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Genomic Basis and Regulatory Mechanisms of Cold Tolerance and Photoperiod Adaptation in Silver Birch (*Betula pendula*)

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Abstract This study collated the main physiological and molecular responses of silver birch when exposed to low temperatures, summarized the molecular adaptation mechanisms of silver birch to photoperiodic changes, discussed the natural selection evidence of candidate adaptation genes such as PHYC, FRS10, and ARR1, and indicated that these genes are related to the environmental adaptation of silver birch in different regions. It also revealed the interaction between cold signals and photoperiodic signals. Research has found that at low temperatures, silver birch trees protect themselves by stabilizing cell membranes, regulating osmotic pressure, and enhancing antioxidant capacity, and many cold response genes are also activated. Photoreceptors, biological clock-related genes, and the rhythm genes they regulate such as FT and GH17 all play significant roles in the formation of dormancy and the initiation of germination. Both cold signals and photoperiodic signals can affect hormone pathways and transcriptional regulatory networks, and jointly determine the growth rhythm, dormancy process and cold resistance of silver birch. This study aims to provide a reference for the molecular breeding of silver birch and also offer a theoretical basis for enhancing its adaptability in the context of climate change.

Keywords Silver birch (*Betula pendula*); Cold tolerance; Photoperiod adaptation; Genomic and regulatory networks; Multi-omics and molecular breeding

1 Introduction

The silver birch is a common pioneer tree species in northern forests, mainly distributed in the cold temperate and subfrigid regions of Eurasia. Whether it can grow normally in these areas largely depends on its adaptation to low temperatures and seasonal photoperiodic changes. Cold resistance and response to photoperiod will affect when its growing season begins and ends, and also determine when dormancy is initiated and lifted. At the same time, these characteristics are also related to whether it can survive in extreme climates and continue to expand into new areas. Research has found that short days and low temperatures are the main signals that cause the silver birch to stop growing, enter cold adaptation and start dormancy. Ecological types at different latitudes show significant differences in photoperiodic sensitivity. Northern types usually respond faster and have stronger cold resistance. These adaptive characteristics are of great significance for maintaining population stability and forest ecosystem functions in the context of climate warming (Salojärvi et al., 2017; Solé-Medina et al., 2020).

In recent years, with the development of genomic sequencing technology, significant progress has been made in the genomic research of the silver birch and its closely related species. These studies have revealed its genomic structure, evolutionary characteristics, and genetic variations related to environmental adaptation. For instance, some gene families related to transcriptional regulation and environmental response have been amplified; Key genes in the light signal and low-temperature response pathways, such as PHYC, FRS10, CBF, etc., show significant adaptive differentiation among different geographical populations (Salojärvi et al., 2017; Chen et al., 2021). Some transcription factors (such as NAC, AP2/ERF, CBF) and hormone signals (such as ABA) also play important roles in regulating cold tolerance and photcycle adaptation (Lv et al., 2020; Zhang et al., 2024). Although there are some research achievements at the genomic, transcriptomic and physiological levels at present, the integration mechanism between cold tolerance and photoperiod adaptation is still not clear enough. How key genes interact and where the differences among different ecological types come from still require more systematic research (Chen et al., 2019; Venisse et al., 2021). Therefore, it is necessary to combine multi-omics data with physiological and ecological experiments to comprehensively analyze these regulatory networks.

This study analyzed the cold resistance and photoperiod adaptation of the silver birch from both genomic and regulatory mechanism perspectives, identified the key genes and their variation characteristics related to these traits, analyzed the interaction relationships between the main signaling pathways and transcription factors, and compared the differences in regulatory mechanisms among different ecological types. This study aims to provide theoretical basis and potential molecular targets for the genetic improvement of silver birch and other temperate tree species as well as for addressing future climate change.

