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Research Article

Bacterial Endophytes as Elicitors of Drought Stress Responsive Genes Expression in Wheat (*Triticum aestivum* L.)

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Abstract

Drought stress is one of the major abiotic stresses, which adversely affects plant growth and grain yield. This study aims to examine the effect of 11 different drought-tolerant plant growth promoting endophytic bacterial strains in expression of seven drought responsive genes in wheat using quantitative real-time PCR. Genes *DREB2A, CAT1* and *APX1* showed up-regulation in non-inoculated drought stressed (NC) wheat plants, while majority of the endophytic bacteria primed seedlings, displayed reduced transcript accumulation signifying their role in expression of these genes under drought stress conditions. Expression analysis of *HSP 17.8* and *SAMS1* genes also showed up-regulation in NC seedlings, while majority of the bacterial endophytes primed seedlings showed down-regulation under drought stress. Transcript accumulation of *TaCYP707A1* gene was lower in NC seedlings compared to positive control, PC (non-inoculated with water supply) seedlings but it was still higher than majority of the endophytic bacteria primed seedlings. In case of *DHN*, expression in NC was higher than PC and majority of the bacteria primed seedlings. Consequently, bacterial strains namely *Priestia aryabhattai* (KDT-WRB2), *Priestia* sp. (KDT-WRB4), *P. megaterium* (KDT-WRB5), *Bacillus subtilis* (KDT-WRB7), *B. safensis* (KDT-WRB8)and *B. zhangzhouensis* (KDT-WRB13) were recorded to alleviate the deleterious effects of the drought stress in wheat plants.

Keywords: Bacterial endophyte, drought, stress-responsive genes, wheat

1. Introduction

Global warming has led to extreme weather conditions like drought, extreme temperatures (heat or cold) and incessant rains leading to floods, posing a major threat to the agriculture worldwide. Among these, drought is one of the most widespread and unpredictable abiotic stresses, adversely affecting plant growth, physiological and metabolic processes, and ultimately leading to substantial reductions in crop productivity and yield (Vadez *et al.,* 2024). Drought mainly reduces water availability to the plants, hence affects cell expansion, photosynthesis and nutrient uptake. Further, it affects plant water potential and turgor, leading to interference with normal plant functions, and changes in physiological and morphological traits of plants (Vurukonda *et al.,* 2016). With changing climatic conditions, drought frequency and severity are projected to increase, with nearly 70% of global land area is expected to experience declining soil moisture by mid-century under a moderate-emissions scenario (OECD, 2025). Therefore, to address the challenges of increasing drought situation, adoption of sustainable practices is pivotal for ensuring long-term agricultural productivity. Out of different viable approaches, utilizing beneficial microorganisms for improving both the crop yield and soil health under drought stress is a smart and

sustainable approach. Other approaches include the development of drought-tolerant cultivars, conservation tillage, mulching, deficit irrigation, crop residue retention, and integrated nutrient management, all of which help in enhancing water-use efficiency, maintain soil moisture, and improve crop resilience under drought conditions (Fereres and Soriano, 2007; Wang and Shangguan, 2015; Yadav *et al.,* 2018).

