BIOPENDIX: Journal of Biology, Education and Applied Sciences
Volume 13, Issue 2, October 2026
Page: 114-124
https://doi.org/10.30598/biopendixvol13issue2page114-124
P-ISSN: 2407-4969
E-ISSN: 2684-8341

Original Article

OPEN ACCESS

The Role and Engineering of DREB Genes in Improving Drought and Salinity Resistance in Plants: A Systematic Literature Review

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Submitted: March 17, 2026; Accepted: March 25, 2026; Available online: July 8, 2026; Published:October 31, 2026

Abstract. This study aims to systematically examine the role, molecular mechanisms, and effectiveness of DREB (Dehydration-Responsive Element Binding) gene engineering in increasing plant resistance to drought and salinity stress. The method used is the Systematic Literature Review (SLR) method guided by PRISMA guidelines through a search of Scopus databases. Based on the results of a systematic literature review of 18 primary articles, the DREB gene has been shown to play an important role as an important factor in increasing plant resistance to abiotic stress. This gene works by activating various stress response genes through binding to DRE/CRT elements in the promoter region, thereby triggering cell protection mechanisms such as increased proline and soluble sugar accumulation, enhanced antioxidant enzyme activity (SOD, CAT, POD), and decreased ROS and MDA levels. The results of the study indicate that DREB gene engineering, especially through overexpression approaches and the use of inducible promoters, generally shows increased tolerance, although the response depends on the gene subtype and the genetic context of the plant. However, its effectiveness is greatly influenced by the type of DREB gene used, the genetic background of the plant, and environmental conditions. Therefore, appropriate selection of gene variants and field-scale testing remain necessary to ensure that increased tolerance of safe tests can be accompanied by sustained stability of results.

Keywords: DREB; Drought; Genetic Engineering; Salinity Resistance

How to cite this article:
Muarifah, M., Maghfirah, Y. M., & Hala, Y. (2026). The Role and Engineering of DREB Genes in Improving Drought and Salinity Resistance in Plants: A Systematic Literature Review. *BIOPENDIX: Jurnal Biologi, Pendidikan dan Terapan, 13*(2), 114-124. https://doi.org/10.30598/biopendixvol13issue2page114-124

Journal home page: https://ojs3.unpatti.ac.id/index.php/biopendix
Journal email: jbiopendix@gmail.com

INTRODUCTION

Global climate change has triggered extreme weather events that have a devastating impact on the sustainability of the agricultural sector and food security worldwide. Among the various environmental threats, abiotic stresses such as drought and soil salinity are two major limiting factors that drastically reduce the growth, biomass, and productivity of agricultural commodities. Plants often face these two stresses simultaneously, with the combination of drought and salinity having a synergistic negative impact that is far more damaging than either stressor acting individually (Alghamdi, 2024). Physiologically, drought triggers stomatal closure, regulated by abscisic acid (ABA) signals, to reduce water loss. This also inhibits the absorption of essential nutrients and reduces turgor pressure, which is crucial for cell division. On the other hand, high salinity not only causes osmotic stress but also triggers ionic imbalances within cells. The accumulation of toxic ions such as sodium interferes with the absorption of essential nutrients and massively triggers the production of *Reactive Oxygen Species* (ROS), which damage chloroplasts, drastically reducing the rate of photosynthesis (Alghamdi, 2024). The threat of a food crisis due to increasingly extreme environmental conditions demands the intervention of cutting-edge technology that is faster, more precise, and more efficient than conventional breeding methods.

In response to these challenges, molecular biotechnology through genetic engineering approaches offers a highly promising strategic solution for developing adaptive crop varieties (*climate-resilient crops*). These biotechnological solutions continue to evolve, ranging from single gene isolation and overexpression, promoter manipulation, gene silencing *,* to more complex approaches such as co *-overexpression* (Sugumar et al., 2024). One of the main and most effective focuses in current plant resistance engineering is the genetic modification of genes encoding transcription factors (TFs). These transcription factors act as control centers or "master regulators" *that* control the activity of many genes simultaneously. When plants experience environmental stress, these proteins activate various protective genes simultaneously so that plants can respond and survive adverse conditions (Sugumar et al., 2024; Ma et al., 2024).

