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# Salt Tolerance Domestication in Pitaya: Genetic Regulation of Ion Homeostasis, Osmoregulation, and Root System Architecture

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**Abstract** Pitaya, due to its heat, drought and poor soil tolerance, is widely cultivated in saline-alkali lands in Southeast Asia, the Middle East and other regions. But, salt stress remains an important factor affecting its yield and growth. To enhance its adaptability in saline-alkali environments, this study has sorted out the genetic regulatory mechanism of pitayat's salt tolerance, focusing on three major aspects: ion balance, osmotic regulation and root structure. Several key genes, like *HuTZF3*, *HuERF1* and *HuBADH*, have been identified in the research, which play significant roles in regulating ion transport, antioxidant response and root development. Based on transcriptome and functional verification data, a regulatory network of these genes has been initially established. The study also summarized several current strategies for salt-tolerant breeding, including field screening, MAS, GS and gene editing. The results show that, if the salt tolerance potential of wild resources is combined with precise molecular tools, it is expected to accelerate the breeding process of new salt-tolerant varieties. This study provides ideas and technical paths for the in-depth research, and breeding application of pitaya's salt tolerance.

**Keywords** Pitaya; Salt stress; Ion homeostasis; Osmotic regulation; Root system structure; Gene regulation

## 1 Introduction

Pitaya (*Hylocereus* spp.) was originally a tropical crop in Central and South America. It likes high temperatures, is drought-resistant, and is not picky about soil. In recent years, its cultivation range has expanded to many arid areas in Southeast Asia, Africa, and the Middle East (Carvalho et al., 2022; Oliveira et al., 2022; Xu et al., 2023). In marginal areas where water resources are scarce and the soil is saline, other crops are difficult to survive, but pitaya can grow well, so it has gradually become an economic crop that many countries have focused on promoting (Lee and Chang, 2024). Especially in some areas severely affected by salinization, it is seen as an option that can balance economic benefits and ecological restoration. Compared with traditional crops that rely on large amounts of water and fertilizer, pitaya has less demanding resources and is considered to have certain potential in achieving sustainable agriculture.

Pitaya can deal with some salt in the soil, but too much still causes trouble. High salt levels can stop seeds from sprouting well, slow down seedling growth, and cut down the final harvest. Kenanoğlu et al. (2023) reported that, when salt (NaCl) reached 2,500 ppm, the seed germination rate dropped by about 30%. At 5,000 ppm, plant growth went down by around 45%. Salt also made seedlings shorter and weighed less. These problems make it hard to grow pitaya in salty or alkaline soil. Other studies, like those by Carvalho et al. (2022) and Oliveira et al. (2022), have pointed this out too.

Generally speaking, wild pitaya species have richer genetic diversity and stronger stress resistance traits than cultivated species, which may have been partially lost during conventional breeding. Therefore, utilizing the genetic potential of wild relatives and introducing or enhancing salt tolerance traits in cultivated species are crucial to improving the adaptability of pitaya under adverse conditions (Razzaq et al., 2021).

As the area of salinized cultivated land continues to expand, it has become increasingly urgent to improve the salt tolerance of pitaya. It is no longer possible to deal with this problem by conventional planting methods, and more targeted genetic improvement strategies must be introduced. In recent years, progress in genomics and transcriptomics has gradually revealed some genes that are critical to salt stress response, such as *HuTZF3*, *HuERF1*, and *HuBADH* (Nong et al., 2019; Qu et al., 2020; 2023; Xu et al., 2023). These genes play a role in maintaining ion balance, regulating osmotic state, and coping with adversity, providing a specific entry point for subsequent molecular breeding, and biotechnology interventions.

This study focuses on the response of pitaya to salt stress and explores its genetic mechanisms in maintaining ion balance, regulating cell osmotic pressure and shaping root structure. Based on the collation and analysis of related studies on wild species and cultivated species, a number of key genes and their regulatory networks that may be related to salt tolerance traits were screened out. This study hopes to gain a deeper understanding of the salt tolerance mechanism of pitaya and provide a reference direction for genetic improvement to increase its yield and sustainable use in marginal lands such as saline-alkali land.

## 2 Physiological and Morphological Basis of Salt Tolerance in Pitaya

### 2.1 Ion toxicity and osmotic stress effects in pitaya

Under salt stress, the first thing that pitaya is hit by is the imbalance of ion concentration in the body. Especially $Na^+$ and $Cl^-$, once they accumulate excessively in the cells, they will disrupt the internal homeostasis. This not only affects the normal progress of metabolic reactions, but also triggers oxidative stress-cells begin to produce a large amount of reactive oxygen (ROS), resulting in damage to cell membranes, proteins, and even genetic material, and a significant decrease in the overall vitality of the plant (Qu et al., 2020; 2023; Xu et al., 2023). However, plants are not completely passive, they will try to adjust. Antioxidant enzymes, like catalase and peroxidase, will activate defense mechanisms to remove ROS and minimize damage. Although this reaction is a "passive response", it is an important part of plant survival.