Wheat, being one of the most important cereal crops globally, occupies the largest sowing area, and contributes to a substantial grain harvest (FAO, 2021). Drought affects wheat by way of impairing its physiology, growth, development, and reproduction (Gontia-Mishra *et al.,* 2017). However, drought-tolerant plants use different mechanisms to deal with drought stress at different levels of water scarcity (Shi *et al.,* 2017). It includes mechanisms like photosynthesis and gas exchange (Menezes-Silva *et al.,* 2017; Bryant *et al.,* 2021), nutrient translocation (Demidchik, 2015), ROS-scavenging enzymes, and osmo-protectants (Khan and Bano, 2019), transcriptional activity of genes and transposable elements (Makarevitch *et al.,* 2015). An economical and environment friendly approach to impart tolerance against drought is utilising beneficial microbes or plant endophytes. In the plant-endophyte based amelioration system, host plant supplies nutrients and provides residence to their endophytes (Arslan *et al.,* 2017), whereas, the endophytes promote the growth of the host plant through providing important minerals needed for plant growth and health, mediating plant defense system for pathogens, and stimulating contaminant mineralization (Glick, 2010; Khan *et al.,* 2013). Furthermore, they improve plant growth through various innate mechanisms (Pawlik *et al.,* 2017) like helping in better adaptation of their host to biotic and abiotic stresses; facilitating the availability of nitrogen, phosphorus, and iron; producing phytohormones; and protecting the plant against pathogens (Qin *et al.,* 2015; Abbamondi *et al.,* 2016; Santoyo *et al.,* 2016). Plant growth promoting bacteria (PGPB) can stimulate plant growth either with their director indirect involvement. The direct involvement includes production of auxins, [indole-3-acetic acid (IAA)], 1-aminocyclopropane-1 carboxylic acid (ACC) deaminase, cytokinins, gibberellins, atmospheric nitrogen fixation (nitrogenase production), phosphorus solubilization, and iron sequestration (Dobrzyński *et al.,* 2022). The indirect mechanism includes the production of antibiotics (e.g., cyclic lipopeptides), fungal cell wall degrading enzymes (including chitinases and β-1,3 glucanases), and hydrogen cyanide (HCN) and inducing plant resistance (against fungal phytopathogens) (Lipková *et al.,* 2021; Shahid *et al.,* 2021; Mirskaya *et al.,* 2022).

During stress conditions, plants undergo various physiological and biochemical adaptations through precise regulation of their gene activity. PGPRs (Plant Growth Promoting Rhizobacteria) activate genes in response to drought, promoting stress tolerance systems to improve plants' ability to withstand drought stress (Tripathi *et al.,* 2024). Furthermore, gene expression profiling has become an important approach for investigating plant responses to environmental changes by providing insights into transcriptional regulation and stress-responsive molecular mechanisms (Sanku *et al.,* 2024). Abiotic stresses can disrupt protein structure and function by promoting protein misfolding, unfolding, and aggregation, thereby impairing cellular protein homeostasis and normal biological functions (Kasim *et al.* 2013). However, heat shock proteins (HSPs) play a crucial role in mitigating stress-induced cellular damage by functioning as molecular chaperones that facilitate proper protein folding, prevent protein aggregation, and maintain protein stability and cellular homeostasis under adverse environmental conditions (ul Haq *et al.,* 2019; Georgieva and Vassileva, 2023). Similarly, dehydration-responsive element-binding (DREB) proteins constitute an important subfamily of AP2/ERF transcription factors that regulate the expression of numerous stress-responsive genes, thereby enhancing plant tolerance to various abiotic stresses (Zhang and Xia, 2023). Furthermore, dehydrins (DHNs), class II LEA proteins, protect cells under abiotic stress by stabilizing membranes and organelles, and are regulated through ABA-dependent and ABA-independent pathways (Szlachtowska and Rurek, 2023). ABA catabolism occurs mainly through hydroxylation and conjugation. The major pathway is C-8′ hydroxylation catalysed by ABA 8′-hydroxylase (CYP707A), producing 8′-hydroxy-ABA that is further converted to phaseic acid (Kumar *et al.,* 2022). The ABA catabolic enzyme ABA 8′-hydroxylase (ABA8′OH) is encoded by members of the cytochrome P450 707A (CYP707A) gene family, which play important roles in regulating ABA levels during seed development and consequently influence seed dormancy and germination (Kumar *et al.,* 2022). The *CYP707A*

