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INTEGRATED COMPREHENSION OF HEAT STRESS TOLERANCE IN WHEAT: MOLECULAR, GENETIC, MORPHOLOGICAL, AND OMICS PERSPECTIVES

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ABSTRACT: Heat stress (HTS) being one of the most important abiotic factors affects wheat's growth, development and yield formation to some extent. This is particularly the case since heat stress is most likely to exert its negative effects during two of the plant's most developmental periods – flowering and grain fill. These lethal hazards require stabilization and wheat plants developed various physiological, biochemical and molecular defence mechanisms. Of these, heat stress responsive genes are the most important category of thermotolerant genes identified to date. Some of the genes and their regulation systems that are important in relation to heat stress are HSPs, HSFs and other typically stress-responsive gene in this review in wheat. Also, we outline recent discoveries in identifying and characterizing these genes with omics methods, and their potential applications to breed heat-resistant wheat varieties. Comprehending the intricate regulatory mechanisms and roles of heat stress genes can facilitate wheat's adjustment to worldwide climate fluctuations.

KEYWORDS: Heat Stress, Wheat, Climate Change, Plants.

Introduction

Background and Importance

Wheat ranks as one of the world's key staple crops supplying most of the planet's daily calorie intake. Yet rising global temperatures and frequent heat waves threaten wheat production. Wheat have a negative effect by heat stress at different stages of growth, which lowers biomass, production of grains and quality. Heat stress is the result of temperatures above the range that is favourable for plant growth. The impact is damaging during the flowering and grain filling phases when high temperatures can cause pollen sterility smaller grain size, and reduced grain numbers. (Zampieri et al., 2017; Sehgal et al., 2018).

Mechanisms of Heat Stress Reaction

In response to heat stress, wheat plants have evolved morphological, physiological, and biochemical responses in addition to other coping methods. Activating genes that react to heat stress constitutes one of these; it is vital for the induction of defence mechanisms that enhance thermotolerance. These specific genes create heat shock proteins (HSPs), heat shock factors (HSFs), and other stress-responsive

proteins that help maintain cellular homeostasis under adverse situations. (Kumar et al., 2019; Hassan et al., 2016).

Heat-shock proteins (HSPs) and heat-shock factors (HSFs)

A substantial category of proteins produced by heat stress is called HSPs. As molecular chaperones, they help ensure that developing proteins fold correctly, refold denatured proteins, and stop proteins from clumping together. According to Kumar et. al. (2019), based on their size, they include; Tiny HSPs (sHSPs), HSP70, HSP90 and others which actively contribute to the prevention of heat damage on cellular structures. HSPs are, therefore, regulated by gene transcription factors known as HSFs, which are regulated temperature changes. Wheat has multitudes of HSFs, and in the bosom of a web of reactive signalling they are all involved in the control of stress responses. (Gupta et al., 2017). Heat stress, heat shock proteins (HSPs), and heat shock factors (HSFs) are related to each other and result in cellular responses, as explained in Figure 1.



Figure 1 illustrates the relationship between heat stress, heat shock proteins (HSPs), heat shock factors (HSFs), and the ensuing cellular responses.

Progress in Omics Methodologies

The fields of proteomics, metabolomics, transcriptomics, genomics, and other omics technologies have advanced recently and contributed significantly to our understanding of wheat's responses to heat stress. The above techniques have allowed researchers to discover new heat-responsive genes, investigate regulatory networks, and locate rapid shifts in how genes and proteins express themselves in response to heat stress (Zhang et al., 2022). The integration of omics data and conventional breeding methods permits the creation of heat-resistant wheat cultivars. (Liu and colleagues, 2020).

Review objectives

Presenting an in-depth comprehension of the role, regulation, and potential breeding implications of wheat heat stress genes is the aim of this paper. We will summarise the most important discoveries from current research, draw attention to the functions of different omics techniques, and suggest next lines of inquiry for this field. Improving wheat's resistance to heat stress and maintaining sustainable production in the face of global climate change would require addressing the molecular and genetic foundations of heat stress responses.

Wheat phenological and morphological variations during exposure to heat stress Reactions Morphological

Wheat plants that are subjected to heat stress undergo significant morphological modifications that lessen the direct effects of heat and conserve water. These types of plants grow smaller leaves that can change orientation to allow for reduced heat absorption. up order to reach water, the roots may simultaneously go longer and deeper, which could cause the plant to take up more water. Further, heat stress can occur in a manner that grain yield is affected by presenting spikelets per spike, bracts, or stems much shorter than usual. This adaptive response means the plant can only survive under conditions of high temperature, hence an assurance of its growth and productivity. (Bita and Gerats, 2013).

Phenological changes

High temperatures can alter wheat phenology, including key growth stages and their timing of development. This type of adaptation mechanisms to heat stress has a negative effect on the grain-filling duration, usually characterized by grains that are small and light (Prasad et al., 2011).

The extant styles for adding Wheat parentage and inheritable forbearance to heat Stress

• The traditional parentage: Using phenotypic webbing in hot conditions, heat-tolerant genotypes are named.

• Marker- supported Selection (Mamas) : Effective parentage is accomplished by using molecular labels associated with heat forbearance rates (Pinto et al., 2010).

• Genomic Selection (GS) : Using genome-wide labels to prognosticate parentage line performance in order to quicken the product of heat-tolerant cultivars (Gupta et al., 2017).

Progressive Biotechnologies

CRISPR/Cas9 Genome Editing: The aim is to target specific genes involved in heat stress tolerance, like TaHSFA1 and HSP genes, for boosting heat tolerance (Wang et al., 2016).
To enhance Wheat's resistance against heat stress; genes from different heat tolerant species can be incorporated using transgenic techniques (Qin et al., 2015).

