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KEY TRANSCRIPTION FACTOR FAMILIES IN ABIOTIC STRESS TOLERANCE

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ABSTRACT

Plants are often exposed to abiotic stresses such as drought, salinity, temperature extremes, and oxidative stress, which markedly impair growth and productivity. Being sessile, plants depend on complex molecular mechanisms for stress adaptation, with transcription factors (TFs) playing a pivotal role in regulating stress-responsive gene expression. Major TF families, including AP2/ERF, NAC, bZIP, MYB, WRKY, HSF, and bHLH, have been widely reported as key regulators of abiotic stress tolerance in crops and model plants. These TFs modulate processes such as osmotic adjustment, ROS scavenging, ion balance, and stress signaling via ABA-dependent and independent pathways.

KEYWORDS: ABA, abiotic stress tolerance transcription factors, stress-responsive gene

INTRODUCTION

Plants, being immobile, are constantly challenged by environmental stresses such as drought, salinity, extreme temperatures, and oxidative damage. These abiotic stresses strongly influence their growth, development, and yield. Since plants cannot move away from stress like animals, they have evolved complex molecular systems to adapt and survive. A key part of this adaptation is controlled by transcription factors (TFs)-proteins that attach to specific DNA sequences and regulate the activity of stress-related genes, working like switches to turn protective responses on or off.

In the last twenty years, researchers have discovered many important TF families that help plants tolerate stress, both in model species like Arabidopsis thaliana and in crops such as rice, wheat, and maize. Among these, the AP2/ERF (DREB/CBF), NAC, bZIP, MYB, WRKY, HSF, and bHLH families play especially crucial roles. These TFs are organized into stress-responsive pathways that can be broadly divided into ABA-dependent and ABA-independent mechanisms. This article highlights the major transcription factors, their functional pathways, and their applications in developing stress-resilient crops.

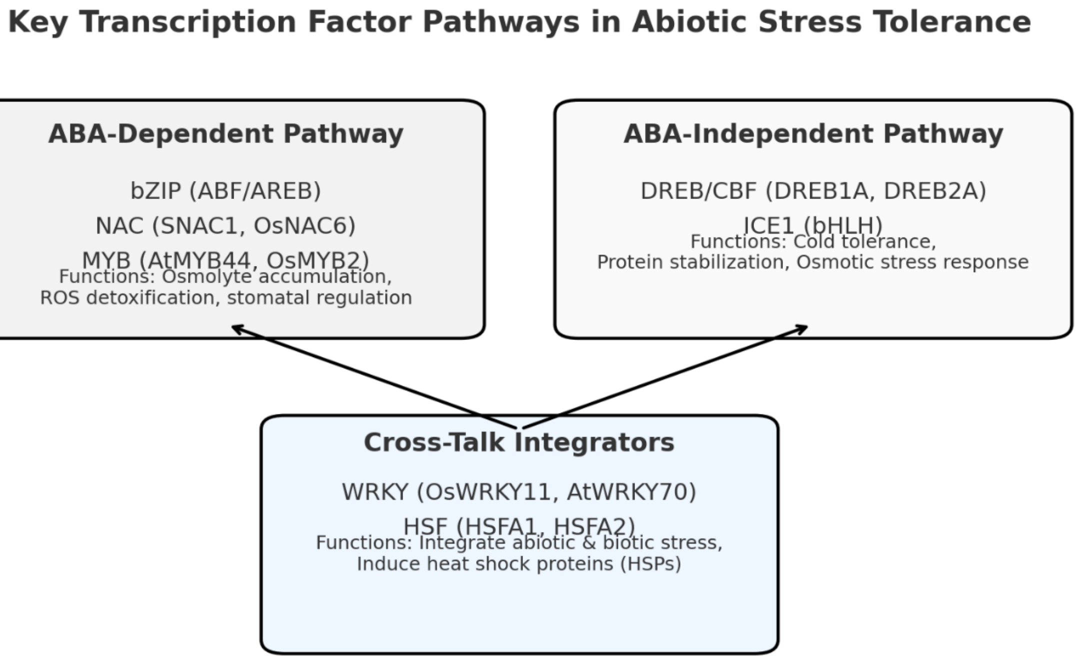

Fig: The schematic diagram showing how key transcription factors operate in ABA-dependent, ABA-independent, and cross-talk pathways for abiotic stress tolerance.