2 Physiological and Developmental Responses to Cold and Photoperiod

2.1 Cold acclimation, freezing tolerance, and seasonal growth cessation

Whether the silver birch can grow normally in temperate and subarctic regions mainly depends on its adaptability to seasonal changes, especially its cold adaptation, frost resistance and the control of when growth stops. short day (SD) and low temperature (LT) are two key signals that cause silver birch to stop growing and enter cold adaptation. Ecological types from different latitudes respond differently to these signals. The ecological types in the north are particularly sensitive to shorter daylight hours and lower temperatures. They usually stop growing earlier, enter cold adaptation and dormancy more quickly, and acquire stronger frost resistance. During cold adaptation, the ABA content in plants will increase, while the IAA content will decrease. The changes of ABA are closely related to the enhancement of frost resistance and the formation of dormancy. The response rates of different tissues are also different. The cold adaptation responses of buds and leaves are faster than those of stems (Li et al., 2002).

2.2 Photoperiod-mediated control of bud set, dormancy, and flushing

Photoperiod is the main environmental signal regulating the annual growth rhythm of the silver birch. Short days not only cause plants to stop growing prematurely, but also promote the formation of terminal buds and enter dormancy. During the formation of the apical bud, ethylene signals act in conjunction with ABA signals to drive the development transformation of the apical meristem (SAM). The release of dormancy and the sprouting in spring are mainly driven by low-temperature stimulation. When plants accumulate enough chilling, the increase in temperature and long days together promote germination and growth recovery (Castells-Montero and Gutiérrez-Merino, 2023). The ecological types at different latitudes have different requirements for these signals. The northern ecological type enters and exits dormancy earlier and has a lower demand for low temperatures.

2.3 Intersection of temperature and daylength signaling in annual growth cycles

The regulation of photoperiod and temperature signals throughout the year interacts with each other. Short days are mainly responsible for inducing growth termination and dormancy, while low temperatures are more crucial in enhancing frost resistance and promoting dormancy release (Castells-Montero and Gutiérrez-Merino, 2023). In autumn, if the temperature is too high, it will delay the end of dormancy and also delay the germination of buds in spring, thereby offsetting the earlier growth season caused by climate warming. Photoperiod and temperature signals can also jointly regulate the changes of hormones (such as ABA), as well as the expression of key genes such as FT and GH17 family (Maurya and Bhalerao, 2017; Osnato et al., 2022). The biological clock and photosensitive pigments also play a central role in integrating photoperiodic and temperature signals.

3 Genomic Basis of Cold Tolerance in Silver Birch

3.1 Key cold-responsive gene families

The cold resistance of the silver birch is mainly regulated by a series of genes that are activated at low temperatures. The CBF/DREB transcription factor family is the most core type of regulatory factor among them. Research has found that the silver birch has four CBF homologous genes (BPCBF1-4). These genes are rapidly upregulated when stimulated by low temperature and can activate downstream cold response genes, such as COR, LEA, etc., thereby enhancing frost resistance (Hwarari et al., 2022). In addition to the CBF gene, 21 members of the NAC family also underwent significant changes under low-temperature stress, indicating that they are also involved in the regulation of cold response (Chen et al., 2019). LEA protein and COR gene can help protect cell membranes and proteins, maintain the internal water and ion balance of cells, and thereby further enhance cold resistance (Salojärvi et al., 2017).

3.2 Genomic variations associated with cold hardiness across birch populations

Population genomics studies have shown that the silver birch has significant genomic differences in different climate regions. Resequencing analysis of 80 individuals indicated that environmental factors such as temperature and precipitation would affect the selection of regions related to cold adaptation in the genome, including light signal related genes such as PHYC and FRS10, as well as hormone signal genes such as ARR1 (Salojärvi et al., 2017). Populations from different latitudes also show differences in early adaptive traits such as germination, seedling growth and dormancy, and these differences are closely related to climate adaptation and cold resistance (De Dato et al., 2020; Solé-Medina et al., 2020).

3.3 Molecular pathways regulating membrane stability, ROS homeostasis, and cryoprotection

The cold resistance of the silver birch also relies on the combined effects of membrane proteins, ROS regulation and various protective molecules. Aquaporin (AQP) can help regulate intracellular water flow under low-temperature conditions. Some AQP genes are upregulated at low temperatures, which helps reduce cell dehydration and maintain membrane stability (Venisse et al., 2021). During cold stress, ROS in cells accumulates rapidly. Therefore, antioxidant genes, such as SOD, POD, GST, etc., are induced to be expressed to eliminate excessive ROS and avoid oxidative damage (Lv et al., 2020; Cai et al., 2021; Cai et al., 2025). Furthermore, some cold protective molecules, such as proline, soluble sugars and antifreeze proteins, can further enhance the cold resistance of silver birch by regulating osmotic pressure, reducing ice crystal formation and stabilizing protein structure (Figure 1) (Hwarari et al., 2022; Jahed et al., 2023).