High salt environments, also cause osmotic stress, which means that although there is water in the soil, the plant cannot absorb it. After the cells lose water, the state will deteriorate rapidly - the seeds will not germinate, the seedlings will grow slowly, and the biomass of the whole plant will be significantly reduced. A study on red-skinned pitaya (*H. costaricensis*) found that, under a salt concentration of 6.6 dS/m, the total dry weight of the seedlings decreased by more than 40% (Oliveira et al., 2022). This is not an extreme case. Other experiments have also shown that under higher salinity, the overall growth of pitaya may only be 70% of the original level, and the seed germination rate will also drop significantly (Orozco et al., 2017; Carvalho et al., 2022; Kenanoğlu et al., 2023). Obviously, in the entire life cycle of pitaya, the early stages are particularly sensitive to osmotic imbalance, which cannot be ignored.

### 2.2 Pitaya root system adaptations under salinity

Under salt stress, pitaya roots will become thicker and have more branches. These changes help expand the range of soil exploration and enhance the ability to obtain water and nutrients from limited soil. Experiments have been verified. Sousa et al. (2021) treated *Hylocereus undatus* seedlings with water of two salinities, 0.3 dS/m and 5.0 dS/m, and also combined shading and full light settings. The results showed that under “shading + low” salt conditions, the root dry weight increased significantly. This change may indicate that the roots of pitaya can "stimulate potential" under certain stress combinations. Although there is still a lack of direct observational evidence for the formation of structures such as aerenchyma, transcriptome data have given clues: many stress-related genes are active in the roots (Nong et al., 2019; Xu et al., 2023).

A common strategy for pitaya to cope with salt stress is to adjust the root-to-crown ratio, that is, to "invest more resources underground." The roots grow, but the aboveground parts do not necessarily grow. This tendency has been clearly observed in experiments. Oliveira et al. (2022) conducted a 120-day salt stress experiment and set four different salt concentrations (0.6, 2.6, 4.6, and 6.6 dS/m). The results showed that although the overall growth of the plants was inhibited, the proportion of root dry weight continued to increase, and the root/stem dry weight ratio also increased significantly. In other words, pitaya chooses to "keep roots" under stress in order to absorb water and regulate ions more effectively. Similar changes also include increases in root length and root volume (Orozco et al., 2017), which further enhances its ability to survive in high-salt environments.

### 2.3 Salt exclusion and tissue tolerance mechanisms

Pitaya has ways to protect itself from salt damage. One way is by stopping too much sodium ($Na^+$) and chloride ($Cl^-$) from getting into the parts of the plant that are more sensitive. It chooses which ions to take in and puts the extra salt into safer places. Some studies have found that genes, like *HuTZF3* and *HuERF1,* help with this. These genes help the plant move ions around and send out stress signals, so it can handle salty soil better (Nong et al., 2019; Xu et al., 2023). Pitaya also stores extra salt in vacuoles or in certain tissues. This helps the plant keep its ion levels steady and makes sure its cells can keep working normally.

In addition, the upregulation of osmotic regulation-related genes (such as *HuBADH*) can promote the synthesis of compatible solutes such as glycine betaine, thereby enhancing the tolerance of tissues to high salt environments (Qu et al., 2023). The *HuBADH* gene of *Hylocereus undatus* was cloned and transformed into Arabidopsis. The results showed that under salt stress, the betaine content of the transgenic strain was 70%-80% higher than that of the wild type, and 32%-36% higher under no stress.

## 3 Genetic Regulation of Ion Homeostasis in Pitaya

### 3.1 Ion transporters involved in salt tolerance in pitaya

Ion homeostasis is a key component of plant salt tolerance, which is mainly maintained by regulating the transport of sodium ions ($Na^+$) and potassium ions ($K^+$) to maintain intracellular ion balance (Shen et al., 2015). At present, the specific ion transporters in pitaya have not been systematically identified, but the research on related species and the discovery of stress-responsive genes in pitaya indicate that it may have similar regulatory mechanisms. Under salt stress conditions, the effective regulation of ion transporters is of great significance for reducing ion toxicity and maintaining normal physiological functions of plants.

