of subarctic scrub communities [55]. Then, silver birch (*B. pendula*) was sequenced and a reference genome from a fourth-generation inbred line was assembled, which showed high similarity with *B. platyphylla* [56]. Recently, researchers sequenced the *B. platyphylla* genome and assembled the sequences into 14 chromosomes, which facilitated the identification of important and essential genes governing important traits of trees and genetic improvement of *B. platyphylla* [57].

### 3.2 Molecular Marker-Assisted Breeding

Molecular markers are essential tools for genetic improvement, which can be applied to germplasm evaluation, genetic analysis and marker-assisted breeding. Multiple molecular markers were effectively used for genetic diversity, population structure and marker-trait association analysis of *B. platyphylla*. Random amplified polymorphic DNA (RAPD) is a convenient method to detect genetic diversity, which is based on the polymerase chain reaction (PCR) using randomly synthesized oligonucleotides (10 bp) as primers. The provenance division and genetic variation among 13 provenances of *B. platyphylla* in China were studied by using RAPD. The results showed that the differentiation of the percentage of polymorphic loci (PPL) among different provenances was evident, ranging from 20.17% to 32.19%. Among them, Maoershan provenance and Qingyuan provenance had the higher percentages of PPL; in contrast, Chuoer provenance had the lowest PPL percentage [58]. The fragment BFL significantly related to fiber length was selected from 100 *B. platyphylla* individuals with long-fiber using the RAPD technology. Then, BFL was successfully transformed into a sequence characterized amplified region (SCAR) marker by which the identification rate of long fiber *B. platyphylla* was more than 70% [59]. Using simple sequence repeat (SSR), four amplified fragments related to fiber length were identified in *B. platyphylla* [60]. In addition, genetic diversities of 41 white birch genotypes collected from 6 different geographical regions were analyzed using SSR markers. The result indicated that 111 selected SSR loci showed low to moderate similarity (0.025–0.610); by UPGMA-based clustering analysis of the allelic constitution, the six different geographical regions were further separated into four clusters: Cluster I, Huanren and Liangshui provenances; Cluster II, Xiaobeihu and Qingyuan provenances; Cluster III, Finland provenance; Cluster IV, Maoershan provenances [61]. Using ISSR (inter-simple sequence repeat) markers, 15 provenances from the provenance trial in Maoershan, and the result showed the range of the percentages of polymorphic loci was 48.03%~62.20% [62]. Furthermore, some studies about genetic linkage maps of *B. platyphylla* were also based on molecular markers, such as ISSR and AFLP (Amplified fragment length polymorphism) [63].

### 3.3 Genetic Engineering Breeding

Genetic engineering has emerged as a method with high potential to modify traits more precisely and made functional genomics studies more efficiently. In the last decade, improving plant traits through genetic engineering has become an area of increased focus. Tree genetic engineering has advanced to the point at which genes for desirable traits can now be introduced and expressed efficiently [64,65]. Here,

we describe major scientific discoveries on genetic engineering in terms of insect resistant, abiotic stress, wood property modification and flowering in *B. platyphylla*.

### 3.3.1 Insect-Resistant and Stress-Resistant Genetic Engineering

Unfortunately, *B. platyphylla* forests always were invaded by insects due to the abundance of secondary metabolites. It is an effectively pollution-free way to control plant pests by introducing insect-resistance genes. In 2001, a Chinese investigator obtained the first transgenic insect-resistant *B. platyphylla* by overexpressing chimeric sequences of C peptide of *Bt* gene and spider insecticide peptide [66]; the transgenic birch could restrain the development of *Lymantia dispar* [67].

Researchers have found that there are many stress resistance genes in plants, and their functions could be studied in detail to understand the stress-resistant mechanism. In recent years, some resistance genes of *B. platyphylla* have been identified consecutively. The transgenic *B. platyphylla* plants with overexpressing *BpMYB46* improved salt and osmotic tolerance by affecting gene expressions included *SOD*, *POD* and *P5CS* to increase reactive oxygen species scavenging and proline levels [68]. *BpNAC012* positively activated the core sequence CGT(G/A) to induce *SOD* and *POD* genes, and the overexpression lines showed increased *SOD* and *POD* activities under salt and osmotic stress [69]. Moreover, the expression of *BpARF1* was significantly up-regulated by drought stress, and the silencing of *BpARF1* could improve the drought tolerance of *B. platyphylla* [70]. Compared with the wild type and *BpERF11*-overexpression lines, *BpERF11* RNAi-silence in *B. platyphylla* showed increased ROS scavenging capability, reduced proline accumulation and enhanced water loss rate under salt and severe osmotic stress [71].

