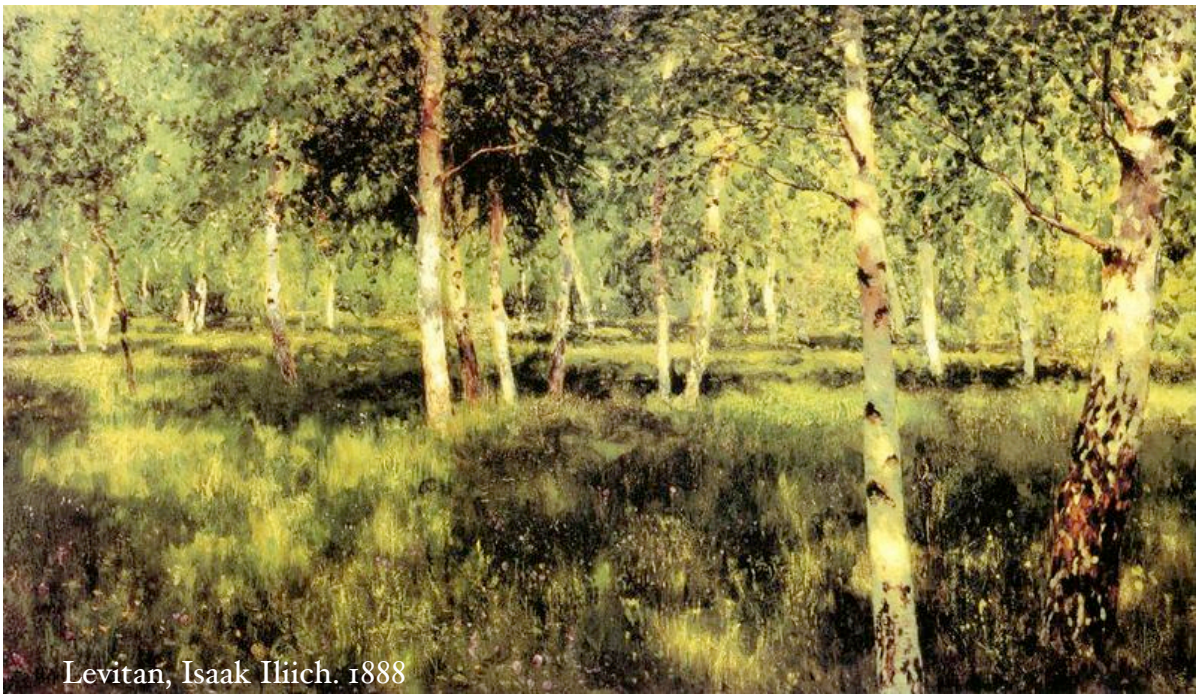
GENETICALLY MODIFIED POPLARS IN CHINA

A situation analysis



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Abstract

China has vast areas of poplar plantations serving as wind shelter, erosion control facility and industry resource. The intensive utilization of clonal forestry with its minimal genetic diversity has aroused serious pest infestation. To solve this problem and ultimately eliminate insect-caused losses, genetically engineered pest-resistant poplar has been introduced in a large scale planting. This made China the first and only country allowing genetically modified (GM) trees to be released into open environment.

Images of Populs spp.

However, the long life span of trees is likely to increase the chance in detecting transgene instability and increasing the danger to biodiversity, especially genetic diversity. It should be highlighted that the open-pollinated mating system of poplar would speed the gene dispersal of these GMO genotypes and issues related to potential environmental consequences and biosafety issues caused by gene flow and transgene escape need to be addressed in a comprehensive manner. In this article, I will analyze the condition of GM poplars released in China, review the major concerns and raise some proposals on how to eliminate the likelihood of transgene escape under the current situation. In my perspective, a prudent approach that considers the consequences of releasing GM trees, large-scale commercialization with a monitoring and risk assessing system is preferred, and corrections should not be hesitated to be made.

Key Words: Poplar; Genetic modification; Genetic diversity; Genetic Contamination

1. Introduction

1.1 Background

Forest harbours a great amount of the planet's biodiversity while serving significant ecological, social and economical functions, without which neither the ecosystem nor the social construction could last. During the industrialisation and population booming, China has experienced serious deforestation in the recently passed decades (Ewald et al. 2006). Poplar, with certain advanced characters against other tree species, majored the gigantic afforestation project in China, during which the massive plantation of artificial forests constructed with excessively used tree species cost severe pest infestation: 23.7% of the total forest plantation were under biotic disturbance resulting in an economic loss approaching 1 billion dollar (Ewald et al., 2006). In searching for the solution that would hopefully solve the problem efficaciously forever, Chinese forestal researchers employed the star of the biotech era — Genetic Modification. Thus, in the early 1990s gene transformation targeting trees within the *Populus* genus prevailed in China as well as across the world, and the goals were not limited within biotic disturbance resistance, but extended into aspects like environmental stress tolerance, wood quality modification and growth alternation (Tian & Tan, 2009).

As widely spread genus, *Populus* has an impressive natural distribution that covers from tropical to sub-polar climate zones in the Northern hemisphere and provides habitats for local and migrating wild lives as well as insects and micro-organisms, serves as air exchanging agents, water cycle tache and ecosystem holders. It also embraces great heterogeneity and includes many long cultivated and intensively used tree species across the world, which is both a virescence material, an industrial raw material and a conservation tool (Hu et al., 2010).

Poplars were broadly planted world-wide for wind shelters, erosion control / water-soil conservation, phytoremediation, landfill covers, biofuel production, pulp and logs (Acker et al. 2011; Marmiroli et al., 2011; Zalesny & Bauer, 2007). Meanwhile, favoured by their simple clonal propagation, relatively rapid growth rate and considerably small genome size among woody spe-

cies, they are one of the major model plants used in both scientific and industrial forestal research (Bradshaw et al., 2000; Polle & Douglas, 2010).

China, with a rich flora of the genus and the biggest crop of poplars through the globe, has been using poplar plantation as an efficient approach several environmental and social issues arose along the industrialisation of the country (Weisgerber & Han, 2001). Historically, poplars have been closely associated with human civilisation and extensively utilised in agroforestry/ silvopastoral systems on the land for hundreds of years, resulting in the overall present distribution of poplars, including native species, to be considerably transformed from its natural distribution (Sigaud, FAO). Hybrid clones are widely planted in China for their various functions mentioned above. One of the marked purposes lays in the protection against wind and desertification, poplar is one of the major material constructing the Three-North Shelter-belt, a massive shelter-belt grid horizontally across North China covering a 4480 km dimension east to west reserving planting area over 25 mil. ha., Figure 1-1.), while in the eastern provinces of the country the planting aims at commercial wood and biomass production (Sigaud, FAO). In the major afforestation programmes in China, poplar is estimated to occupy 60% of the total tree planting area (National Poplar Commission, 1996) and 80% of windbreak shelters of the Three North have been established with poplars (Sigaud, FAO). By 2006, artificial plantation area of poplars has exceed 7 million hectare in China, which is about 19% of its total artificial forest area (Lu & Hu, 2006), 5% of the total forest cover (Ewald, et al., 2006) and is steadily increasing. It is predictably hard for such enormous scale of artificial plantation constituted with clones from limited cultivars to perform well under the stress of insects and diseases. After witnessing great mortality under biotic disturbance, Chinese foresters took GM as a possible solution to eliminate the eco and commercial loss and overcome China's lack of pest resistant poplar germplasm resources (Hu et al., 2010), however, whether there is indeed a lack of pest resistant genetic resources remains to be discussed. The purpose of this paper is to interpret poplars breeding in China in an overall picture, given the situation of the rapid development in genetic modification and the already taken place commercialisation of GM cultivars, and provide a preventive, as well as remedial insight through the issue.

1.2 Taxonomy, Distribution, Basic Botany and Molecular physiology of poplars

The Taxonomy Lineage of poplars (Chao et al., 2009):

Kingdom: *Plantae*
Phylum: *Angiosperms*
Class: *Eudicots*
Order: *Malpighiales*
Family: *Salicaceae*
Subfamily: *Populoideae*
Genus: *Populus*

Populus is a genus of six sections (*Leuce*, *Tacamahaca*, *Aigeiros*, *Turanga, Populus* and *Leucoides*), a member of *Salicaceae,* which have been placed under the *Malpighiales* in the recent cladistic analysis of the angiosperms, while various classifications still exist (FOC, 1999; Bradshaw et al. 2000; Sterck et al., 2005). It is naturally distributed through most terrestrial areas within the Northern Hemisphere and has a small representation in tropical Africa (FOC, 1999; Polle & Douglas, 2010). There are about 100 species worldwide, including species applied with various common names such as poplar, aspen, and cottonwood (FOC, 1999; URGI, 2010).

China is among countries with a highly multifarious indigenous flora; based on its ample genetic variation of poplar species, there are germplasm resources with the conserved ability to survive, reproduce and settle in divergent habitats after long periods of adaptation processes (Weisgerber & Han, 2001). Out of over 100 *Populus* species found in nature, 71 species (47 endemic) are distributed in China, including at least nine hybrids (FOC). Among them, 37 are distributed in North China (Sigaud, FAO, Table 1.), which have been intensively researched and utilised through the history of Chinese agroforestry. Meanwhile, comprehensive contemporary studies of the genus *Populus* looked into the mountain ranges of the Qinghai-Tibet Plateau , and uncovered concentrated genetic diversity of poplars in the subtropical mountainous regions of Southwest China: 3 sections, 17 species and 15 varieties have been recorded, described and taxonomically classified there. They grow within board altitudes between 1500 m and 4300 m above sea level. Many of these poplar sources are notable for their remarkable site adaptation potential in harsh habitats

and vigorous growth under acceptable conditions (Weisgerber & Han, 2001). As summarised by Bradshaw et al. (2000), with the capability of rapidly invading disturbed sites, many poplar species occupy habitats in the dynamic environment of riverine floodplains, where they form a key component of riparian forests (Braatne et al., 1996). Others, such as the aspens, commonly colonise upland areas after intense, initialising fires (Burns & Honkala, 1990).

Populus plants are deciduous broadleaf trees that can grow from 15 to 50 meters in height, with trunk diameters up to 2.5 meter (URGI, 2010). The majority species under the genus are dioecious with pendulous catkins formed by flowers of neither calyx nor corolla, which is adapted to wind pollination; the female plants produce tiny capsules with filament around the bottom, a typical seed structure established for wind and water dispersal (FOC, 1999; Chao et al., 2009).

The heteromorphic plants' fertilisation method is typical chalazogamy, and they perform an obligate outcrossing mating system with self-incompatibility mechanism and interspecific recognition, thus inbred strains rarely occur and haplotypic polymorphisms were expected (Knox et al., 1972; Valda & Murray, 1981; Tuskan et al., 2006). Certain proteins in its pollen grain walls are essential for pollen germination and altering the interspecific incompatibility system, which determines whether pollen tubes develop sufficiently. This system lays barriers in the hybridisation between some poplar species, for instance, between the section *Leuce* and *Aigeiros* (Knox et al., 1972).

Also, plants in *Populus* are all capable of reproducing asexually, often by sprouting from the root collar of killed trees or from detached branches that have been kept in moist condition and become embedded in the soil; some species propagate through sucker shoots that arise from horizontal roots, mostly after clear-cut and abiotic disturbance, especially fire (Bradshaw et al., 2000; Ghazoul, 2004). This property of poplars would typically result in clonal stands up to a few hectares, and recurrent fires can maintain the generation of such clones for centuries (Bradshaw et al., 2000). Such eco-association with fire made it a good choice for regenerate and conserve fire damaged forest land.

All species within this genus are diploids (2n=38) and can be breed for many fertile hybrids with highly targeted characteristics that enrich the diversity of the natural germplasm and benefits the human society (Marmiroli et al., 2011). As suggested by Marmiroli et al., the small size of the haploid *Populus* genome (ca. 480 to 550 Mbp, only four times that of *Arabidopsis*, and 400 times smaller than that of *Pinus*) has favoured the creation of 25 genetic maps and the development of various molecular resources in different species (Cervera et al., 2004; Tuskan et al., 2006; Markussen et al., 2007; Gaudet et al., 2008; Polle & Douglas, 2010), which forms an efficient complement to plant researches based on *Arabidopsis,* since many plant species found in nature are more similar to *Populus* than to *Arabidopsis,* life-historically and genetically (URGI, 2010).

2. Experimental approach towards poplar breeding

2.1 The genome sequencing project and genetic maps of *Populus* species

The genome sequencing of *Populus trichocarpa* conducted by Tuskan et al. (2006) is a milestone of forest sciences' successfully employing biotechnology, which opened doors and paved the way for molecular-scoped breeding and research on and around poplars. With the sophisticating biotechnical tools, the detailed interpretation of its genomic information and its favoured nature, *Poplus* has become a well accepted model system (Polle & Douglas, 2010). During the sequencing, a wealth of biotechnics and several genomic databases are adhibited to draft the *P. trichocarpa* genome, which enabled and facilitated the investigation of cellular and molecular mechanisms in long-lived forest trees by providing a thoroughly studied model system (Tuskan et al., 2006, Polle & Douglas, 2010).

The research group adopted whole-genome shot gun strategy for sequencing and assembling, and augmented it by constructing a physical map "based on BAC restriction fragment fingerprints, BAC-end sequencing, and extensive genetic mapping based on simple sequence repeat (SSR) length polymorphisms" (Tuskan et al., 2006). In order to assemble as many of substantial frac-

tions derived from the shotgun reads as possible and assess the nature of the sequences in the fraction of the genome, the group proforem wu-BLAST searches against online databases (eg. NCBI, etc.). After that BAC clones were fingerprinted with an agarose gel based method and the BAC-end sequence were compared with the shotgun assembly through BLAST. With the linkage groups already discovered by previous researchers added in, the map was drafted (Tuskan et al. 2006). After getting the map, the research group constructed genome-wide pairwise DNA alignments between *Populus* and assemblies of *Oryza* and *Arabidopsis* with VISTA pipeline infrastructure for detailed information. Thus, with following refinement, further prediction and annotation, whole-genome microarray analyses, related RNA verification and statistic analysis, the millstone project that laid the foundation of transgenic tree breeding was carried out (some major results demonstrated in figures are attached in Appendix II). This initiative approach did not only answered the questions on how perennial plants are different from annual ones, what makes a tree to have the unique biology and how should the future breeding of trees be conducted, but set a completely new agenda for forest research (Bhalerao et al., 2003).

2.2 Current commercial breeding objectives and pertinent breeding approaches

Currently the breeding of poplars mainly aims at insect and disease resistance, environmental adaptation, biotic and abiotic stress tolerance, lignin and cellulose content modification, rapid growth with high biomass production, phytoremediation and aesthetic value for virescence (Hu et al., 2010; Marmiroli et al., 2011; Weisgerber & Han, 2001). The classical breeding programmes are continued while molecular methods start to draw growing attention (Weisgerber & Han, 2001).

For classical breedings, the major approaches are domestication of plants, deliberate crossing and targeting properties selecting, which relies on homologous recombination between chromosomes and mutants to generate genetic diversity that allows for desirable traits to occur (Kingsbury, 2009). Since we entered the biotech era, classical breedings are no longer limited in nurseries and fields; procedures could also take place partially for entirely in the lab, benefiting from bio-

technics such as hormonal regulation, tissue culture, hydroponic culture, protoplast fusion and mutagenesis, etc. One of the major achievement in classical poplar breeding is the recognition pollen method developed for successful interspecific breeding. As mentioned previously, some species within the *Populus* genus are interspecific incompatible, thus one species' pollen might not sufficiently germinate on a stigma from another species even though they are within the same genus. To come across this barrier and breed hybrid poplar cultivars, conventional tree breeders used recognition pollen technique to overcome the barrier (Knox et al. 1972): by mixing viability reduced compatible pollens achieved by repeated freezing and thawing, gamma-radiation or chemical treatment into the viable incompatible pollens and bringing in the proteins that enables them to germinate, Knox et al. obtained highly successful hybridisation from the cross *P. alba* x *P. deltoides* repeatedly.

For modern breedings, molecular biotechnics are involved in enlarging the gene pool, desired trait selecting for desired traits and eventually enhancing the efficiency of breeding (Kingsbury, 2009). The major approaches are marker assisted selection, reverse breeding, doubled haploidy and genetic engineering (Gepts, 2002, Kingsbury, 2009). With decades of endeavour of the scientists and breeders, molecular markers and genetic maps are available for most important crop plants and marker-trait association have been establish for a diverse array of traits (Dwivedi et al., 2007), which provides information and visions for poplar breeding nowadays. Main attempts in genetic modification in poplars includes transfer of single genes into poplars and transformation of combined multi-genes for targeted traits (Ewald et al., 2006). The transferred sections came from a wealth of sources, from the bacteria to insect, and got engineered into certain poplar cultivars' gene pool with molecularized methods. The two most common transformation methods are Agrobacterium-mediated DNA transfer, and bombardment with DNA-coated microprojectiles, so-called "biolistic" transformation. By the beginning of this century, transformation systems were further developed, but progress was mostly limited to a few poplar hybrids that were selected for ease of transformation. Nowadays, routine transformation procedures utilising A. *tumefaciens* or A. *rhizogenes* are conducted on most poplar species and hybrids even for recalcitrant genotypes such as cottonwoods (Frankenhuyzen & Beardmore, 2004).

Wu and Fan (1991) carried out the first gene transfer project in China inserting single Bt genes into poplars and created anti-defoliator poplars, following which various of genetic engineering took place in China. Meanwhile, genetic modification of crop plants, fruits and vegetables as well as trees are happening as a new way towards food security and biomass mass sufficiency to satisfy the world with booming population (Dwivedi et al., 2007). By now, genetically modified poplar cultivars have been processed to have many purposeful customised novel traits, which will be introduced in the following section.

3. Genetically Modified poplars

3.1 Evolutionary background and phylogenetic relationship with its related wild / cultivated species

Although *Populus* has been cultivated and studied for a long time, the exact phylogenetic information about the genus is still under discussion; the classification sections was majorly relying on morphological, reproductive characters and interspecific crossability (Hamzeh & Dayanandan, 2004; Cervera et al., 2005): members of the same section can hybridise with each other naturally or artificially (Zsuffa, 1975; Cervera et al., 2005). Classic taxonomic analysis, has been under great difficulties posed by high intraspecific diversity, wide natural crossability, and the convergent morphology shown by hybrids and their parental species (Cervera et al., 2005).

To overcome the difficulties, molecular methods was brought in. Cervera et al. (2005) tried to determine the intergeneric, intersectional, interspecific, and intraspecific genetic and phylogenetic relationships among species and hybrids of the *Populus* genus molecularly by using AFLP markers, and concluded *Populus* species generally group along their classical section lines, with markable exceptions observed, such as the placement of *P. nigra* in the *Aigeiros* section (Fig. 3-1-4). Meanwhile Hamzeh and Dayanandan (2004) approached the phylogeny by nucleotide sequences of certain chloroplast and nuclear genes (chloroplast *trn*T-*trn*F region and rDNA), and

proposed a phylogeny trees of the genus which fits into the molecular interpretations towards the interspecific phylogenetic relationship of the genus from three different angle (Fig. 3-1-3). Combining the molecular analysis with the traditional evolutionary analysis, the researches conducted by Cervera, as well as Hamzeh and Dayanandan proved the suggestion of Eckenwalder: since the progenitor species are generally of higher genetical diversity than the derived species do, *Populus* species under the *Leuce* and *Aigeiros* section are reckoned to be the oldest and the most recent poplar species, respectively (Eckenwalder, 1996).

With the refined information evolutionary back ground and phylogenetic relationship provided, the breeding within the species and the genetic modification targeting species within the genus are under going a way with more directions. It would provide information for both traditional and modern poplar breeding. One example of phylogenetic background knowledge helps throwing light upon poplar breeding is the developing and utilisation of Poplar 741. For many poplar transgenic experiments conducted in China, hybrid-clone 741, which is a complex cross of several poplars [*Populus alba* L. × (*P. davidiana* Dode + *P. simonii* Carr.) × *P. tomentosa* Carr.], is used to diminish gene flow of transgenes into the environment and natural population, since the formation of seeds in 741 Poplar is restricted and these seeds possess no capability to germinate under natural condition (Ewald et al., 2006). Finding this base material, increased the efficiency and reduced the cost of the experiments on transgenic poplars.

3.2 Why do Chinese foresters create and release GM poplars?

With such improved technology to facilitate breeding, and the public concerns on genetic engineering both scientifically and ethically, why are GM poplars still created and why is it even developed with considerably or even concernably high pace?

Improvement of trees through conventional breeding is constrained by the long reproductive cycles and complex reproductive characteristics of woody plants, even with the help with *in vito* technologies, it takes a relatively long period to stable or maintainable cultivars with favoured

characteristics (Fladung, 2006), especially with the interspecific incompatibility system in some poplar species. Thus, when genetic engineering offers an attractive addition to conventional breeding by permitting the transfer of genes coding for preferred traits into selected cultivars without compromising their desirable genetic background, while taking the waiting through several life cycles out of the breeders way (Frankenhuyzen & Beardmore, 2004), the industry jumped for it.

Genetic engineering is expected to bring great traits into poplar cultivars, which will majorly benefit the intensively managed short-rotation plantations with clonally propagated species, in contrast to conventional breeding, which is limited to sexually accessible variation with complex, sometimes combined traits that typically depend on a large number of interacting genes, recombinant-DNA technology presented an almost infinite gene pool for breeders' to find and use genes coding for favourable traits. Concluded by Frankenhuyzen and Beardmore, endogenous genes already present in the tree genome can be modified to improve certain traits, such as fibre content and wood quantity, while exogenous genes can be transferred from unrelated organisms to provide entirely novel traits, such as resistance to herbicides, diseases or pests. The targeting traits are expected to positively affect the economics of plantation forests (improved growth, reduced rotation, promoted wood yield and quality, lowered cost of pest control), or confer various environmental benefits associated with forestry production (reduced pesticide and herbicide use) or processing (improved pulping, reduced inputs of hazardous chemicals and energy). (Frankenhuyzen & Beardmore, 2004)

By reducing the harvesting pressures on natural forest and meeting the industrial demands, GM tree breeding is now seen as an important future forest conservation strategies by its supporters (Adams et al. 2002).

3.2.1 Modification of wood production

The same as in most areas in the world, there is an urgent demand in wood and wood products to be met in China. The country is now, the largest importer of industrial logs and the second largest

importer of forest products globally, reported by FAO (Lu, 2004). At the same time, the protection of natural forests, which had become necessary because of the severe deforestation caused by industrialisation and environmental degradation, contributed to a shortage in wood production (Ewald et al., 2006).

To achieve maximised economic benefits, there are two basic directions in modifying wood production: quantitively and qualitatively. The first one is usually achieved by altering the plant metabolism and increase the growth rate thus to obtain increased biomass production. The latter could be achieved by modifying the lignin / cellulose synthesis mechanism (Fladung, 2006). While modification of wood parameters and growth are traditionally a major goal in forest breeding programs, the material is as complex as the formation process, thus targets are extremely hard to be accomplish through the time and resources consuming methods of conventional breeding; even when cultivars are established, their performance is largely dependent on ambient conditions (Fladung, 2006).

Genetically modified trees with reduced lignin composition have been proposed as a strategy to potentially reduce environmental impacts from chemically harsh pulping practices, maximise operation efficiency and minimise the environmental footprint in the paper industry (Sponza, 2003).

3.2.2 Abiotic Stress Tolerant

Along with the megatrend of global climate change, desertification, salinization and accumulation of toxic substances in soils (Frankenhuyzen & Beardmore, 2004), one of the serious problems confronting Chinese forestry is soil salinity (Ewald et al, 2006), as well as dry out and pollution of the limited water supply, which makes the already limited land resources for forest habitat conservation and industrial plantation even more stretched. Poplars as tested phytoremediating and water-soil conserving species (Marmiroli, 2011), are propagated as a fixation of the situation, which will make the primary salinized land productive, put the secondary salinized land on the way of recovering and becoming arable and detoxify the polluted soil to a certain

degree. However, the mechanism is very complexed and only by transcriptomes comparison and pathway analysis can scientists understand the establishment of such stress tolerance mechanisms through evolutionary adaption (Janz et al., 2010). Thus, genetic engineering becomes the most efficient way to combine preferred traits and realise them in single cultivars, so as to keep the land productivity within salinised areas, or with the plantation still functioning in phytoremediation, which is considered an approach towards ease the dilemma of mitigating the shortage of land resource contradicting the unfulfilled huge forest biomass demands in China.

Another main abiotic stress affecting poplar plantations in China is frost. To over come this issue, alternations in poplar phenology were often conducted. Usually, breeders try to put back the budding time to avoid cold damage to the newly germinated parts. With conventional breeding, the goal of achieving cold hardness as well as high productivity is constrained by limited germplasm resources within the genus and interspecific incompatibility. To remove frost as a growth limiting factor for plantations and to adapt to the capricious weather under the influence of global climate change, as well as to meet the urgent need of forestry product by the booming population, gene transfer became the most economic solution.