genes are also reported to play a role in mediating plant response to environmental stresses such as salt, osmotic and drought stresses (Son *et al.,* 2016). PGPRs can alleviate osmotic stress in plants by modulating physiological and metabolic defence mechanisms, including the accumulation of compatible osmolytes such as amino acids and soluble sugars, thereby enhancing plant tolerance to drought stress (Chieb and Gachomo, 2023). S-adenosyl-L-methionine (SAM) is a central metabolite in one-carbon metabolism and serves as a universal methyl-group donor for numerous methyl transferase-mediated reactions involved in the biosynthesis and regulation of diverse plant metabolites (Jardine *et al.,* 2025). Therefore, it reduces the damage caused by reactive oxygen species (ROS) by boosting the activities of various ROS-scavenging enzymes like superoxide dismutase (SOD), peroxidase (POD), catalase (CAT), ascorbate reductase (APX), and glutathione reductase (GR) (Vurukonda *et al.,* 2016; Ghosh *et al.,* 2018; Carlson *et al.,* 2020). There are bacteria which help in detoxifying ROS accumulation by producing enzymatic antioxidants like SOD, POX, CAT, and APX and glutathione-S-transferases (GSTs) (Sessitsch *et al.,* 2012; Alquéres *et al.,* 2013).

The study was hypothesised to prove that endophytic bacteria may play a role in enhancing drought stress tolerance in wheat by modulating the expression level of stress-responsive genes. It was aimed to study the expression levels of stress-related genes (*DREB2A*, *CAT1*, *APX1*, *DHN*, *TaCYP707A1, HSP17.8* and *SAMS1*) in wheat seedlings exposed to eleven drought tolerant endophytic bacteria with drought endurance properties in wheat grown under artificially created drought conditions, and to relate the expression levels of these genes with their roles in drought tolerance in wheat.

2. Material and Methods

2.1 Background

Eleven endophytic bacterial strains KDT-WRB1, KDT-WRB2, KDT-WRB3, KDT-WRB4, KDT-WRB5, KDT-WRB6, KDT-WRB7, KDT-WRB8, KDT-WRB13, KDT-WRB15 and KDT-WRB16 were isolated from the roots of drought tolerant wheat genotypes *viz*., C306, NI5439, DBW110, WH1142, MP3288) grown in the Rain Out Shelter facility at ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India (29°43′N, 76°58′E, 245 m MSL). The strains listed above were identified as *Priestia megaterium, Priestia aryabhattai, Priestia megaterium, Priestia* sp., *Priestia megaterium, Bacillus pumilus, Bacillus subtilis, Bacillus safensis, Bacillus zhangzhouensis, Bacillus australimaris* and *Bacillus safensis,* respectively, on the basis of 16S rRNA gene sequencing. These gene sequences were submitted to NCBI GenBank under the accession numbers *viz*., PQ164414, PQ164417, PQ182242, PQ164427, PQ187422, PQ164430, PQ178994, PQ164436, PX312804, PX215769, respectively except strain KDT-WRB15. These strains possessed multiple plant growth-promoting traits like IAA and siderophore production, ACC deaminase activity in *in vitro*, phosphate and potassium solubilisation (data not shown). Drought mitigating effects of these bacterial strains in wheat have been studied in pots as well as under rainfed-field conditions, and plant physiological, morphological as well as yield-related traits have been studied.

2.2 Expression analysis of genes involved with drought response

The expression analysis of *DREB2A* (dehydration-responsive element binding proteins), *CAT1* (catalase), *DHN* (dehydrins), *TaCYP707A1* (cytochrome P450 monooxygenase 707A1) and *APX1* (ascorbate peroxidase), *HSP17.8* (heat shock protein) and *SAMS1* (S-adenosyl-methionine synthetase) genes was performed using quantitative reverse transcriptase polymerase chain reaction (qRT-PCR). Seedlings were grown in sterilized soil: sand mixture (3:1, w/w) under controlled conditions. Drought stress was imposed by withholding irrigation for 7 days to simulate moderate-to-severe transient drought conditions, followed by 3 days of rewatering recovery treatment. Leaf samples were collected at the seedling (two-leaf) stage immediately after completion of drought stress and recovery treatments. Total RNA was isolated from the leaf tissue of non-inoculated seedlings with water supply (positive control, PC), non-inoculated seedlings with drought induction (negative control, NC) and bacteria-inoculated seedlings using RNeasy plant mini kit (QIAGEN, Hilden, Germany). Three independent samples of each treatment were used. cDNA was synthesized in a 20 µL reaction volume using QuantiTect Reverse Transcription Kit (QIAGEN) following the manufacturer's instructions, and diluted five-fold with deionised water before using as template in qRT-PCR. 18S rRNA gene was used as an internal control to normalize