Among the crucial transcription factors, the AP2/ERF (*APETALA2/Ethylene Responsive Factor*) gene family is a plant-specific protein family that is highly dominant in regulating abiotic stress responses. A subfamily of this family, the DREB (*Dehydration-Responsive Element-Binding*), has been widely identified as an essential component in molecular adaptation mechanisms (Ma et al., 2024). Anatomically, DREB proteins possess a highly conserved AP2 DNA-binding domain, consisting of a YRG region that primarily functions for DNA binding, and a RAYD element that mediates inter-protein interactions (Yadav et al., 2023). Specifically, DREB proteins work by recognizing and binding to the DRE/CRT core sequence (with the base sequence A/GCCGAC) in the promoter region of various stress-responsive downstream genes (Ma et al., 2024; Nakashima et al., 2025).

The DREB genetic regulatory network is divided into several subclasses with specific roles. The DREB1 (or CBF) gene is generally more responsive in mediating tolerance to cold and drought, while DREB2A acts as a key controller, actively responding to high salinity and dehydration stress (Nakashima et al., 2025; Yadav et al., 2023). Binding of these transcription factors to the promoter region activates the expression of specific protective genes, such as those encoding the LEA (*Late Embryogenesis Abundant*) protein, proline synthase, and betaine synthase (Yadav et al., 2023). The accumulation of osmoprotectant compounds such as proline and sugars is crucial for maintaining cell turgor, maintaining membrane stability, and neutralizing free radicals (ROS) during dehydration and osmotic stress (Todingan et al., 2025). In addition, evolutionary studies have shown that DREB genes in cereal crops are often intronless *,* a high-level adaptation that allows these genes to be transcribed very rapidly when plants face sudden stress (Yang et al., 2025).

DREB gene engineering efforts have been widely applied, particularly to secure the productivity of strategic food crops such as cereals and other monocots, which have been shown to have a very strong evolutionary relationship with DREB genes (Yang et al., 2025). At the physiological level of transgenic cereals, the presence of this gene enables plants to maintain a high Relative Water Content (*RWC*). Plants are able to regulate partial stomata closure to minimize water loss, while maintaining minimal transpiration levels to cool the leaf canopy from accompanying heat stress (Todingan et al., 2025).

The development of DREB gene research in Indonesia in recent years has shown a strong focus on the exploration and characterization of the *OsDREB2A gene* in local rice varieties as a candidate gene for drought and salinity tolerance. Research by Chrisnawati et al. (2022) analyzed *OsDREB2A gene polymorphism* in local rice varieties from Lampung and found nucleotide sequence variations that have the potential to be molecular markers of drought tolerance. Therefore, the identification of genetic variations in regulatory genes such as DREB can be utilized in marker-based selection for stress-tolerant rice breeding programs. A more comprehensive study was conducted by Yuliza et al. (2024) who explored the *OsDREB2A gene* in nine local

Indonesian rice varieties from Java, Kalimantan, Aceh, and West Sumba, with the analysis results showing that all samples had 100% *query cover* against the tolerant cultivar Pokkali and a high level of similarity (>99%) with several reference tolerant cultivars, without any changes in *the DNA-binding domain* (AP2/ERF domain) which plays an important role in regulating stress responses, and is localized on chromosome 1 at the *LOC_Os01g07120 locus* . These findings indicate that local Indonesian varieties have the potential to have a genetic basis for drought tolerance comparable to international tolerant cultivars.

Regarding salinity, research by Zakiyah et al. (2021) showed that *OsDREB2A polymorphism* in local Banten rice does not directly determine salinity tolerance, confirming that salinity tolerance is polygenic and involves complex interactions between DREB and other gene pathways such as the SOS system and hormone regulation. Meanwhile, Rini (2019) reported that *DREB2 gene sequence variations* can be used as molecular markers to identify drought-tolerant plants, thus strengthening the molecular approach in mapping candidate stress tolerance alleles as a basis for precision breeding in Indonesia. In general, DREB gene research in Indonesia has shown progress in the exploration and characterization stages of genes, particularly *OsDREB2A* in local rice varieties that have the potential to support drought and salinity tolerance. However, most studies are still limited to molecular analysis and have not yet progressed to functional validation or field testing. This condition indicates the need for more comprehensive studies to map the effectiveness and regulatory strategies of DREB genes in more depth.