3.2.3 Biotic Disturbance resistance

Insect attacks and diseases are the main factors for economic losses in forestry. According to incomplete statistics dating back to the 1950s, the 1960s and the 1990s, an annual increase of losses of 25% was calculated in Chinese forestal economy (Su et al. 2003).

Insect resistance is among the major goal, if not the most important one, of Chinese modern forestry, since pest infection is one of the main causes of forest damage, especially in artificial plantations and the insects are often a limiting factor for tree growth and biomass production (Ewald et al., 2006). The control of forest pests with insecticides is only capable on smaller scales, such as in nurseries, but has detrimental ecological effects (Ewald et al., 2006). The Three North Shelterbelts Project, which, as mentioned previously, is established with intensely duplicated clones of very limited cultivars, has already been threatened by insect attacks. The reduction in timber

production of Chinese forestry due to pests has been estimated to be around 17 million cubic metres per year that results in a huge economic loss. A spread of these insects from plantations into natural forests, causing a loss in both forest coverage and biodiversity in the surrounding ecosystem is of great possibility (Su et al. 2003).

Meanwhile, the resistance and resilience against diseases caused by virus, fungus and bacteria are attracting increasing attention in China. The diseases do not only cause forest mortality, damaged wood quality and reduced aesthetic value, but often spread around fleetly and tend to be associated with insects, which made it extremely hard to be taken under control once happened, usually requiring intense chemical treatment that potentially do harm to micro-organisms, the rhizosphere, the local environment and affects broader area through the water-soil system.

Therefore, efficient solutions for overcoming the problems in an economic way is under urgent call and biotechnology offers a real and fast solution (Ewald et al., 2006), both the breeders and the stakeholders jump at having the insect resistant genes engineered into poplar and have the cultivars commercialised to take the severe loss under control, and maybe make some benefit within the shortest time. This would not only ease the economic issue, but will also approach towards solving the biomass resource security issue of the nation, since it is not a secure way for long term operation to rely that much on imported wood.

3.3 Impacts and concerns in both long- and short-terms

3.3.1 Genetic contamination

Since poplars have a relatively long life span, and the metabolism and reproduction process of GM poplar will leave tissues and secretions containing novel genes in the local ecosystem to be accumulated through their life cycle. Suggested by Li (unpublished), the transferred genes left in the rhizospheric soil system is testable and stable for approximately three years, while the metabolism of the trees is always happening. Also, routes of novel gene transfer and exotic protein

obtain could be established in the forest soil system, which links litter decomposition and nutrient cycling dynamically, and where novel proteins could be transmitted through the network constructed by soil, soil microflora, mycorhizal and plant root (Frankenhuyzen & Beardmore, 2004). Thus, with the continually inflow of engineered DNAs and novel proteins into the soil, concerns on the direct and indirect effects of novel gene leftovers are rising from the very beginning of tree genetic engineering, which are mainly addressed on impacts of toxin-encoding transgenes on population levels of competitors, preys, hosts, sybionts, predators, parasites, pathogens and soil microbes, as well as the influence of novel genes and toxic proteins on non-target organisms (Lu, 2008).

Apart from this, the invasive escape and vertical gene flow from GM clones towards their non-GM counter-species, varieties, cultivars, landraces, as well as wild relatives has intimidated tremendous debate worldwide (Snow, 2002). Transgenic species and their offsprings are concerned to turn into weeds, since the super competitive characters brought in by the transgenes greatly increased the invasiveness of its carrier, for instance by conferring early stage herbicides resistance into certain cultivar (Frankenhuyzen & Beardmore, 2004). Then, they might take over the habitat of the wild species or traditional varieties resulting in biodiversity losses and increased conservational cost. The concern is not a presumption but a lesson learn form the history of exotic tree species cultivation and plantation, for example, more than 19 species of pines have escaped cultivation and become invasive weeds in the southern hemisphere during the last decades costing huge losses in economic and ecological values (Richardson, 1998; Frankenhuyzen & Beardmore, 2004). Moreover, the novel genes could flow to nontransgenic individuals within the same species through sexual reproduction, such as pollination, which is already observed by Stewart et al. (2003) and many other scientists in GM annual crop plants, and as stated by Smouse et al. (2007), transgene flow by propagules was seen in GM forest trees. In addition, transgenes could be passed on to the wild relatives without interspicific incompatibility through out-breeding and gene introgression (Snow, 2002; Stewart et al., 2003).

Concerns have also been addressed on horizontal novel gene transferring from GM plants to unrelated organisms, sometimes even a cross-kingdom gene transfer, through nonsexual means, like feed and digestion or biosynthesis. The most common example is from plants to parasite or micro-organisms (Lu, 2008; Frankenhuyzen & Beardmore, 2004). A recent research conducted by Zhang et al. (2012) found out that exogenous plant miRNAs were present in the sera and tissues of various animals, which were primarily acquired orally through food intake; they stated that their findings demonstrated that exogenous plant genetic material in food can regulate expression of target genes in mammals. Suddenly, the discussion of biosafty risks brought by commercialising GM crops and trees reached a new peak in vehemence.

3.3.2 Ecological pressure

Even if transgenes are well restricted within the carriers, they might still have it's influence on the holding environment (Frankenhuyzen & Beardmore, 2004). The large existence of transgenic trees with engineered traits and a long life span draws significant ecological pressure on its living habitat, which includes the selection pressure on both targeting and non-targeting organisms in the local habitat and the ecosystem and the possible niche shift caused by their over-competing surrounding plant species and the influence on their associated species. All of these implicate a predictable loss in biodiversity, especially genetic diversity both within the species and among the ecosystem. Thus, they might as well affect critical ecosystem processes like decomposition and nutrient cycling (Frankenhuyzen & Beardmore, 2004).

Insects and pathogens have extremely short life cycles comparing with trees, thus within a pest or disease resistant GM poplar site, the evolution of resistant pest or pathogen biotypes stand a great chance of exceeding both the sustainability of the habitat and the function of the engineered traits (Strauss et al., 1991; Brunner et al., 2007). Selection pressures resulting from GM trees with superb characteristics could also affect non targeting insect species within the same habitat, which might be achieve by altering the food chain or breaking the equilibrium in competition (Frankenhuyzen & Beardmore, 2004). Thus, possible consequences on pest competitive suppression and trophic interactions (Schuler et al. 2001) that might shift arboreal organism com-

munity dynamic and local biodiversity should be precautiously examined before the release of anti-insect transgenics.

There are still some unknown mechanism, involvements and routes in biogeochemical process. Significant interactions between engineered traits and the environment might come within our sight anytime. Further studies and observations are necessary before stepping forward (Lu, 2008).

3.3.3 Food and feed safety

Directly affecting ourselves are the food and feed safety issues caused by GM plants. The main concerns are about toxicity, allergy and long tern effect on human and other living creatures' health caused by products from or under the impacts of GM plants.

Plenty of genes used in genetic modification are of the ability to cause toxicity, for example antibiotic marker gene, anti-insect genes that encoding for insecticidal protein or neurotoxins and genes coding for antibacterial chemicals all have a potential toxicity towards livestocks that depends on poplar leaves and young tissues, and then humans (Liu et al., 2001; Anon, 2008; Séralini et al., 2011). Allergy is usually caused by pollens from GM plants. It may affect not only humans and animals within the forest stand, but also have the influence delivered with the distance travel pollens and seeds, and the anaphylaxis could be caused by direct contact with plant tissue or pollen, feeding on GM contaminated food and applying personal care products derived from GM plants or plant materials contaminated by GMOs (Madsen & Sandøe, 2008; Antignac et al., 2010; Domingo & Bordonaba, 2011). Although, the concerns about subchronic and chronic health effects has been raised for GMOs, especially those containing pesticides, either produced from their engineered insect tolerance mechanism or gained from the external application of chemicals based on their pesticide tolerance, and some statistically significant findings on the toxicity of GMOs on rodent have been revealed (Séralini et al., 2009; 2012), most relevant studies indicate no obvious deleterious effect. However, the no-obvious-effect situation is believed to be a consequence of insufficient studies limited by time and methods (Séralini et al., 2012).

3.4 Status quo of GM poplars in China

Leple et al. reviewed all genetically engineered *Populus* species and hybrids by the year of 2000 worldwide (Table 3-3). Eight herbicides resistant lines, 5 insect resistant lines and 10 growth alternated lines, as well as 6 lines developed for wood quality modification. There are two cultivars of transgenic poplars commercialised in China by 2003: one is Poplar Hybrid 741 with *Bt, Cry1* and *API* genes inserted, the other is *Populus nigra* with single Bt inserted, and they are both engineered to resistant leaf-eating insects (Sigaud, FAO). By 2010, nineteen insect-resistant GM poplar lines was created in China (Hu et al., 2010) possessing genes or combination of genes encoding the production of proteinase inhibitors, insecticidal proteins, lectin or neurotoxin, all efficient in fighting against insects (Ewald et al., 2006).

While the research and application of genetic modification are developing rapidly, the relative policies in China remained brief and deficient. Table 4 reviewed major policy measures related to biotechnology carried out in China from early 1980s (Huang & Wang, 2002), from which we see the refining process of the national policies, however, it is still way too loose comparing with that of the EU (Jaffe, 2004). Also, based on my observation, the public awareness and participation are relatively low. There is barely no local NGO or community advocacy for genetic safety issues. This unbalanced situation might enlarge the nation's chance in confronting with genetic contamination and related negative ecological changes.

4. A proposal of "What we can do before it's too late"

4.1 Transparency

First of all, I advocate for transparency in policy making procedures, which should not only be known within the high-level authority, as well as the data and information facilitating the decision making, which should not be kept within the authority group. The consumers have the right to informations that may benefit their choice and the farmers and foresters have the right to the

genetic resources on their land. It is not fair for the policy makers to keep them from knowing what they should know.

Also, I advocate for marketing transparency. Labelling products containing GM materials and products harvested or processed in and near GM poplar forests and nurseries, for example economic agriculture products harvested from undergrowth layer of forest stands constructed with GM poplars. What's more important, the labels should be obvious and easy to find. Based on my observation, GMO products in the market in China are either labeled ambiguous or the label is extremely small and hard to find. People who is not conscious about GMO related issues, or seniors and kids without sensitive observational ability may never notice the information, which is supposed to be carried out to each consumer. Every purchase and consume on GMO related products should be conducted by people who is fully aware of it, or it is no difference than market fraud. The government should standardise the labelling in the market with uniform marks. Not only should GM poplar products be labelled, GM poplar surrounding products should also be labelled. If a carton of mushroom is non-GMO itself but is harvested from GM poplar logs, the information should be clearly conducted to the customers. With such board scale of GM plants released and commercialised in China, no blind buying and trading of GM related products is still tolerable.

If the people cannot choose whether they want GMOs to be released and commercialised in their country, they should at least be ensured their access to information about what is going on exactly and their right of choosing whether to buy and used such product should be respected.

4.2 Develop well established risk assessment and regulation system

With all the concerns reviewed previously, insufficient risk assessing mechanism and the lack of efficient regulatory methods for the consequences of potential genetic contamination, the release and commercialisation of GM poplars were still carried out in China, which brought up the ur-

gent demand for a sensitive monitoring system as well as complementarity risk assessing and regulating mechanism.

To assess the risk and find regulatory methods, the foresters need to understand the condition first, and to really know what is going on with plantations containing GM poplars and the nature forests near the plantations, GIS monitoring is a great tool for risk assessment, record keeping, forest management and geographical genetics conservation (Fan, 2001).

However, it is very hard and costly to genotyping all the major poplar forest stand routinely and mark every genetic information on different layers in GIS to monitor the stability of target genes, the potential gene flow and both the long and short terms of ecological pressures. To lower the cost and increase the feasibility I suggest using asymmetry data as an indicator. Asymmetry datas of plants is often fluctuating through its life history reflecting the living condition of the plant and could indicate their fitness, developmental stability and the stress level (ecotoxicity, competition, inbreeding, etc.) they are under (Clark et al., 1986; Jones, 1987; Graham et al., 1993; Kozlov et al., 1996; Rettig et al., 1997). Also, fluctuating asymmetry (FA) is more sensitive than life historical parameters, and is able to quantify the impact of GM poplars, especially the ecological pressure (Zhai, 2001), which made it suitable for combination with GIS. As the mensuration and analysis of FA data are relatively easy to conduct and there is no need for high-priced instruments, the data collecting could be done with hearing co-op students, which on one hand, will lower the labour costs, on the other hand will provide students with a hand-on experience in forest management and research, as well as better understanding in the forest ecosystem.

Many other risk assessment mechanisms are proposed by multiple authors. Most of them are laboratory operations, micro mimic nature system models (usually for microbes) and mathematical models that predict or determine the impacts and development trends of GM poplars (Domingo & Bordonaba, 2011). A combination of both field and laboratory assessment gives foresters better information and chance to regulate potential consequences of GM popler releasing.

4.3 Do not become too relied on genetic engineering

Even though biotic disturbances resistant GM poplars are currently performing well in tolerating the attacks from insects and weedy, Chinese forestry should not rely entirely on transgenes to solve the issues. In some small scaled plantation and plantation close to nature forests, bio-pesticide and bio-herbicide, which are not as toxic to the surrounding ecosystems as chemical compounds could be used in case of insect attack or weed overgrowth.

Also, planting prescriptions could help with increasing the insect resistance of traditional cultivars and natural species of poplars. A common approach is mix planting. Pointed out by Ewald et al. (2006) Asian longhorn beetle (*Anoplophora glabripennis*) is the major damage causing pest for poplars in China. However, mix-plant non-GM poplars with *Ailanthus altissima* helps the stand resist against *Anoplophora spp*. (Jin, 2008), which tend to be a good solution for stands not planted for maximum biomass production.

Meanwhile, both commercial and researching organic farming and foresting should be encouraged, as a preservation of genetic resources, a life style choice for people and a research potential.

4.4 Approaching the problems through "Traditional breeding" of poplars

Since Chinese forestry is confronted with several dilemmas mentioned in section 3.2, to become less relied on genetic engineering, Chinese foresters should try to breed certain non-transgenic poplar cultivars that is capable of solving part of the problems.

The first step of a breeding plan is to select for the suitable germplasm. In the breeding plan I am going to propose, the key species is *Populus euphratica.* It is a broadly distributed tree species in central Asia, of whom the natural habitats in China are located in the deserted area in Gansu, Qinghai, Xinjiang, Ningxia and Inner Mongolia (Peng et al., 2009; Zhang, 2009). *P. euphratica*

evolved from the harsh deserted habitat process great quality of salinity tolerance, waterlog tolerance, drought tolerance and sandstorm resistance. Also, it is no leaf feeding *lepisoptera* species hosting on *Populus euphratica* distributed in China (Table 5, Robinson et al., 2010).

Populus euphratica is the only species under the section *Turanga*, so the hybrid between it and any other *Populus* species will be characterised under distant hybridisation, which is highly affected by its interspecific incompatibility. To overcome the barrier, breeders employed artificial pollination on stigmas previously treated with female parental pollen extracts, in vitro ovule culture, and hybrid seedlings in vitro propagation technics to force hybridisation. Based on the result achieved by multiple combinations tries through different breeding methods, when using *P. euphratica* as the pollen source, the hybrid progenies tend to possess more desired traits in *P. euphratica* (Peng et al., 2009). Also, the survival rate of seed germinated seedlings are much higher than that of the clones developed from sprout tillers, thus some asexual propagation might not be suitable for establishing hybrid *P. euphratica* stands (Shen et al., 2009). With the germplasm selected, the breeding methods developed and relative mechanism studied, the preferable cultivars will not remain hard to create for very long.

4.5 A PROSPECT

I my perspective, a desirable future condition of GM poplar forestry in China is constructed with three elements: well established risk assessing and regulating mechanism, elaborative record keeping and monitoring system and carefully restricted plantation area gradually replaced by mix-planting or traditional hybrids with no less biomass production making the utmost of the nature biodiversity. From scopes other than forestry, I am looking forward to see the government could hold on to its own word of valuing the principle of freedom of science, but advances in science must serve, not harm humankind, and will actually “mull over new rules and regulations to guide, promote, regulate, and guarantee a healthy development of science”, promoting the technology while showing appropriate precaution for biosafety, environmental health, food safety, and the commercialisation of biotechnology (Huang & Wang, 2002).

Conclusion

Genetic modification is a double-edged sword, from which we knew exactly what we would be benefiting, but what damage would it do were never thoroughly understood. The extensive cultivation of GM poplars in China has generated great benefits and helped solving a variety of issues both ecologically and economically. However, even while we are in the biotech era, the current information and data are not sufficient in showing the exact long-term influence of GM poplars on both bio-safety and human health. Great issues have been raised concerning GMO deployment at large. The fact that GM trees are already widely planted in China and the present risk assessment system is not adequate in addressing these concerns, then the establishing of a sophisticated risk assessment system is urgently needed. The plethora of available knowledge did not only provide us a way to deal with the present, but also should assist us to use biotechnology in a sustainable manner to save the future for all the living creatures. While benefiting from genetic engineering, an integrated standing system of research, monitoring, evaluating and readjusting should be established.

Appendix I

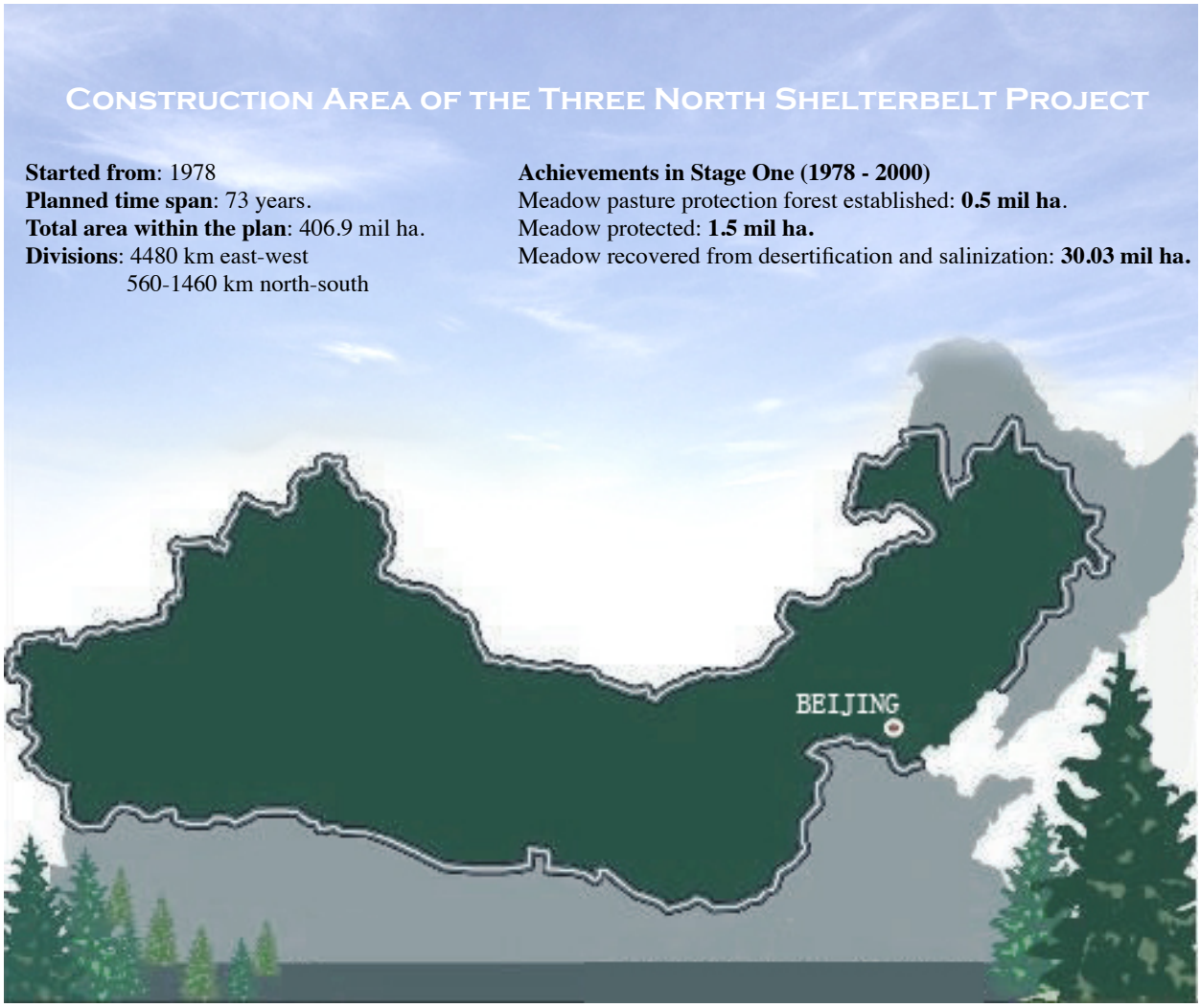

Figure 1-1. Construction area of the Three North Shelterbelt Project. (Edited from the original illustration by Ding, M. & Zhang, Y. Publish by Xinhua News Agency)

Table 1. Distribution of poplar species in North China. (Derived by Sigaud, FAO., based on Xu, 1988)

SPECIES	North East			Central North			North West					ALTITUDE (m)
	Heil	Jil	Liao	Mon	Heb	Shan	Shaa	Gan	Nin	Qing	Xinj	
P. afghanica											√	1400 - 2800
P. alba											√	450 - 750
P. amuyensis	√			√								600 - 800
P. canescens											√	600 - 700
P. cathayana			√	√	√	√	√	√		√	√	800 - 3200
P. charbinensis	√											300 - 500
P. davidiana	√	√	√	√	√	√	√	√	√	√	√	200 - 3800
P. euphratica				√				√	√	√	√	2500 - 2900
P. gansuensis								√				1800 - 2000
P. girinensis	√	√										300 - 400
P. hopeiensis					√	√	√	√	√	√		700 - 1600
P. hsinganica	√			√	√							300 - 700
P. iliensis											√	600 - 750
P. jrtyschensis											√	200 - 2000
P. koreana	√	√	√									400 - 1100
P. lasiocarpa							√					1300 - 3500
P. laurifolia											√	1200 -1700
P. maximowiczii	√	√	√	√	√		√	√				400 - 2000
P. nakaii	√	√	√	√	√							600 - 900
P. nigra											√	400 - 800
P. ningshanica						√	√					600 - 1000
P. pamirica											√	1800 - 2000
P. pilosa											√	1600 - 2300
P. pruinosa											√	300 - 1500
P. przewalskii				√			√		√			500 - 1500
P.pseudomaximowiczii					√		√					1000 - 1600
P. pseudosimonii	√	√	√	√	√	√	√	√		√		300 - 2300
P. pseudotomentosa						√						300 - 1400
P. purdomii					√		√	√				700 - 3300
P. simonii	√	√	√	√	√	√	√	√	√	√	√	600 - 2300
P. suaveollens	√			√								200 - 400
P. szechuanica							√	√				1100 - 4000
P. talassica											√	500 - 1800
P. tomentosa					√	√	√	√				200 - 1800
P. tremula											√	700 - 2300
P. ussuriensis	√	√	√									300 - 1400
P. wilsonii							√	√				1300 - 3300
NUMBER BY PROVINCE	12	8	8	11	11	8	14	12	5	6	16	37

* ***Heil*** - Heilongjiang Province; ***Jil*** - Jilin Province; ***Liao*** - Liaoning;
Mon - Inner Mongolia Municipality; ***Heb*** - Hebei Province; ***Shan*** - Shanxi Province;
Shaa - Shaanxi Province; ***Gan*** - Gansu Province; ***Nin*** - Ningxia Municipality;
Qing: Qinghai Province; ***Xin*** - Xinjiang Municipality

