Molecular Signaling Pathways Involved in Drought Stress Tolerance in Wheat

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ABSTRACT

Wheat (Triticum aestivum L.) drought is the most restrictive abiotic stress, resulting in significant losses in growth, photosynthesis and grain output. Complex molecular signaling networks that detect a water deficiency and trigger protective reactions regulate tolerance. This mini-review summarizes the primary pathways: (i) ABA-dependent PYL-PP2C-SnRK2 signaling (ii) ABA-independent DREB/CBF regulation (iii) ROS, calcium (Ca2+) and mitogen-activated protein kinase (MAPK) signaling and (iv) downstream transcription factor (TF) networks comprising NAC, MYB, WRKY and bZIP. Stomatal closure, osmolyte accumulation, antioxidant defense, root remodeling and LEA/dehydrin protein production are all coordinated by crosstalk between these modules. Comprehending these pathways offers molecular targets for transgenic, genome-editing and marker-assisted selection methods to create wheat that is climate robust.

INTRODUCTION:

Bread wheat provides about 20% of global dietary calories and protein, but its productivity is highly vulnerable to drought. Even moderate water deficit at tillering, anthesis and grain-filling reduces tiller number, photosynthetic rate, grain number and thousand-grain weight, with yield losses of 20–60% in arid and semi-arid regions. Climate change is increasing the frequency and severity of such episodes, making drought tolerance a priority breeding trait.

Drought tolerance is quantitative and involves sensing of osmotic stress, generation of second

messengers, protein phosphorylation cascades and massive transcriptional reprogramming. Two widely interacting systems are identified in wheat: ABA-dependent signaling which mainly regulates stress-gene expression and stomatal aperture and ABA-independent signaling which is mediated by DREB/CBF, MAPK, Ca2+ and ROS and activates cellular defense and growth adaptation. Important receptors, kinases, TFs and effector genes that are conserved with rice and Arabidopsis but have wheat-specific homoeolog regulation have been found in recent transcriptome, proteomic and functional studies of hexaploid wheat. This review concisely integrates different signaling networks and their phenotypic effects to propose targets for improving wheat resilience.

1. Core Molecular Signaling Pathways for Drought Tolerance

1.1 ABA-dependent pathway: PYL-PP2C-SnRK2 core module

Abscisic acid rapidly accumulates under drought via up-regulation of 9-cis-epoxycarotenoid dioxygenase (NCED) and suppression of ABA 8′-hydroxylase. In wheat, ABA is perceived by TaPYL receptors that sequester clade-A TaPP2C phosphatases, releasing SNF1-related protein kinases TaSnRK2s (e.g., TaSnRK2.4, TaSnRK2.8, TaOST1). In order to reduce transpirational loss, activated TaSnRK2s phosphorylate two downstream targets: (a) ion channels like SLAC1 for stomatal closure and (b) bZIP TFs TaABF/TaAREB that bind ABA-responsive elements (ABRE) to induce LEA, dehydrin (DHN, Wrab) and osmolyte biosynthesis genes like Δ1-pyrroline-5-carboxylate synthase (TaP5CS). Overexpression of TaSnRK2.8 and TabZIP60 enhances stomatal sensitivity, water-use efficiency and grain yield under water deficit, confirming this module as the central drought switch.

1.2 ABA-independent pathway: DREB/CBF regulation

Parallel to ABA signaling, dehydration-responsive element-binding (DREB) TFs activate genes containing DRE/CRT cis-elements without requiring ABA. TaDREB1, TaDREB2 and TaCBF14/15 are strongly induced by drought and cold in wheat leaves and roots. They increase the expression of genes that stabilize membranes and proteins such as COR, LEA, heat-shock and aquaporin. Transgenic wheat overexpressing TaDREB2 or TaERF3 shows improved proline accumulation, chlorophyll retention and root biomass under drought. Importantly, DREB and ABF pathways converge on common effectors and exhibit crosstalk through Mediator and SnRK-mediated phosphorylation, providing fine-tuned and redundant control.

Table 1. Major signaling components involved in drought tolerance in wheat

Signaling Pathway	Key Genes / Proteins in Wheat	Function in Drought Tolerance
ABA core module	TaPYL, TaPP2C, TaSnRK2.4/2.8, TaABF/AREB	Stomatal closure, ABRE-gene activation
ABA-independent	TaDREB1/2, TaCBF14/15, TaERF3	LEA, dehydrin, COR gene induction
MAPK cascade	TaMAPKKK, TaMKK1/3, TaMPK3/6	ROS balance, growth–stress trade-off
Ca2+ signaling	TaCBL, TaCIPK, TaCDPK, TaCaM	Ion homeostasis, guard-cell regulation
ROS scavenging	TaRBOH, TaSOD, TaCAT, TaAPX	Detoxification, redox signaling
TF networks	TaNAC69, TaMYB33, TaWRKY19, TabZIP60	Osmolytes, root growth, cuticle wax

Note: Representative genes validated by expression or transgenic studies in wheat; many have A, B and D homoeologs with overlapping functions.