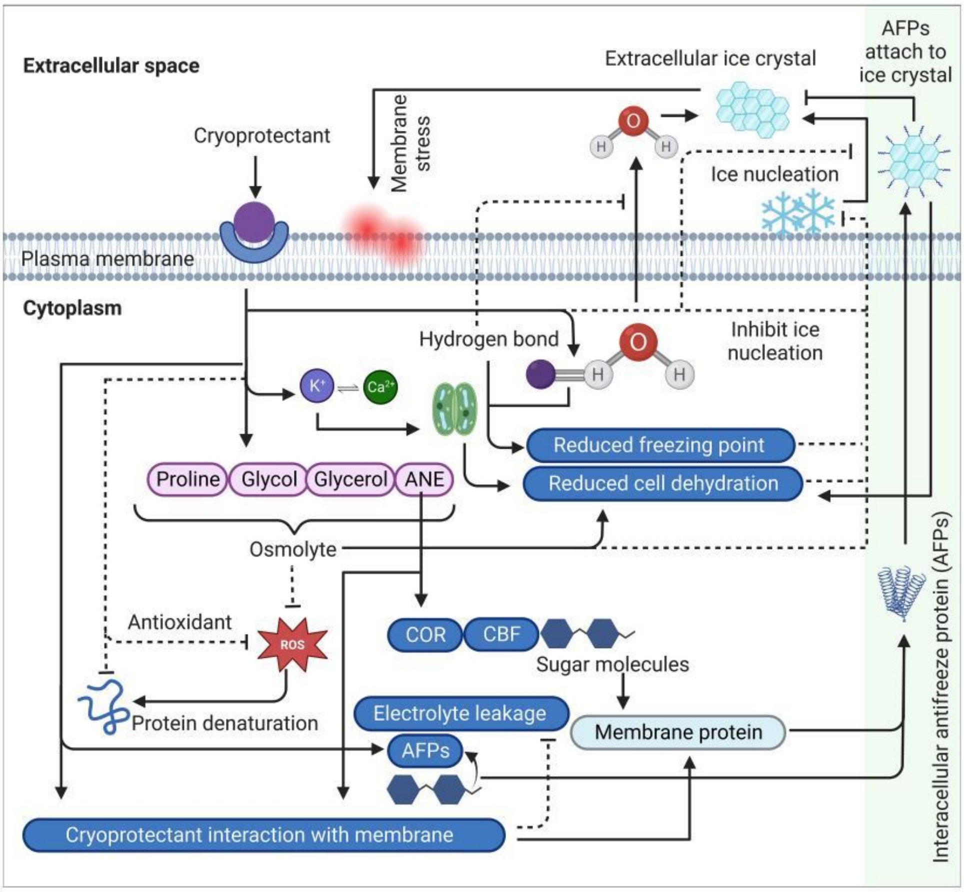

Figure 1 A comprehensive schematic summary of cryoprotectants mechanism of action and cold stress modulation in plants (Adopted from Jahed et al., 2023)

4 Regulatory Mechanisms of Photoperiod Adaptation

4.1 Core circadian clock components and their roles

The circadian clock of plants is mainly composed of several core genes, among which the most important ones include the LHY, TOC1 and PRR families. These genes control the rhythm through a set of feedback loops. The expression levels of LHY and CCA1 are the highest in the morning, and they can inhibit TOC1. In the evening, after TOC1 increases, it will in turn suppress LHY and CCA1 (Hu et al., 2024; Jang et al., 2024). In addition, LHY and CCA1 can also promote the expression of PRR7 and PRR9, while PRR7 and PRR9 can inhibit the transcription of LHY, making the entire rhythm present a clear temporal sequence regulation. The PRR protein can also work together with transcription factors such as BBX19 to further finely regulate the rhythm and affect the photoperiodic regulated growth process (Yuan et al., 2021). These clock genes not only respond to photoperiod, but also participate in temperature regulation and environmental adaptation (Hu et al., 2024; Jang et al., 2024).