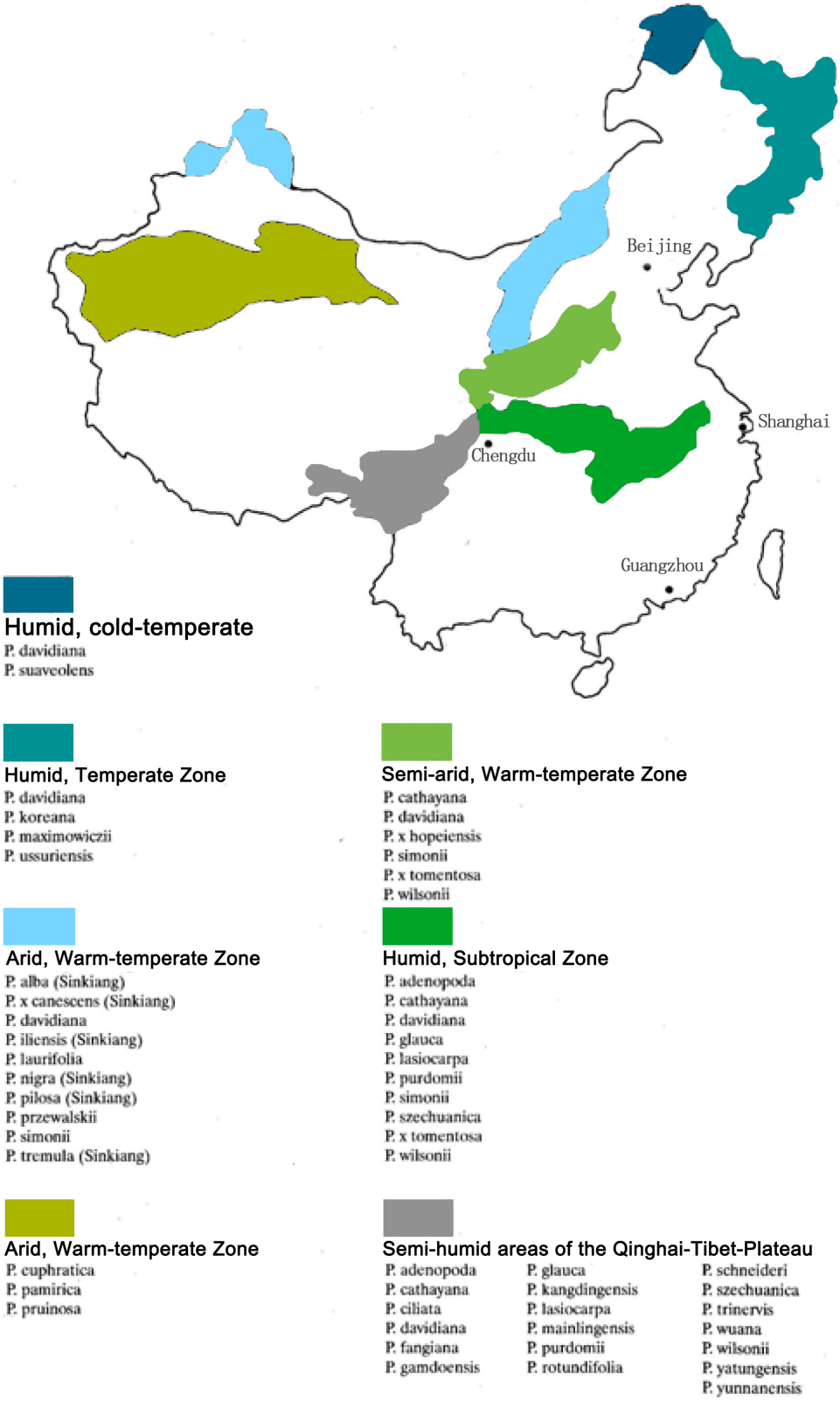

Figure 1-2. Classification and distribution of indigenous poplar species of China according the climatic zones (Weisgerber & Zhou, 1997. Translated from German to English and edited by the author)

Appendix II

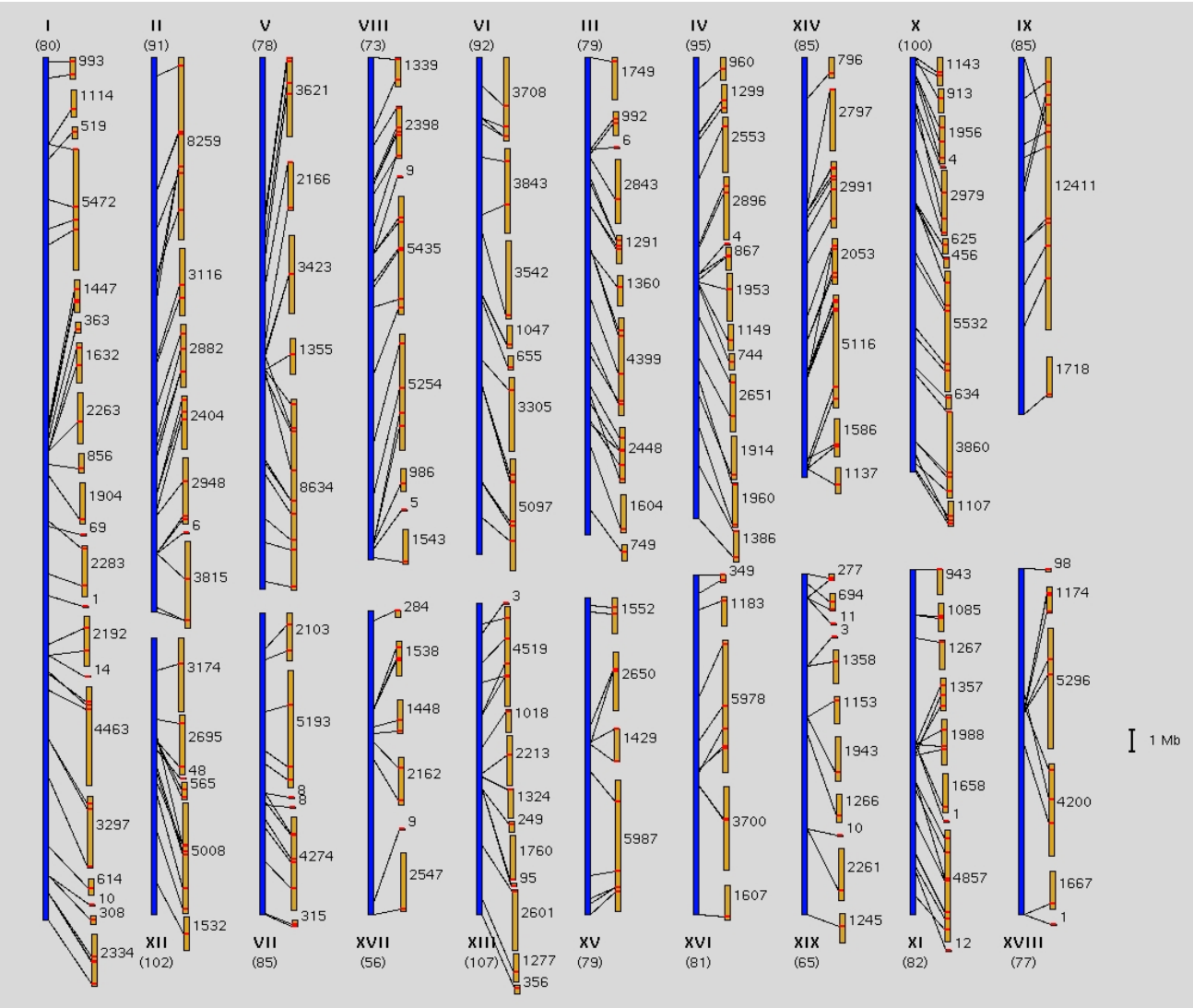

Figure 2-1. Representation of the 335 Mb of *Populus* genomic sequence contained in 155 Scaffolds aligned and oriented to a genetic map of the 19 *Populus* linkage groups (indicated by Roman numerals I - XIX) (Tuskan et al., 2006)

* Each scaffold (yellow bars) was mapped to a chromosome (blue bars) using micro-satellite markers with unique sequence locations (red lines). Numbers in parentheses are estimates of the percentage of the linkage group covered by assembled sequence (assuming uniform physical: genetic distance across the genome). Approximate size (in kb) is indicated to the right of each Scaffold. Gaps between scaffolds are known size.

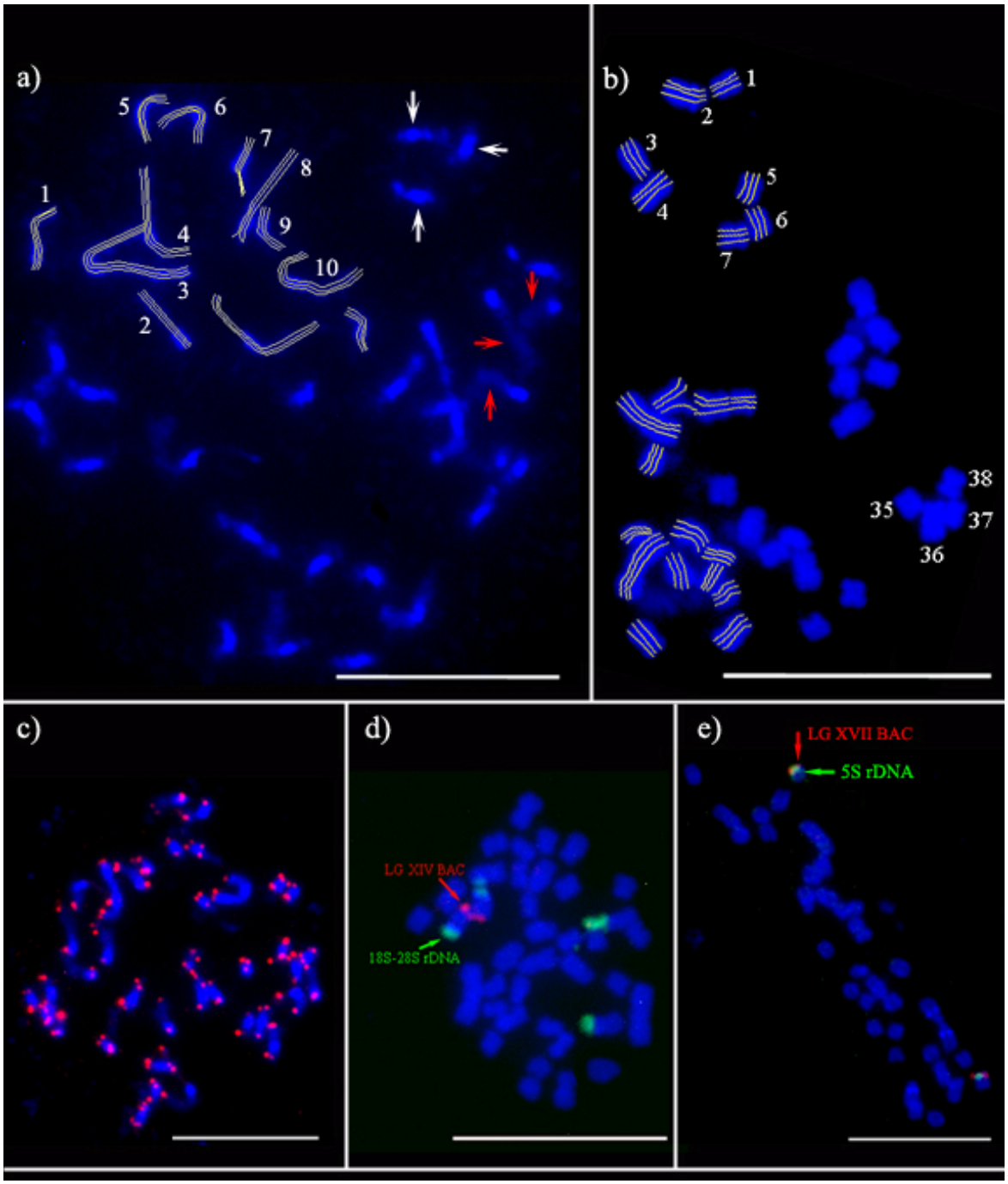

Figure 2-2. DAPI stained a) prophase and b0 metaphase *Populus* somatic chromosomes and FISH using Arabidopsis-tyoe telomere repeat sequence (A-type TRS), 18S-28S rDNA, 5S rDNA and linkage group (LG) specific Poplulus BAC clones as probes. (Tuskan et al., 2006)

* White and red arrows a) show heterochromatic (A-T rich, brightly stained) and euchromatic regions, respectively. For data collection, chromosomes were numbered arbitrarily from 1 to 38 in each cell and chromosome length was measured three times per chromosome (shown by white trace lines) using Optimas v6. c) A-type TRS FISH signals are observed at the end all chromosome arms. d) BACs from

LGXIV are found to be co-localized with an 18S-28S rDNA site and e) BACs from LGXVII are found to be co-localised with the 5S rDNA site. Bar is 10 µm.

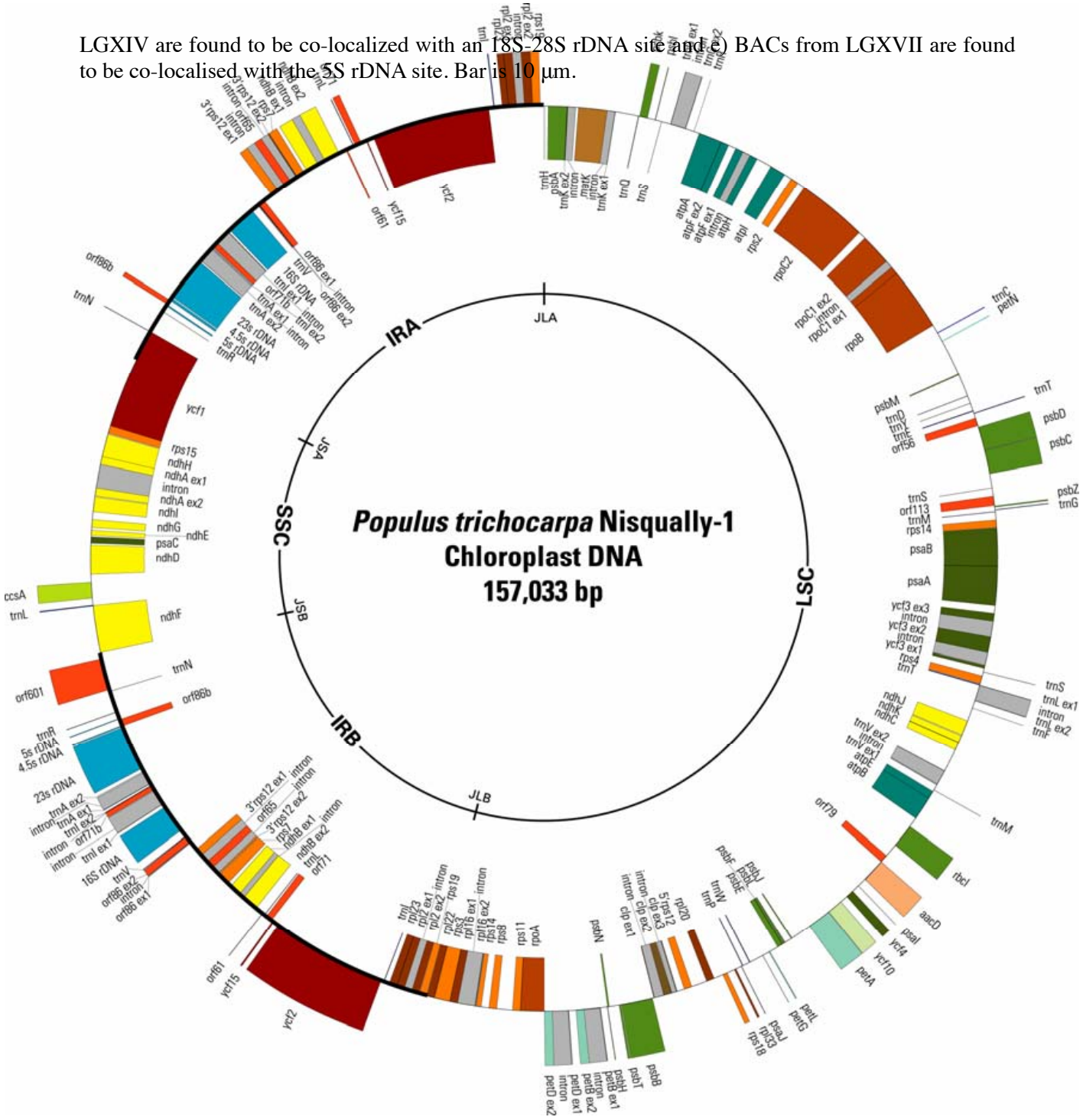

Figure 2-3. Graphic representation of the de novo whole-genome shotgun sequence assembly and annotation for the *Poplulus trichocarpa* chloroplast. (Tuskan et al., 2006)

* Each nucleotide is represented by an average of 410 sequence reads at a quality score of 40 or higher. Gene Models were predicted based on the Glimmer program at Oak Ridge National Laboratory.

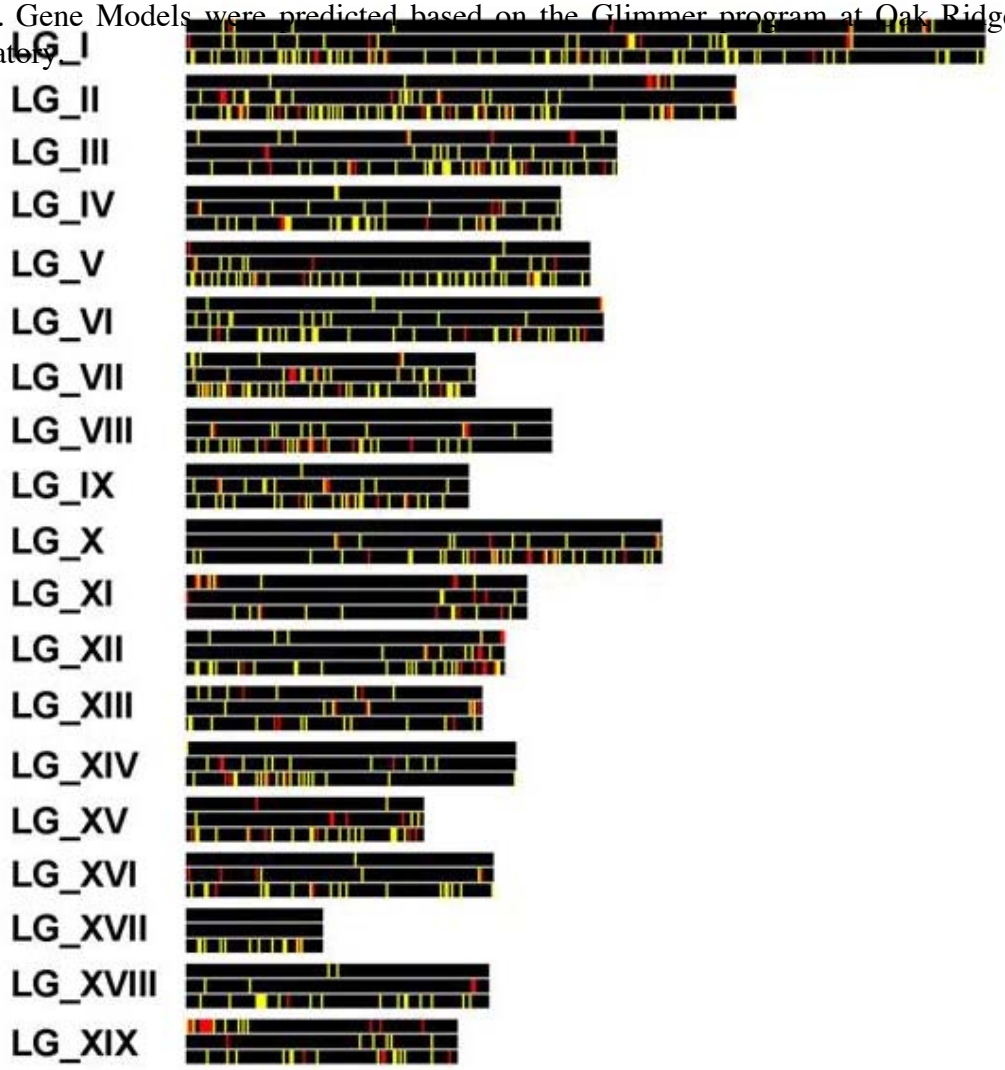

Figure 2-4. Chromosomal localization designated by linkage groups (LG), for disease resistance genes (top), genes coding for P450 enzymes (middle) and transcription factors (bottom). (Tuskan et al., 2006)

* Yellow denotes a single gene in a 100 kb window, red 2 or more genes in a 100 bp window.

Appendix III

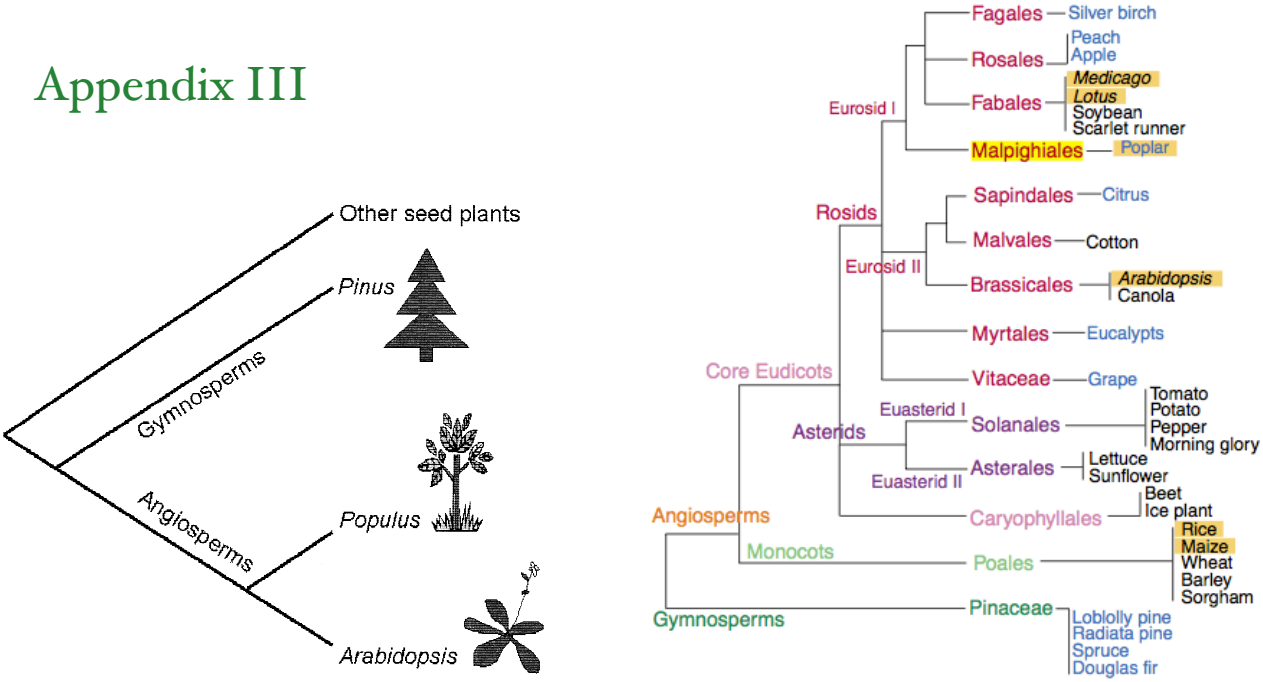

Figure 3-1-1. Phylogeny of *Populus*, which indicates poplars diverged relatively recently from other angiosperms, such as Arabidopsis. (Bradshaw et al., 2000; Brunner et al., 2004)

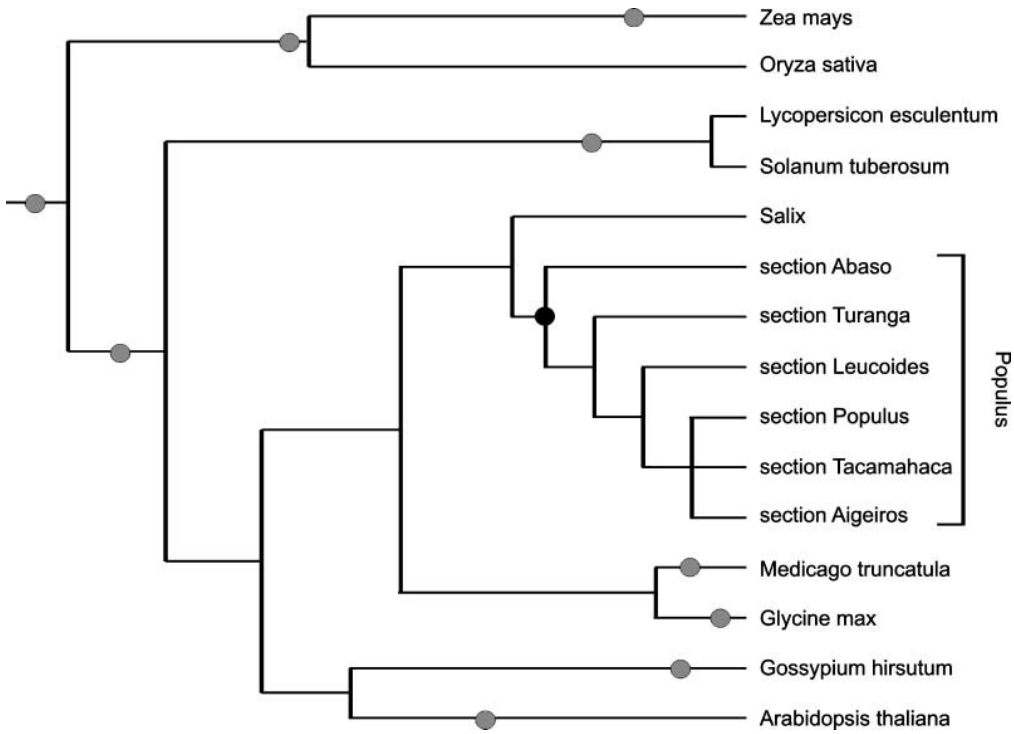

Figure 3-1-2. Intersectional phylogenetic relationship of the genus *Populus*. Schematic representation of the phylogeny of the genus *Populus* and some relevant plant species (Sterck et al., 2005).

