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EXPLORING HEAT SHOCK PROTEIN RESPONSE IN BREAD WHEAT WITH DIVERSE HEAT SENSITIVITY

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SUMMARY

The heat shock protein (HSP) plays an essential role in adaptation mechanisms under heat stress conditions. This work aimed to explore the response of HSP across seven diverse bread wheat (*Triticum aestivum* L.) cultivars. The utilized dual approach combined biochemical assessment via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) with molecular analysis through a quantitative RT-PCR. Seedlings of seven wheat commercial cultivars sustained exposure to thermal shock conditions of 45 °C for 4 h compared with a control temperature of 25 °C to elicit HSP production in significant quantities. Among the tested cultivars, Sids.1, Misr.2, and Giza.168 exhibited the highest levels of heat shock proteins, with distinct bands observed at 83, 71, 37, 36, and 31 kDa. Conversely, Gemmeiza.11 displayed the least heat shock proteins, characterized by a single band at 32 kDa. Furthermore, the thermal shock treatment affected the quantity and diversity of proteins produced by Gemmeiza.10 and Gemmeiza.7 by reducing observed bands under treated conditions. Real-time qPCR analysis proceeded to evaluate the expression of *HSP* genes utilizing RNA extracts from Sids.1 and Gemmeiza.10. The Sids.1 exhibited robust gene expression while Gemmeiza.10 displayed a low gene expression. The detected expression of HSP22 suggests a plausible involvement in conferring heat tolerance in bread wheat.

Keywords: read wheat (*T. aestivum* L.), differential heat shock response, heat shock proteins, gene expression analysis, environmental stress adaptation

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Key findings: Bread wheat (*T. aestivum* L.) cultivar Sids.1 exhibited resilience to heat stress, contrasting with the other genotype Gemmeiza.10, which showed higher susceptibility. Tolerant genotypes to heat stress displayed increased *HSP* gene expression compared with sensitive varieties.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a cornerstone of global food security, serving as a vital staple for a considerable portion of the world's population (Alomari *et al.*, 2023). It is a primary winter cereal crop cultivated in subtropical regions (Wang *et al.*, 2020). Despite its importance, it is highly sensitive to various climatic challenges, which can severely impact essential physiological processes (Yadav *et al.*, 2022). Global warming amplifies these challenges as elevated temperatures threaten wheat development and productivity (Rezaei *et al.*, 2023). Rising temperatures and the escalating frequency of heat stress threaten yield reduction and global food security, with projections suggesting a heightened incidence of heat events in the future (Becker *et al.*, 2023). The adverse effects of heat stress during critical growth stages demonstrate compromised yields and diminished grain quality, exacerbating concerns regarding wheat production and food sustainability (Yanagi, 2024). Hence, exploring adverse impacts of heat stress on wheat and planning effective mitigation strategies are essential steps in sustaining food security policies (Tadesse *et al.*, 2017).

The plant's response to heat stress involves various mechanisms, including inhibition of translation and transcription, heightened expression of heat shock proteins (HSP), and development of thermotolerance (Guo *et al.*, 2016). Notably, the elevation of HSP levels is pivotal in adaptation, regulated by heat shock transcription factors (HSF) (Divya *et al.*, 2019). Recent advancements in molecular genetics have shed light on the intricate genetic pathways governing plant responses to heat stress, unveiling complex multigene families encoding HSFs and HSPs (Chandra *et al.*, 2023). Across a broad spectrum of plants, the induction of HSPs is a prevalent phenomenon spanning various developmental stages. Remarkably, key HSPs display striking structural similarities across diverse plants, highlighting their evolutionary significance and functional conservation (de la Fuente and Novo, 2022). The induction of HSPs is a universal defense mechanism against temperature stress, protecting against detrimental effects at molecular and cellular levels. This adaptive response is crucial for enhancing plant resilience, enabling them to withstand environmental fluctuations and maintain cellular homeostasis (Kumar *et al.*, 2023).

Previous studies demonstrated HSPs are vital for plant thermotolerance, acting as molecular chaperones stabilizing and refolding denatured proteins during heat stress. In this context, Kumar and Rai (2014), Sarkar *et al.* (2021), Yadav *et al.* (2022), and Shahbaz (2024) depicted HSPs significantly protect cellular structures and maintain homeostasis under elevated temperatures. However, when subjected to heat stress conditions, sufficient information existed on the differential expression of HSPs among diverse wheat cultivars. Some studies indicate variability in HSP expression levels, suggesting certain wheat cultivars may possess unique mechanisms or enhanced capabilities for heat stress adaptation. Hence, comprehensive comparative analyses and a thorough understanding of the molecular mechanisms underlying wheat response to heat stress are pivotal for developing resilient cultivars capable of withstanding extreme thermal conditions. Therefore, this study aimed to integrate molecular analysis using biochemical assessment via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and quantitative RT-PCR and elucidate the dynamics of HSP expression in response to heat shock.