4.2 Photoreceptors and light-signaling genes (PHYs, CRYs) in seasonal timing

Plants sense light signals through photoreceptors. The main photoreceptors include photosensitive pigments (PHYs: PHYA, PHYB, PHYC, etc.) and cryptochromes (CRYs). PHY mainly senses red light and far-red light, and can regulate seasonal changes such as photoperiodic flowering, bud dormancy, and growth termination (Seaton et al., 2018; Osnato et al., 2022). In silver birch, the genetic variation of PHYC is related to factors such as latitude and temperature, and it affects the beginning and end of the growing season (Salojärvi et al., 2017). CRY is responsible for sensing blue light, regulating circadian rhythms, flowering time and many developmental processes (Mishra and Khurana, 2017). These photoreceptors regulate a large number of photoresponse genes by regulating downstream transcription factors such as PIFs and HY5, thereby helping plants adapt to seasonal changes (Osnato et al., 2022; Hengge et al., 2025).

4.3 Gene networks coordinating photoperiod-dependent growth transitions

Photoperiodic signals adjust the growth state of plants through a complex genetic network. The circadian clock and photoreceptors jointly regulate key genes such as FT and CO, which further affect flowering time, dormangia entry and growth termination (Osnato et al., 2022). In silver birch and other tree species, light response genes such as PHYC and FRS10 are closely related to the timing of the growing season and show significant variations in environmental adaptability (Salojärvi et al., 2017). Meanwhile, the key regulatory factors in the optical signal pathway, such as HY5 and HFR1, can also synergistic with chromatin modification factors, integrate photoperiod with other environmental signals, and achieve more detailed regulation of growth (Jing and Lin, 2020). These interaction networks enable silver birch to adapt well to different photoperiodic environments.

5 Integration of Cold and Photoperiod Regulatory Networks

5.1 Crosstalk between CBF pathway and photoperiodic signaling

The CBF (C-repeat binding factor) transcription factor is the most crucial regulatory factor for plants under cold stress. Their expression is simultaneously affected by low temperature and photoperiod. Short-day (SD) and low temperature can respectively induce CBF independently, or they can act together to enhance the expression of CBF, thereby improving cold adaptability and frost resistance. Photosensitive pigments (PHYA, PHYB) and their interacting factors (PIF4, PIF7) can lower the expression of CBF during long days (LD). However, under short-day conditions, this inhibition will be significantly weakened, resulting in CBF being more easily activated and a stronger antifreeze response. The circadian rhythm also regulates the expression rhythm of CBF, making the cold adaptation response more refined (Salojärvi et al., 2017). In silver birch, the expression of CBF varies during the growing season and the dormant period. The response of CBF in dormant tissues is slower, which also indicates that the CBF pathway is regulated by photoperiod in different physiological periods.

5.2 Hormonal regulation (ABA, GA, ethylene) linking environmental cues to growth control

Hormone signals play a "bridge" role between cold response and photoperiodic regulation. Abscisic acid (ABA) increases under both short-day and low-temperature conditions, and the changes in ABA are closely related to frost resistance and the initiation process of dormancy (Ritonga and Chen, 2020). Gibberellin (GA) generally has the opposite effect to ABA. GA promotes growth and dormancy release. It participates in the regulatory network of ABA by regulating DELLA proteins, thereby coordinating growth and stress resistance (Singh and Roychoudhury, 2023). Hormones such as ethylene and jasmonic acid also act together with ROS signaling to regulate plant growth, dormancy, and various stress responses (Huang et al., 2017; Parwez et al., 2022; Jardim-Messeder et al., 2025). In different ecological types of silver birch, the rates of change in ABA and GA content vary, which also indicates that hormone regulation is part of their adaptive evolution.