the expression levels. Gene-specific primers for each gene used for qRT-PCR analysis were designed from sequences of the respective genes downloaded from the previous studies (Table 1). The AriaMx Real-Time PCR platform (Agilent, Santa Clara, US) and Maxima SYBR Green qPCR kit Master Mix (2X) Universal (Thermo Fisher Scientific) were used for the qRT-PCR following the manufacturer's instructions. qRT-PCR cycling conditions were: initial denaturation at 95 °C for 10 min, 95 °C for 30 s and 55 °C for 1 min for 40 cycles, followed by melt curve analysis at 95 °C for 1 min, 60°C for 30 s and 95 °C for 30 s. The $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001) was used to calculate the relative expression levels of the target genes normalised to the expression level of 18S rRNA from cycle threshold values.

Table 1. Gene-specific primers used in qRT-PCR analysis

Genes	Primer Sequences	Reference
DREB2A	Forward: 5'-GAATGGATCCCGGAAAGCAC-3' Reverse: 5'-GGGAATGAACCAAGCCACAG-3'	Gontia-Mishra *et al.* (2016)
CAT1	Forward: 5'-CCATCTGGCTCTCCTACTGG-3' Reverse: 5'-AGAACTTGGACGACGGCCCTGA-3'	Moloudi *et al.* (2013)
APX1	Forward: 5'-GGAGGCTTCCTGATGCTG-3' Reverse: 5'-CGGCGTAGTCCTTGAAGAAT-3'	Kasim *et al.* (2013)
TmSAMS1	Forward: 5'-GACCCAGGTGACTGTGGAGT-3' Reverse: 5'-AGGCACGCCAATAGCATAAG-3'	Kasim *et al.* (2013)
HSP17.8	Forward: 5'-AGGATGTTCGGACTGGAGAC-3' Reverse: 5'-ACGAACTTGCGCATCATCT-3'	Kasim *et al.,* (2013)
DHN	Forward: 5'-ATGGAGCACCAGGGGC-3' Reverse: 5'-GCAGCTTGTCCTTGATCTTG-3'	Licaj *et al.* (2023)
TaCYP707A1	Forward: 5'-GCCAGGAAGCGGAACAAG-3' Reverse: 5'-AAGA GGTGCGCCTGAGTA-3'	Son *et al.* (2016)
18S rRNA	Forward: 5'-AAACGGCTACCACATCCAAG-3' Reverse: 5'-CCTTCAATGGATCCATCGTTA-3'	Stolf-Moreira *et al.* (2011)

2.3 Statistical analysis

The results of the experiment were presented as the average of three replications. The mean data obtained were statistically analysed by one-way analysis of variance (ANOVA) using OPSTAT (Sheoran *et al.,* 1998). The critical difference (CD) values were calculated at $P = 0.05$ to find significant differences between means for bacterial treatment under control and drought stress.

3. Results and Discussion

3.1 Drought mitigation and growth promotion by root Endophyles

Efficient strains of wheat root endophytic bacteria such as *Priestia aryabhattai* KDT-WRB2, *Priestia* sp. KDT-WRB4, *P. megaterium* KDT-WRB5, *Bacillus subtilis* KDT-WRB7, *B. safensis* KDT-WRB8, and *B. zhangzhouensis* KDT-WRB13 were identified as promising bio-inoculants for improving drought tolerance in wheat. Unlike previously reported PGPR studies, primarily focused on rhizospheric bacteria and physiological responses, these strains are unique due to their isolation as drought-tolerant wheat root associated endophytes and their ability to simultaneously regulate multiple drought-responsive genes under stress conditions. Drought stress is a major constraint to wheat productivity, with its effects on growth and grain yield depending largely on the timing, severity, and duration of water deficit (Poggi *et al.,* 2023). In the present study, inoculation with drought-tolerant endophytic bacteria significantly improved plant growth under stress conditions, as evidenced by 20–40% higher relative water content, 35–100% higher fresh biomass and 18–44% higher dry biomass at the seedling stage compared to uninoculated stressed plants. Mean plant height under drought stress increased from 82.0 cm in uninoculated plants to 87–95 cm in inoculated plants, while spike length increased by 10–13%. These findings align with previous reports demonstrating that plant growth-promoting rhizobacteria (PGPR) enhance plant performance and mitigate drought stress effects