MATERIALS AND METHODS

Plant material and experimental conditions

The latest study used seven commercial wheat (*T. aestivum* L.) cultivars (Table 1). Wheat genotypes' sowing in climate-controlled greenhouses commenced at the Faculty of Agriculture, Ain Shams University, Egypt. Planting of 10 seeds continued in pots containing 2 kg of soil. The seedlings' maintenance had 25 °C and 15 °C temperatures during the day and night, respectively, with approximately 14 h day length and an average relative humidity of 65%. Fourteen-day-old wheat seedlings' exposure to heat shock stress had temperatures of 35 °C and 45 °C for 4 h for heat shock induction, while a control group remained at 25 °C. The plants received watering by hand to preserve the soil close to field capacity**.** No significant effects occurred at 35 °C compared with the control group at 25 °C. Consequently, the extraction of heat shock proteins came from seedlings exposed to 45 °C treatments.

Extraction of heat shock proteins

Seedling samples bore homogenizing with 1 ml of sample extraction buffer utilizing a mortar and pestle. The homogenate, transferred to Eppendorf tubes, sustained incubation at 4 °C overnight. Following incubation, samples reached centrifugation at 12000 rpm for 10 min at 4 °C. The resulting supernatants, containing water-soluble heat shock proteins, got collected and stored at –80 °C until further analysis.

SDS - protein electrophoresis

The SDS-PAGE proceeded to isolate and separate heat shock proteins extracted from the seven treated wheat cultivars, along with their respective control samples. Protein fractionation commenced using a vertical slab gel system, following the protocol, as described by Studier (1973).

RNA extraction and cDNA synthesis

Total RNA extraction resulted from two wheat cultivars, Sids.1 (tolerant parent) and Gemmeiza.10 (sensitive parent), with their respective controls subjected to a 4-h treatment at 45 °C. The ISOLATE II RNA Mini Kit (Bioline, Germany) served for extraction following the manufacturer's instructions**.**

The extracted RNA, then reverse-transcribed into cDNA, used the Tetro cDNA Synthesis Kit (Bioline, Germany). Conducting the first-strand cDNA synthesis generated cDNA templates for subsequent two-step reverse transcriptase polymerase chain reaction (RT-qPCR) analysis. Before use, all reagents and samples incurred thorough mixing and brief centrifuging, followed by storage on ice to maintain sample integrity.

Table 1. Name, origin, and pedigree of seven wheat cultivars used in this study highlighting their genetic backgrounds.

No.	Name	Origin	Pedigree
1	Gemmeiza.7	Egypt	CMH74A.630/5x//Seri 82/3/AgentCGM611-2GM-3GM-1GM-0GM
2	Gemmeiza.10	Egypt	MAYA74S/ON//160-147/3/BB/GLL/4/CHAT "S"/5/CROW"S"GM5820-3GM-1GM-2GM- 0GM
3	Gemmeiza.11	Egypt	BOWSKVZS//7C/SERI82/3/ GIZA168/SAKH61.GM7982-2GM-1GM-2GM-1GM-0GM.
4	Sakha.93	Egypt	Sakha 92TR 810328 S 8871-1S-2S-1S-0S
5	Sids.1	Egypt	HD2172/PAVONS// 1158.57/ MAYA 74S. SD46-4SD-2SD-ISD-OSD
6	Misr.2	CIMMYT	BAV92/ SKAUZ
7	Giza.168	Egypt	MRL/Buc//SERICM93046-8M-0Y -0M-2Y-0B

Quantitative polymerase chain reaction (qPCR)

The qPCR represents a robust and precise method for detecting specific mRNA molecules and quantifying their expression levels. Moreover, the qPCR enables the comparison of transcript levels across different samples. In the presented study, utilizing a primer targeting hsp22 helped detect the hsp22 mRNA and quantify its expression fold**.**

Novel primer pairs, designed based on the wheat hsp22 mRNA sequence (GenBank accession: AF035460), used the Geneious 8.1 software. The forward primer, Mm-F1291 (5' ATGGCTTCCATTGTCGCTTCCAGGAG 3'), and the reverse primer, Mm-R1567 (5' CTACTCGACGTTGACTTGGAACACGTC 3'), underwent synthesis by Invitrogen, UK. Employing the Primer-3 online tool assessed the designed primers' hairpin formation and self annealing. The in silico PCR tool (University of California, Santa-Cruz, http://genome.ucsa.edu) verified primer specificity, revealing the expected DNA fragment size to be 277 bp**.**