Agricultural Technologies

Optimized Irrigation: Water management practices alleviate the impact of heat stress. Other practices that reduce the temperature of the soil and shield the plant from very high temperatures include mulching and shading. Plant Growth Regulators: Growth regulators can be applied, salicylic acid, and abscisic acid improve the tolerance of plants to heat (Reynolds et al., 2012).

The Omics Strategies to Abolish Heat Stress

There are different strategies that play significant role to control heat stress. **Transcriptomics**

The transcriptome examines changes that occur in the levels of gene expression due to the impact of heat stress. RNA-Seq plays a pivotal role. RNA sequencing identifies genes responding to heat as well as regulatory networks. Differential Expression Analysis is useful for genes taking part in the heat stress responses that are upregulated or downregulated (Liu et al., 2015). Moreover, transcription factors are proteins that control gene expression in response to environmental stimuli, such as heat stress. Wheat has several TF families involved in its heat stress response, including HSFs, DREB/CBF, NAC, and MYB families (Zhang et al., 2013). Recent advances have identified specific TFs that may enhance heat tolerance, such as TaHSFA1 overexpression, which activates heat-responsive genes (Li et al., 2018).

Proteomics

The proteomic study has hence reflected the expression of protein with post-translational modification due to heat stress. Plants respond to high-temperature challenge by induction of heat shock proteins. HSPs protect cells by behaving as a molecular chaperone that helps in stabilising and refolding of denatured proteins against heat-induced cellular damage. Wheat HSPs are categorized into several groups, including HSP70, HSP90, and small HSPs, according to molecular weight classification. (Chauhan et al., 2012). These proteins are induced rapidly under heat stress. Mechanism and Function: HSPs play an important role in cellular homeostasis during heat stress through interactions with denatured proteins.It has recently been demonstrated that overexpressing some HSPs in wheat is linked

to a significant improvement in heat tolerance. TaHSP70, for illustration, appears to be linked to acquired thermotolerance by preserving photosynthetic protein stability in the context of heat stress (Xue et al., 2014).

Metabolomics

Detailed research in metabolism has shown the first how a modern organism configures metabolic pathways not to offer advantage over one another but rather stress-induced and metabolite accumulation coping. The principal two metabolites are:

Primary metabolites: The profile includes primary metabolites such as sugars, amino acids and organic acid-based molecules used both for energy production and osmoprotection.

Characterization of antioxidative chemical compounds including flavonoids and phenolics collectively named as secondary metabolites (Smith and Jones., (2021).

Epigenomics and Genomics are Interrelated

Combining Genomic and Epigenomics Approaches Provided a Global Picture in Genetic and Epigenetic Regulations of Heat Stress Responses.

One of the most important applications to use GWA studies is associated with finding genetic loci involved in heat tolerance-related wheat traits. To pinpoint the exact DNA areas, called loci associated with heat tolerance, it analyzes variation across whole genome of different wheat populations. To achieve this, genetic polymorphisms such as SNPs are associated with phenotypes in the context of heat stress. These loci were found to be important for understanding the genetic basis of heat tolerance (Zhang et al., 2020) and further used in breeding programs using gene introgression or marker-assistant selection for development high temperature stress tolerant wheat varieties. In summary, our GWAS has bridged important gaps in knowledge about genetic contributions to thermotolerance underlying food yield maintenance sustainability into the future amidst global warming (Liu et al., 2021).

Epigenetic

Epigenetic variation refer to a heritable changes in gene expression that do not involve alterations of the DNA sequence.

Several epigeneticisms such as DNA methylation, histone modifications and non-coding RNAs that are also involved in heat stress response have been isolated only a few wheat plants (Liu et al., 2015).

DNA Methylation – DNA methylation patterns have been shown to be influenced by heat stress which in turn could activate or repress the expression of specific responsive genes. Several studies have demonstrated that the hypermethylation of certain gene promotor region affected expression under heat stress. Histone modifications, i.e. acetylation and methylation of the N-terminal tails of histones H3H4 or_K9,K27 _,K36), are associated with chromatin remodeling processes important for controlling gene expression. For example, several histone modifications have been associated with the expression and activation of heat stress-responsive genes in wheat.

MicroRNAs (miRNAs) and long non-coding RNAs (lncRNA): miR-NAM-0-mi2585, as well as lacy5083 were discovered to mediate the post-transcriptional regulation of gene expression under heat stress in loach. For example, details of miRNAs that target mRNAs encoding HSPs and other stress-related proteins in wheat have been well established.

Recent Developments: Recent studies have shown that the heat stress tolerance is imparted by epigenetic modifications. Wheat may be able to withstand greater temperatures by modifying these epigenetic markers (Tang et al., 2020).

Future Perspectives

The Data Integration-Omics Approaches, using Integration of data from transcriptomics, proteomics, metabolomics, and genomics will give a comprehensive view of the heat stress responses and define critical regulatory networks. Furthermore, precision breeding method advances in genomic selection and genome editing provide ways for the exact breeding of heat-tolerant wheat varieties (Varshney et al., 2017). Into the bargain Climate-Smart Agriculture method, the development of climate-smart agricultural practices through the deployment of heat-tolerant varieties along with optimized management practices will enhance wheat resilience against heat stress. Additionally global collaboration is the best way. This will require international collaboration and data sharing to accelerate the research and development process of heat-tolerant wheat varieties (Whitford et al., 2013).

Conclusion

Improved understanding of morphological and phenological responses of wheat to heat stress, in combination with recent developments in breeding and biotechnology, along with omics technologies, opens new perspectives for the improvement of heat tolerance. These studies in the future should integrate omics data, precision breeding techniques, and climate-smart agricultural practices for sustainable wheat production under rising global temperatures.

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