Although publications on the isolation and engineering of DREB genes demonstrate tremendous potential, the application of transgenic engineering in the field still faces several fundamental challenges that create a research gap. Interventions in DREB genes sometimes trigger unexpected pleiotropic effects on other biosynthetic pathways, or even gene silencing (Yadav et al., 2023). Furthermore, constitutive overexpression of DREB genes has been reported to deplete plant metabolic energy, leading to phenotypic abnormalities and reduced yields or *growth penalties* (Todingan et al., 2025; Nakashima et al., 2025). To overcome this, precise regulatory strategies are needed, such as the use of stress *-inducible promoters* (Todingan et al., 2025). Currently, there is still no comprehensive synthesis of the latest literature that maps the effectiveness, specific regulatory methods, and dynamics of DREB gene interactions across various host plant taxa amidst the complexity of plant hormone *crosstalk.* Therefore, this *Systematic Literature Review* was prepared to examine and synthesize the literature on the role and engineering of DREB genes in improving drought and salinity resistance in plants, in order to provide a solid theoretical foundation for future precision plant breeding programs.

MATERIALS AND METHODS

This study used the *Systematic Literature Review* (SLR) method. *Systematic Literature Review* (SLR) is a research methodology used to collect, identify, and critically analyze various available research studies through systematic procedures. The literature search and screening process was carried out in a structured manner following the *Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines* (Kadir et al., 2025). The keyword combinations used by the researchers were ("DREB") AND ("overexpression" OR "transgenic") AND ("drought" OR "salinity"). This strategy helped researchers obtain literature relevant to the topic of the Role and Engineering of the DREB Gene in Improving Drought and Salinity Resistance in Plants.

The initial identification process through the Scopus database resulted in 145 articles relevant to the search keywords. Furthermore, the publication year was limited to the 2021–2026 range, reducing the number of articles to 130. The next stage was filtering based on *subject areas*, namely *Agricultural and Biological Sciences and Biochemistry*, *Genetics and Molecular Biology*, resulting in 102 articles. Further filtering was carried out by narrowing the keywords to the terms *DREB*, *transgenic*, *drought*, and *salinity*, resulting in 67 articles that were more specific to the research topic. The final stage, inclusion criteria were carried out in the form of open access *to* ensure the availability of full - *text*. Based on this filtering process, the number of articles declared eligible and eligible for analysis in this study was 18 articles. The PRISMA flowchart can be seen in Figure 1 below.

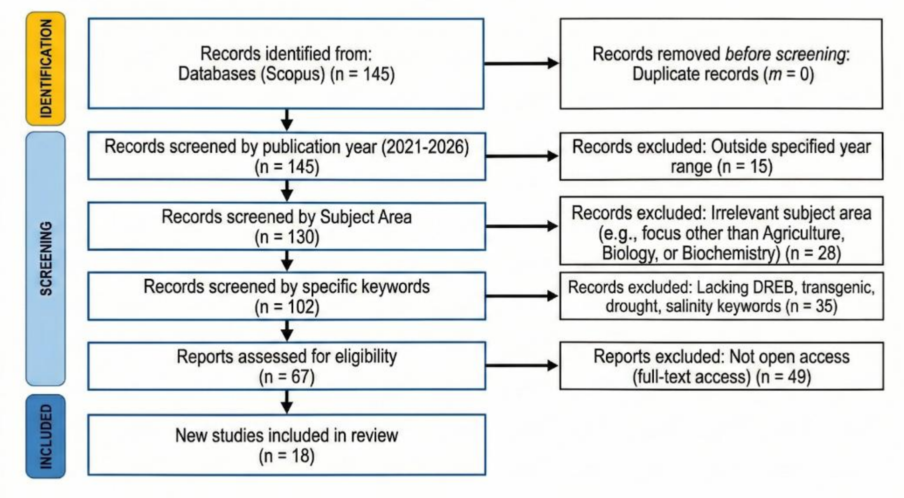

Figure 1. PRISMA Flowchart

RESULTS AND DISCUSSION

Dehydration-Responsive Element Binding (DREB) Gene

Dehydration-Responsive Element Binding (DREB) genes are a group of transcription factors in plants that play a crucial role in regulating responses to abiotic stresses, including drought, salinity, and extreme temperatures (Warsi et al., 2023). As key regulators, DREBs control the expression of various stress-response genes, enabling plants to adapt to adverse environmental conditions (Wu et al., 2022).