(Khan and Bano, 2019). Physiological parameters including NDVI (0.57), chlorophyll fluorescence (0.775), and relative chlorophyll content (54.3 SPAD unit) were also consistently higher, while canopy temperature was reduced by nearly 12–16% in bacteria-inoculated plants indicating enhanced photosynthetic efficiency. Higher tiller number (94.7 tillers m^{-1}), grain yield and biomass (enhanced by approximately 30–35%) and grain number and thousand grain weight (increased by 16–42%) further support the positive role of endophytic bacteria in enhancing plant yield traits under drought stress. These beneficial effects can be attributed to the plant growth-promoting traits of the isolates, including nutrient solubilization [phosphate (by 10 strains) and potassium (by 6 strains)], siderophore production (by 3 strains), indole-3-acetic acid (IAA) synthesis (ranging up to 10.6 µg mL^{-1}), and ACC deaminase activity (reaching 0.421 µmol α-ketobutyrate $\mu g^{-1} h^{-1}$), as reported for similar bacterial species such as *Bacillus pumilus* (Chakraborty *et al.,* 2013; Upadhyay *et al.,* 2019).

3.2 Relative quantification of stress-responsive genes

To elucidate the molecular basis of drought tolerance, the expression of seven stress-responsive genes (Table 1) was analysed using qRT-PCR in non-inoculated drought-stressed seedlings (NC), inoculated drought-stressed seedlings, and well-watered uninoculated control seedlings (PC). Drought stress alone (NC) resulted in significant upregulation of APX1 (13.4-fold), DREB2A (6.5-fold), CAT1 (6.2-fold), and DHN (2.0-fold) compared to PC plants, indicating activation of intrinsic stress defence mechanisms. However, inoculation with endophytic bacteria modulated the expression of these genes, generally leading to their downregulation relative to NC plants. The transcription factor *DREB2A,* a key regulator of drought-responsive pathways, was markedly induced under stress but significantly repressed in inoculated seedlings (3.7–6.2-fold reduction) (Fig. 1), suggesting that bacterial association alleviates stress perception and reduces the need for activation of stress signalling pathways. Similar trends have been reported in wheat under drought conditions (Chu *et al.,* 2014; Gontia-Mishra *et al.,* 2016; Tiwari *et al.,* 2016).

A comparable pattern was observed for antioxidant-related genes. *CAT1*, involved in hydrogen peroxide detoxification, showed strong induction under drought stress but was downregulated (0.7–6.2-fold) following bacterial inoculation, except in strain KDT-WRB3 (Fig. 2). Likewise, *APX1*, a key enzyme in the ascorbate–glutathione cycle, was repressed (1.4–12.4-fold) in most inoculated treatments (Fig. 3), with a few strain-specific exceptions (KDT-WRB3, KDT-WRB15, KDT-WRB16). These results suggest reduced accumulation of reactive oxygen species (ROS) in inoculated plants, indicating improved cellular homeostasis. Inoculation with endophytic bacterial strains KDT-WRB7, KDT-WRB13, and KDT-WRB16 led to a reduction in *DHN* gene expression (0.5–1.4-fold) in drought-stressed seedlings compared to the negative control (NC). In contrast, seedlings inoculated with other bacterial strains exhibited an increase in *DHN* transcript accumulation ranging from 1.3- to 22.2-fold (Fig. 4). This differential modulation of *DHN*, which encodes protective dehydrin proteins, indicates strain-specific regulation, with some bacteria suppressing while others enhancing its expression under stress conditions. Reduced expression of these antioxidant and protective genes implies that endophytic bacteria contribute to the mitigation of oxidative stress, consistent with recent evidence that root-endophytic bacteria enhance antioxidant defence and reduce lipid peroxidation in drought-stressed wheat (Pushpad *et al.,* 2025).