* Grey dots indicate large-scale duplication events; the black dot denotes the large-scale duplication event in poplar proposed in the current study.

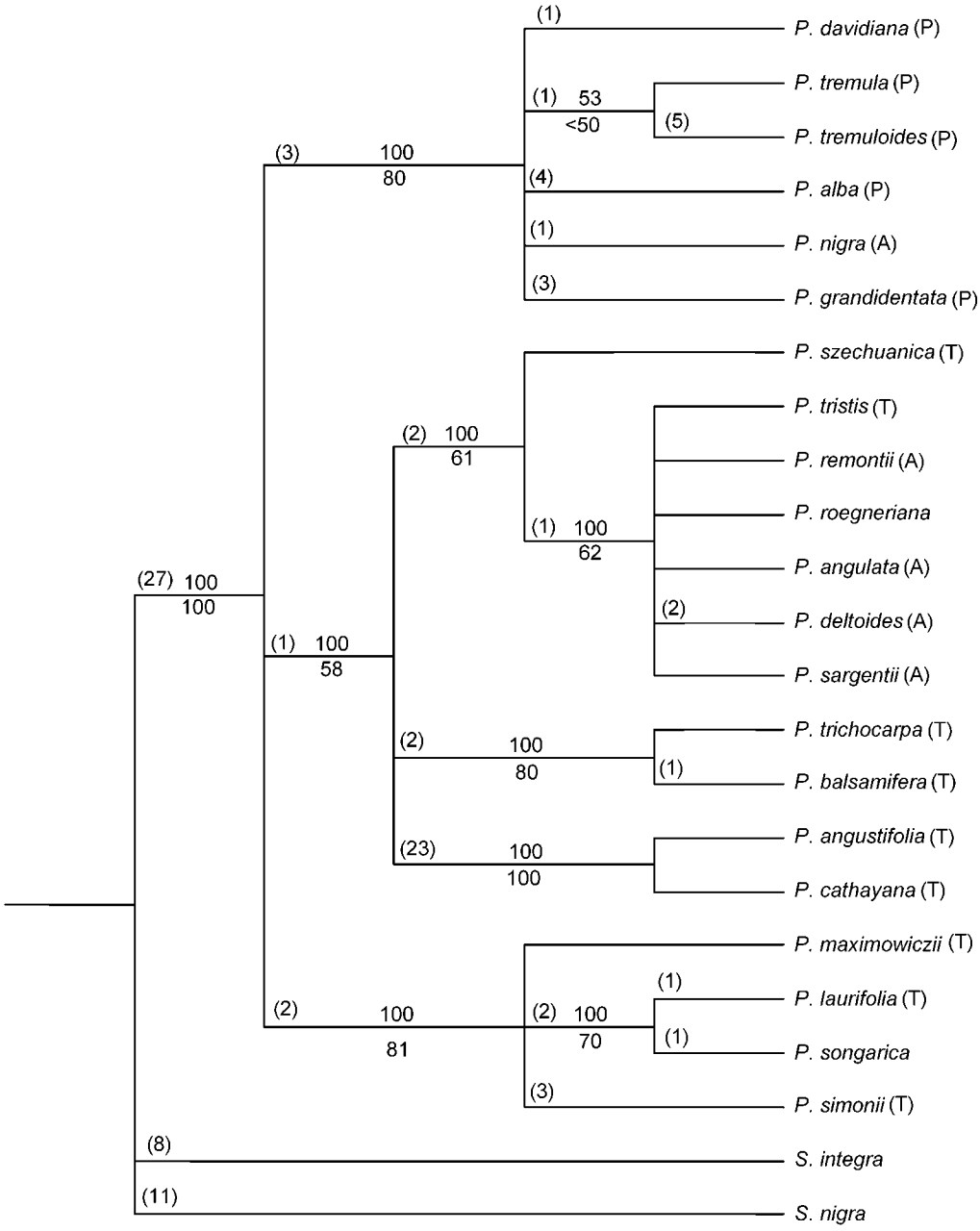

Figure 3-1-3-a. Interspecific phylogenetic relationship of the genus *Populus*. (Hamzeh & Dayanandan, 2004)

The majority rule consensus tree of 30,939 equally parsimonious trees (tree length 118; consistency index = 0.924) based on three noncoding regions of trnT-trnF of cpDNA sequences from *Populus* species.

* Numbers above branches show the frequency of occurrence in 50% majority rule consensus tree, and numbers below branches indicate bootstrap percentage values.
* Numbers in brackets show branch lengths (number of nucleotide substitution).
* **A**, *Aigeiros*; **P**, *Populus*; **T**, *Tacamahaca*.

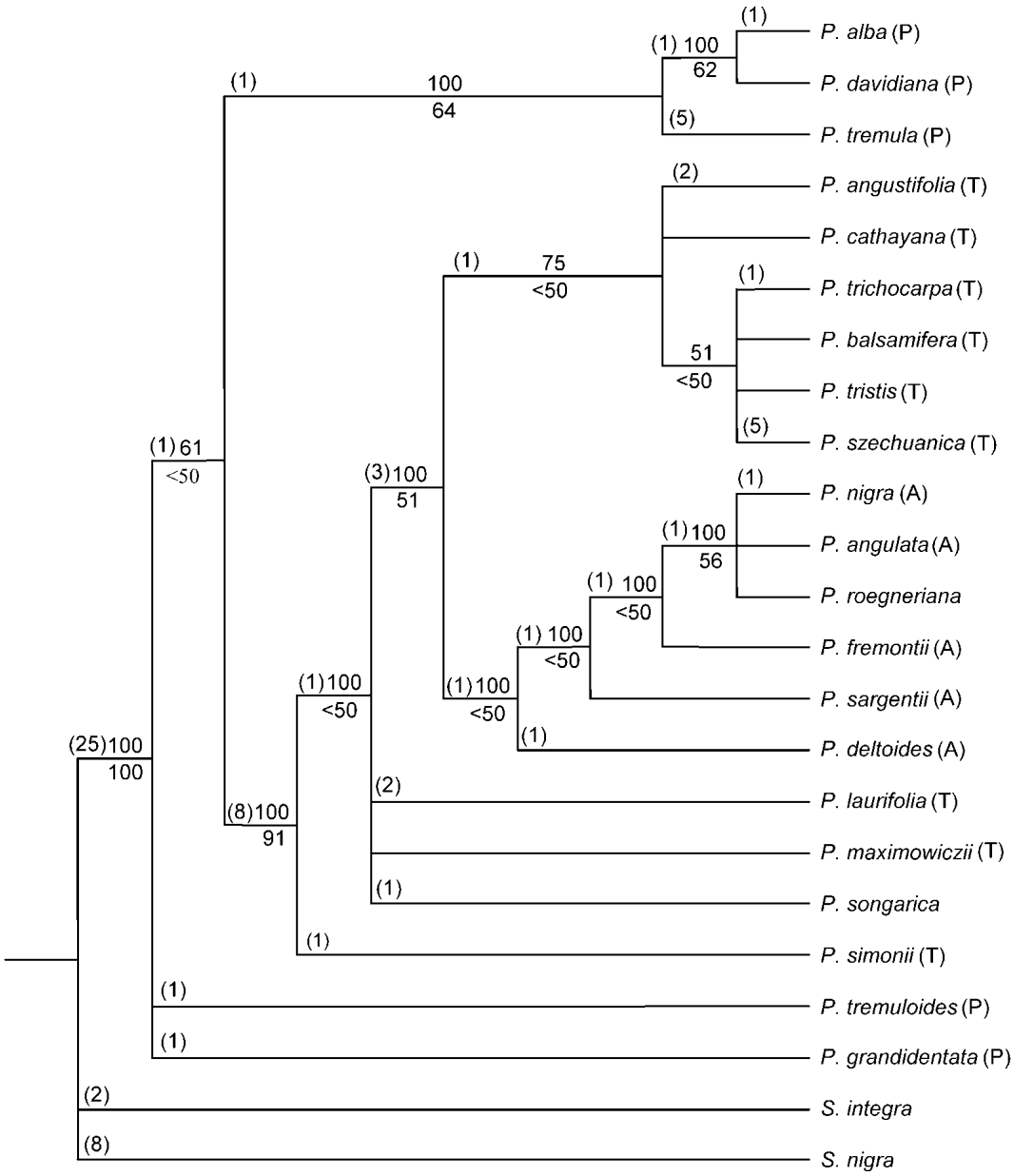

Figure 3-1-3-b. Interspecific phylogenetic relationship of the genus *Populus*. (Hamzeh & Dayanandan, 2004)

The majority rule consensus tree of 497 equally parsimonious trees (tree length 94; consistency index = 0.851) based on partial 5.8S RNA gene, ITS1 and ITS2 and part of 28S subunit sequences from Populus species.

* Numbers above branches show frequency of occurrence in 50% majority rule consensus tree, and numbers below branches indicate bootstrap percentage values.
* Numbers in brackets show branch lengths (number of nucleotide substitution).
* **A**, *Aigeiros*; **P**, *Populus*; **T**, *Tacamahaca*.

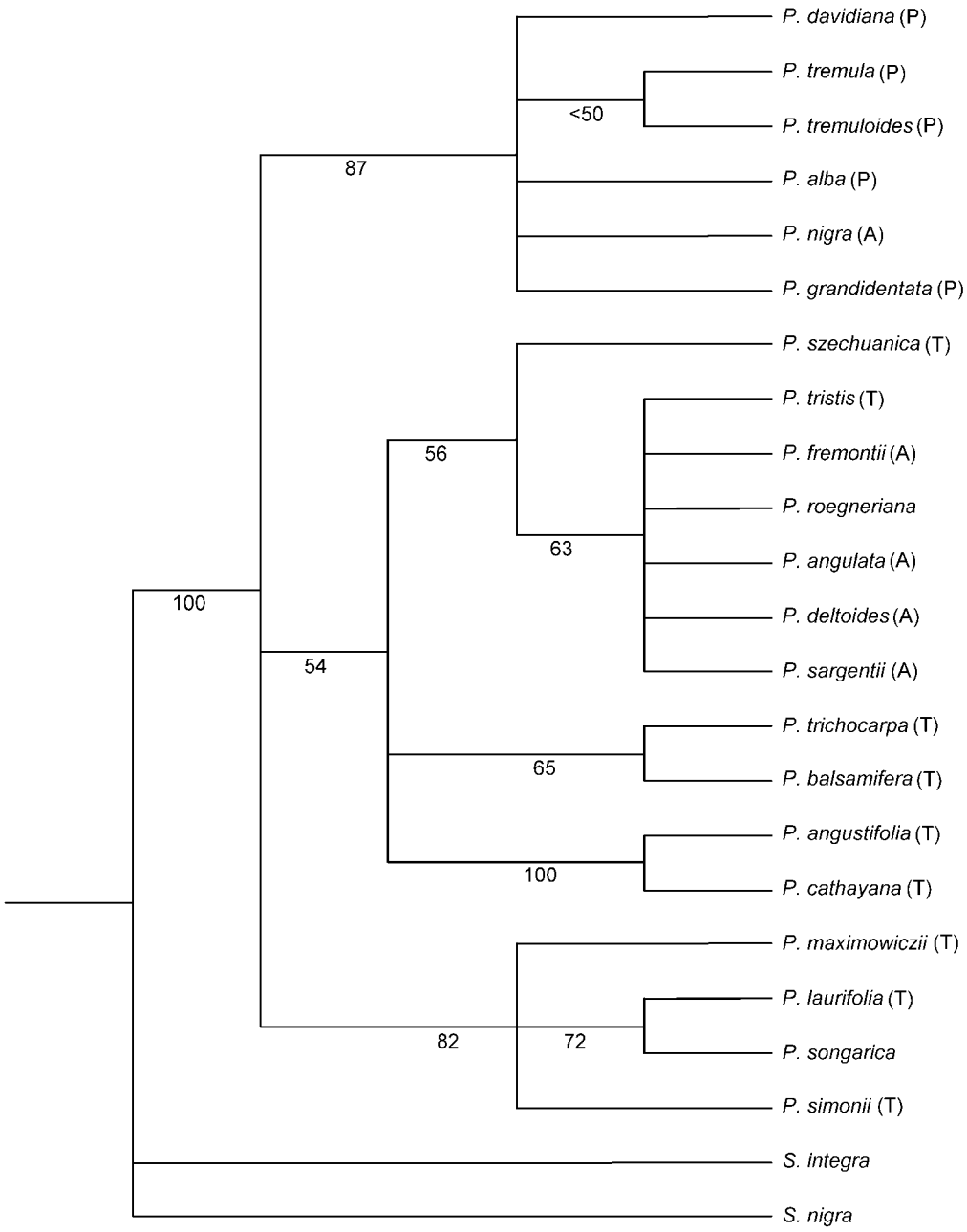

Figure 3-1-3-c. Interspecific phylogenetic relationship of the genus Populus. (Hamzeh & Dayanandan, 2004)

Maximum likelihood tree based on three noncoding regions of trnT-trnF of cpDNA sequences from Populus species.

* Numbers below branches show bootstrap percentage values.
* **A**, *Aigeiros*; **P**, *Populus*; **T**, *Tacamahaca*.

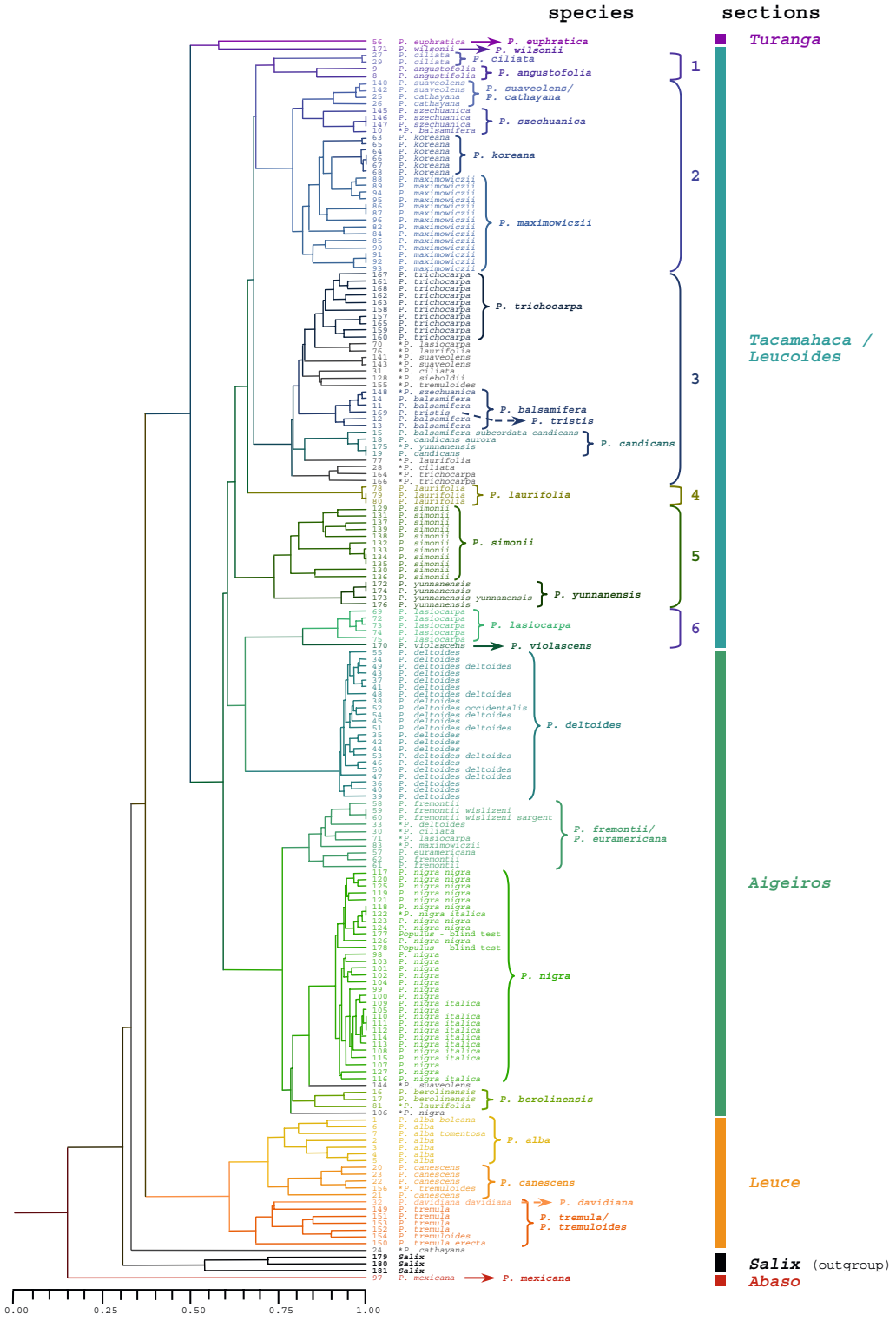

Figure 3-1-4. Dendrogram of *Populus* accessions with *Salix* as an outgroup, constructed from AFLP fragment similarities (Dice coefficient) with the UPGMA clustering method, and based on AFLP markers resolved by five primer combinations. (Cervera et al., 2005)

* Accessions marked with an asterisk are potentially mislabeled species or hybrids. Species are marked by brackets and arrows, whereas lines group sections.

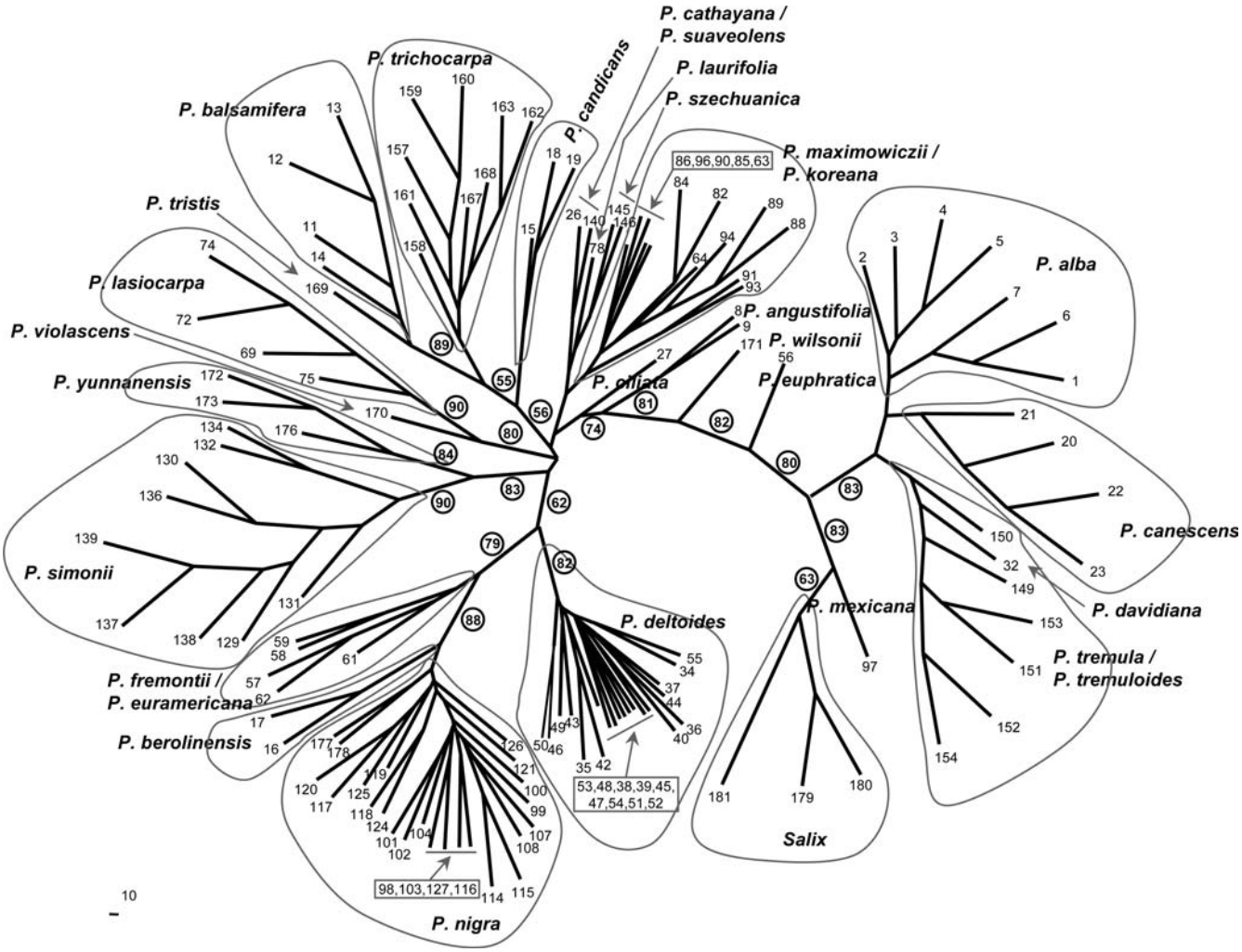

Figure 3-2. The single most parsimonious bifurcating unrooted tree, based on the Wagner method, representing the phylogeny of *Populus*. Plain and circled numbers correspond to accession codes (Table 3-1) and bootstrap values (only those above 50% are shown for main branches, grouping several species), respectively. (Cervera et al. 2005)

Table 3-1. Information on individual poplar accessions of 32 typical *Populus* species and hybrids within 5 main sections analysed in Fig. 3-1-4 & Figure 3-2. (Cervera, 2005)

Accession number	Species	Variety or cultivar	Clone name	Origin	Provider	New tentative assignation[e]
1	*P. alba*	*boleana*			CN	
2	*P. alba*		603.02		FR, INRA	
3	*P. alba*		A.L05.010	IT	IT, ISP	
4	*P. alba*		BO-1	IT	IT, ISP	
5	*P. alba*		Villafranca	IT	IT, ISP	
6	*P. alba*		B	BE	BE, VIB-UG	
7	*P. alba*	*tomentosa*			FR, INRA	
8	*P. angustifolia*		46/69		DE, HLFWW	
9	*P. angustifolia*		ANG		FR, INRA	
10	*P. balsamifera*[c]		1-5	US, MN	BE, IBW	*P. szechuanica*
11	*P. balsamifera*		8-6	US, MN	BE, IBW	
12	*P. balsamifera*		21-7	US, WI	BE, IBW	
13	*P. balsamifera*		15-5	US, MI	BE, IBW	
14	*P. balsamifera*		19-2	US, MI	BE, IBW	
15	*P. balsamifera*	*subcordata candicans*		BE, IBW	*P. candicans*	
16	*Populus* × *berolinensis*				BE, arboretum Kalmthout	
17	*Populus* × *berolinensis*		19870019	FR	BE, arboretum Meise	
18	*P. candicans*	*aurora*	19860364		BE, arboretum Meise	
19	*P. candicans*		19810762		BE, arboretum Meise	
20	*Populus* × *canescens*		90000054		BE, arboretum Meise	
21	*Populus* × *canescens*		limbrichterbos		BE, arboretum Kalmthout	
22	*Populus* × *canescens*		Grauwe abeel 1		BE, IBW	
23	*Populus* × *canescens*		Grauwe abeel 2		BE, IBW	
24	*P. cathayana*[c]		E6		IE, Teagasc	unclassified
25	*P. cathayana*[b]		306-52		DE, HLFWW	
26	*P. cathayana*				US, Washington University	
27	*P. ciliata*		72-085		IT, ISP	
28	*P. ciliata*[c]		65-017		IT, ISP	*P. trichocarpa* × *P. maximowiczii*
29	*P. ciliata*[a]		72-085		FR, INRA	
30	*P. ciliata*[c]		102L7		IE, Teagasc	*Populus* × *canadensis*
31	*P. ciliata*[c]		D1D4E3		IE, Teagasc	intrasectional *Tacamahaca* hybrid
32	*P. davidiana*	*davidiana*			FR, INRA	
33	*P. deltoides*[c]		V12	US, IL	BE, IBW	*Populus* × *canadensis*
34	*P. deltoides*		V1	CA, ONT	BE, IBW	
35	*P. deltoides*		V2	CA, ONT	BE, IBW	
36	*P. deltoides*		V3	US, MN	BE, IBW	
37	*P. deltoides*		V7B	US, MO	BE, IBW	
38	*P. deltoides*		S174-1	US, ND	BE, IBW	
39	*P. deltoides*		S197-1	CA, ON	BE, IBW	
40	*P. deltoides*		S329-31	US, OH	BE, IBW	
41	*P. deltoides*[b]		S333-53	US, MI	BE, IBW	
42	*P. deltoides*		S235-3	US, IL	BE, IBW	
43	*P. deltoides*		S193-1	US, ND	BE, IBW	
44	*P. deltoides*		DO-006	US, TX	IT, ISP	
45	*P. deltoides*		DI-180A	US, OH	IT, ISP	
46	*P. deltoides*		S336-4	US, CT	BE, IBW	
47	*P. deltoides*	*deltoides*	D37	CA, ON[g]	CA, O.P. Rajora	
48	*P. deltoides*	*deltoides*	D43	CA, ON[g]	CA, O.P. Rajora	
49	*P. deltoides*	*deltoides*	D68	US, IN[g]	CA, O.P. Rajora	
50	*P. deltoides*	*deltoides*	D70	US, IL[g]	CA, O.P. Rajora	
51	*P. deltoides*	*deltoides*	D56	CA, ON[g]	CA, O.P. Rajora	
52	*P. deltoides*	*occidentalis*	D87	US, KS[g]	CA, O.P. Rajora	
53	*P. deltoides*	*deltoides*	D109	US, MS[g]	CA, O.P. Rajora	
54	*P. deltoides*	*deltoides*	D121	US, IL[g]	CA, O.P. Rajora	
55	*P. deltoides*		S9-2	US	BE, IBW	
56	*P. euphratica*			CN	VIB-UG	

Table 3-1. (Continued).