DREB proteins recognize the DRE/CRT cis-elements in target gene promoters and trigger the activation of adaptive genes through abscisic acid-dependent and -independent pathways (Tang et al., 2026; Dong et al., 2022). The DREB subfamily within the AP2/ERF family is classified into six subgroups, A1 to A6, with DREB1 and DREB2 being the most studied in response to low temperature and drought (Yang et al., 2025).

The crucial role of DREBs in a wide range of plants, from model to cultivated, makes them a prime target in genetic engineering research to improve tolerance to abiotic stresses (Tang et al., 2026). Furthermore, preliminary studies have shown that subgroup variation and interactions between genes influence DREB effectiveness, providing insight into their potential and limitations before being applied to genetic engineering (Warsi et al., 2023; Wu et al., 2022).

DREB Gene Engineering in Plants

DREB gene engineering in plants has been carried out through overexpression and genome editing approaches to enhance the regulation of responses to drought and salinity stress. Several studies have shown that increasing DREB expression can enhance the expression of genes involved in drought and salinity tolerance (Chen et al., 2022). However, most research has been conducted under controlled conditions in greenhouses or laboratories. These conditions do not fully reflect the dynamic field environment, so their effectiveness in real-world cultivation systems requires further testing. Plant responses to drought and salinity in the field are often complex and gradual, so results under controlled conditions may not be entirely consistent.

The use of constitutive promoters generally results in a strong increase in gene expression, but can potentially cause growth impairment under non-stress conditions. In contrast, drought- and salinity-inducible promoters offer a more physiologically appropriate approach (Kodackattumannil et al., 2023), although their effectiveness can vary across species and genetic backgrounds. Regulation of the expression system is crucial for maintaining the balance between increased tolerance and stable plant growth.

The development of genome editing technologies such as CRISPR/Cas offers the opportunity to more precisely modify endogenous DREB genes without introducing foreign genes. This approach allows for enhanced regulatory function of DREBs while maintaining the plant's genetic character. However, a deeper understanding of the regulatory network controlled by DREBs is still needed to prevent unintended consequences from changes in gene expression.

Variations in engineering approaches, promoter types, plant species, and evaluation parameters used in various studies indicate differences in results between studies. Therefore, a systematic synthesis is needed to assess the consistency and effectiveness of DREB gene engineering in improving drought and salinity tolerance. A *Systematic Literature Review* (SLR) approach was conducted to map the methods, results, and limitations of reported studies. Table 1 below presents a summary mapping of DREB gene engineering in various crops, including the type of engineering and the main results reported.

Table 1. Mapping of DREB Gene Engineering in Various Plants

No.	Researchers	Year	Plant Name	DREB Engineering Types	Findings
1	Zhou et al.	2026	Sunflower (*Helianthus annuus* L.) & *Arabidopsis thaliana*	*HaDREB1D* gene overexpression	Increase tolerance to drought stress by increasing survival & activity of antioxidant enzymes, and reducing cell damage (MDA).
2	Tang et al.	2026	Canola (*Brassica napus* L.) & *Arabidopsis thaliana*	Overexpression of *the BnaA6.TINY gene*	Increases tolerance to drought stress by stimulating stomatal closure, increasing proline, and suppressing ROS & MDA.
3	Cheng et al.	2026	Eucalyptus (*Eucalyptus grandis*) & *Arabidopsis thaliana*	Overexpression of the *EgrDREB3 gene*	Increases tolerance to salinity (and drought) stress by delaying leaf senescence, increasing photosynthetic efficiency & biomass.
4	Van der Vyver et al.	2025	Sugarcane (*Saccharum* spp.)	Overexpression of *the AtBBX29 gene* (triggers DREB)	Enhances tolerance to drought stress by delaying senescence & maintaining photosynthetic function via ABA-independent pathway.
5	Wang et al.	2024	*Lotus japonicus* & *Arabidopsis thaliana*	Overexpression of the *LjDREB2B gene*	Increases tolerance to drought stress by suppressing oxidative damage & stimulating protective antioxidant enzymes.
6	Xu et al.	2024	Banana (*Musa acuminata* L.) & *Arabidopsis thaliana*	Overexpression of the *MaDREB14 gene, 22, 51*	Increases tolerance to drought stress by reducing chlorophyll & MDA damage, and increasing proline.
7	Kodackattumannil et al.	2023	Date Palm (*Phoenix dactylifera* L.) & Tobacco (*Nicotiana tabacum*)	*PdDREB1G* Promoter Cloning	Increase tolerance to drought and salinity stress through a spatiotemporal promoter that is active only during stress with a strength of 2-4 times.