The expression of *HSP17.8*, a small heat shock protein involved in protein stabilization under stress, was slightly upregulated (1.1-fold) in NC plants compared to PC plants but generally downregulated (0.03–1.03-fold) in inoculated seedlings, with minor upregulation (0.75- to 0.31-fold) observed in strain KDT-WRB3 and KDT-WRB6 (Fig. 5). Since HSPs function as molecular chaperones that protect proteins from stress-induced damage, their reduced expression in inoculated plants may indicate a lower cellular stress burden and reduced requirement for protein-folding and stabilization mechanisms, suggesting effective stress mitigation by endophytic bacteria (Wang *et al.,* 2023). Drought stress also influences hormonal balance, particularly abscisic acid (ABA), which regulates stomatal closure and water conservation (Lim *et al.,* 2015). The *TaCYP707A1* gene, encoding ABA 8′-hydroxylase involved in ABA catabolism, was downregulated (0.69-fold) under drought stress and further suppressed (0.03–0.29-fold) in most inoculated treatments (Fig. 6). This indicates that endophytic bacteria may modulate ABA homeostasis, contributing to improved drought tolerance.

The involvement of CYP707A-mediated ABA catabolism in regulating ABA levels and plant responses to abiotic stress has been well documented (Kumar *et al.,* 2022), although contrasting evidence highlights the complexity of ABA-mediated regulation (Ji *et al.,* 2011). Osmotic adjustment, a key adaptive response under drought, was reflected in the expression of *SAMS1*, which encodes S-adenosylmethionine synthase and participates in SAM-dependent metabolic processes associated with plant stress responses (Mega *et al.,* 2023). SAMS1 was upregulated (2.59-fold) in NC plants, indicating activation of osmotic stress responses, consistent with the reported involvement of S-adenosylmethionine synthetase in the response of wheat seedlings to drought stress (Licaj *et al.,* 2023). However, its expression was reduced (0.62–2.47-fold) in most inoculated seedlings (Fig. 7), except KDT-WRB1 (up-regulated by 2.20-fold), suggesting that bacterial inoculation alleviates osmotic imbalance and reduces the metabolic demand for osmolyte biosynthesis.

Overall, the results demonstrate that endophytic bacteria enhance drought tolerance in wheat by modulating stress-responsive gene expression, reducing oxidative stress, regulating hormonal balance, and improving osmotic adjustment. The general downregulation of key stress-inducible genes in inoculated plants compared to non-inoculated stressed controls indicates that bacterial association alleviates stress at both physiological and molecular levels, enabling improved growth and productivity under drought conditions. Unlike earlier studies focused mainly on physiological and biochemical responses, the present study comprehensively evaluated 11 drought-tolerant endophytic bacterial strains for their ability to modulate the expression of seven drought-responsive genes in wheat under drought stress conditions. The study uniquely demonstrates that bacterial endophytes can modulate multiple stress-responsive pathways by reducing the stress-induced overexpression of genes associated with oxidative stress (CAT1 and APX1), dehydration response (DREB2A and DHN), heat shock response (HSP17.8), ABA catabolism (TaCYP707A1), and methyl metabolism (SAMS1). The findings contribute significantly in understanding the gene-level interactions between endophytic bacteria and host plants under drought stress and support the development of eco-friendly strategies for climate-resilient wheat production.