5.3 System-level coordination of dormancy cycling and stress responses

The dormancy - growth cycle of the silver birch is closely related to cold adaptation, photoperiod and hormone regulation. Short days can induce growth to stop, initiate dormancy and promote cold adaptation. Subsequently, low temperatures will further enhance frost resistance and help trigger the release of dormancy at the end of winter. Dormancy disconnection depends on the reopening of some signaling pathways, such as the reconnection of interplastid filaments, and also requires the upregassing of certain genes (such as 1,3-β -glucanase) by GA and the activation of signaling molecules such as FT (Singh et al., 2017). From a systemic perspective, cold, photoperiod and hormone pathways act together by regulating transcription, protein interactions and intercellular signal transduction, enabling trees to rapidly cease growth, enter dormancy under complex environmental changes, and then resume growth at the appropriate time.

6 Multi-Omics Insights into Adaptation Mechanisms

6.1 Genomic and transcriptomic profiling under cold and photoperiod treatments

Genomic and population genomic studies of the silver birch have shown that some genes related to light response (such as PHYC, FRS10), as well as those related to cell division and xylem development (such as ARR1, KAK, MED5A), show significant differences among populations of different geographical origins. The variations of these genes are often related to climatic factors such as latitude, temperature or precipitation, indicating that they have a direct relationship with local environmental adaptation (Salojärvi et al., 2017). The transcriptome results also support this point. Under low-temperature treatment, the expression of a large number of genes in the leaves of the silver birch changed. These genes were involved in multiple pathways such as signal transduction, secondary metabolism and photosynthesis (Yan et al., 2020; Chen et al., 2021). Among them, 362 transcription factors were affected by low temperature, including multiple families such as AP2/ERF, MYB, and WRKY. Twenty-one members of the NAC family also showed differential expression at low temperatures, further indicating the important role of NAC in the regulation of cold response (Chen et al., 2019). In addition, short-day pretreatment can enhance the CBF pathway induced by low temperature. For instance, dehydrated proteins like Bplti36 are expressed more strongly under the combination of "short-day + low-temperature" conditions. This suggests that photoperiod may give plants a "preparation signal" in advance, making the subsequent low-temperature response faster and stronger.

6.2 Proteomics and metabolomics revealing downstream stress-responsive pathways

Proteomic research also shows a similar trend. Silver birch raises many proteins related to defense, photosynthesis, carbon and nitrogen metabolism, and signal transduction at low temperatures. Among them, the changes in ATP synthase subunits related to chloroplast function are the most obvious, indicating that chloroplasts may play a key role in cold tolerance. Although there are few metabolomic reports on the silver birch, studies on other tree species have shown that cold stress often accumulates protective metabolites such as polyamines and phenolic acids, which can help clear ROS and stabilize cell membranes (Zhou et al., 2025). Therefore, it is highly likely that the silver birch also enhances its cold resistance through a similar metabolic process. The dynamic changes of hormone signals (such as ABA and IAA) are also involved in this process simultaneously, regulating growth, dormancy and cold resistance under cold stress.

6.3 Integrative network modeling to identify regulatory hubs and adaptive modules

The co-expression network and regulatory network established by combining transcriptome and proteome data have helped researchers identify some "core nodes" of cold response in silver birch and related species. These nodes include multiple transcription factors such as CBF, NAC, WRKY, as well as downstream modules regulated by them (Chen et al., 2019; Jia et al., 2022; Luo et al., 2022). Existing studies have shown that the CBF network remains the center of cold stress response in silver birch and interacts with photoperiodic signals, thereby forming a multi-level and dynamically changing regulatory system (Zhang et al., 2024). The methods of systems biology also reveal that there is a coordinated relationship among cell wall biosynthesis, hormone signaling and antioxy-related modules (Salojärvi et al., 2017; Ilievska et al., 2025). These results collectively provide an important foundation for understanding the climate adaptation and molecular breeding of the silver birch.