8	Zha et al.	2023	Grapes (*Vitis vinifera* L.) & *Arabidopsis thaliana*	Overexpression of the *VvDREB2c gene*	Increase tolerance to drought stress by maintaining photosynthetic efficiency, increasing photoprotective responses, and suppressing ROS accumulation which generally increases in water deficit conditions.
9	Warsi et al.	2023	Cowpea (*Vigna unguiculata*), Green Bean (*Vigna radiata*), Tomato (*Solanum lycopersicum*), Rice (*Oryza sativa*), etc.	Overexpression of various specific genes (e.g. *VuDREB2A*)	Increased tolerance to drought and salinity stress through regulation of stress response genes, increased proline accumulation, and activation of protective antioxidant systems.
10	Wu et al.	2022	Wucai Vegetables (*Brassica campestris* L.) & *Arabidopsis thaliana*	Overexpression of the *BrDREB2B gene*	Increases tolerance to drought and salinity stress by stimulating root growth and suppressing oxidative damage.
11	Mei et al.	2022	Wheat (*Triticum aestivum* L.)	Overexpression of the superior allele *TaDTG6-B^Del574*	Enhancing tolerance to drought stress without phenotypic abnormalities through activation of the protective gene *TaPIF1* .
12	Chen et al.	2022	Sugarcane (*Saccharum* sp.) & Tobacco (*Nicotiana benthamiana*)	*the ScDREB2B-1* gene	Increases tolerance to drought stress by maintaining water levels via activation of the ABA signaling pathway & antioxidant enzymes.
13	Zhou et al.	2022	Wheat (*Triticum aestivum* L.) & Soybeans (*Glycine max*)	Overexpression of the *GmTDN1 gene* into Wheat	Increase tolerance to drought stress which has a direct impact on increasing the rate of photosynthesis & crop *yield* .
14	Geng et al.	2022	Rose (*Rosa chinensis*) & *Arabidopsis thaliana*	Silencing & Overexpression of *RcTINY2 gene*	Silencing of the RcTINY2 gene reduces tolerance to salinity and drought stress in roses, suggesting a positive role for this gene in stress responses. The differential responses in Arabidopsis indicate that DREB regulation is species-specific in response to drought and salinity.

15	Dong et al.	2022	Tobacco (*Nicotiana tabacum*)	Overexpression & Silencing of *NtDREB-1BL1 gene*	Increases tolerance to drought stress by stimulating the biosynthesis of protective carotenoids to reduce ROS levels.
16	Liu et al.	2022	Desert Moss (*Syntrichia caninervis*) & *Arabidopsis thaliana*	Overexpression of the *ScDREB5 gene*	Increases tolerance to salinity stress by regulating ion homeostasis & triggering Jasmonic Acid (JA) biosynthesis.
17	Samtani et al.	2022	Wheat (*Triticum aestivum* L.)	Overexpression of the *HVA1 gene* (triggers DREB)	Increases tolerance to drought stress by improving root growth & regulating protective transcription factor genes.
18	Yu et al.	2022	Wheat (*Triticum aestivum* L.)	*TaERF-6-3A* gene	Under salinity and drought stress, this gene acts as a negative regulator that suppresses antioxidant genes, making plants more susceptible.

Based on the data mapping in Table 1, gene engineering of the DREB family has been applied to various plant groups, ranging from model plants to high-value cultivated plants. In strategic food crops such as wheat (*Triticum aestivum* L.) and rice (*Oryza sativa*), DREB gene engineering showed increased tolerance to drought and salinity by strengthening the regulation of protective genes. Plantation and industrial crops such as sugarcane (*Saccharum* spp.), soybean (*Glycine max*), canola (*Brassica napus* L.), and eucalyptus (*Eucalyptus grandis*) also showed a similar pattern of increased tolerance. Consistent results were also found in horticultural crops, including bananas (*Musa acuminata* L.), grapes (*Vitis vinifera* L.), dates (*Phoenix dactylifera* L.), roses (*Rosa chinensis*), and wucai vegetables (*Brassica campestris* L.). In addition, studies in model organisms such as *Arabidopsis thaliana*, *Lotus japonicus*, and tobacco (*Nicotiana tabacum*) strengthen the understanding of the regulatory mechanisms of DREB in response to drought and salinity.