ABA-DEPENDENT PATHWAYS: GUARDIANS OF DROUGHT AND SALINITY

Abscisic acid (ABA) is a central hormone in plant stress signaling, especially under drought and salinity conditions. Transcription factors that respond to ABA play a crucial role in regulating water balance, osmolyte production, and the accumulation of protective proteins.

1. bZIP family (ABF/AREB factors): These TFs bind to ABA-responsive elements (ABREs) in promoter regions. For example, AREB1 and ABF3 in Arabidopsis regulate drought-inducible genes. In rice, OsbZIP23 plays a similar role, enhancing drought and salt tolerance.
2. NAC family: Many NAC proteins, such as SNAC1 and OsNAC6, respond to ABA accumulation. They modulate stomatal closure, ROS detoxification, and cuticle reinforcement.
3. MYB factors: Several MYBs, including AtMYB44 and OsMYB2, integrate ABA signaling with osmotic stress responses, contributing to drought adaptation.

Together, these TFs act as the first responders to water deficit by ensuring plants conserve water and maintain cellular homeostasis.

ABA-INDEPENDENT PATHWAYS: COLD AND OSMOTIC STRESS DEFENCES

1. Some transcription factors bypass ABA signaling, directly activating stress-protective genes.

2. DREB/CBF proteins: Perhaps the best studied, these TFs recognize dehydration-responsive elements (DRE/CRT) in promoters. DREB1/CBFs regulate cold-responsive genes (COR15A, RD29A) and are essential for freezing tolerance. DREB2 members respond to drought and heat stress by mediating the production of osmo-protectants and chaperones.
3. ICE1 (bHLH family): This TF activates CBF genes under cold stress, serving as a critical upstream regulator of the cold stress pathway.
4. These TFs represent the independent warriors of stress adaptation, functioning even when ABA levels remain low.

INTEGRATORS OF MULTIPLE SIGNALS

Some TFs do not strictly follow ABA-dependent or independent categories but instead act as crosstalk mediators.

1. **WRKY proteins:** Traditionally linked to pathogen defense, several WRKYs (e.g., OsWRKY11, AtWRKY46) also enhance drought and salt tolerance, suggesting a dual role in integrating biotic and abiotic stress responses.
2. **Heat Shock Factors (HSFs):** While best known for heat tolerance (HSFA1, HSFA2), HSFs also regulate oxidative stress responses, making them versatile protectors.
3. **NAC-MYB-WRKY interactions:** Many studies reveal that these TFs physically interact or regulate each other's expression, forming transcriptional hubs that balance growth, defense, and stress resilience.

TRANSCRIPTIONAL NETWORKS AND CROSS-TALK

The strength of plant stress responses lies in network-level regulation rather than the action of a single TF.

- Under drought stress, ABA levels rise, triggering bZIPs, NACs, and MYBs.
- Under cold stress, ICE1 activates CBF/DREB genes independently of ABA.
- WRKYs and HSFs link abiotic stress signaling with biotic defense and ROS detoxification.

This layered regulatory system allows plants to fine-tune their responses based on stress intensity, duration, and overlap with other stresses

APPLICATIONS IN CROP IMPROVEMENT

Harnessing TFs has become a promising strategy in crop improvement:

- Transgenic approaches: Overexpression of DREB, NAC, or bZIP TFs has enhanced stress tolerance in rice, wheat, maize, and tomato.

- Genome editing (CRISPR/Cas): Targeted modifications of TFs now allow precise control of stress-responsive networks. For example, editing negative regulators of ABA signaling can improve drought tolerance without yield penalties.
- Marker-assisted breeding: Natural allelic variations in TFs (such as drought-responsive NAC genes in rice) are increasingly used in breeding programs

CONCLUSION

Abiotic stress tolerance in plants is orchestrated by a concert of transcription factors that regulate stress-responsive genes through ABA-dependent and ABA-independent pathways. Key players such as DREB/CBF, NAC, bZIP, MYB, WRKY, HSF, and ICE1 act as master regulators, ensuring survival under drought, salinity, heat, and cold. Future agricultural sustainability will depend on integrating knowledge of these transcriptional networks into breeding and biotechnological strategies. By manipulating transcription factors, scientists can design crops that are not only resilient to environmental stresses but also capable of maintaining yield stability in a changing climate.

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