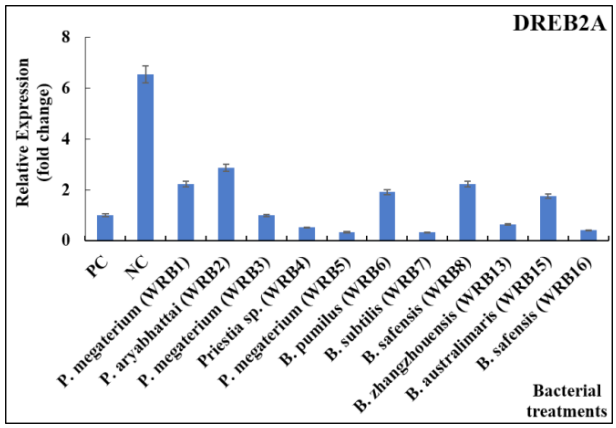

Fig. 1. Relative expression level of *DREB2A* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

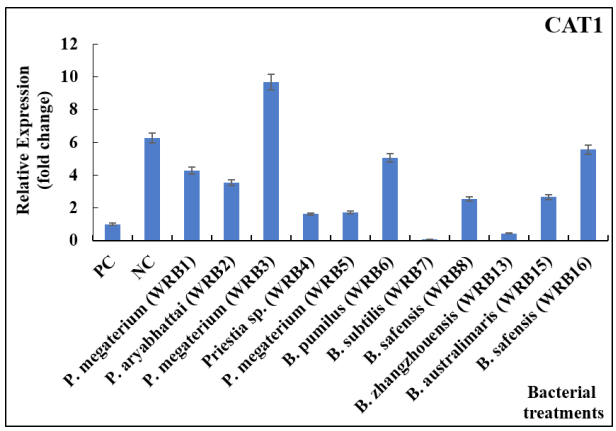

Fig. 2. Relative expression level of *CAT1* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

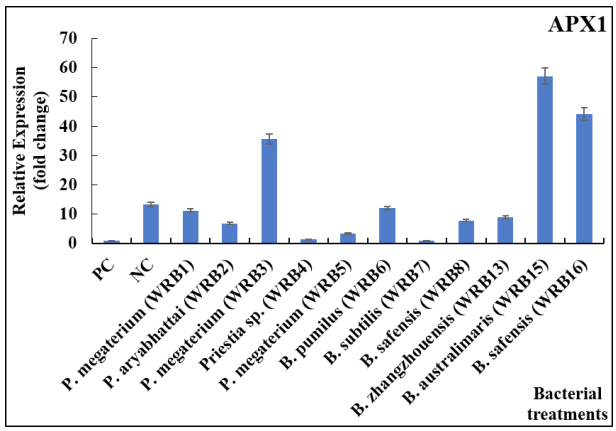

Fig. 3. Relative expression level of *APX1* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

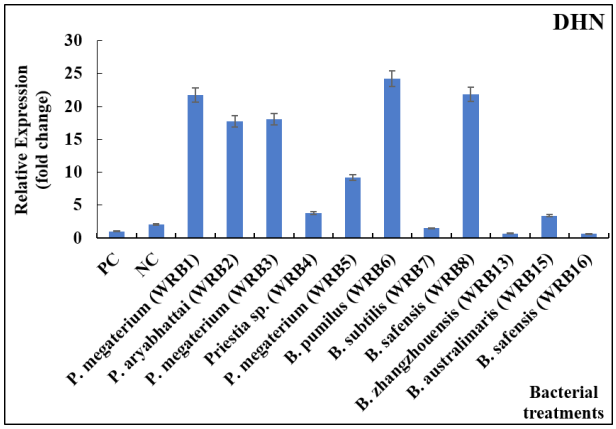

Fig. 4. Relative expression level of *DHN* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

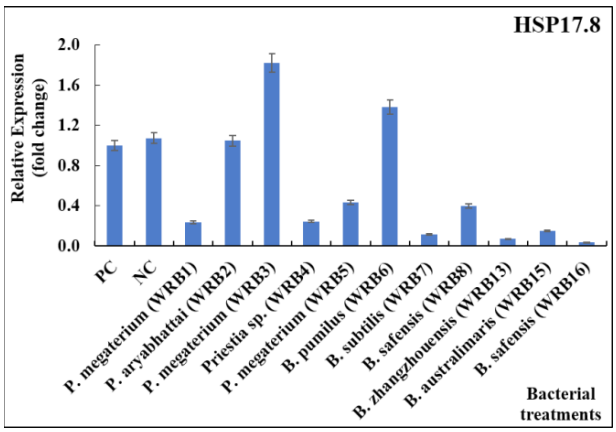

Fig. 5. Relative expression level of *HSP17.8* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