In general, most studies indicate that DREB genes function as positive regulators in increasing tolerance to drought and salinity. However, an exception was found in study 18, where overexpression of the TaERF-6-3A gene in wheat acted as a negative regulator, suppressing the activity of antioxidant genes, thereby increasing plant susceptibility. This finding confirms that the effects of DREB gene engineering are not always uniform. The resulting response is strongly influenced by the specific characteristics of the genes and their interactions within the host plant genome.

Molecular Mechanism of DREB Genes in Drought and Salinity Response

DREB transcription factors work by binding to the cis-acting DRE/CRT elements found in the promoter regions of target genes. This binding activates the expression of various stress response genes that play a role in coping with drought and salinity stress. One example is the interaction of DREB with the promoter of certain genes, such as PSY, which has been reported to increase carotenoid biosynthesis as part of the cell's protective response to environmental stress (Dong et al., 2022). This mechanism suggests that DREB plays a key regulatory role in coordinating gene expression when plants experience abiotic stress.

One important response regulated by DREB is the activation of the antioxidant defense system. Drought and salinity can increase the production of *reactive oxygen species* (ROS), which can potentially damage membranes and other cellular components. Increased DREB expression has been reported to be associated with increased activity of antioxidant enzymes such as superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT). This increase in enzyme activity is accompanied by decreased levels of malondialdehyde (MDA), an indicator of membrane lipid damage (Chen et al., 2022).

DREB also plays a role in osmotic adjustment by increasing the accumulation of osmoprotectants, particularly proline. This compound helps maintain cell osmotic balance, maintains turgor pressure, and supports protein and membrane stability when plants are under water deficit or exposed to high salt (Chen et al., 2022). Furthermore, the DREB regulatory pathway interacts with the plant hormone signaling network. Analysis shows that overexpression of DREB can affect the biosynthesis of hormones such as jasmonic acid (JA) and regulate the expression of other stress response genes (Liu et al., 2022). This interaction strengthens the coordination of plant responses to abiotic stresses.

However, not all members of the DREB family have the same effects. Some subtypes have been reported to act as negative regulators in the stress response. These subtypes can suppress the expression of protective genes such as RD29A and the gene involved in proline synthesis, P5CS1(Yu et al., 2022). These differences in function suggest that the role of DREBs is specific depending on the type of gene being expressed.

Effectiveness of DREB Genes against Drought

Transgenic plants expressing DREB exhibit higher tolerance to drought, with improved root growth, increased survival, and relatively maintained water content compared to control plants (Chen et al., 2022; Zhou et al., 2022). Various studies have shown that increased DREB gene expression is associated with increased plant tolerance to drought. Transgenic plants expressing DREB exhibit higher survival rates, improved root growth, and are able to maintain water content relative to wild-type plants under water stress conditions (Chen et al., 2022). These results indicate that DREB activation significantly contributes to plant resilience during drought periods.

At the physiological level, DREB expression promotes increased accumulation of osmoprotectants such as proline and soluble sugars, which function to maintain water balance within cells. The activity of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and peroxidase (POD) also increases, thereby suppressing the accumulation of reactive oxygen species (ROS) and reducing malondialdehyde (MDA) levels, a marker of membrane damage (Chen et al., 2022). The expression of genes such as RD29 and LEA also helps maintain protein and membrane stability during dehydration (Tang et al., 2026).

DREB also interacts with hormone signaling pathways, particularly abscisic acid (ABA), through both ABA-dependent and -independent mechanisms (Tang et al., 2026). However, improving these physiological parameters does not necessarily directly increase crop yield. Most research is still conducted in the vegetative phase and under controlled conditions, so its effects on the reproductive phase and final plant productivity still require further study.

Agronomically, several DREB alleles with *gain-of-function traits* have been reported to increase drought tolerance without reducing plant growth or yield (Mei et al., 2022). These findings demonstrate the potential use of DREB genes in developing drought-tolerant varieties. However, further testing is needed to ensure that these increased tolerances are consistent across various environmental conditions.