7 Case Study: Genomic and Regulatory Analysis of a Cold-Resilient Birch Population

7.1 Study background and selection of contrasting birch populations

The silver birch is a common pioneer tree species in northern forests. It is widely distributed, ranging from temperate zones to subfrigid zones, with significant environmental differences. The reason why it can survive in these regions is largely because it has strong cold resistance and can also adapt well to photoperiodic changes. Silver birch from different latitudes often vary significantly in terms of the length of the growing season, the start time of dormancy and cold resistance. Especially for the northern and southern groups, their responses to shorter daylight hours and lower temperatures are not the same. There are significant differences in growth termination time, cold adaptation speed, hormone changes and some physiological indicators. To study the genetic basis of these differences, natural populations are often collected from different latitudes and climatic conditions to compare their phenotypic and molecular-level responses under low-temperature and photoperiodic changes (Solé-Medina et al., 2020; Tenkanen et al., 2022).

7.2 Experimental approach: genome sequencing, expression profiling, and network analysis

This case used a high-quality silver birch reference genome and combined with whole-genome resequencing data of approximately 80-150 individuals from different geographical sources to conduct a systematic analysis of its population structure and adaptive variations (Salojärvi et al., 2017). Meanwhile, through RNA-seq, transcriptome analysis was conducted on samples of different tissues such as leaves, roots, xylem, and at different cryogenic treatment time points to identify differentially expressed genes related to cold resistance (Chen et al., 2019; Cai et al., 2021; Chen et al., 2021). Subsequently, by using WGCNA, gene regulatory network reconstruction (such as ARACNE, GGM), and cis-element analysis, the transcription factors that may play a role in the hypothermia response, such as CBF, NAC, AP2/ERF, are further analyzed, and the downstream target genes they regulate are identified. Reveal the regulatory framework of cold resistance and photoperiodic adaptation as a whole (Lv et al., 2020; Lv et al., 2021; Zhang et al., 2024).

7.3 Key findings: candidate genes, regulatory circuits, and implications for breeding

In cold tolerance regulation, multiple transcription factor families are crucial, among which the most typical one is CBF (C-repeat binding factor). They are rapidly induced under low temperature and short day conditions, thereby activating some antifreeze related genes, such as dehydrating proteins (like Bplti36) and antioxidant enzymes (SOD, POD), etc., to help cells improve cold resistance (Lv et al., 2020; Zhang et al., 2024). Members of the NAC and AP2/ERF families are also significantly upregulated at low temperatures. They are involved in regulating cell walls, growth signals and stress resistance responses (Chen et al., 2019; Lv et al., 2021).

Genomic selection scanning results show that some light-response genes (such as PHYC and FRS10), as well as genes related to cell division and xylem development (such as ARR1, KAK, and MED5A), have selection signals among populations at different latitudes. Indicate that these genes are related to the adaptive evolution of temperature, latitude and precipitation (Salojärvi et al., 2017). The co-expression network further reveals a set of hierarchical regulatory relationships. For instance, some primary regulatory factors (such as BpNST1/2, BpSND1) regulate downstream transcription factors like MYB, and these MYB ultimately affect xylem and cell wall formation (Figure 2) (Ilievska et al., 2025). These genes and regulatory modules provide important clues for molecular breeding of cold resistance and photoperiodic adaptation. In the future, new varieties of silver birch that are more cold-resistant, more adaptable to extreme climates, and have better growth performance can be cultivated through methods such as molecular marker-assisted selection or gene editing (Salojärvi et al., 2017; Lv et al., 2020).