Accession number	Species	Variety or cultivar	Clone name	Origin	Provider	New tentative assignation[e]
114	*P. nigra*	'Italica'	PI88-058	TR	IT, ISP	
115	*P. nigra*	'Italica'	PI88-063	BG	IT, ISP	
116	*P. nigra*	'Italica'	Zaragoza	ES	ES, SIA	
117	*P. nigra*	*nigra*	N13	CZ[h]	CA, O.P. Rajora	
118	*P. nigra*	*nigra*	N19	NL[h]	CA, O.P. Rajora	
119	*P. nigra*	*nigra*	N20	FR[h]	CA, O.P. Rajora	
120	*P. nigra*	*nigra*	N29	NL[h]	CA, O.P. Rajora	
121	*P. nigra*	*nigra*	N40	NL[h]	CA, O.P. Rajora	
122	*P. nigra*[b]	*nigra*	N84	DE[h]	CA, O.P. Rajora	
123	*P. nigra*[b]	*nigra*	N85	DE[h]	CA, O.P. Rajora	
124	*P. nigra*	*nigra*	N96	CZ[h]	CA, O.P. Rajora	
125	*P. nigra*	*nigra*	N100	CZ[h]	CA, O.P. Rajora	
126	*P. nigra*	*nigra*	N102	CZ[h]	CA, O.P. Rajora	
127	*P. nigra*		Ghoy	BE	BE, IBW	
128	*P. sieboldii*[c]		Sie	GB	IE, Teagasc	*P. trichocarpa* × *P. balsamifera*
129	*P. simonii*		1/9		BE, IBW	
130	*P. simonii*		81-001-003	CN	IT, ISP	
131	*P. simonii*		81-002-003	CN	IT, ISP	
132	*P. simonii*		108/49		DE, HLFWW	
133	*P. simonii*[b]		57/65		DE, HLFWW	
134	*P. simonii*		147/65		DE, HLFWW	
135	*P. simonii*[b]		141/66		DE, HLFWW	
136	*P. simonii*		58/90		DE, HLFWW	
137	*P. simonii*		59/90		DE, HLFWW	
138	*P. simonii*		60/90		DE, HLFWW	
139	*P. simonii*	*fastigiata*			BE, VIB-UG	
140	*P. suaveolens*		21/65		DE, HLFWW	
141	*P. suaveolens*[c]		15/74		DE, HLFWW	*P. trichocarpa* × *P. balsamifera*
142	*P. suaveolens*[a]		21/65		DE, HLFWW	
143	*P. suaveolens*[a,c]		15/74		DE, HLFWW	*P. trichocarpa* × *P. balsamifera*
144	*P. suaveolens*[c]		20/65		DE, HLFWW	*P.* × *canadensis* × *P. nigra*
145	*P. szechuanica*		SZC		FR, INRA	
146	*P. szechuanica*		275/49		DE, HLFWW	
147	*P. szechuanica*[b]		67/65		DE, HLFWW	
148	*P. szechuanica*[c]		144/65		DE, HLFWW	*P. balsamifera*
149	*P. tremula*		130-19		FR, INRA	
150	*P. tremula*	*erecta*			BE, arboretum Beveren	
151	*P. tremula*		1H		BE, IBW	
152	*P. tremula*		2H		BE, IBW	
153	*P. tremula*		3H		BE, IBW	
154	*P. tremuloides*		210-22		FR, INRA	
155	*P. tremuloides*[c]		HI-10		IE, Teagasc	intrasectional *Tacamahaca* hybrid
156	*P. tremuloides*[c]				BE, arboretum Kalmthout	*Populus* × *canescens*
157	*P. trichocarpa*		FPL		FR, INRA	
158	*P. trichocarpa*		19-73		FR, INRA	
159	*P. trichocarpa*		36-77		FR, INRA	
160	*P. trichocarpa*		101-74		FR, INRA	
161	*P. trichocarpa*		S3-31		BE, IBW	
162	*P. trichocarpa*		V509		BE, IBW	
163	*P. trichocarpa*		V510		BE, IBW	
164	*P. trichocarpa*[c]	'Fritzi Pauley'	V235	US, WA	BE, IBW	*P. trichocarpa* × *P. maximowiczii*
165	*P. trichocarpa*[b]		212-161		FR, INRA	
166	*P. trichocarpa*[a,c]	'Fritzi Pauley'			BE, arboretum Kalmthout	*P. trichocarpa* × *P. maximowiczii*
167	*P. trichocarpa*	'Trichobel'			BE, IBW	
168	*P. trichocarpa*	'Columbia river'	V24	US, OR	BE, IBW	
169	*P. tristis*		24/65		DE, HLFWW	

Table 3-1. (Continued).

Accession number	Species	Variety or cultivar	Clone name	Origin	Provider	New tentative assignation[e]
170	*P. violascens*		19860054	UK	BE, arboretum Meise	
171	*P. wilsonii*		19820416	DE	BE, arboretum Meise	
172	*P. yunnanensis*		82001		FR, INRA	
173	*P. yunnanensis*	*yunnanensis*			FR, INRA	
174	*P. yunnanensis*[b]		V535		BE, IBW	
175	*P. yunnanensis*[c]				BE, arboretum Beveren	*P. candicans*
176	*P. yunnanensis*				BE, arboretum Beveren	
177	*Populus-unknown*[d]		22616		BE, arboretum Kalmthout	*P. nigra*
178	*Populus-unknown*[d]		22031		BE, arboretum Kalmthout	*P. nigra*
179	*Salix*				BE, VIB-UG	
180	*Salix*				BE, VIB-UG	
181	*Salix*		22010		BE, arboretum Kalmthout	

* Countries are abbreviated according to ISO 3166-1-Alpha-2 code (***BE*** Belgium, ***BG*** Bulgaria, ***CA*** Canada [ON Ontario], ***CN*** China, ***CZ*** Czech Republic, ***DE*** Germany, ***DK*** Denmark, ***ES*** Spain, ***FR*** France, ***IE*** Ireland, ***IT*** Italy, ***JP*** Japan, ***MX*** Mexico, ***NL*** The Netherlands, ***TR*** Turkey, ***GB*** United Kingdom, ***US*** United States [IL Illinois, IN Indiana, KS Kansas, MN Minnesota, MO Missouri, MS Mississippi, ND North Dakota, OH Ohio, OR Oregon, TX Texas, WA Washington State, WI Wisconsin], ***YU*** Yugoslavia).

* ***HLFWW*** Hessian Forest Center for Management, Planning, Research and Ecology (Munden, Germany),
IBW Instituut voor Bosbouw en Wildbeheer (Geraardsbergen, Belgium),
INRA Institut National de la Recherche Agronomique (Orleans, France),
ISP Istituto di Sperimentazione per la Pioppicoltura (Casale Monferrato, Italy),
SIA Servicio de Investigacion Agroalimentaria Diputacion General de Aragon (Zaragoza, Spain), Teagasc Irish Agriculture and Food development Authority (Dublin, Ireland),
VIB-UG Vlaams Interuniversitair Instituut voor Biotechnologie-Universiteit Gent (Gent, Belgium).

* Accessions in bold were used to perform the phylogenetic analysis

a. Samples known to be duplicates before the start of the analysis and confirmed by AFLP

b. Accessions showing GS of ≥ 0.98 based on AFLP fragment similarities

c. Possibly mislabeled and/or misclassified accessions based on AFLP analysis

d. Based on morphological descriptors (blind test). These clones showed AFLP patterns typical of *P. nigra*

e. Tentative assignation of misclassified accessions based on AFLP patterns, GS values and the dendrogram in Fig. 3-1-3

Table 3-2. Interspecific and intraspecific GS among pairs of *Populus* and *Salix*, with average similarities between parentheses. (Cervera, 2005)

	P. euphratica (1)	*P. ciliata* (2)	*P. lasiocarpa* (5)	*P. alba* (7)	*P. davidiana* (1)	*P. sieboldii* (1)	*P. tremula* (5)	*P. tremuloides* (1)	*P. angustifolia* (2)	*P. balsamifera* (5)	*P. candicans* (4)	*P. cathayana* (2)	*P. laurifolia* (3)	*P. maximowiczii* (14)
P. euphratica	–													
P. ciliata	0.50–0.51 (0.51)	0.99												
P. lasiocarpa	0.46–0.47 (0.47 ± 0.01)	0.56–0.59 (0.58 ± 0.01)	0.90–0.99 (0.95 ± 0.03)											
P. alba	0.29–0.45 (0.36 ± 0.05)	0.29–0.4 (0.32 ± 0.04)	0.34–0.44 (0.40 ± 0.03)	0.70–0.95 (0.81 ± 0.06)										
P. davidiana	0.40	0.35	0.36–0.38 (0.38 ± 0.01)	0.57–0.65 (0.60 ± 0.03)	–									
P. sieboldii	0.48	0.62	0.60–0.62 (0.61 ± 0.01)	0.39–0.47 (0.44 ± 0.03)	0.43	–								
P. tremula	0.34–.047 (0.40 ± 0.04)	0.36–0.43 (0.39 ± 0.02)	0.35–0.49 (0.41 ± 0.04)	0.53–0.70 (0.59 ± 0.04)	0.71–0.78 (0.74 ± 0.03)	0.38–0.51 (0.46 ± 0.05)	0.67–0.86 (0.75 ± 0.07)							
P. tremuloides	0.39	0.37	0.37–0.43 (0.41 ± 0.02)	0.52–0.66 (0.59 ± 0.05)	0.71	0.47	0.63–0.90 (0.77 ± 0.11)	–						
P. angustifolia	0.54–0.60 (0.57)	0.72–0.76 (0.74 ± 0.02)	0.57–0.66 (0.62 ± 0.03)	0.34–0.55 (0.43 ± 0.06)	0.40–0.45 (0.43)	0.65–0.67 (0.66)	0.4–0.50 (0.45 ± 0.03)	0.42–0.43 (0.42)	0.86					
P. balsamifera	0.46–0.53 (0.50 ± 0.03)	0.58–0.67 (0.64 ± 0.03)	0.57–0.65 (0.62 ± 0.02)	0.33–0.47 (0.39 ± 0.03)	0.35–0.43 (0.40 ± 0.03)	0.80–0.88 (0.85 ± 0.03)	0.31–0.51 (0.43 ± 0.06)	0.40–0.47 (0.45 ± 0.03)	0.61–0.72 (0.67 ± 0.03)	0.89–0.99 (0.94 ± 0.03)				
P. candicans	0.51–.052 (0.51 ± 0.01)	0.67–0.72 (0.69 ± 0.02)	0.66–0.70 (0.68 ± 0.01)	0.37–0.52 (0.41 ± 0.05)	0.44–0.47 (0.45 ± 0.01)	0.80–0.85 (0.82 ± 0.02)	0.35–0.49 (0.45 ± 0.05)	0.44–0.45 (0.45 ± 0.01)	0.64–0.73 (0.68 ± 0.03)	0.75–0.87 (0.81 ± 0.03)	0.94–1.00 (0.97 ± 0.02)			
P. cathayana	0.44	0.67–0.73 (0.70 ± 0.03)	0.54–0.63 (0.58 ± 0.03)	0.30–0.45 (0.34 ± 0.05)	0.38–0.41 (0.40)	0.65–0.70 (0.68)	0.32–0.46 (0.40 ± 0.04)	0.40–0.43 (0.42)	0.59–0.69 (0.64 ± 0.04)	0.62–0.72 (0.68 ± 0.03)	0.65–0.73 (0.69 ± 0.03)	0.89		
P. laurifolia	0.39–0.40 (0.40 ± 0.01)	0.63–0.65 (0.64 ± 0.01)	0.47–0.54 (0.51 ± 0.02)	0.26–0.38 (0.31 ± 0.03)	0.33–0.35 (0.34 ± 0.01)	0.67–0.68 (0.68 ± 0.01)	0.31–0.41 (0.37 ± 0.03)	0.36–0.37 (0.37 ± 0.01)	0.56–0.61 (0.58 ± 0.02)	0.60–0.66 (0.64 ± 0.02)	0.61–0.67 (0.63 ± 0.02)	0.69–0.72 (0.70 ± 0.02)	0.99–1.00 (0.99 ± 0.01)	
P. maximowiczii	0.45–0.52 (0.47 ± 0.02)	0.69–0.74 (0.71 ± 0.02)	0.52–0.62 (0.58 ± 0.02)	0.27–0.49 (0.35 ± 0.05)	0.37–0.44 (0.42 ± 0.02)	0.60–0.69 (0.66 ± 0.03)	0.30–0.49 (0.41 ± 0.04)	0.40–0.44 (0.42 ± 0.02)	0.62–0.73 (0.68 ± 0.03)	0.59–0.73 (0.67 ± 0.03)	0.62–0.75 (0.68 ± 0.03)	0.73–0.86 (0.81 ± 0.03)	0.64–0.71 (0.68 ± 0.02)	0.73–1.00 (0.85 ± 0.06)
P. koreana	0.44–0.45 (0.45 ± 0.01)	0.67–0.69 (0.68 ± 0.01)	0.55–0.61 (0.58 ± 0.02)	0.31–0.47 (0.35 ± 0.05)	0.41–0.43 (0.42 ± 0.01)	0.63–0.67 (0.65 ± 0.01)	0.36–0.45 (0.41 ± 0.02)	0.41–0.45 (0.42 ± 0.02)	0.63–0.72 (0.68 ± 0.03)	0.60–0.71 (0.67 ± 0.03)	0.65–0.70 (0.67 ± 0.02)	0.78–0.84 (0.82 ± 0.02)	0.65–0.71 (0.68 ± 0.02)	0.79–0.91 (0.86 ± 0.03)
P. simonii	0.34–0.46 (0.39 ± 0.04)	0.48–0.62 (0.55 ± 0.05)	0.49–0.63 (0.56 ± 0.03)	0.27–0.45 (0.34 ± 0.04)	0.38–0.44 (0.41 ± 0.02)	0.53–0.62 (0.57 ± 0.02)	0.36–0.45 (0.45 ± 0.03)	0.33–0.41 (0.39 ± 0.02)	0.54–0.62 (0.59 ± 0.03)	0.50–0.69 (0.59 ± 0.03)	0.60–0.68 (0.63 ± 0.02)	0.56–0.73 (0.65 ± 0.06)	0.50–0.58 (0.55 ± 0.03)	0.49–0.72 (0.62 ± 0.06)
P. suaveolens	0.44	0.70–0.73 (0.72 ± 0.01)	0.57–0.63 (0.60 ± 0.01)	0.30–0.46 (0.35 ± 0.05)	0.41	0.70	0.37–0.47 (0.41 ± 0.03)	0.43	0.60–0.67 (0.64 ± 0.04)	0.63–0.72 (0.69 ± 0.04)	0.69–0.73 (0.70 ± 0.01)	0.91–0.98 (0.94 ± 0.04)	0.67–0.70 (0.69 ± 0.01)	0.75–0.84 (0.81 ± 0.03)
P. szechuanica	0.45–0.49 (0.47 ± 0.02)	0.67–0.70 (0.68 ± 0.01)	0.57–0.61 (0.59 ± 0.01)	0.30–0.47 (0.34 ± 0.05)	0.37–0.39 (0.38 ± 0.01)	0.64–0.71 (0.66 ± 0.03)	0.32–0.48 (0.39 ± 0.04)	0.39–0.44 (0.40 ± 0.03)	0.63–0.71 (0.66 ± 0.03)	0.63–0.73 (0.69 ± 0.03)	0.66–0.72 (0.68 ± 0.02)	0.82–0.86 (0.84 ± 0.02)	0.69–0.76 (0.71 ± 0.02)	0.70–0.82 (0.76 ± 0.03)
P. yunnanensis	0.42–0.45 (0.44 ± 0.02)	0.62–0.65 (0.64 ± 0.02)	0.58–0.66 (0.62 ± 0.03)	0.32–0.49 (0.39 ± 0.04)	0.45–0.48 (0.46 ± 0.02)	0.63–0.67 (0.65 ± 0.02)	0.36–0.51 (0.45 ± 0.05)	0.46–0.49 (0.48 ± 0.02)	0.61–0.68 (0.65 ± 0.03)	0.56–0.69 (0.64 ± 0.03)	0.66–0.72 (0.68 ± 0.02)	0.68–0.76 (0.73 ± 0.03)	0.55–0.61 (0.59 ± 0.02)	0.62–0.75 (0.69 ± 0.04)
P. trichocarpa	0.40–0.50 (0.48 ± 0.03)	0.62–0.70 (0.67 ± 0.02)	0.58–0.75 (0.65 ± 0.03)	0.30–0.48 (0.40 ± 0.04)	0.38–0.47 (0.41 ± 0.02)	0.82–0.89 (0.86 ± 0.02)	0.32–0.55 (0.45 ± 0.05)	0.41–0.51 (0.46 ± 0.04)	0.62–0.76 (0.70 ± 0.04)	0.71–0.87 (0.81 ± 0.04)	0.74–0.87 (0.80 ± 0.03)	0.63–0.78 (0.69 ± 0.03)	0.63–0.68 (0.66 ± 0.01)	0.58–0.76 (0.67 ± 0.04)
P. deltoides	0.41–0.49 (0.44 ± 0.02)	0.52–0.61 (0.56 ± 0.02)	0.61–0.72 (0.66 ± 0.02)	0.30–0.44 (0.37 ± 0.03)	0.37–0.45 (0.40 ± 0.02)	0.57–0.64 (0.59 ± 0.02)	0.28–0.43 (0.37 ± 0.04)	0.39–0.42 (0.41 ± 0.01)	0.54–0.69 (0.61 ± 0.04)	0.53–0.66 (0.60 ± 0.03)	0.68–0.81 (0.75 ± 0.03)	0.54–0.71 (0.59 ± 0.03)	0.49–0.60 (0.53 ± 0.02)	0.53–0.66 (0.60 ± 0.03)
P. × euramericana	0.37–0.45 (0.43 ± 0.03)	0.53–0.64 (0.59 ± 0.03)	0.53–0.64 (0.59 ± 0.02)	0.26–0.42 (0.35 ± 0.04)	0.35–0.42 (0.39 ± 0.02)	0.58–0.65 (0.63 ± 0.02)	0.27–0.46 (0.38 ± 0.04)	0.36–0.40 (0.39 ± 0.02)	0.58–0.71 (0.65 ± 0.04)	0.51–0.67 (0.61 ± 0.04)	0.64–0.79 (0.74 ± 0.03)	0.50–0.66 (0.60 ± 0.04)	0.50–0.56 (0.53 ± 0.01)	0.52–0.68 (0.61 ± 0.03)
P. nigra	0.41–0.48 (0.45 ± 0.02)	0.53–0.61 (0.57 ± 0.02)	0.45–0.53 (0.49 ± 0.01)	0.22–0.38 (0.29 ± 0.03)	0.30–0.40 (0.34 ± 0.02)	0.59–0.65 (0.62 ± 0.02)	0.31–0.42 (0.35 ± 0.03)	0.29–0.39 (0.32 ± 0.02)	0.58–0.67 (0.61 ± 0.02)	0.51–0.66 (0.59 ± 0.03)	0.57–0.67 (0.62 ± 0.02)	0.49–0.61 (0.55 ± 0.03)	0.50–0.55 (0.52 ± 0.02)	0.50–0.64 (0.57 ± 0.03)
P. violascens	0.49	0.69	0.79–0.83 (0.82 ± 0.02)	0.36–.46 (0.39 ± 0.04)	0.41	0.69	0.40–0.46 (0.42 ± 0.02)	0.43	0.67–0.70 (0.68)	0.61–0.69 (0.67 ± 0.03)	0.77 (± 0.01)	0.70 (0.70)	0.58–0.59 (0.58 ± 0.01)	0.65–0.75 (0.71 ± 0.04)
P. wilsonii	0.58	0.61–0.62 (0.61)	0.58–0.61 (0.59 ± 0.01)	0.38–0.47 (0.42 ± 0.03)	0.41	0.66	0.39–0.48 (0.44 ± 0.03)	0.41	0.65	0.59–0.68 (0.65 ± 0.04)	0.59–0.63 (0.61 ± 0.02)	0.56–0.59 (0.57)	0.46	0.55–0.65 (0.58 ± 0.03)
P. tristis	0.51	0.66–0.67 (0.66)	0.61–0.65 (0.63 ± 0.01)	0.37–0.45 (0.41 ± 0.03)	0.40	0.89	0.36–0.51 (0.45 ± 0.06)	0.50	0.71–0.72 (0.71)	0.88–0.96 (0.93 ± 0.03)	0.80–0.87 (0.83 ± 0.03)	0.67–0.72 (0.70)	0.63–0.64 (0.63 ± 0.01)	0.65–0.73 (0.69 ± 0.03)
P. berolinensis	0.41–0.43 (0.42 ± 0.01)	0.60–0.66 (0.63 ± 0.03)	0.49–0.54 (0.51 ± 0.02)	0.26–0.37 (0.33 ± 0.03)	0.31–0.37 (0.33 ± 0.03)	0.60–0.64 (0.62 ± 0.02)	0.33–0.40 (0.37 ± 0.02)	0.34–0.35 (0.35 ± 0.01)	0.60–0.64 (0.61 ± 0.02)	0.51–0.63 (0.59 ± 0.04)	0.62–0.67 (0.63 ± 0.02)	0.59–0.69 (0.65 ± 0.04)	0.64–0.68 (0.66 ± 0.01)	0.52–0.69 (0.63 ± 0.04)
P. × canescens	0.35–0.39 (0.37 ± 0.2)	0.31–0.41 (0.38 ± 0.04)	0.37–0.43 (0.40 ± 0.02)	0.63–0.79 (0.72 ± 0.04)	0.61–0.66 (0.64 ± 0.02)	0.44–0.46 (0.45 ± 0.01)	0.57–0.72 (0.65 ± 0.05)	0.58–0.64 (0.61 ± 0.03)	0.42–0.5 (0.47 ± 0.03)	0.34–0.46 (0.41 ± 0.03)	0.36–0.46 (0.42 ± 0.04)	0.33–0.42 (0.38 ± 0.03)	0.31–0.36 (0.34 ± 0.02)	0.29–0.41 (0.35 ± 0.03)
P. mexicana	0.14	0.13 (0.13)	0.13–0.17 (0.14 ± 0.02)	0.05–0.14 (0.10 ± 0.04)	0.26	0.16	0.12–0.20 (0.16 ± 0.03)	0.14	0.11–0.16 (0.13)	0.10–0.13 (0.12 ± 0.01)	0.14–0.16 (0.16 ± 0.01)	0.09–0.12 (0.11)	0.23–0.26 (0.25 ± 0.02)	0.10–0.16 (0.13 ± 0.02)
Salix	0.31–0.38 (0.34 ± 0.04)	0.17–0.29 (0.25 ± 0.05)	0.25–0.35 (0.31 ± 0.03)	0.26–0.44 (0.33 ± 0.06)	0.29–0.36 (0.32 ± 0.04)	0.29–0.34 (0.31 ± 0.03)	0.22–0.32 (0.28 ± 0.03)	0.26–0.35 (0.30 ± 0.04)	0.27–0.35 (0.31 ± 0.03)	0.26–0.37 (0.32 ± 0.04)	0.30–0.37 (0.33 ± 0.02)	0.24–0.30 (0.28 ± 0.02)	0.28–0.33 (0.31 ± 0.02)	0.23–0.37 (0.29 ± 0.04)

Table 3-2. (Continued).