The qPCR reactions, performed in a total volume of 20 µl, contained 10 µl of 2x Sensi-FAST-SYBR® NoRox-kit (Bioline-Germany), 0.5 µl of reverse primer, 0.5 µl of forward primer, one µl of 100 ng cDNA template, and nuclease free water to reach 20 µl. The Stratagene MX3000 P machine (Agilent Technologies) had the following programmed steps: an initial denaturation at 92 °C for 2 min, followed by 40 cycles of denaturation at 92 °C for 5 s, annealing at 56 °C for 15 s, and an extension at 72 °C for 26 s. The conducted dissociation test was from 95 °C to 50 °C at 10-min intervals to assess dimerization.

Data analysis

Quantitative Polymerase Chain Reaction (qPCR) cycle threshold (CT) values' utilization estimated the relative expression levels of the *hsp22* gene. The experiment calibration used a standard concentration of 100 ng RNA across all samples to ensure consistency. ΔCT, ΔΔCT, and gene copy number's calculation used simple subtraction equations, as follows:

$$\Delta CT = CT\ HGK - CT\ HSP$$

$$\Delta\Delta CT = \Delta CT\ control\ \Delta CT\ treatment$$

$$Gene\ copy\ number = 2^{-(\Delta CT)}$$

RESULTS AND DISCUSSION

Screening using HSP through SDS-PAGE

Heat stress induces significant adjustments in plants to mitigate its detrimental effects. One crucial adaptation at the cellular and molecular levels is the synthesis of heat shock proteins (HSPs). These proteins protect cellular functions and reduce damage from high temperatures (Abasi *et al.*, 2023). In the presented study, seedlings exposed to heat stress substantially increased heat shock protein production when subjected to 45 °C compared with 25 °C (Table 2)**.** Among the assessed bread wheat (*T. aestivum* L.) cultivars, Sids.1, Misr.2, and Giza.168 demonstrated robust heat shock protein synthesis when exposed to 45 °C. The cultivars Sids.1, Misr.2, and Giza.168 exhibited the highest expression of heat shock proteins, with bands observed at molecular weights of 83, 71, 37, 36, and 31 kDa (Table 2). In contrast, Gemmeiza.10, Sakha.93, and Gemmeiza.7 gave negligible production of heat shock proteins compared with the control treatment at 25 °C**.** Moreover, Gemmeiza.11 displayed the lowest expression, with only one band observed at 32 kDa**.** Furthermore, the proteins produced in Gemmeiza.10 and Gemmeiza.7 notably received thermal shock influences, with a reduced bands' number observed under the heat treatment versus the control treatment. These findings underscore the significance of HSPs, indicating both the diversity of HSPs among cultivars and their potential role in conferring tolerance to heat stress. The obtained results are consistent with previously published reports, such as, Sarkar *et al.* (2021), who suggested early proteins and newly synthesized proteins may confer protective effects at 45 °C, thereby, facilitating healthy growth in wheat plants during recovery. Moreover, Yan *et al.* (2020)

Table 2. Electrophoretic bands of water-soluble proteins in seven wheat cultivars under control (CON, 25 °C) and heat-stress (HS, 45 °C) conditions.

Bands		Sakha.93		Gemmeiza.7		Gemmeiza.10		Gemmeiza.11		Misr.2		Sids.1		Giza.168	
No.	MW (kDa)	CON	HS	CON	HS	CON	HS	CON	HS	CON	HS	CON	HS	CON	HS
1	123	+	+	+	-	+	+	+	+	+	-	+	+	+	+
2	110	+	+	+	+	+	+	+	+	+	+	+	+	+	+
3	96	+	+	+	+	+	+	+	+	+	+	+	+	+	+
4	83	-	-	-	-	-	-	-	-	-	+	-	-	-	-
5	79	+	+	+	+	+	+	+	+	+	+	+	+	+	+
6	71	-	-	-	-	-	-	-	-	-	+	-	-	-	-
7	69	+	+	+	+	+	+	+	+	+	+	+	+	+	+
8	60	+	+	+	-	+	+	+	+	+	+	+	+	+	+
9	53	+	+	+	+	+	+	+	+	+	+	+	+	+	+
10	42	+	+	+	-	+	-	+	+	+	-	+	+	+	-
11	46	+	+	+	+	+	+	+	+	+	+	+	+	+	+
12	37	+	+	+	+	+	+	-	-	+	-	-	+	-	-
13	36	-	-	-	-	-	-	-	-	-	-	-	-	-	+
14	35	+	+	-	-	-	-	-	-	-	-	-	-	-	-
15	32	+	+	+	-	+	-	+	-	-	-	+	-	+	-
16	31	-	-	-	-	-	-	-	-	-	-	-	-	-	+
17	28	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Total bands		13	13	12	8	12	10	11	10	11	10	11	11	11	11