Effectiveness of DREB Genes on Salinity

Salinity stress causes osmotic stress due to difficulty in water uptake by plants, as well as ion toxicity due to sodium accumulation in cells. Genes from the DREB family are known to play a crucial role in helping plants cope with these conditions. This role was demonstrated through gene silencing experiments. When DREB gene expression is suppressed, plants exhibit decreased tolerance and become more susceptible to salinity stress (Geng et al., 2022). These results indicate that DREB plays a crucial role in cellular defense mechanisms against salinity.

The effects of this regulation are evident in the physiological and morphological responses of plants. Plants that overexpress DREB *generally* have higher survival rates under salinity conditions. Primary root growth also tends to be better than control plants (Wu et al., 2022). Maintained root growth helps plants absorb water and nutrients even in environments with high salinity.

High salinity can disrupt ion balance within cells. Under these conditions, overexpression of the DREB gene has been reported to upregulate the Salt Overly Sensitive gene pathway, namely SOS1, SOS2, and SOS3 (Liu et al., 2022). Activation of this pathway plays a role in reducing excess ion accumulation within cells, thereby suppressing damage caused by ion toxicity.

Furthermore, increased DREB expression is also associated with a plant's ability to maintain relative water content. This is supported by increased accumulation of proline, an osmoprotectant, and increased antioxidant enzyme activity, which helps suppress reactive oxygen species (ROS) accumulation and reduce membrane damage (Chen et al., 2022).

Although numerous studies have demonstrated a positive role for DREBs in salinity tolerance, their effectiveness depends on the gene subtype used. Some DREB subtypes have been reported to act as negative regulators. Under high salinity conditions, such as exposure to 300 mM NaCl, overexpression of certain subtypes actually reduces plant resistance and causes severe wilting and even death (Yu et al., 2022). These findings demonstrate that the selection of DREB gene variants in genetic engineering programs must be selective and based on scientific evidence.

Advantages and Challenges of DREB Gene Engineering

Efforts to increase plant tolerance to drought and salinity stress through transcription factor manipulation are increasingly being developed because responses to both stresses involve the integrated regulation of multiple genes. *Dehydration-Responsive Element Binding* (DREB) genes act as key regulators in the drought and salinity response network. DREB proteins work by binding to the DRE/CRT cis-elements in the promoter regions of target genes, thereby simultaneously activating the expression of multiple protective genes (Wu et al., 2022). This approach is considered more effective than manipulating a single structural gene because it can regulate multiple stress-responsive genes through a single regulatory mechanism.

However, this broad regulatory capability can lead to pleiotropic effects if DREB expression is not properly regulated. Constitutive expression has the potential to disrupt plant growth by increasing resource allocation to stress responses. Under prolonged drought and salinity conditions, this can lead to reduced growth as a consequence of increased tolerance. Therefore, the success of DREB gene engineering is determined not only by increased stress tolerance but also by balanced regulation of gene expression.

The superiority of DREB is also evident in its ability to work through both ABA-dependent and ABA-independent pathways (Tang et al., 2026). The involvement of these two pathways allows plants to respond more adaptively to drought and salinity stress. However, the resulting response is still influenced by genetic factors and environmental conditions. Some DREB alleles have been reported not to cause significant growth reduction (Mei et al., 2022), but the consistency of this response still requires further testing at the field scale and across various growing seasons. Therefore, the application of DREB gene engineering requires consideration of the expression system, plant genetic background, and environmental cultivation conditions.

CONCLUSION

Based on the results of a systematic literature review of 18 articles, the DREB (Dehydration-Responsive Element Binding) gene plays an important role as a transcription factor in increasing plant resistance to drought and salinity stress. This gene works by activating various stress response genes through binding to the DRE/CRT element in the promoter region, thereby triggering cell protection mechanisms such as increased accumulation of proline and soluble sugars, strengthening the activity of antioxidant enzymes (SOD, CAT, POD), and reducing ROS and MDA levels.

The study results indicate that DREB gene engineering, particularly through overexpression approaches and the use of inducible promoters, generally improves plant tolerance without causing significant growth impairment. However, its effectiveness is influenced by the type of DREB gene used, the plant's genetic background, and environmental conditions. Therefore, selecting the appropriate gene variant and field-scale testing are still necessary to ensure that increased stress tolerance is accompanied by sustained yield stability.

ACKNOWLEDGEMENTS

The authors would like to thank colleagues who have provided valuable input and suggestions during the preparation of this systematic literature review.

CONFLICT OF INTEREST

The authors declare no conflict of interest and take full responsibility for the content of the article, including the implications of AI-generated content.

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