1.3 MAPK, calcium and ROS signaling

Osmotic signals are sent to nuclear targets by mitogen-activated protein kinase (MAPK) cascades (MAPKKK–MKK–MPK). Drought and H2O2 activate TaMPK3/6 and TaMKK1 in wheat, controlling lateral root development and antioxidant enzymes. Guard-cell turgor and stress-gene expression are regulated by calcium, which functions as a second messenger. Drought-induced cytosolic Ca2+ spikes are decoded by TaCBL–TaCIPK complexes, TaCDPKs and calmodulins. Reactive oxygen species are produced by NADPH oxidases (TaRBOH) and serve as both hazardous byproducts and signaling molecules. By coordinating the development of superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX) and the ascorbate–glutathione cycle, tolerant genotypes minimize membrane lipid peroxidation while allowing ROS-mediated ABA and MAPK crosstalk.

1.4 Transcription factor networks and crosstalk

Large TF families coordinate adaptation downstream of kinases. TaMYBs control cuticular wax and flavonoid antioxidants, TaWRKYs adjust the balance of ABA and jasmonate, TabZIPs combine light and drought signals and TaNACs (e.g., TaNAC69, TaNAC2) encourage root elongation and proline synthesis. These TFs control a variety of effector suites including osmolytes (proline, trehalose, glycine betaine), LEA/dehydrins (TaDHN, TaLEA), aquaporins and expansins for water transport and cell-wall flexibility (Figure 1). Stomatal versus growth responses are further altered by hormonal interactions with ethylene, brassinosteroids and jasmonate. Hexaploidy allows homoeologs to be sub-functionalized for stage-specific tolerance in addition to providing functional buffering.

Figure 1. Overview of drought stress signaling in wheat

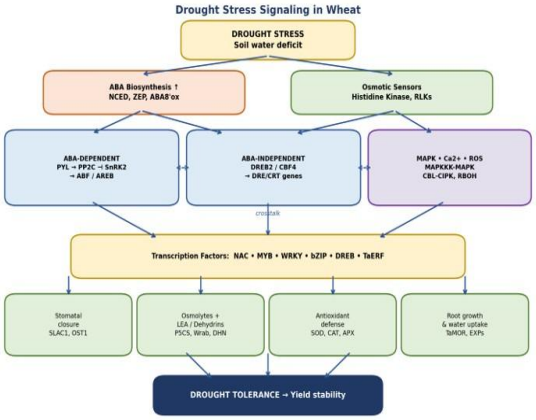


Figure 1. Drought perception triggers ABA biosynthesis and osmotic sensors that activate ABA-dependent (PYL-PP2C-SnRK2-ABF), ABA-independent (DREB/CBF) and MAPK–Ca2+–ROS modules. These converge on NAC, MYB, WRKY, bZIP and ERF transcription factors to induce stomatal closure, osmolyte and LEA accumulation, antioxidant defense and root growth, collectively conferring drought tolerance and yield stability.

CONCLUSION

Drought tolerance in wheat emerges from coordinated ABA-dependent and ABA-independent signaling, amplified by MAPK, Ca2+ and ROS messengers and executed by NAC, MYB, WRKY and bZIP transcriptional programs. No single gene confers full tolerance rather, balanced regulation of water loss, cellular protection and root architecture is critical. Future progress will depend on (i) functional validation of homoeolog-specific alleles using CRISPR/Cas (ii) integration of high-throughput phenotyping with genomic selection for signaling haplotypes and (iii) pyramiding complementary modules e.g., TaSnRK2-mediated stomatal control with TaDREB-driven cellular protection and TaNAC-mediated root traits to achieve stable yields under increasingly variable climates.

REFERENCES

Abhinandan K, Skori L, Stanic M, Hickerson NMN, Jamshed M, Samuel MA. Abiotic stress signaling in wheat – an inclusive overview of hormonal interactions during abiotic stress responses. Agronomy. 2018;8(12):267.

Gahlaut V, Jaiswal V, Kumar A, Gupta PK. Transcription factors involved in drought tolerance and their possible role in developing drought tolerant cultivars with emphasis on wheat. Theor Appl Genet. 2016;129(11):2019-2042.

Kulkarni M, Soolanayakanahally R, Ogawa S, Uga Y, Selvaraj MG, Kagale S. Drought response in wheat: key genes and regulatory mechanisms controlling root system architecture and transpiration efficiency. Front Chem. 2017;5 :106.

Sallam A, Alqudah AM, Dawood MFA, Baenziger PS, Börner A. Drought stress tolerance in wheat and barley: advances in physiology, breeding and genetics research. Int J Mol Sci. 2019;20(13):3137.