(+) means presence and (-) means absence of band.

demonstrated the temporal dynamics of soluble protein mobilization during early germination in wheat genotypes varied depending on the nature of the applied stress factors. Furthermore, Yildiz and Terzi (2008) investigated the impact of heat stress on soluble proteins from leaf tissues of various bread wheat cultivars. They found variations in small heat shock proteins (sHSPs) among cultivars sharing the same genome, with heat-tolerant cultivars exhibiting more sHSPs than heat-susceptible ones. Additionally, certain sHSPs were specific to particular cultivars**.**

Park and Seo (2015) emphasized the critical role of heat shock proteins (HSPs) as molecular chaperones involved in protein folding, translocation, assembly, and degradation during stress conditions, alongside their essential roles in regular cellular processes. These proteins play a crucial role in maintaining the quality control of plasma membrane resident PRRs (pattern recognition receptors) and intracellular R proteins (resistance proteins) against potential pathogens**.** In this context, Satbhai *et al.* (2016) conducted a study examining the SDS-PAGE protein profile in wheat genotypes exposed to sub-lethal to lethal heat stress (ranging from 40 °C for 2 h to 46 °C for 3 h). They observed the appearance of small molecular weight proteins with varying intensity during temperature induction treatments. Furthermore, they noted the synthesis of most normal proteins reached suppression when normal wheat seedlings sustained temperatures exceeding five degrees above the optimum growth temperature (25 °C). In contrast, inducing the translation of new proteins happens. These findings underscore the intricate molecular responses of wheat to heat stress conditions and highlight the importance of understanding the underlying mechanisms for improving heat stress tolerance in wheat breeding programs**.**

Genetic reaction to thermal stress and HSP gene expression

Candidate heat shock protein (*HSP*) gene expression assessment used RNA extracts from Sids.1 and Gemmeiza.10, employing qPCR. Identifying heat stress responsive genes in this work improves understanding of the molecular mechanisms underlying heat tolerance in diverse wheat cultivars, paving the way for future heat tolerance improvements in wheat

Table 3. Ct Values, Delta-Ct, Delta Delta-Ct, and estimated gene copy number of relative expression for two genotypes: Sids.1 (1) and Gemmeiza.10 (2).

	CT	delta Ct	ddCt	Relative expression
1C-HSP	30.65	1.71	1. 57	1.00
1T-HSP	29.08	0.14		2.97
1C-HKG	28.94			
1T-HKG	28.94			
2C-HSP	31.18	7.27	4.3	0.02
2T-HSP	32.47	2.97		0.42
2C-HKG	23.91			
2T-HKG	29.5			

C: Control, T: Treatment, HSP: Heat Shock Protein, HKG: Housekeeping gene.

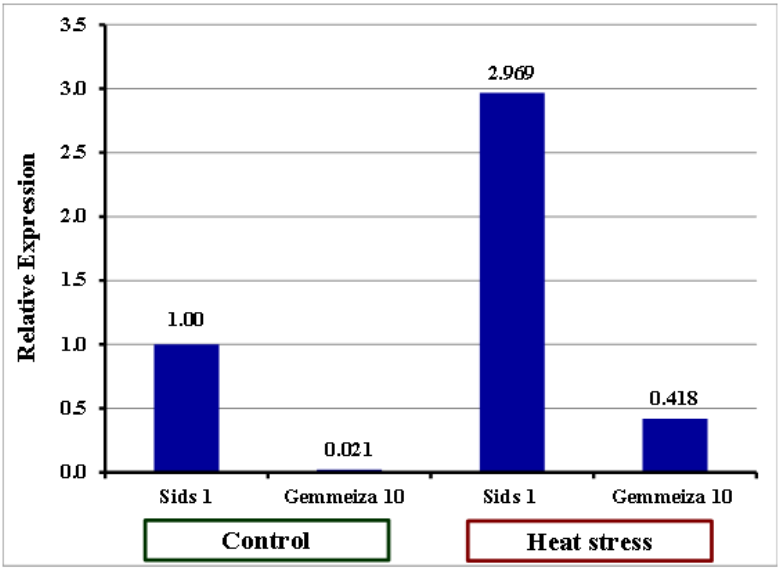

Figure 1. Relative expression of *HSP22* gene for two wheat cultivars, Sids.1 and Gemmeiza.10.