### 3.3.2 Genes Involved in Wood Formation

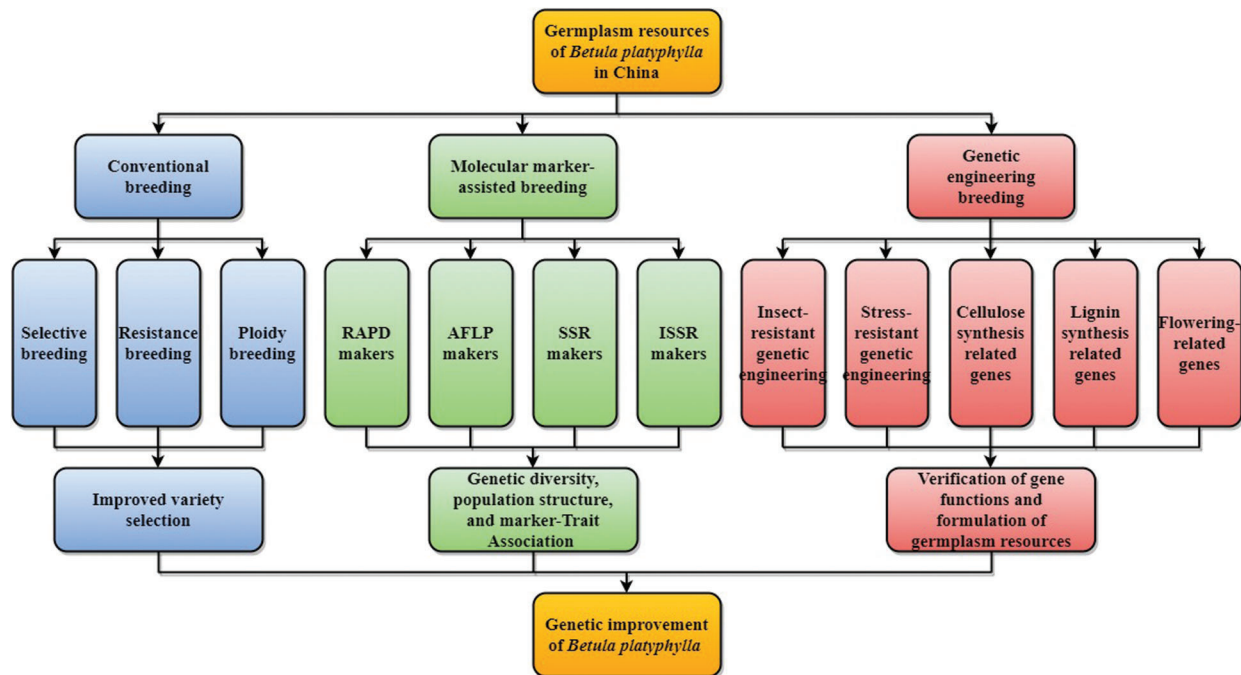
The properties of wood are determined by the composition and characteristics of the xylem secondary cell wall. *B. platyphylla* is one of the main pulpwood species; however, pulping yields for pulping industry were affected due to the high lignin content. Therefore, it is of great significance to study the lignin and cellulose biosynthesis for the genetic improvement of forest trees. The main mechanism of cellulose biosynthesis is that the thousands of glucose residues are combined into a full length chain by the glycosyltransferase. In the cDNA library of the *B. platyphylla* cambium, the gene for the glycosyltransferase was highly expressed during the important periods for wood formation [72]. Four Cellulose Synthase (*CESA*) genes from *B. platyphylla* were identified. *BpCESA7* and *BpCESA4* may be related to the formation of a cellulose synthase complex and participate mainly in secondary cell wall biosynthesis. *BpCESA3* was possibly involved in primary cell wall biosynthesis and homogalacturonan synthesis [73]. Expression analysis of the cellulose synthase gene promoter in *B. platyphylla* has also been conducted. The promoter of *BpCESA7* gene was cloned and the histochemical assays indicated that *BpCESA7* may play an important role in growth and development of *B. platyphylla* [74]. Furthermore, studies of lignin synthesis genes have made a great progress recently. The Cinnamoyl-CoA reductase (*CCR*) gene was the key enzyme of the lignin-specific pathway, and its homologous gene *BpCCR1* was isolated from *B. platyphylla*. Compared with WT, the higher lignin contents in overexpressed *BpCCR1* *B. platyphylla* seedlings, indicated that the *BpCCR1* gene was related to the lignin synthesis [75]. *BpCCoAOMT*, isolated from *B. platyphylla*, played an important role in the precursor synthesis of G-lignin units. Compared with WT, the antisense *BpCCoAOMT* transgenic tobaccos showed the characteristics of decreased lignin content and reduced S-lignin content [76]. Besides enzyme genes, some transcription factors were reported to be involved in lignin synthesis. Ectopic expression of *BpMYB4* in *A. thaliana* conferred lower lignin deposition and increased cellulose content [77]. Compared with the nontransgenic plants, the *BpMADS12*-overexpressing lines had higher lignin levels. There were differentially expressed genes involved in lignin and brassinosteroid biosynthesis, suggesting that *BpMADS12* promoted the expression of lignin synthesis enzyme genes in response to brassinosteroid signaling [78]. In addition, the above-mentioned *BpNAC012* and *BpMYB46* were involved in the abiotic