	P. koreana (6)	*P. simonii* (11)	*P. suaveolens* (2)	*P. szechuanica* (4)	*P. yunnanensis* (4)	*P. trichocarpa* (10)	*P. deltoides* (22)	*Populus* × *canadensis* (10)	*P. nigra* (31)	*P. violascens* (1)	*P. wilsonii* (1)	*P. tristis* (1)	*P.* × *berolinensis* (3)	*P.* × *canescens* (5)	*P. mexicana* (1)
P. euphratica															
P. ciliata															
P. lasiocarpa															
P. alba															
P. davidiana															
P. sieboldii															
P. tremula															
P. tremuloides															
P. angustifolia															
P. balsamifera															
P. candicans															
P. cathayana															
P. laurifolia															
P. maximowiczii															
P. koreana	0.85–1.00 (0.92 ± 0.07)														
P. simonii	0.51–0.74 (0.63 ± 0.06)	0.75–1.00 (0.83 ± 0.07)													
P. suaveolens	0.80–0.84 (0.83 ± 0.01)	0.57–0.73 (0.64 ± 0.06)	0.98												
P. szechuanica	0.74–0.79 (0.76 ± 0.01)	0.52–0.71 (0.61 ± 0.07)	0.80–0.83 (0.81 ± 0.01)	0.87–1.00 (0.93 ± 0.05)											
P. yunnanensis	0.67–0.71 (0.69 ± 0.01)	0.67–0.79 (0.74 ± 0.04)	0.71–0.76 (0.74 ± 0.02)	0.63–0.67 (0.66 ± 0.02)	0.91–1.00 (0.95 ± 0.03)										
P. trichocarpa	0.61–0.74 (0.68 ± 0.03)	0.54–0.72 (0.63 ± 0.04)	0.65–0.78 (0.70 ± 0.03)	0.60–0.74 (0.66 ± 0.03)	0.58–0.75 (0.69 ± 0.04)	0.91–1.00 (0.95 ± 0.03)									
P. deltoides	0.57–0.65 (0.60 ± 0.02)	0.51–0.66 (0.56 ± 0.02)	0.56–0.72 (0.61 ± 0.03)	0.57–0.72 (0.61 ± 0.02)	0.57–0.71 (0.62 ± 0.02)	0.54–0.68 (0.60 ± 0.03)	0.89–0.99 (0.94 ± 0.02)								
P. × *canadensis*	0.53–0.66 (0.61 ± 0.03)	0.54–0.73 (0.61 ± 0.04)	0.54–0.66 (0.62 ± 0.03)	0.50–0.64 (0.58 ± 0.03)	0.57–0.71 (0.65 ± 0.02)	0.54–0.71 (0.63 ± 0.03)	0.67–0.83 (0.75 ± 0.03)	0.78–1.00 (0.87 ± 0.02)							
P. nigra	0.53–0.64 (0.59 ± 0.02)	0.48–0.78 (0.59 ± 0.06)	0.52–0.61 (0.57 ± 0.02)	0.53–0.62 (0.57 ± 0.02)	0.53–0.63 (0.56 ± 0.02)	0.54–0.68 (0.61 ± 0.03)	0.45–0.60 (0.53 ± 0.02)	0.68–0.87 (0.76 ± 0.03)	0.84–1.00 (0.93 ± 0.03)						
P. violascens	0.71–0.72 (0.72 ± 0.01)	0.56–0.65 (0.61 ± 0.03)	0.70–0.72 (0.71)	0.65–0.69 (0.68 ± 0.02)	0.69–0.73 (0.72 ± 0.02)	0.66–0.76 (0.71 ± 0.03)	0.64–0.71 (0.67 ± 0.03)	0.59–0.68 (0.65 ± 0.03)	0.52–0.58 (0.55 ± 0.02)	–					
P. wilsonii	0.54–0.59 (0.56 ± 0.02)	0.43–0.55 (0.49 ± 0.05)	0.56–0.59 (0.58)	0.59–0.62 (0.61 ± 0.01)	0.50–0.54 (0.52 ± 0.02)	0.59–0.68 (0.64 ± 0.03)	0.46–0.55 (0.50 ± 0.02)	0.43–0.52 (0.49 ± 0.03)	0.45–0.54 (0.49 ± 0.02)	0.58	–				
P. tristis	0.67–0.71 (0.69 ± 0.01)	0.52–0.64 (0.58 ± 0.04)	0.70–0.72 (0.71)	0.69–0.71 (0.70 ± 0.01)	0.65–0.69 (0.67 ± 0.02)	0.80–0.87 (0.84 ± 0.03)	0.62–0.68 (0.64 ± 0.02)	0.58–0.68 (0.65 ± 0.03)	0.60–0.67 (0.63 ± 0.02)	0.69	0.66	–			
P. berolinensis	0.57–0.73 (0.67 ± 0.05)	0.55–0.74 (0.62 ± 0.05)	0.63–0.68 (0.66 ± 0.02)	0.55–0.63 (0.59 ± 0.03)	0.60–0.68 (0.63 ± 0.02)	0.57–0.69 (0.64 ± 0.03)	0.48–0.55 (0.52 ± 0.02)	0.67–0.78 (0.72 ± 0.03)	0.73–0.85 (0.79 ± 0.02)	0.61–0.65 (0.63 ± 0.02)	0.45–0.51 (0.48 ± 0.03)	0.59–0.64 (0.61 ± 0.03)	0.84–0.94 (0.88 ± 0.05)		
P. canescens	0.34–0.40 (0.37 ± 0.02)	0.27–0.46 (0.38 ± 0.04)	0.33–0.44 (0.40 ± 0.04)	0.31–0.41 (0.36 ± 0.03)	0.34–0.49 (0.42 ± 0.04)	0.37–0.53 (0.44 ± 0.04)	0.28–0.41 (0.34 ± 0.03)	0.27–0.41 (0.35 ± 0.03)	0.24–0.47 (0.34 ± 0.04)	0.38–0.44 (0.42 ± 0.02)	0.40–0.51 (0.46 ± 0.04)	0.39–0.46 (043 ± 0.03)	0.34–0.41 (0.37 ± 0.02)	0.73–0.94 (0.85 ± 0.07)	
P. mexicana	0.13–0.15 (0.14 ± 0.01)	0.14–0.23 (0.18 ± 0.03)	0.09	0.11–0.14 (0.11 ± 0.02)	0.16–0.18 (0.16 ± 0.01)	0.12–0.19 (0.17 ± 0.02)	0.13–0.18 (0.15 ± 0.01)	0.15–0.20 (0.17 ± 0.02)	0.15–0.22 (0.18 ± 0.02)	0.14	0.12	0.10	0.21–0.22 (0.22 ± 0.01)	0.08–0.14 (0.10 ± 0.03)	–
Salix	0.23–0.31 (0.26 ± 0.03)	0.20–0.34 (0.29 ± 0.05)	0.24–0.30 (0.27 ± 0.03)	0.27–0.36 (0.32 ± 0.03)	0.25–0.43 (0.35 ± 0.06)	0.24–0.38 (0.30 ± 0.03)	0.26–0.42 (0.34 ± 0.04)	0.22–0.40 (0.32 ± 0.06)	0.20–0.41 (0.30 ± 0.05)	0.28–0.36 (0.32 ± 0.04)	0.24–0.34 (0.30 ± 0.05)	0.29–0.37 (0.32 ± 0.04)	0.23–0.33 (0.28 ± 0.04)	0.24–0.38 (0.30 ± 0.05)	0.13–0.16 (0.15 ± 0.02)

The number of accessions analyzed per species is indicated between *parentheses* in the heading

Table 3-3. Overview of traits introduced into poplar *via* genetic engineering (Leple et al., 2000)

Species/hybrid	Methods	Transgenes[a]	Characteristics	Reference
Resistance to herbicides				
P. alba × *P grandidentata*	Fillatti et al. (1987)	*aroA*	Glyphosate resistance	Fillatti et al. (1987)
P. tremula × *P. alba*	De Block (1990)	*bar*	Basta resistance	De Block (1990)
P. trichocarpa × *P deltoides*	De Block (1990)	*bar*	Basta resistance	De Block (1990)
P. tremula × *P. alba*	Devillard (1992)	*bar*	Basta resistance	Devillard (1992)
P. tremula × *P. alba*	Brasileiro et al. (1991) Leplé et al. (1992)	*crs1-1*	Chlorsulfuron resistance	Brasileiro et al. (1992)
P. tremula × *P. alba*	Chupeau et al. (1994)	*crs1-1*	Chlorsulfuron resistance	Chupeau et al. (1994)
P. tremula × *P. alba*	Chupeau et al. (1994)	*bar*	Basta resistance	Chupeau et al. (1994)
P. alba × *P grandidentata*	Fillatti et al. (1987)	*aroA*	Glyphosate resistance	Donahue et al. (1994)
Resistance to insects				
P. alba × *P grandidentata*	McCown et al. (1991)	*cryIA(a)*	*Malacosoma disstria* (L)[b] *Lymantria dispar* (L)	McCown et al. (1991)
P. nigra	Tian et al. (1993)	*cryIA(c)*	*Lymantria dispar* (L) *Apochemia cinerarius* (L)	Wang et al. (1996)
P. tremula × *P. tremuloides*	Leplé et al. (1992)	*cryIIIA*	*Chrysomela tremulae* (C)	Cornu et al. (1996)
P. tremula × *P. tremuloides*	Brasileiro et al. (1991) Leplé et al. (1992)	*ocI*	*Chrysomela tremulae* (C)	Leplé et al. (1995)
P. alba × *P. grandidentata*	Klopfenstein et al. (1991)	*pinII*	*Lymantria dispar* (L)	Hcuchelin et al. (1997)
Flower development				
P. tremuloides	Nilsson et al. (1992)	*leafy*	Precocious flowering	Weigel and Nilsson (1995)
Alteration of metabolism				
P. tremula × *P. alba*	Leplé et al. (1992)	*ipt*	Cytokinin content	Von Schwartzenberg et al. (1994)
P. tremula × *P. alba*	Nilsson et al. (1992)	*iaaM, iaaH*	Hormone metabolism	Tuominen et al. (1995)
P. tremula × *P. tremuloides*	Nilsson et al. (1992)	*rolC*	Hormone metabolism	Nilsson et al. (1996)
P. tremula × *P. tremuloides*	Fladung et al. (1996)	*rolC*	Hormone metabolism	Ahuja and Fladung (1996)
P. tremula × *P. alba*	Leplé et al. (1992)	*gor*	Glutathione metabolism	Foyer et al. (1995)
P. tremula × *P. alba*	Leplé et al. (1992)	*gshII*	Glutathione metabolism	Foyer et al. (1995); Strohm et al. (1995); Arisi et al. (1997)
P. tremula × *P. alba*	Leplé et al. (1992)	*gshI*	Glutathione metabolism	Noctor et al. (1996) Arisi et al. (1997)
P. tremula × *P. alba*	Leplé et al. (1992)	AS *comt*	Lignin composition	Van Doorsselaere et al. (1995)
P. tremula × *P. alba*	Leplé et al. (1992)	AS *cad*	Lignin extractability	Baucher et al. (1996a)
Promoter studies				
P. tremula × *P. grandidentata*	Klopfenstein et al. (1991)	p*pin2/cat*	Wound-induced expression	Klopfenstein et al. (1991)
P. tremula × *P. alba*	Leplé et al. (1992)	p*cad/gus*	Xylem-specific expression	Feuillet et al. (1995)
P. tremula × *P. tremuloides*	Nilsson et al. (1992)	p*rolC/gus*	Seasonal-specific expression	Nilsson et al. (1996)
P. tremula × *P. alba*	Leplé et al. (1992)	p-SAM/gus	Tissue-specific expression	Mijnsbrugge et al. (1996)
P. tremula × *P. tremuloides*	Nilsson et al. (1992)	p35S/*gus*	Constitutive expression	Nilsson et al. (1996)
Transposable elements				
P. tremula × *P. tremuloides*	Fladung et al. (1996)	p35S/Ac/*rolC* p*rbcs*/Ac/*rolC*	Phenotype modification	Ahuja and Fladung (1996)

* ***aroA***: mutant EPSP synthase (glyphosate resistance);
bar: phosphinotricin acetyl transferase (phosphinotricin resistance);
cad: cinn3myllilcohol dchydrogenllse;
cat: ehloramphenieal acetyl transferase; ***comt***: caffeic acid *O*-methyl transferase; ***crs1-1***: mutant actetolactate synthase (chlorsulfuron resistance);
cry*IA(c)*, cry*IA(a)*, cry*IIIA*: *BacilluJ thuringiensis* **δ**-endotoxins genes;
gshl: **γ**-glutamylcysteine synthetase;
gshIl: glutathione synthetase; *gor*: glutathione reductasc;
gus: **β**-glueuronidase;
ipt: isopenteny transferase;
iaaH: indole-3-aectamide hydrolase;
iaaM: tryptophan-2-mono-oxygenase;
luxF2: lucifcrase; *ocl*: cysteine proteinase inhibitor from rice (oryzacystatin);
p: promoter;
pinll: potato protease inhibitor II.

* L: Lepidoptera; C: Coleoptera.

Appendix IV

Table 4. Major policy measures related to biotechnology in China since the early 1980s (Huang & Wang, 2002).

Key Breakthrough Science & Technology Projects	Started in 1982 by SDPC. Updated every five years. One of major components of these projects is biotechnology R&D.
Patent system	Patent law promulgated 1985. A total of 1,599 applications on genetic engineering for invention patents were filed between 1985 and 1999.
National Biotechnology Development Policy Outline	Prepared by scientists and officials led by MOST, SDPC, and others in 1985. Formally issued by the State Council in 1988. The Outline defined the research priorities, development plan and measures to achieve targets.
National Key Laboratories (NKLs) on Biotechnology	Started in 1985 under MOST. Thirty National Key Laboratories in biotechnology (15 on agriculture or agriculture related) have been established. NKLs are open laboratories, inviting both domestic and international visiting fellows.
The Climbing Program	A National Program for Key Basic Research Projects, including biotechnology program, initiated in the early 1980s.
High Technology Research and Development Plan (863 Plan)	Approved in March 1986 with 10 billion RMB for 15 years to promote high-technology R&D in China. Biotechnology is one of seven supporting areas, with a total budget of about 1.5 billion RMB from 1986-2000.
Natural Science Foundation of China	Established in 1986 to support basic science research. Life science and agronomy are two support areas related to agrobiotechnology.
Biosafety regulations	MOST issued the Biosafety Regulations on Genetic Engineering in July of 1993, which include the biosafety grading and safety assessment, application and approval procedure, safety control measures, and legal regulations.
Agricultural biosafety regulations	MOA issued the Safety Administration, Implementation, and Regulations on Agricultural Biological Genetic Engineering in July 1996.
973 Plan	Initiated in March 1997 to support basic science and technology research. Life science is one of the key supporting areas.
Agricultural GMO Biosafety Committee	Ministry-level Agri GMO Biosafety Committee was set up in MOA in 1997. The Committee was updated in 2002 to national level with its office in MOA.
Special Foundation for Transgenic Plant Research and Commercialization	A five-year program launched in 1999 by MOST to promote the research and commercialization of transgenic plants in China. The total budget of this program in the first five years is 500 million RMB.
Key Science Engineering Program	Started in the late 1990s under MOST and SDPC to promote basic research, including biotechnology program. The first project on biotech (crop germplasm and quality improvement) was funded in 2000 with 120 million RMB.
Foundation for high-tech commercialization	A special program supported by the SDPC to promote the application and commercialization of technologies, started from 1998.
Seed Regulation and Law	Regulation on the Protection of New Varieties of Plants was issued in 1999. The first Seed Law was issued in 2000.
Updated and amended agricultural biosafety regulations	1996 MOA's biosafety regulation was amended and issued by the State Council in May 2001. Three regulations on the biosafety management, trade, and labeling of GM farm products were issued by MOA to take effect after March 20, 2002.
Foreign investment in GMOs	In April 2002, the SDPC, State Economic and Trade Commission, and MOTEC jointly issued a Guideline List of Foreign Investment, which puts GMO as a prohibited area for foreign investment

Appendix V

Table 5. All *lepisoptera* species feeding on *Populus euphratica* and their distribution (Robinson et al., 2010).

Lepidoptera Family	Lepidoptera Name	Hostplant Family	Hostplant Name	Country
Gelechiidae	*Istrianis squamodorella*	Salicaceae	*Populus euphratica*	Iraq
Gelechiidae	*Istrianis squamodorella*	Salicaceae	*Populus euphratica*	Palaearctic
Gracillariidae	*Phyllonorycter pruinosella*	Salicaceae	*Populus euphratica*	Palaearctic
Noctuidae	*Helicoverpa armigera*	Salicaceae	*Populus euphratica*	India
Noctuidae	*Helicoverpa armigera*	Salicaceae	*Populus euphratica*	India
Sesiidae	*Synanthedon ommatiaeformis*	Salicaceae	*Populus euphratica*	India
Sesiidae	*Synanthedon ommatiaeformis*	Salicaceae	*Populus euphratica*	Oriental
Tortricidae	*Eucosma hapalosarca*	Salicaceae	*Populus euphratica*	India
Tortricidae	*Eucosma hapalosarca*	Salicaceae	*Populus euphratica*	Iran
Tortricidae	*Eucosma hapalosarca*	Salicaceae	*Populus euphratica*	Iraq
Tortricidae	*Eucosma hapalosarca*	Salicaceae	*Populus euphratica*	Palaearctic
Tortricidae	*Eucosma xerophloea*	Salicaceae	*Populus euphratica*	India
Tortricidae	*Eucosma xerophloea*	Salicaceae	*Populus euphratica*	Oriental
Tortricidae	*Gypsonoma riparia*	Salicaceae	*Populus euphratica*	India
Tortricidae	*Gypsonoma riparia*	Salicaceae	*Populus euphratica*	Oriental
Tortricidae	*Gypsonoma riparia*	Salicaceae	*Populus euphratica*	Oriental
Tortricidae	*Gypsonoma riparia*	Salicaceae	*Populus euphratica*	Pakistan

BIBLIOGRAPHY

Abril, N., Gion, J.-M., Kerner, R., Müller-Starck, G., Cerrillo, R. M. N., Plomion, C., & Jorrin-Novo, J. V. (2011). Proteomics research on forest trees, the most recalcitrant and orphan plant species. Phytochemistry, 72(10), 1219-1242. doi:10.1016/j.phytochem.2011.01.005

Acker, V.R., Storme, V., Goeminne, G., Ivens, B., Custers, R., Aerts, D., & Boerjan, W. (2011). Science, society and biosafety of a field trial with transgenic biofuel poplars. BMC Proceedings, 5(Suppl 7), I23. doi:10.1186/1753-6561-5-S7-I23

Ahuja, M. R. (2009). Transgene stability and dispersal in forest trees. Trees, 23, 1125–1135. doi:10.1007/s00468-009-0362-8

Ahuja, M. R. (2011). Fate of transgenes in the forest tree genome.Tree Genetics & Genomes,7(2), 221-230. doi:10.1007/s11295-010-0339-1

Anon. (2008). Safety and nutritional assessment of GM plants and derived food and feed: The role of animal feeding trials, Food and Chemical Toxicology, 46, S2-S70. doi:10.1016/j.fct.2008.02.008

Antignac, E., Nohynek, G., Re, T., Clouzeau, J., & Toutain, H. (2011). Safety of botanical ingredients in personal care products/cosmetics. Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association. doi:10.1016/j.fct.2010.11.022

Aranda, I., Forner, A., Cuesta, B., & Valladares, F. (2012). Species-specific water use by forest tree species: From the tree to the stand. Agricultural Water Management, 114, 67-77. doi:10.1016/j.agwat.2012.06.024

Arimura, G.-I., Huber, D., & Bohlmann, J. (2004). Forest tent caterpillars (Malacosoma disstria) induce local and systemic diurnal emissions of terpenoid volatiles in hybrid poplar (Populus trichocarpa x deltoides): cDNA cloning, functional characterization, and patterns of gene expression of (-)-germacrene D synthase, PtdTPS1. The Plant journal: for cell and molecular biology. Retrieved from http://onlinelibrary.wiley.com/resolve/openurl?genre=article&sid=nlm:pubmed&issn=0960-7412&date=2004&volume=37&issue=4&spage=603

Auld, G., & Bull, G. (2003). The institutional design of forest certification standards initiatives and its influence on the role of science: the case of forest genetic resources. Journal of environmental management. doi:10.1016/S0301-4797(03)00118-X

Barriere, Y., Thomas, J., & Denoue, D. (2008). QTL mapping for lignin content, lignin monomeric composition, p-hydroxycinnamate content, and cell wall digestibility in the maize recombinant inbred line progeny F838 x F286. Plant Science, 175(4), 585-595. doi:10.1016/j.plantsci.2008.06.009

Barritt, J., Brenner, C., Willadsen, S., & Cohen, J. (2000). Spontaneous and artificial changes in human ooplasmic mitochondria. Human reproduction (Oxford, England). doi:10.1093/humrep/15.suppl_2.207

Beringer, J. (1999). Keeping watch over genetically modified crops and foods. The Lancet, 353(9153), 605-606. doi:10.1016/S0140-6736(99)00041-0

Bhalerao, R., Nilsson, O., & Sandberg, G. (2003). Out of the woods: forest biotechnology enters the genomic era.Current Opinion in Biotechnology, 14(2), 206-213. doi:10.1016/S0958-1669(03)00029-6

Bi, Y., Qin, M., Wang, J., Shi, X. & Zhuge, Q. (2009). Cloning of SRK2C genes and its genetic transformation in poplar. Molecular Plant Breeding 7(3), 513-518 (in Chinese with English abstract)

Boerjan, W. (2005). Biotechnology and the domestication of forest trees. Current opinion in biotechnology, 16(2), 159-66. doi:10.1016/j.copbio.2005.03.003

Borevitz, J. O., & Chory, J. (2004). Genomics tools for QTL analysis and gene discovery. Current Opinion in Plant Biology, 7(2), 132-136. doi:10.1016/j.pbi.2004.01.011

Borzan, Ž. &Schlarbaum, S.E. (2004). GENETICS AND GENETIC RESOURCES | Cytogenetics of Forest Tree Species, Encyclopedia of Forest Sciences, Burley, J. (eds), Elsevier, Oxford, 2004, Pages 204-214, doi:10.1016/B0-12-145160-7/00077-6. (http://www.sciencedirect.com/science/article/pii/B0121451607000776)

Braatne, J.H., Rood, S.B. & Heilman, P.E. (1996). Life history, ecology, and conservation of riparian cottonwoods in North America. Biology of Populus and its implications for management and conservation. Stettler, R.F., Bradshaw, H.D. Jr., Heilman, P.E., Hinckley, T.M. (eds). Ottawa: NRC Research Press. 57–85.

Bradshaw, H. D., Ceulemans, R., Davis, J., & Stettler, R. (2000). Emerging Model Systems in Plant Biology: Poplar (Populus) as A Model Forest Tree. Journal of Plant Growth Regulation, 19(3), 306-313. doi:10.1007/s003440000030

Brunner, A. M., Li, J., DiFazio, S. P., Shevchenko, O., Montgomery, B. E., Mohamed, R., & Strauss, S. H. (2007).

Genetic containment of forest plantations. Tree Genetics & Genomes, 3(2), 75-100. doi:10.1007/s11295-006-0067-8

Brunner, A., Busov, V., & Strauss, S. (2004). Poplar genome sequence: functional genomics in an ecologically dominant plant species. Trends in plant science. doi:10.1016/j.tplants.2003.11.006

Brush, S. (1992). Farmer's rights and genetic conservation in traditional farming systems.World Development, 20(11), 1617-1630. Retrieved from http://www.sciencedirect.com/science/article/pii/0305750X9290018Q

Burczyk, J., DiFazio, S.P. & Adams, W.T. (2004). Gene flow in forest trees: how far do genes really travel? Forest Genetics 11(3-4), 179-192.

Burns, R.M. & Honkala, B.H. (1990). Silvics of North America. Vol. 2, hard-woods. U.S. Forest Service Agriculture Handbook No. 654. (technical coordinators)

Cashore, B., Auld, G., & Newsom, D. (2003). Forest certification (eco-labeling) programs and their policy-making authority: explaining divergence among North American and European case studies. Forest Policy and Economics 5, 225–247. Retrieved from http://www.sciencedirect.com/science/article/pii/S1389934102000606

Cervera, M. T., Storme, V., Soto, A., Ivens, B., Montagu, M., Rajora, O. P., & Boerjan, W. (2005). Intraspecific and interspecific genetic and phylogenetic relationships in the genus Populus based on AFLP markers. Theoretical and Applied Genetics, 111(7), 1440-1456. doi:10.1007/s00122-005-0076-2

Cervera, M.T., Sewell, M.M., Faivre-Rampant, P., Storme, V. & Boerjan, W. (2004). Genome mapping in Populus. Molecular Genetics and Breeding of Forest Trees. Kumar, S. & Fladung,, M. (eds). Food Product Press, New York, 387–410. doi:10.1093/treephys/tpr090

Chao, N., Liu, J. & Gong. G.-T. (2009). On the classification and distribution of the subfamily Populoideae (Salicaceae). Journal of Wuhan botanical Research, 27(1), 23-40 (in Chinese with English abstract)

Chen, C. & Zhan, J. (2007). 国外转基因标识政策的比较及其对中国转基因标识政策制定的思考. World Agriculture 343, 21-24 (in Chinese)

Chen, K., Xu, Z., Yan, L. & Fang, X. (2009). Primary rish assessment of transgenes escape of transgenic peanut in field. Chinese Jurnal of Oil Crop Sciences 31(3), 383-385 (in Chinese with English abstract)

Cheng, Q., Pan, H., Xu, L., Zhuge, Q., Wang, M. & Huang, M. (2009). The poplar genome project and progress in poplar molecular biology studies. Journal of Nanjing Forestry University (Natural Sciences Edition) 33(1), 131-135 (in Chinese with English abstract)

Clarke, G.M. (1995). Relationships Between Developmental Stability and Fitness: Application for Conservation Biology. Conservation Biology, 9(1), 18-24.