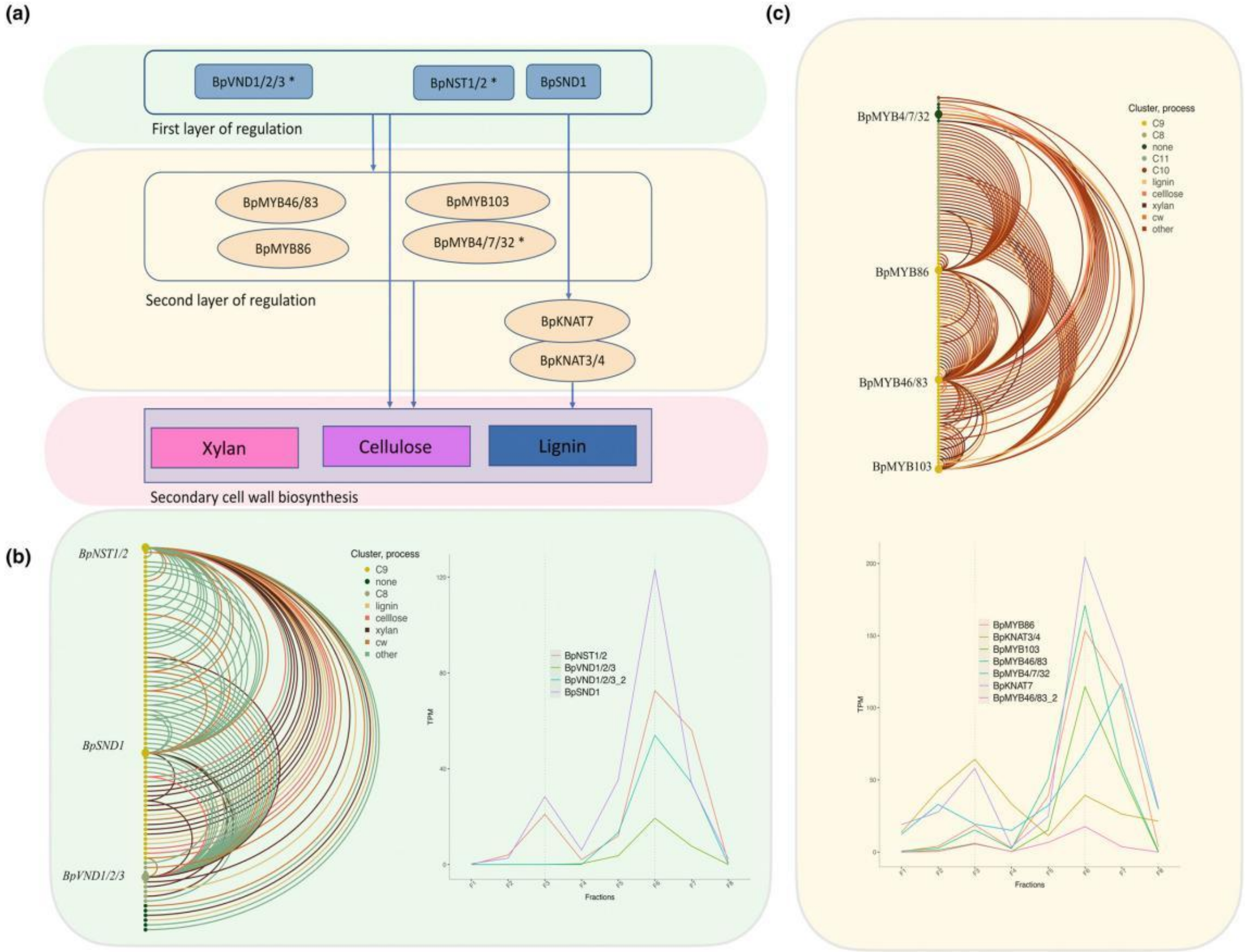

Figure 2 Cell wall biosynthesis regulatory network in birch (Adopted from Ilievska et al., 2025)

8 Applications in Breeding and Forest Management

8.1 Genomic markers for cold tolerance and photoperiod sensitivity

The cold resistance and adaptation to photoperiod of the silver birch are closely related to a series of genetic changes. GWAS and population genomics studies have pointed out that variations in the light response genes PHYC and FRS10 vary with latitude, temperature and precipitation. These variations are also related to photcycle sensitivity and cold resistance, and thus are often regarded as available molecular markers (Salojärvi et al., 2017). Meanwhile, the CBF (C-repeat binding factor) family is rapidly induced under low-temperature and short-day conditions, and they can activate downstream cold response genes, such as dehydrating protein Bplti36. The expression patterns of these genes can well reflect the cold resistance level of the plants and can also be used as cold resistance markers (Lv et al., 2020; Zhang et al., 2024). The expression of these genes varies significantly among silver birch in different regions, providing a practical basis for molecular marker-assisted selection (MAS).