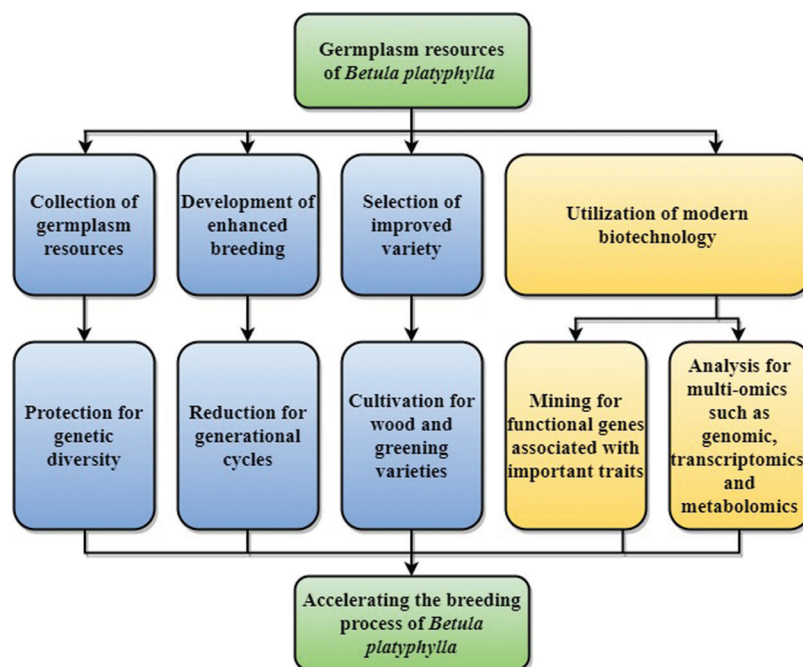
resistance of the regulated secondary wall biosynthesis as well [68,69]. For instance, *BpNAC012* activated the expression of secondary wall-associated downstream genes (such as *MYB46*, *MYB54*, *CCR1*, *4CL1* and *CesA3*), resulting in ectopic secondary wall deposition in the transgenic stem epidermis.

### 3.3.3 Flowering-Related Genes

Flowering is the transformation process from vegetative to reproductive growth and plays a vital role in life cycle of plants. However, *B. platyphylla* had a long juvenile period, which constrained breeding programs, and a few studies have focused on their floral development. The first reported case in birch flower development suggested that *BpSPL1* (a SBP-box gene from *B. pendula*) was expressed in inflorescences as well as in shoots and leaves [79]. Subsequently, *BplSPL1*, the homologous gene of *BpSPL1*, was identified in *B. platyphylla*. Further studies showed that *35S::BplSPL1* transgenic *A. thaliana* had the early-flowering phenotype and the expression levels of flowering time genes and flower meristem identity genes had changed [80]. Early-flowering birches were generated by genetic transformation of *35S::BpAPI1*, and the inflorescences of the transgenic lines emerged miraculously beginning 2 months after transplanting. The male inflorescences rarely produced pollen, whereas the female inflorescences developed normally. The hybrid progeny by using the transgenic birch as female parent also completed flowering within only one year [81]. A similar early-flowering phenotype was observed in *35S::BpSEP4* transgenic *A. thaliana*, which changed the expression of flowering time genes and flower meristem identity genes. Moreover, the ectopic expression of *BpSEP4* in *A. thaliana* caused aberrant floral organ development and delayed flower abscission [82].



**Figure 2:** Genetic improvement progress of *B. platyphylla* in China



**Figure 3:** Genetic improvement strategies of *B. platyphylla*

#### 4 Conclusions

In summary, a great deal of work has been done in China on the genetic improvement of *B. platyphylla* (Fig. 2), and some achievements have been made: (1) Many planting varieties with elite characteristics were cultivated through conventional breeding methods such as selection and hybridization. (2) Modern biotechnology has been widely used in the genetic improvement of *B. platyphylla*, and many transgenic *B. platyphylla* plants with stress resistance or economic traits have been bred. Nevertheless, there also have the following shortcomings: (1) Not enough attention has been paid to the utilization of *B. platyphylla* resources in many areas, and the *B. platyphylla* forest has been severely damaged. (2) The research on *B. platyphylla* in China started relatively late, most of the research results have not been widely used in production practice. (3) Breeding and spreading of excellent varieties are still at an early stage, and the economic benefits they reap have not been enough to produce a virtuous circle. (4) Despite the whole-genome sequencing of *B. platyphylla* has already been completed, transcriptome and metabolomics analyses for specific traits are still lacking.

Given the above problems, further active measures should be taken to protect and utilize *B. platyphylla* resources in China (Fig. 3). (1) The genetic diversity of *B. platyphylla* should be protected, a safe utilization plan should be formulated, and the collection of germplasm resources should be strengthened. (2) The construction of intensive seed orchards for *B. platyphylla* should be strengthened for growth-promoting and shortening the generational cycle. (3) The breeding and promotion of *B. platyphylla* elite varieties should be strengthened, and attention should be paid to the cultivation of wood and greening varieties. (4) Further research involving multi-omics such as genomics, transcriptomics, and metabolomics should be developed to accelerate the breeding process of *B. platyphylla*.

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**Conflicts of Interest:** The authors declare that they have no conflicts of interest to report regarding the present study.

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