Clarke, G.M., Brand, G.W., & Whitten, M.J. (1986). Fluctuating asymmetry: a technique for measuring developmental stress caused by inbreeding. Biology Science, 39, 145-153

Cockburn, A. (2002). Assuring the safety of genetically modified (GM) foods: the importance of an holistic, integrative approach. Journal of biotechnology. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/12126808

Cotton, S., & Wedekind, C. (2007). Control of introduced species using Trojan sex chromosomes.Trends in ecology & evolution. doi:10.1016/j.tree.2007.06.010

Daniels, J. D. (1984). Role of tree improvement in intensive forest management. Forest Ecology and Management, 8(3-4), 161-195. doi:10.1016/0378-1127(84)90052-5

de Koning, D.-J., Carlborg, O., & Haley, C. S. (2005). The genetic dissection of immune response using gene-expression studies and genome mapping. Veterinary Immunology and Immunopathology, 105(3-4), 343-352. doi:10.1016/j.vetimm.2005.02.007

Dinus, R. (2001). Genetic improvement of poplar feedstock quality for ethanol production. Retrieved from http://link.springer.com/article/10.1385/ABAB%3A91-93%3A1-9%3A23

Domingo, J., & Giné Bordonaba, J. (2011). A literature review on the safety assessment of genetically modified plants. Environment international. doi:10.1016/j.envint.2011.01.003

Dona, A. & Arvanitoyannis, I.S. (2009). Health risks of genetically modified foods. Critical Reviews in Food Science and Nutrition, 49(2). doi:10.1080/10408390701855993

Douglas, C., & DiFazio, S. (2010). The Populus Genome and Comparative Genomics. Genetics and Genomics of Populus. doi:10.1007/978-1-4419-1541-2_4. Retrieved from http://link.springer.com/chapter/10.1007/978-1-4419-1541-2_4

Doull, J., Gaylor, D., Greim, H., Lovell, D., Lynch, B., & Munro, I. (2007). Report of an Expert Panel on the reanalysis by of a 90-day study conducted by Monsanto in support of the safety of a genetically modified corn variety (MON 863). Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association. doi:10.1016/j.fct.2007.08.033

Du, L. & Han, R. (2011). V Series transgenic Salix alba var tristis and non - transgenic preliminary analysis of poten-

tial head. Northen Environment 23(3), 85-87 (in Chinese with English abstract)

Du. Z. (2010). Study on ecological risk of genetically modified organism technology and countermeasures. Journal of Anhui Agriculural Sciences 38(19), 9961-9964 (in Chinese with English abstract)

Dwivedi, S.L., Crouch, J.H., Mackill, D.J., Xu, Y., Blair, M.W., Ragot, M., Upadhyaya, H.D., Ortiz. R. (2007). The Molecularization of Public Sector Crop Breeding: Progress, Problems, and Prospects. Advances in Agronomy, Sparks, D.L. (eds). Academic Press. 95,163-318. doi:10.1016/S0065-2113(07)95003-8. (http://www.sciencedirect.com/science/article/pii/S0065211307950038)

El-Kassaby, Y. & Prado. J.A. (2010). Forests and genetically modified trees. FAO, Rome.

Ellis, H.M. & Horvitz, H.R. (1986). Genetic control of programmed cell death in the nematode C. elegans. Cell, 44, 817-829

Ewald, D. & Han, Y. (2000). Field trials with transgenic poplar in China. Workshop "Release of transgenic trees – present achievements, problems, future prospects", Berlin, 52–57

Ewald, D., Hu, J. & Yang, M. (2006). Transgenic Forest Trees in China. Tree Transgenesis: Recent Development. Fladung, M. & Ewald, D. (eds). Springer - Verlag Berlin Heidelberg. doi:10.1007/3-540-32199-3_2

Eyzaguirre, P. B., & Dennis, E. M. (2007). The Impacts of Collective Action and Property Rights on Plant Genetic Resources. World Development. doi:10.1016/j.worlddev.2006.05.017

Fan, L. (2001). GIS for plant transgene escape: a proposal. Biotechonlogy information 2001(3), 1-3 (in Chinese with English abstract)

Fan, L., Zhou, X., Hu, B., Shi, C. & Wu, J. (2001). Gene dispersal risk of transgenic plants. Chinese Journal of Applied Ecology 12(4), 630-632 (in Chinese with English abstract)

Fang, J-Y., Song, Y-C., Liu, H-Y. & Piao, S-L. (2002). Vegetation-climate relationship and its application in the division of vegetation zone in China. Acta Botanica Sinica, 44(9), 1105-1122

Finkeldey, R., Leinemann, L., & Gailing, O. (2010). Molecular genetic tools to infer the origin of forest plants and wood. Applied Microbiology and Biotechnology, 85(5), 1251-1258. doi:10.1007/s00253-009-2328-6

Fladung, M. (2006). Modification of cellulose in wood Tree Transgenesis: Recent Development. Fladung, M. & Ewald, D. (eds). Springer - Verlag Berlin Heidelberg.

Fladung, M., Nowitzki, O., Ziegenhagen, B., & Kumar, S. (2003). Vegetative and generative dispersal capacity of field released transgenic aspen trees. Trees - Structure and Function. 17, 412–416. doi:10.1007/s00468-003-0253-3

FOC. (1999). Populus. Flors of China, 4, 139-162. Accessed from http://www.efloras.org/florataxon.aspx?flora_id=2&taxon_id=126537 in Feb. 2012

Frankenhuyzen, K. van, & Beardmore, T. (2004). Current status and environmental impact of transgenic forest trees. Canadian Journal of Forest Research, 34, 1163-1180. doi:10.1139/X04-024

Frost, C., Mescher, M., Dervinis, C., Davis, J., Carlson, J., & De Moraes, C. (2008). Priming defense genes and metabolites in hybrid poplar by the green leaf volatile cis-3-hexenyl acetate. The New phytologist, 180. 722-734. doi:10.1111/j.1469-8137.2008.02599.x

Gailing, O., Vornam, B., Leinemann, L., & Finkeldey, R. (2009). Genetic and genomic approaches to assess adaptive genetic variation in plants: forest trees as a model.Physiologia Plantarum, 137(4), 509-519. doi:10.1111/j.1399-3054.2009.01263.x

Gallardo, F., Fu, J., Jing, Z. P., Kirby, E. G., & Canovas, F. M. (2003). Genetic modification of amino acid metabolism in woody plants. Plant Physiology and Biochemistry, 41(6-7), 587-594. doi:10.1016/S0981-9428(03)00081-0

Gaston, C., Globerman, S., & Vertinsky, I. (1995). Biotechnology in forestry: Technological and economic perspectives, 50, 79-92. Retrieved from http://www.sciencedirect.com/science/article/pii/004016259400084A

Gaudet, M., Jorge, V., Paolucci, I., Beritognolo, I., Scarascia-Mugnozza, G. & Sabatti, M. (2008). Genetic linkage maps of Populus nigra L. including AFLPs, SSRs, SNPs, and sex trait. Tree Genet. Genomes, 4, 25–36.

Gepts, P. (2002). A comparison between crop domestication, classical plant breeding, and genetic engineering. Crop Science. 42, 1780–1790. doi:10.2135/cropsci2002.1780

Geraldes, A., Pang, J., Thiessen, N., Cezard, T., Moore, R., Zhao, Y., Tam, A., et al. (2011). SNP discovery in black cottonwood (Populus trichocarpa) by population transcriptome resequencing. Molecular ecology resources, 11(1), 81-92. doi:10.1111/j.1755-0998.2010.02960.x

Ghazoul, J. (2004). ECOLOGY | Reproductive Ecology of Forest Trees. Encyclopedia of Forest Sciences, Burley, J. (eds). Elsevier, Oxford, 63-68, doi:10.1016/B0-12-145160-7/00020-X. (http://www.sciencedirect.com/science/article/pii/B012145160700020X)

Graham, J. H., Emlen, J. M., & Freeman, D. C. (1993). Developmental stability and its applications in ecotoxicology. Ecotoxicology, 2(3), 175-184. doi:10.1007/BF00116422

Groeneveld, C. N., Hakkert, B. C., Bos, P. M. J., & Heer, C. (2004). Extrapolation for Exposure Duration in Oral Toxicity: A Quantitative Analysis of Historical Toxicity Data. Human and Ecological Risk Assessment: An International Journal. doi:10.1080/10807030490484318

Groover, A. T. (2005). What genes make a tree a tree?Trends in Plant Science, 10(5), 210-214. doi:10.1016/j.tplants.2005.03.001

Grunewald, W., & Bury, J. (2013). Comment on "Long term toxicity of a Roundup herbicide and a Roundup-tolerant genetically modified maize" by Séralini et al. Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association. doi:10.1016/j.fct.2012.10.051

Gu, Z., Zhang, D. & Huang, Q. (2010). Transgenic modification on pulp plants by key genes regulating lignin biosythesis. Journal of Central South University of Forestry & Technology 30(3), 67-74 (in Chinese with English abstract)

Gupta, A., & Sankararamakrishnan, R. (2009). Genome-wide analysis of major intrinsic proteins in the tree plant Populus trichocarpa: Characterization of XIP subfamily of aquaporins from evolutionary perspective.BMC Plant Biology,9(1), 134. doi:10.1186/1471-2229-9-134

Hamrick, J. (2004). Response of forest trees to global environmental changes. Forest Ecology and Management. doi:10.1016/j.foreco.2004.05.023

Hamzeh, M. & Dayanandan, S. (2004). Phylogeny of populus (Salicaceae) based on nucleotide sequences of chloroplast trnT-trnF region and nuclear rDNA. American Journal of Botany 91(9), 1398-1408.

Harfouche, A., Meilan, R., & Altman, A. (2011). Tree genetic engineering and applications to sustainable forestry and biomass production. Trends in Biotechnology, 29(1), 9-17. doi:10.1016/j.tibtech.2010.09.003

Harfouche, A., Meilan, R., Kirst, M., Morgante, M., Boerjan, W., Sabatti, M., & Scarascia Mugnozza, G. (2012). Accelerating the domestication of forest trees in a changing world. Trends in Plant Science, 17(2), 64-72. doi:10.1016/j.tplants.2011.11.005

Hasebe, A. (1999). Assessment and management of field testing of transgenic crop plants in east asian countries. Methods for Risk Assessment of Transgenic Plants. III.Ecological risks and propspects of transgemc plants. Ammann, K., Jacot, Y., Simonsen, V., & Kjellsson G.(eds). 1999 Birkhauser Verlag Basel/Switzerland

Hehui, L., Xiaohua, S., & Bingyu, Z. (2011). Research Progress in Genetic Evaluation of Populus L. Germplasm Resources. CHINESE BULLETIN OF BOTANY. doi:10.3724/SP.J.1259.2011.00586

Ho, P., Vermeer, E.B. and Zhao, J.H. 2006. Biotech and food safety in China: consumers' acceptance or resistance? Development and Change, 37(1), 227-253. Retrieved from http://agbioforum.org/v7n4/v7n4a02-ho.htm

Houllier, F.,Novotny, J., Paivinen, R., Rosen, K., Scarascia-Mugnozza, G. & K.V. Teuffel. (2005). Future forest research strategy for a knowledge based forest cluster: an asset for a sustainable Europe. European Forest Institute Discussion Paper 11

Hu, J., Li, S., Lu, M., Li, J., Li, L., Sun, X. & Zhao, Z. (2007). Stability of insect-resistance of Bt transformed Populus nigra plantation and its effects on the natural enemies of insects. Forest Research 20(5), 656-659 (in Chinese with English abstract)

Hu, J., Yang, M. & Lu, M. (2010). Advances in biosafety studies on transgenic insect-resistant poplars in China. Biodiversity Science, 18(4), 336-345 (in Chinese with English abstract)

Hu, J., Zhang, Y., Lu, M., Zhang, J. & Zhang, S. (2004). Transgene stability of transgenic Populus nigra and its effects on soil microorganism. Scientia Silvae Genetica 40:105–109

Hu, X., & Li, B. (2002). Linking evolutionary quantitative genetics to the conservation of genetic resources in natural forest populations. Silvae genetica. Frankfurt am Main: JD Sauerlander, 1957-. Retrieved from http://allgemeineforstundjagdzeitung.com/fileadmin/content/dokument/archiv/silvaegenetica/51_2002/51-5-6-177.pdf

Huang, J. & Wang, Q. (2002). Agricultural biotechnology development and policy in China. AgBioForum, 5(4), 122-135

Irwin, R. & Jones, P.B.C. (2006). Biosafety of Transgenic Trees in the United States. Managing Forest Ecosystems. William, C.G. (eds). 245-261. doi:10.1007/1-4020-3869-0_14

Ishii, K. and Lu., M. (2008). Testing the possibility of horizontal transfer of introduced neomycin phosphotransferase(nptII) gene of transgenic Eucalyptus camaldulensis into soil bacteria. Forestry Studies in China, 10(2), 134-136. doi:10.1007/s11632-008-0017-7

Jackson, R. B., Schenk, H. J., Jobbagy, E. G., Canadell, J., Colello, G. D., Dickinson, R. E., & Sykes, M. T. (2000). Belowground consequences of vegetation change and their treatment in models. Ecological Applications,10(2), 470-483.

doi:10.1890/1051-0761(2000)010[0470:BCOVCA]2.0.CO;2

Jaffe, G. (2004). Regulating Transgenic Crops: A Comparative Analysis of Different Regulatory Processes.Transgenic Research, 13(1), 5-19. doi:10.1023/B:TRAG.0000017198.80801.fb

Jaiwal, P.K., Sahoo, L., Singh, N.D. & Singh, R.P. (2002). Sreategies to deal with the concern about marker genes in transgenic plants: some environment-friendly approaches. Current Science, 83(2), 128-137

Janssen, J. (1999). Property rights on genetic resources: economic issues. Global Environmental Change, 9, 313-321. Retrieved from http://www.sciencedirect.com/science/article/pii/S0959378099000254

Jansson, S., & Douglas, C. J. (2007). Populus: A Model System for Plant Biology. Annual Review of Plant Biology, 58(1), 435-458. doi:10.1146/annurev.arplant.58.032806.103956

Janz, D., Behnke, K., Schnitzler, J.-P., Kanawati, B., Schmitt-Kopplin, P., & Polle, A. (2010). Pathway analysis of the transcriptome and metabolome of salt sensitive and tolerant poplar species reveals evolutionary adaption of stress tolerance mechanisms. BMC Plant Biology, 10(1), 150. doi:10.1186/1471-2229-10-150

Jiang, W., Liu, J. & Li, C. (2011). Studay on community structure of arthropod in transgenic poplar with mixed cultivating. Journal of Shandong Agricultural University (Natural Science) 42(3), 383-387 (in Chinese with English abstract)

Jiang, W., Liu, J., Zhang, F. & Gao, B. (2009). Oppulation dynamic of target pests, non-target pests and major natural enemies in trandgenic hybrid Poplar 741. Journal of Shandong Agricultural University (Natural Science) 40(2), 195-199 (in Chinese with English abstract)

Jin, Y. (2008). 园林景观设计. Liaoning Science and Technology Publishing House. ISBN: 9787538149654 (in Chinese)

Johnson, K., Raybould, A., Hudson, M., & Poppy, G. (2007). How does scientific risk assessment of GM crops fit within the wider risk analysis? Trends in plant science. doi:10.1016/j.tplants.2006.11.004

Jones, J. S. (1987). An asymmetrical view of fitness. Nature, 325, 298-299. doi:10.1038/325298a0

Kikuchi, A., Yu, X., Shimazaki, T., Kawaoka, A., Ebinuma, H., & Watanabe, K. N. (2009). Allelopathy assessments for the environmental biosafety of the salt-tolerant transgenic Eucalyptus camaldulensis, genotypes codA12-5B, codA 12-5C, and codA 20C. Journal of Wood Science. doi:10.1007/s10086-008-1007-z

Kingsbury, N. (2009). Hybrid: the history & science of plant breeding. The University of Chicago Press, Chicago and London. ISBN-13: 978-0-226-43704-0

Knox, R. B., Willing, R. R., & Ashford, A. E. (1972). Role of Pollen-Wall Proteins as Recognition Substances in Interspecific Incompatibility in Poplars. Nature, 237, 382-383. doi:10.1038/237381a0

Knox, R. B., Willing, R. R., & Pryor, L.D. (1972). Interspecific hybridization in poplars using recognition pollen. Silvae Genetica, 21, 3-4.

Knudsen, I., & Poulsen, M. (2007). Comparative safety testing of genetically modified foods in a 90-day rat feeding study design allowing the distinction between primary and secondary effects of the new genetic event. Regulatory toxicology and pharmacology: RTP. doi:10.1016/j.yrtph.2007.07.003

Knudsen, I., Søborg, I., Eriksen, F., Pilegaard, K., & Pedersen, J. (2008). Risk management and risk assessment of novel plant foods: concepts and principles.Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association. doi:10.1016/j.fct.2008.01.022

Kooten, G. C. van, Nelson, H. W., & Vertinsky, I. (2005). Certification of sustainable forest management practices: a global perspective on why countries certify.Forest Policy and Economics,7(6), 857-867. doi:10.1016/j.forpol.2004.04.003

Koskela, J., Lefevre, F., Schueler, S., Kraigher, H., Olrik, D. C., Hubert, J., & Ditlevsen, B. (2013). Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. Biological Conservation, 157, 39-49. doi:10.1016/j.biocon.2012.07.023

Koski,V. (2004) GENETICS AND GENETIC RESOURCES | Genetic Systems of Forest Trees, Encyclopedia of Forest Sciences, Burley, J. (eds), Elsevier, Oxford, 2004, Pages 175-182, doi:10.1016/B0-12-145160-7/00075-2. (http://www.sciencedirect.com/science/article/pii/B0121451607000752)

Kozlov, M.V., Wilsey, B.J., Koricheva, J. & Haukioja, E. (1996). Fluctuating asymmetry of birch leaves increases under pollution impact. Journal of Applied Ecology, 33, 1489-1495

Kuiper, H. A., Noteborn, H. P., & Peijnenburg, A. A. (1999). Adequacy of methods for testing the safety of genetically modified foods. The Lancet, 354(9187), 1315-1316. doi:10.1016/S0140-6736(99)00341-4

Kuparinen, A., Savolainen, O., & Schurr, F. M. (2010). Increased mortality can promote evolutionary adaptation of forest trees to climate change. Forest Ecology and Management, 259(5), 1003-1008. doi:10.1016/j.foreco.2009.12.006

Lefèvre, F. (2004). Human impacts on forest genetic resources in the temperate zone: an updated review.Forest Ecology and Management, 197(1-3), 257-271. doi:10.1016/j.foreco.2004.05.017

Leplé, J.C., Pilate, G., & Jouanin, L. (2000). Transgenic poplar trees (Populus species). Transgenic trees: biotechnology in agriculture and forestry 44, Bajaj, Y.P.S., (eds). Springer-Verlag, Berlin. 221–244.

Li, S. (2011). Bio-safety of transgenic papaya resistant against Papaya ring spot virus. Plant Protection 37(6), 59-63 (in Chinese with English abstract)

Li, X. (unpublished). Insect bioassay and tentative analysis of effevts on soil microbial flora of transgenic Populus eramericana cv 'nanlin 895' with Bt or CpTI gene. Master Dissertation, Nanjing Forestry University, 2008.

Li, Y., Xu, Q., Liu, J., Yang, X., & Nakagawa, T. (2007). A transfer-function model developed from an extensive surface-pollen data set in northern China and its potential for palaeoclimate reconstructions. The Holocene, 17(7), 897-905. doi:10.1177/0959683607082404

Liu, H., Wu, X.Q., Ren, J.H. & Ye, J.R. (2011). Isolation and identification of phosphobacteria in poplar rhizosphere from different regions of China. Pedosphere, 2l(1),90-97.

Liu, H., Zhang, C., Zheng, Y., Jia, Z. & Ma, M. (2010). Biological effects of aqueous extract from fresh leaves of insect-resistant transgenic populus nigra. Journal of Northeast Forestry University 38(12), 27-30 (in Chinese with English abstract)

Liu, H., Zhou, J., Zhang, C., Feng, J. & Zheng, Y. (2011). A multiplex polymerase chain reaction method for rapid detection of foreign genes in insect-resistant transgenic Populus nigra. Forest Research 24(3), 334-339 (in Chinese with English abstract)

Liu, J., Gao, B., Zhang, F. & Jiang, W. (2009). Life table of population of target insect in the stands of transgenic hybrid Poplar 741. Scientia Silvae Sinicae 45(5), 102-108 (in Chinese with English abstract)

Liu, K. & Wu, L.(2010). 转基因农产品推广中的论理原则探讨. Science and Technology Management Research 9, 237-240 (in Chinese)

Liu, S., Tan, J., Sun, Z., Shen, J. & Zhang, H. (2011). 转基因成份在肉鸡体内的代谢残留及对生化指标、器官发育的影响. Feed Industry. 32(9), 19-25 (in Chinese)

Lu, B. (2008). Transgene escape from GM crops and potential biosafety consequences: an environmental perspective. Retrieved from http://www.icgeb.org/~bsafesrv/pdffiles/Bao-Rong.pdf

Lu, M.-Z., & Hu, J.-J. (2011). A brief overview of field testing and commercial application of transgenic trees in China.BMC Proceedings, 5(7), O63. doi:10.1186/1753-6561-5-S7-O63

Lu, M., Han, Y. & Du, S. (1999). Risk assessment and safety management of the genetic engineered trees. Forest Research 12(3), 17-24 (in Chinese with English abstract)

Lu, M.Z. & Hu, J.J. (2006). Current status of research and development of transgenic poplars in China. Forestry Science and Technology Development, 20(6), 1–4. (in Chinese)

Luan, H., Su, X. & Zhang, B. (2011). Research progress in genetic evaluation of Populus L. germplasm resources. Chinese Bulletin of Botany 45(5), 586-595 (in Chinese with English abstract)

Luo, K., Duan, H., Zhao, D., Zheng, X., Deng, W., Chen, Y., Stewart, C., et al. (2007). "GM-gene-deletor": fused loxP-FRT recognition sequences dramatically improve the efficiency of FLP or CRE recombinase on transgene excision from pollen and seed of tobacco plants. Plant biotechnology journal, 5, 263-274. doi:10.1111/j.1467-7652.2006.00237.x

Madsen, K. & Sandøe, P. (2008). The Bioethics and Biosafety of Gene Transfer. Agrobacterium: From Biology to Biotechnology, Tzfira, T. & Citovsky, V. (eds). Springer New York. doi:10.1007/978-0-387-72290-0_19

Major, I. T., & Constabel, C. P. (2006). Molecular analysis of poplar defense against herbivory: comparison of wound- and insect elicitor-induced gene expression. New Phytologist, 172(4), 617-635. doi:10.1111/j.1469-8137.2006.01877.x

Markussen, T., Pakull, B. & Fladung, M. (2007). Positioning of sex-correlated markers for Populus in a AFLP- and SSR-marker based genetic map of Populus tremula × tremuloides. Silvae Genet, 56,180 –184.

Marmiroli, M., Pietrini, F., Maestri, E., Zacchini, M., Marmiroli, N., & Massacci, A. (2011). Growth, physiological and molecular traits in Salicaceae trees investigated for phytoremediation of heavy metals and organics. Tree Physiology, 31(12), 1319-1334. doi:10.1093/treephys/tpr090

Martin-Trillo, M. & Martinez-Zapater, J.M. (2002). Growing up fast: manipulating the generation time of trees. Current Opinion in Biotechnology, Elsevier Science Ltd, 13, 151–155

Matyssek, R., Sandermann, H., Wieser, G., Booker, F., Cieslik, S., Musselman, R., & Ernst, D. (2008). The challenge of making ozone risk assessment for forest trees more mechanistic. Environmental Pollution, 156(3), 567-582. doi:10.1016/j.envpol.2008.04.017

Megalos, M. (2006). Private forests and transgenic forest trees. Managing Forest Ecosystems. William, C.G. (eds). 209-225. Retrieved from http://link.springer.com/content/pdf/10.1007/1-4020-3869-0_12

Meilan, R. (2004). GENETICS AND GENETIC RESOURCES | Molecular Biology of Forest Trees, Encyclopedia of Forest Sciences, Burley, J.(eds), Elsevier, Oxford, 2004, Pages 229-236, doi:10.1016/B0-12-145160-7/00076-4. (http://www.sciencedirect.com/science/article/pii/B0121451607000764)

Meng, X., Pan, H., Zhang, B., Wang, S. & Huang, M. (2009). Molecular biology applied in the improvement process of forest trees. Scientia Silvae Sinicae 45(1), 136-143 (in Chinese with English abstract)

Merkle, S. A., & Dean, J. F. (2000). Forest tree biotechnology. Current Opinion in Biotechnology, 11(3), 298-302. doi:10.1016/S0958-1669(00)00099-9

Metz, P., Stiekema, W., & Nap, J. (1998). A transgene-centered approach to the biosafety of transgenic phosphinothricin-tolerant plants. Molecular Breeding, 4, 335–341. Retrieved from http://link.springer.com/article/10.1023/A%3A1009695124173

Miranda, M., Ralph, S., Mellway, R., White, R., Heath, M., Bohlmann, J., & Constabel, C. (2007). The transcriptional response of hybrid poplar (Populus trichocarpa x P. deltoides) to infection by Melampsora medusae leaf rust involves induction of flavonoid pathway genes leading to the accumulation of proanthocyanidins. Molecular plant-microbe interactions: MPMI. doi:10.1094/MPMI-20-7-0816

Morse, S., Mannion, A. M., & Evans, C. (2012). Location, location, location: Presenting evidence for genetically modified crops. Applied Geography, 34, 274-280. doi:10.1016/j.apgeog.2011.08.015

National Poplar Commission of the PR of China. (1996). National Report on Activities Related to Poplar and Willow Cultivation (1991 – 1996). Document prepared for the XXth Session of the International Poplar Commission, Budapest, Hungary.