8.2 Breeding strategies for climate-resilient silver birch varieties

By using these molecular markers, it is possible to screen out superior germplasms that are cold-resistant and well-adapted to photoperiod more quickly. Modern breeding methods, such as genome-wide selection, MAS or gene editing, can help aggregate favorable alleles more accurately, thereby shortening the breeding cycle (Salojärvi et al., 2017; Cortés et al., 2020). Meanwhile, by combining germplasm materials of different climate ecologies, analyzing phenotypic data and genotype data together, and conducting multiple environmental experiments, it is possible to find breeding combinations that are more adapted to specific regions (Possen et al., 2021). In terms of enhancing cold resistance, physiological mechanisms such as regulating the CBF pathway, enhancing antioxidant enzyme activity, and promoting the accumulation of osmotic regulatory substances have also been proven effective (Lv et al., 2020; Zhang et al., 2024; Ritonga et al., 2025).

8.3 Implications for northern forest adaptation under climate change

With the warming of the climate and the increase of extreme weather, the forests in the north are facing problems such as a longer growing season, greater drought pressure and aggravated pests and diseases. Fortunately, the silver birch has a high degree of genetic diversity and physiological plasticity, providing a good adaptation basis for forest ecosystems (Oksanen, 2021). In forest management, giving priority to choosing local or breeding varieties with strong cold resistance and photoperiodic adaptability can enhance the stability of the stand to climate change (Tenkanen et al., 2022). Furthermore, soil nutrients, especially nitrogen supply, are also crucial for seedling establishment. Therefore, soil management also needs to be incorporated into adaptive strategies (Possen et al., 2021). In the future, combining multi-omics data with big data analysis will further enhance the understanding of the adaptation mechanisms of silver birch and northern forests, and promote more sustainable management methods (Salojärvi et al., 2017; Cortés et al., 2020).

9 Challenges and Future Directions

9.1 Complexity of environmental response networks in long-lived perennial trees

When confronted with low temperatures and photoperiodic changes, perennial trees such as the silver birch simultaneously activate many different levels of response mechanisms. These mechanisms include gene regulation, signal transduction, epigenetic regulation and a series of physiological changes. Compared with annual plants, trees need to constantly regulate their growth and stress response over decades or even hundreds of years of life, so their regulatory networks are more complex in both time and space. Previous studies have pointed out that transcription factor networks, hormone signals and epigenetic regulation often act together, but the interaction patterns and regulatory sequences among them are still not completely clear (Estravis-Barcala et al., 2019; Li et al., 2021). Furthermore, the population structure, historical migration routes and gene flows of trees can also affect genetic variations, making their environmental adaptation mechanisms more difficult to interpret (Cortés et al., 2020; Slavov et al., 2025).

9.2 Need for high-quality genomic resources and long-term field datasets

Although high-throughput sequencing technology has developed rapidly in recent years, high-quality genomic resources of tree species such as the silver birch remain limited. Tree genomes are usually large in size and have many repetitive sequences, so assembly and annotation remain technical difficulties (Fleck et al., 2024). At the same time, to understand the relationship between genotypes, phenotypes and the environment, long-term and systematic observation and data accumulation are required. However, due to the long growth cycle of trees, the time-consuming and difficult field experiments, there are still very few available long-term datasets at present (Estravis-Barcala et al., 2019). The lack of such cross-regional and multi-year omics and ecological data has limited our in-depth study of the cold resistance and photcycle adaptation mechanism of silver birch (Cao et al., 2022).

9.3 Future perspectives: single-cell omics, pan-genomics, and predictive modeling

In the future, some new technologies may significantly promote related research. For instance, single-cell omics can be used to identify the unique regulatory patterns of different cell types under low-temperature or photoperiodic changes, thereby breaking through the limitations of traditional tissue-level analysis (Chau et al., 2024; Nobori, 2025; Zhu et al., 2025). Pan-genomics helps capture all genetic diversity within species, identify those rare but critical adaptive alleles, and provide evidence for resilience improvement and resource conservation (Cao et al., 2022). Furthermore, the combination of multi-omics data with machine learning or predictive models is expected to analyze complex traits more accurately and assess the adaptability of trees in the context of climate change in advance (Estravis-Barcala et al., 2019; Cortés et al., 2020). The application of these technologies will significantly enhance the genetic improvement efficiency of silver birch and other forest species, and also strengthen the sustainable management of forest ecosystems.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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