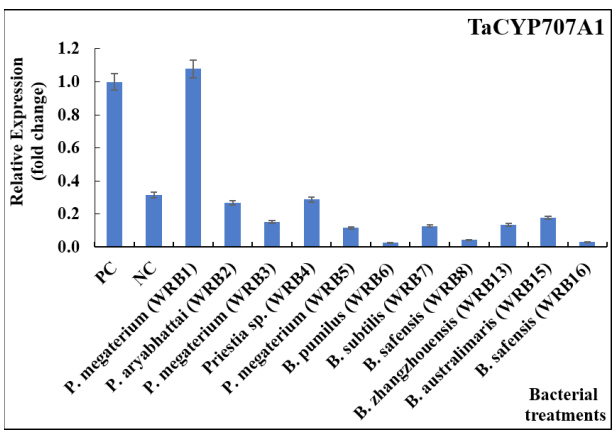

Fig. 6. Relative expression level of *TaCYP707A1* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

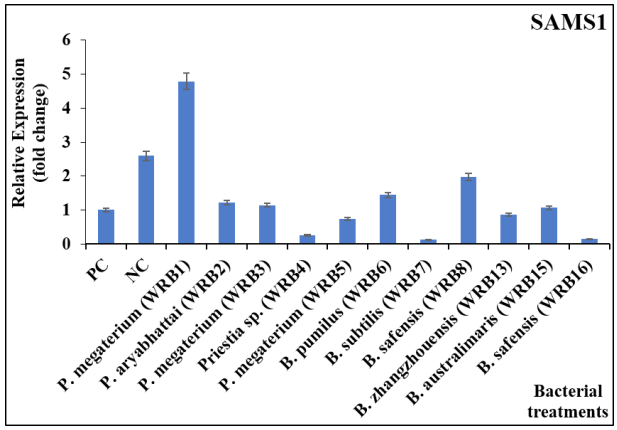

Fig. 7. Relative expression level of *SAMS1* gene in wheat seedlings inoculated with different endophytes under drought stress. Error bars show the standard deviation of the mean values of three replicates.

4. Conclusion

It can be concluded that plants survive and sustain physiological activities under severe drought stress conditions through modulation of gene regulation and metabolic pathways to reduce or repair the resulting stress damage. Here, we demonstrated that the use of potential endophytic bacteria proves to be an economical and environment friendly approach for alleviating the drought stress in sensitive wheat genotypes under stress conditions. Endophytic bacteria used in present study stimulated the stress tolerance mechanisms of wheat plants by modifying the expression of genes related to drought stress. *Priestia aryabhattai* (KDT-WRB2), *Priestia* sp. (KDT-WRB4), *P. megaterium* (KDT-WRB5) *B. subtilis* (KDT-WRB7), *B. safensis* (KDT-WRB8) and *B. zhangzhouensis* (KDT-WRB13) were the potential drought tolerant bacteria (previous study). These endophytic bacterial strains helped stressed seedlings by regulating expression of many stress-inducible genes (*DREB2A*), ROS-scavenging enzymes (*APX1* and *CAT1*), maintaining protein functionality (*HSP17.8*), free-radical scavenging (*DHN*), osmotic adjustments (*SAMS1*) and regulating ABA levels (*TaCYP707A1).* This resulted in enhanced drought tolerance and improved morphology, physiology and metabolism in host wheat plants. Based on their plant growth promoting (previous study) and drought stress alleviating properties, these endophytic bacteria can be potential candidates as bioinoculant for promoting wheat growth under adverse drought conditions.

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Conflict of interest

The authors declare that they have no conflict of interest in the publication.

Author contributions

NW – conceptualization, formal analysis, methodology and original draft writing; OPA - conceptualization, funding acquisition, project administration and review & editing; AY - review & editing; SS - review & editing

Ethical Approval

The article doesn't contain any data involving ethical approvals.

Generative AI or AI/Assisted technologies used in manuscript preparation

No

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