Nelson, C. D., & Johnsen, K. H. (2008). Genomic and physiological approaches to advancing forest tree improvement. Tree Physiology, 28(7), 1135-1143. doi:10.1093/treephys/28.7.1135

Nobs, B., Lamb, R. & Pythoud, F. (2003). The Cartagena Protocol on Biosafety of the Convention on Biological Diversity: overview and future development. Methods for Risk Assessment of Transgenic Plants, Ammann, K., Jacot, Y., & Braun, R. (eds). doi:10.1007/978-3-0348-8033-6_10

Noel, A., Levasseur, C., Le, V. Q., & Seguin, A. (2005). Enhanced resistance to fungal pathogens in forest trees by genetic transformation of black spruce and hybrid poplar with a Trichoderma harzianum endochitinase gene.Physiological and Molecular Plant Pathology, 67(2), 92-99. doi:10.1016/j.pmpp.2005.09.010

Novaes, E., Kirst, M., Chiang, V., Winter-Sederoff, H., & Sederoff, R. (2010). Lignin and Biomass: A Negative Correlation for Wood Formation and Lignin Content in Trees. PLANT PHYSIOLOGY, 154(2), 555-561. doi:10.1104/pp.110.161281

Paoletti, C., Flamm, E., Yan, W., Meek, S., Renckens, S., Fellous, M., & Kuiper, H. (2008). GMO risk assessment around the world: Some examples. Trends in Food Science & Technology. doi:10.1016/j.tifs.2008.07.007

Pautasso, M. (2009). Geographical genetics and the conservation of forest trees.Perspectives in Plant Ecology, Evolution and Systematics, 11(3), 157-189. doi:10.1016/j.ppees.2009.01.003

Peña, L. & Séguin, A. (2001). Recent advances in the genetic transformation of trees. Trends in Biotechnology, 19(12), 500-506. doi:10.1016/S0167-7799(01)01815-7

Peng, R., Zhang, X., Zhao, J., Ji, C., Zhao, D. & Hao, Z. (2009). 胡杨杂交语种研究初报. Journal of Liaoning Forestry Science & Technology, 2, 24-31. Retrived from: http://d.g.wanfangdata.com.cn/Periodical_lnlykj200902009.aspx (in Chinese)

Petry, M. & Wu, B. (2009). Agricultural biotechnology annual—China. Global Agricultural Information Network. USDA Foreign Agricultureal Service.

Pettifer, S., Thorne, D., McDermott, P., Marsh, J., Villeger, A., Kell, D. B., & Attwood, T. K. (2009). Visualising biological data: a semantic approach to tool and database integration.BMC Bioinformatics,10(6), S19. doi:10.1186/1471-2105-10-S6-S19

Philippe, R. N., Ralph, S. G., Klheim, C., Jancsik, S. I., & Bohlmann, J. (2009). Poplar defense against insects: genome analysis, full-length cDNA cloning, and transcriptome and protein analysis of the poplar Kunitz-type protease inhibitor family.New Phytologist,184(4), 865-884. doi:10.1111/j.1469-8137.2009.03028.x

Philippe, R. N., Ralph, S. G., Mansfield, S. D., & Bohlmann, J. (2010). Transcriptome profiles of hybrid poplar (Populus trichocarpa x deltoides) reveal rapid changes in undamaged, systemic sink leaves after simulated feeding

by forest tent caterpillar (Malacosoma disstria). New Phytologist, 188(3), 787-802. doi:10.1111/j.1469-8137.2010.03392.x

Polle, A., & Douglas, C. (2010). The molecular physiology of poplars: paving the way for knowledge-based biomass production. Plant Biology, 12(2), 239-241. doi:10.1111/j.1438-8677.2009.00318.x

Qu, R-Z., L. Hou, L., Lv, H-L. & Li, H-Y. (2004). The gene flow of population genetic structure. Hereditas (Beijing) 26(3), 377-382 (in Chinese with English abstract)

Raddadi, N., Cherif, A., Ouzari, H., Marzorati, M., Brusetti, L., Boudabous, A., & Daffonchio, D. (2007). Bacillus thuringiensis beyond insect biocontrol: plant growth promotion and biosafety of polyvalent strains. Annals of Microbiology, 57(4), 481-494. doi:10.1007/BF03175344

Ralph, S. G., Chun, H. J. E., Cooper, D., Kirkpatrick, R., Kolosova, N., Gunter, L., & Bohlmann, J. (2008). Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. BMC Genomics, 9(1), 57. doi:10.1186/1471-2164-9-57

Ralph, S., Oddy, C., Cooper, D., Yueh, H., Jancsik, S., Kolosova, N., Philippe, R., et al. (2006). Genomics of hybrid poplar (Populus trichocarpax deltoides) interacting with forest tent caterpillars (Malacosoma disstria): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences in poplar. Molecular ecology. doi:10.1111/j.1365-294X.2006.02824.x

Rettig, J.E., Fuller, R.C., Corbett, A.L. & Getty, T. (1997). Fluctuating asymmetry indicates levels of competitioin in an even-aged poplar clone, Oikos, 80, 123-127

Richardson, D.M. (1998). Forestry trees as invasive aliens. Conservation Biology, 12, 18–26.

Ricroch, A. (2012). Assessment of GE food safety using "-omics" techniques and long-term animal feeding studies. New biotechnology. doi:10.1016/j.nbt.2012.12.001

Robinson, G. S., Ackery, P. R., Kitching, I. J., Beccaloni, G. W. & Hernández, L. M. (2010). HOSTS - A Database of the World's Lepidopteran Hostplants. Natural History Museum, London. http://www.nhm.ac.uk/hosts.

Rouhier, N., Couturier, J., & Jacquot, J.-P. (2006). Genome-wide analysis of plant glutaredoxin systems.Journal of experimental botany, 57(8), 1685-1696. doi:10.1093/jxb/erl001

Sampedro, J., Carey, R. E., & Cosgrove, D. J. (2006). Genome histories clarify evolution of the expansin superfamily: new insights from the poplar genome and pine ESTs. Journal of Plant Research, 119(1), 11-21. doi:10.1007/s10265-005-0253-z

Scherrer, D., Bader, M. K.-F., & Korner, C. (2011). Drought-sensitivity ranking of deciduous tree species based on thermal imaging of forest canopies. Agricultural and Forest Meteorology, 151(12), 1632-1640. doi:10.1016/j.agrformet.2011.06.019

Scott, S., & Wilkinson, M. (1999). Low probability of chloroplast movement from oilseed rape (Brassica napus) into wild Brassica rapa. Nature biotechnology, 17(4), 390-2. doi:10.1038/7952

Sederoff, R., Myburg, A., & Kirst, M. (2010). Genomics, Domestication, and Evolution of Forest Trees. Cold Spring Harbor Symposia on Quantitative Biology, 74(0), 303-317. doi:10.1101/sqb.2009.74.040

Séralini, G.-E., Cellier, D., & de Vendomois, J. (2007). New analysis of a rat feeding study with a genetically modified maize reveals signs of hepatorenal toxicity. Archives of environmental contamination and toxicology. doi:10.1007/s00244-006-0149-5

Séralini, G.-E., Clair, E., Mesnage, R., Gress, S., Defarge, N., Malatesta, M., Hennequin, D., et al. (2012). Long term toxicity of a Roundup herbicide and a Roundup-tolerant genetically modified maize. Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association. doi:10.1016/j.fct.2012.08.005

Séralini, G.-E., de Vendômois, J., Cellier, D., Sultan, C., Buiatti, M., Gallagher, L., Antoniou, M., et al. (2009, January 1). How subchronic and chronic health effects can be neglected for GMOs, pesticides or chemicals.International journal of biological sciences. Retrieved from http://www.ijbs.com/v05p0438.htm

Séralini, G.-E., Mesnage, R., Clair, E., Gress, S., Vendômois, J. de, & Cellier, D. (2011). Genetically modified crops safety assessments: present limits and possible improvements. Environmental Sciences Europe. doi:10.1186/2190-4715-23-10

Shao, H., Liang, Z. & Shao, M. (2005). Impact of transgentic living organisms upon ecological environment and their developing tendency. Transaction of the Chinese Society of Agricultural Engineering 21, 691-705 (in Chinese with English abstract)

Shen, Y., Wu, H., Wang, Y., Wu, X. & Jia, X. (2009). 胡杨引种栽培技术试验研究. Modern Agricology, 23, 209-210. Retrived from: http://d.g.wanfangdata.com.cn/Periodical_ahny200923148.aspx (in Chinese)

Sigaud, P. (2011). Poplar Genetic Conservation and Use in China, with Special Attention to North China. FAO. Re-

trieved from http://www.fao.org/forestry/6499-0a5e1e56f46f5c4b81412f38afaffb60f.pdf

Sjodin, A., Street, N. R., Sandberg, G., Gustafsson, P., & Jansson, S. (2009). The Populus Genome Integrative Explorer (PopGenIE): a new resource for exploring the Populus genome .New Phytologist,182(4), 1013-1025. doi:10.1111/j.1469-8137.2009.02807.x

Smouse, P. E., Robledo-Arnuncio, J. J., & González-Martínez, S. C. (2007). Implications of natural propagule flow for containment of genetically modified forest trees.Tree Genetics & Genomes, 3, 141-152. doi:10.1007/s11295-006-0075-8

Snow, A. (2002). Scientific Methods Workshop: Ecological and Agronomic Consequences of Gene Flow from Transgenic Crops to Wild Relatives: Meeting Proceedings. The University Plaza Hotel and Conference Center The Ohio State University Columbus, OH.

Sponza, D. T. (2003). Application of toxicity tests into discharges of the pulp-paper industry in turkey. Ecotoxicology and Environmental Safety, 54(1), 74-86.

Stanton, B. (2004). TEMPERATE ECOSYSTEMS | Poplars. Encyclopedia of Forest Sciences, Burley, J. (eds). Elsevier, Oxford. 1441-1449. doi:10.1016/B0-12-145160-7/00191-5. (http://www.sciencedirect.com/science/article/pii/B0121451607001915)

Sterck, L., Rombauts, S., Jansson, S., Sterky, F., Rouze, P., & Van de Peer, Y. (2005). EST data suggest that poplar is an ancient polyploid. New Phytologist, 167(1), 165-170. doi:10.1111/j.1469-8137.2005.01378.x

Stewart, C., Halfhill, M., & Warwick, S. (2003). Transgene introgression from genetically modified crops to their wild relatives. Nature reviews. Genetics. 4(10), 806-17. doi:10.1038/nrg1179

Strauss, S. H., Howe, G. T., & Goldfarb, B. (1991). Prospects for genetic engineering of insect resistance in forest trees. Forest Ecology and Management, 43(3-4), 181-209. doi:10.1016/0378-1127(91)90127-H

Strauss, S. H., Rottmann, W. H., Brunner, A. M., & Sheppard, L. A. (1995). Genetic engineering of reproductive sterility in forest trees. Molecular Breeding, 1, 5-26. doi:10.1007/BF01682086

Street, N., Jansson, S., & Hvidsten, T. (2011). A systems biology model of the regulatory network in Populus leaves reveals interacting regulators and conserved regulation. BMC plant biology. 11(1), 13. doi:10.1186/1471-2229-11-13

Su, X.H., Zhang, B.Y., Huang, L.J., Zang, X.H. (2003). Advances in tree genetic engineering in China. Paper submitted to the World Forestry Congress, Quebec City, Canada, 1–6 (http://www.fao.org/DOCREP/ARTICLE/WFC/XII/0280-B2.htm; 0280–B2)

Svab, Z., & Maliga, P. (2007, April 24). Exceptional transmission of plastids and mitochondria from the transplastomic pollen parent and its impact on transgene containment. Proceedings of the National Academy of Sciences of the United States of America, 104(17), 7003-7008. doi:10.1073/pnas.0700063104

Swanson, T., & Göschl, T. (2000). Property rights issues involving plant genetic resources: implications of ownership for economic efficiency. Ecological Economics, 32(1), 75-92. doi:10.1016/S0921-8009(99)00072-5

Taylor, G. (2002). Populus: Arabidopsis for Forestry. Do We Need a Model Tree? Annals of Botany, 90(6), 681-689. doi:10.1093/aob/mcf255

Tian, X. & Tan, X. (2009). Research progress and prospect of transgenic Populus. Hunan Forestry Science & Technology 36(2), 71-85 (in Chinese with English abstract)

Tømmerås, B., & Hindar, K. (1999). Assessment of long-term environmental impacts of transgenic trees: Norway spruce as a case study. Retrieved from http://link.springer.com/chapter/10.1007/978-3-0348-8700-7_9

Tuskan, G. A., DiFazio, S., Jansson, S., Bohlmann, J., Grigoriev, I., Hellsten, U., & Salamov, A. (2006). The Genome of Black Cottonwood, Populus trichocarpa (Torr. & Gray). Science, 313(5793), 1596-1604. doi:10.1126/science.1128691

Tuskan, G., DiFazio, S., & Teichmann, T. (2004). Poplar genomics is getting popular: the impact of the poplar genome project on tree research. Plant biology (Stuttgart, Germany). 6(1), 2-4. doi:10.1055/s-2003-44715

Tzfira, T., Zuker, A., & Altman, A. (1998). Forest-tree biotechnology: genetic transformation and its application to future forests.Trends in Biotechnology,16(10), 439-446. doi:10.1016/S0167-7799(98)01223-2

UNGI. (2010). Plant and fungi data integration | Populus. INRA. Accessed from: http://urgi.versailles.inra.fr/Species/Populus , Feb. 2012.

Valda, A., Steven, M. & Murray, B.G. (1981). Studies on heteromorphic self-incompatibility system: the cytochemistry and ultrastructure of the tapetum of Primula Obconica. The Cell Science, 50, 419-431.

Van den Broeck, A. H., Storme, V., Van Slycken, J., Van Bockstaele, E., & Boerjan, W. (2001). Mating system of Populus nigra L. and gene flow with cultivated poplars; implications for in situ restoration. EUFORGEN Populus

nigra NETWORK Report of the Seventh meeting – 22-27 October 2001 – Osijek, Croatia.

Vettori, C., & Fladung, M. (2011). COST Action FP0905: Biosafety of forest transgenic trees: improving the scientific basis for safe tree development and implementation of EU policy directives. BMC Proceedings, 5(Suppl 7), P185. doi:10.1186/1753-6561-5-S7-P185

Viswanath, V., Albrectsen, B. R., & Strauss, S. H. (2012). Global regulatory burden for field testing of genetically modified trees. Tree Genetics & Genomes, 8(2), 221-226. doi:10.1007/s11295-011-0445-8

Wagner, S., Collet, C., Madsen, P., Nakashizuka, T., Nyland, R. D., & Sagheb-Talebi, K. (2010). Beech regeneration research: From ecological to silvicultural aspects.Forest Ecology and Management,259(11), 2172-2182. doi:10.1016/j.foreco.2010.02.029

Wang, L., Han, Y., Hu, J. (2004). Transgenic forest trees for insect resistance. Molecular genetics and breeding of forest trees, Kumar, S., Fladung, M. (eds). Haworth Press, New York, 243–261

Wang, S., Xu, Z. & Wei, Z. (1990). Genetic transformation of leaf explants of Populus tomentosa. Acta Botanica Sinica 32:172–177

Wang, Z. & Yi, Z. (2003). The application of Kanamycin in transgenic plants and the biosafety assessment of Kan Gene. China Biotechnology 23(6), 9-13 (in Chinese with English abstract)

Wang, Z., Liu, S., Wu, X., Meng, F. & Li, W. (2010). Management of field trials of genetically modified crops in U.S.A. Soybean Science 29(3), 530-533 (in Chinese with English abstract)

Wei. W., Qian, Y-Q., Ma, K-P. & Sang, W-G. (1999). Monitoring the ecological risks of genetically modified organisms (GMOs). Chinese Biodiversity 7(4), 312-319 (in Chinese with English abstract)

Weisgerber, H. & Zhou, H. (1997). Afforestation in semiarid regions – Findings and Perspectives. Proceedings of the International Symposium in the People's Republic of China, Datong/Jinshatan. Hann. Münden.

Weisgerber, H., & Han, Y. (2001). Diversity and breeding potential of poplar species in China. The Forestry Chronicle, 77(2), 227-237. Retrieved from http://pubs.cif-ifc.org/doi/abs/10.5558/tfc77227-2

Weisgerber, H., Kownatzki, D., Mussong, M. (1995). Natural poplar resources in China and their significance for breeding and afforestation. Silvae Genetica 44, 298–303

Weng, E.-sheng, & Zhou, G.-sheng. (2006). Modeling distribution changes of vegetation in China under future climate change. Environmental Modeling & Assessment,11(1), 45-58. doi:10.1007/s10666-005-9019-1

Whetten, R., & Sederoff, R. (1991). Genetic engineering of wood. Forest Ecology and Management, 43, 301-316. doi:10.1016/0378-1127(91)90133-G

Wu, N.F. & Fan, Y.L. (1991). Transgenic poplar plants transformed with Bacillus thuringiensis toxin gene. Chinese Science Bulletin, 9, 705–708

Wullschleger, S. D. (2002). Genomics and Forest Biology: Populus Emerges as the Perennial Favorite. THE PLANT CELL ONLINE, 14(11), 2651-2655. doi:10.1105/tpc.141120

Wullschleger, S. D., Tuskan, G. A., & DiFazio, S. P. (2002). Genomics and the tree physiologist. Tree Physiology,22(18), 1273-1276. doi:10.1093/treephys/22.18.1273

Xiang, Y., Cui, P. & Bai, G. (1995). The protection of Xinjiang forestry gene resource in a dry- desert habitat. Forest tree improvement in the Asia-Pacific region, Shen, X. (eds). China Forestry Publishing House, Beijing, 298–299

Xu, C., Wang, W., Zha, L. & Zhuge, Q. (2008). Progress in research of transgenic trees by use of selective biosafety marker genes. Molecular Plant Breeding 6(5), 954-958 (in Chinese with English abstract)

Xu, J. & Yan, Z. (2010). Farmers' cognition of transgenic technology and production intention of transgenic staple foods —— taking Hubei area grainfarmers as investigation objects. Forum on Science and Technology in China 2010(11), 142-148 (in Chinese with English abstract)

Xu, S., Tan, T. & Chen, C. (2010). 发展中国家转基因政策比较及对我国的启示. Jiangsu Agriculture Science 5, 514-516 (in Chinese)

Yadav, R., Arora, P., Kumar, D., Katyal, D., Dilbaghi, N., & Chaudhury, A. (2009). High frequency direct plant regeneration from leaf, internode, and root segments of Eastern Cottonwood (Populus deltoides). Plant Biotechnology Reports, 3(3), 175-182. doi:10.1007/s11816-009-0088-5

Yadav, R., Arora, P., Kumar, S., & Chaudhury, A. (2010). Perspectives for genetic engineering of poplars for enhanced phytoremediation abilities.Ecotoxicology,19(8), 1574-1588. doi:10.1007/s10646-010-0543-7

Yang, M-S., Mi, D., Ewald, D., Wang, Y., Liang, H-Y. & Zhen, Z-X. (2006). The survival and escape of Agrobacterium tumefaciens in triploid hybrid lines of Chinese white poplar transformed with two insect-resistant genes. Acta Ecologica Sinica 26(11), 3555-3561 (in Chinese with English abstract)

Yu, X., Kikuchi, A., Shimazaki, T., Yamada, A., Ozeki, Y., Matsunaga, E., Ebinuma, H., et al. (2013). Assessment of the salt tolerance and environmental biosafety of Eucalyp-

tus camaldulensis harboring a mangrin transgene. Journal of plant research. doi:10.1007/s10265-012-0503-9

Zalesny, R. S., & Bauer, E. O. (2007). Evaluation of Populus and Salix Continuously Irrigated with Landfill Leachate I. Genotype-Specific Elemental Phytoremediation. International Journal of Phytoremediation, 9(4), 281-306. doi:10.1080/15226510701476461

Zalesny, R. S., & Bauer, E. O. (2007). Selecting and Utilizing Populus and Salix for Landfill Covers: Implications for Leachate Irrigation. International Journal of Phytoremediation, 9(6), 497-511. doi:10.1080/15226510701709689

Zeng, F., Qian, J., Kang, J., Wang, H., Wang, Y. & Zhan, Y. (2009). Histochemical study of β-glucuronidase activity in transgenic birch. Chinese Bulletin of Botany 44(4), 484-490 (in Chinese with English abstract)

Zeng, F., Wang, X., Luo, W. & Zhan, Y. (2008). Analysis of pollen vigor, inheritance and expression of foreign genes in transgenic birch(Betula platyphylla Suk.) pollen. Plant Physiology Communications 44(6), 1082-1086 (in Chinese with English abstract)

Zhai, B-P. (2001). Fluctuating asymmetry: an ecological monitor of the rish assessment of gene transgenic plants. Cotton Science 13(1), 45-49 (in Chinese with English abstract)

Zhang, C., Wang, C., Chen, X., Yang, C., Li, K., Wang, J., Dai, J., et al. (2010). Expression profile of microRNAs in serum: a fingerprint for esophageal squamous cell carcinoma. Clinical chemistry. doi:10.1373/clinchem.2010.147553

Zhang, J. (2009). 胡杨、灰叶胡杨种群分布及地理关系的研究. Journal of Zhoukou Normal University, 26(5). Retrived from: http://d.g.wanfangdata.com.cn/Periodical_zksfgdzkxxxb200905032.aspx (in Chinese)

Zhang, L., Hou, D., Chen, X., Li, D., Zhu, L., Zhang, Y., Li, J., et al. (2012). Exogenous plant MIR168a specifically targets mammalian LDLRAP1: evidence of cross-kingdom regulation by microRNA. Cell research. doi:10.1038/cr.2011.158

Zhang, Y., Liu, D., Chen, X., Li, J., Li, L., Bian, Z., Sun, F., et al. (2010). Secreted monocytic miR-150 enhances targeted endothelial cell migration. Molecular cell. doi:10.1016/j.molcel.2010.06.010

Zhang, Z., Wang, J., Zhang, J. & Zhang, S. (2004). Effects of transgenic poplars to the structure of insect community. Scientia Silvae Sinicae 40(2), 84-89 (in Chinese with English abstract)

Zhou, J., Tao, Y., Fu, J. & Zhuge, Q. (2011). Establishment of genetic transformation system with selective marker free for poplar. Molecular Plant Breeding 9(2), 230-237 (in Chinese with English abstract)

Zhou, S. & Cui, Q. (2006). 我国转基因农产品管理中存在的问题及对策建议. Forum on Science and Technology in China 2006(1), 60-63 (in Chinese)

Zhuge, Q., Fang, D., Li, X., Sun, W., Huang, M. & Wang, M. (2006). Transformation of Populus x euramericana cv. "Nanlin895' using Bt and CpTI insect-resistant genes. Molecular Plant Breeding 4(6), 819-824 (in Chinese with English abstract)

Zhuge, Q., Wang, J., Chen, Y., Wu, N., Huang, M., Fan, Y. & Wang, M. (2003). Transgenic plantlets of Populus alba var. pyramidalis by transformation with CpTI gene. Molecular Plant Breeding 1(4), 491-496 (in Chinese with English abstract)

Zou, Y., Shi, J., Zhuge, Q. & Huang, M. (2006). Reacting the silencing genes in the transgenic plants. Molecular Plant Breeding 4(1), 95-102 (in Chinese with English abstract)

Zsuffa, L. (1975). A summary review of interspecific breeding in the genus Populus L. Proceedings of the 14th meeting of the Canadian tree improvement association, part 2. Canadian Forestry Service, Ottawa, 107–123