and other cereals**.** The cultivar Sids.1 exhibited notably high gene expression, with a gene copy number value of 2.97, in contrast to the cultivar Gemmeiza.10 (Table 3 and Figure 1). It indicates mRNA responsible for synthesizing HSPs is a more active transcription under high-temperature conditions of 45 °C. Such differential gene expression profiles provide eminent insights into the genotypic responses to heat stress and offer avenues for targeted molecular breeding strategies to enhance heat tolerance in wheat and related cereal crops**.**

Plant responses to elevated temperatures encompass both inherent resilience, known as basal thermos-tolerance, and the capacity to acquire thermotolerance through acclimation processes. A fundamental aspect of acclimation involves upregulating *HSP* genes, which are pivotal in bolstering plant defense mechanisms against heat stress. Numerous studies have provided compelling evidence linking the induction of *HSP* gene expression to the acquisition of thermotolerance in plants (Andrási *et al.*, 2021; Kan *et al.*, 2023)**.** Furthermore, evidence suggests a specific association between the accumulation of mitochondrial HSP transcripts and the attainment of thermotolerance. This emphasizes the critical role played by HSPs, particularly those localized within mitochondria, in improving the plant capacity to withstand heat stress and

preserve cellular homeostasis under adverse conditions**.** Understanding the intricate interplay between heat shock protein responses and acquiring thermotolerance is crucial for developing strategies to enhance heat resilience in bread wheat and other crop species. By elucidating the molecular mechanisms underlying these responses, researchers can inform targeted breeding efforts to develop heat-tolerant cultivars capable of thriving in increasingly challenging environments, characterized by rising temperatures. (Anwar *et al*., 2024; Juraev *et al*., 2024)**.**

Previous studies have shed light on the role of specific heat shock proteins in plant responses to thermal shock. Wang *et al.* (2020) elucidated the expression of HSP22 might be a critical response mechanism in plant mitochondria under heat stress conditions. Among these proteins, small HSPs (sHSPs) emerge as a prominent family induced by thermal shock across various plant species (Shahbaz, 2024)**.** In the current study, varying degrees of sensitivity to heat stress among two wheat genotypes were evident. The cultivar Sids.1 was an identified heat-tolerant genotype, whereas Gemmeiza.10 seemed heat-sensitive. Notably, the results revealed heat tolerant genotypes displayed elevated expression levels of the *sHSP* gene, particularly TdHSP22 (mitochondrial), compared with their heat sensitive counterparts. This genetic variability detected in the current study holds promise for integration into breeding programs to enhance bread wheat heat tolerance. In this context, Abu-Romman (2016) reported higher expression levels of TdHSPs in heat-tolerant durum wheat genotypes compared with sensitive ones**.** Moreover, reports of similar observations appeared in other cereal crops. Kumar *et al.* (2023) noted significantly higher expression levels of *sHSP* in heat-tolerant rice genotypes than sensitive ones, highlighting the conserved nature of this response mechanism across different plant species**.** Furthermore, Zhao *et al.* (2020) identified transcription factors upregulated by high temperatures, providing valuable insights into the regulatory networks governing plant heat stress responses. These findings underscore the complexity of gene regulation under heat stress conditions and the potential for further characterization of these factors. Zhou *et al.* (2022) explained the intricate interplay between heat shock factor and HSP response pathways under heat. These findings contribute to deeply understanding molecular mechanisms underlying heat-stress responses in bread wheat and other cereal crops, providing valuable insights for developing heat-tolerant genotypes through targeted breeding efforts.

CONCLUSIONS

The promising study assessed the genotypic responses to heat stress across seven bread wheat (*T. aestivum* L.) cultivars, revealing varying degrees of sensitivity among them. Notably, Sids.1 emerged as a heat-tolerant genotype, whereas Gemmeiza.10 displayed a higher sensitivity to heat stress. Furthermore, the investigation unveiled heat-tolerant cultivars displayed elevated expression levels of the *sHSP22* gene compared with heat-sensitive cultivars**.** The genetic variability detected in this work holds significant promise for informing breeding programs aimed at enhancing heat tolerance in bread wheat and related cereal crops like durum wheat. By leveraging this understanding of genotypic responses to heat stress, breeders can selectively incorporate heat-tolerant traits into future cultivars, thus, bolstering agricultural resilience to increasingly challenging environmental conditions, characterized by rising temperatures.

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