

3.3 Role of plant hormones in low-temperature adaptation

Plant hormone signaling is closely linked to cold-stress responses. Cross-species studies have shown that abscisic acid (ABA), auxin, gibberellins, jasmonic acid, salicylic acid, ethylene, brassinosteroids, and cytokinins all participate in plant cold acclimation by regulating gene expression, growth and development, and ROS signaling pathways.

In radish, the ethylene-responsive factor RsERF40 clearly illustrates the integration of hormone signaling and cold signaling. As a member of the AP2/ERF transcription factor family, RsERF40 not only functions in ethylene-related signaling pathways but also regulates cold-induced COR genes and cell wall remodeling processes (Zhou et al., 2025). In addition, transcription factors from the WRKY and MYB families are often regulated by hormonal signals and contribute to balancing plant growth and defense responses under low-temperature conditions (Feng et al., 2025; Qin et al., 2026). Although studies on hormone profile changes in radish under cold stress remain limited, hormone-regulated transcription factors are considered key regulatory nodes linking hormone signaling, ROS homeostasis, and sustained growth.

3.4 Key genes and molecular regulatory pathways associated with cold tolerance

Cold tolerance in radish is regulated by both CBF-dependent and CBF-independent pathways. RsWRKY40 activates RsCBF1 and RsCBF2, while also enhancing RsSPS1 expression, forming a transcriptional regulatory module that links sucrose accumulation with the classical CBF-COR signaling cascade. Similarly, RsWRKY49 transcriptionally activates RsCBF2 and RsNR2, and variations within its promoter region are associated with differences in cold tolerance among genotypes (Chen et al., 2025a).

RsERF40 represents a CBF-independent cold-tolerance pathway. This gene directly upregulates the expression of RsCOR78, RsCOR413PM1, and several cell wall-related genes, thereby promoting cryoprotectant accumulation, maintaining osmotic stability, and supporting fleshy root growth. RsMYB90 binds to the promoter of RsCOR78 and activates RsUFGT expression, enhancing anthocyanin biosynthesis and improving ROS scavenging capacity under low-temperature conditions (Li et al., 2025).

In addition to transcription factors, the GRAS family member RsSHRc is also an important regulator of cold tolerance. Its expression is induced by low temperatures, promoting ROS scavenging, reducing MDA accumulation, and increasing proline content. In this way, it links fleshy root enlargement with stress-defense mechanisms (Li et al., 2022). Radish ICE1-like factors, such as RsICE1, are connected to the widely conserved ICE1-CBF-COR regulatory module found in many plant species. Heterologous expression of RsICE1 in rice enhances cold tolerance by increasing soluble sugar and proline accumulation and reducing membrane damage (Qian, He and Li, 2024).

3.5 Advances in omics studies (transcriptomics and metabolomics)

High-throughput transcriptomic technologies have played a critical role in identifying cold tolerance-related genes in radish. Comparative transcriptome analyses between cold-tolerant and cold-sensitive genotypes revealed that genes such as RsERF40, RsSPS1, RsWRKY40, RsWRKY49, RsCDF3, and RsSHRc are significantly induced under low-temperature conditions and are closely associated with cold-tolerant phenotypes. Therefore, these genes are considered important regulators of cold tolerance (Chen et al., 2025a). In addition, genome-wide analyses of gene families such as RsCDF and RsGRAS have identified several cold-induced members and revealed their expression dynamics during different stages of fleshy root development.

Compared with transcriptomics, metabolomic research in radish is still at a relatively early stage. However, integrated transcriptomic-metabolomic studies in other crops have revealed common patterns. Cold-tolerant genotypes generally accumulate higher levels of soluble sugars, amino acids, polyamines, flavonoids, and lignin-related metabolites. At the same time, their transcriptional regulatory networks are significantly enriched in carbohydrate metabolism, phenylpropanoid/flavonoid biosynthesis pathways, hormone signaling pathways, MAPK cascades, and ROS scavenging systems (Jian et al., 2020; Wang et al., 2021; Gao et al., 2022).