In pitaya, stress-responsive genes related to ion transport may be regulated by transcription factors activated by multiple abiotic stress signals. In the RNA-Seq study, 2 624 differentially expressed transcripts were detected at 3, 7, and 30 hours after 450 mM NaCl treatment, of which 261 were continuously upregulated. These genes are widely involved in pathways such as glycolysis, metabolic regulation, and ion transport (Nong et al., 2019). In-depth research on these genetic regulatory mechanisms will provide important targets for the breeding and biotechnology improvement of salt-tolerant pitaya varieties.

### 3.2 Transcriptional control of ion balance genes in pitaya

In pitaya, transcription factors play a key role in regulating the expression of genes related to ion homeostasis. Hu et al. (2022) systematically identified and analyzed the pitaya NAC transcription factor family at the whole genome level for the first time, identified a total of 64 *HuNAC* genes, and divided them into 15 subclasses through phylogenetic trees. The study found that *HuNAC* genes are unevenly distributed on 11 chromosomes, and family expansion mainly depends on segmental duplication events. Under cold stress treatment, the expression levels of *HuNAC7*, *HuNAC20*, *HuNAC25* and *HuNAC30* were upregulated, indicating that they may be involved in the cold resistance response of plants.

In addition, *HuNAC20*, *HuNAC25* and *HuNAC30* are concentrated in the nucleus in subcellular localization, and exhibit transcriptional activation functions in yeast and tobacco leaves, while *HuNAC7* behaves as a transcriptional repressor. Further functional validation experiments showed that Arabidopsis overexpressing *HuNAC20* and *HuNAC25* showed higher survival rates and lower ion leakage, MDA and ROS levels after low temperature (−6 °C) treatment, indicating that their cold resistance was significantly enhanced.

Molecular analysis showed that the expression of cold-responsive genes (such as *AtRD29A*, *AtCOR15A*, *AtCOR47* and *AtKIN1*) was also significantly upregulated in these transgenic plants, and its mechanisms included reduced ion leakage and improved cell stability. Although the direct targets of these transcription factors in pitaya have not been fully elucidated, their nuclear localization and transcriptional activation properties indicate that they play a central role in regulating the expression of genes that maintain ion homeostasis under abiotic stress.

## 4 Osmoregulation Pathways and Genetic Control in Pitaya

### 4.1 Compatible solutes and osmoprotectants

When pitaya faces salt stress, it uses some special small molecules to keep the water balance inside its cells. One of these important molecules is betaine. The plant makes more of it to help deal with the stress. A key enzyme called betaine aldehyde dehydrogenase helps make betaine, and it's produced by the *HuBADH* gene. This enzyme helps pitaya keep its cell pressure steady and protects the cell from salt damage. Researchers have tested this in other plants by putting the *HuBADH* gene into them. The results showed that these plants had more betaine and were better at handling salty conditions. They also had lower levels of harmful reactive oxygen species (ROS) and stronger activity of antioxidant enzymes (Qu et al., 2023).

When pitaya and genetically modified *A. thaliana* plants face salt stress, the *HuBADH* gene and other related stress-response genes become more active. This shows that these small protective molecules, called compatible solutes, play a role in helping plants deal with salty conditions. They help keep proteins and cell membranes stable, and they also help remove harmful substances like ROS. This helps the cells stay balanced and healthy even under stress.

### 4.2 Signal transduction and hormonal regulation

Signal pathways and plant hormones work together to help pitaya respond to salt stress and stay balanced. One important gene is *HuERF1*. This gene gets turned on when the plant is under salt stress or when it senses ethylene, a common plant hormone (Qu et al., 2020). When scientists made plants produce more *HuERF1*, those plants became better at handling salty conditions. They had less cell damage and stronger antioxidant activity. This means *HuERF1* is likely part of the ethylene signal system that helps the plant fight salt stress (Figure 1).

Li et al. (2022) also found that in fresh-cut pitaya, ethylene pretreatment induced the expression of key genes of the ethylene signaling pathway, such as *HuERF1*, *HuEIN3*, and *HuETR1/2*, which in turn up-regulated the phenylpropane metabolism pathway and promoted the accumulation of total phenolics and flavonoids, contributing to antioxidant and preservation effects.

When *HuERF1* is turned on, it also activates other related genes. This shows how plant hormones help the plant sense changes in the environment and start a protective response. Thanks to this system, pitaya can quickly change how its body works-like adjusting water balance and metabolism-to reduce the harm caused by salt stress (Qu et al., 2020).

## 5 Genetic Basis of Root System Architecture Under Salinity in Pitaya

### 5.1 QTLs and candidate genes controlling root traits

Root traits like depth, angle, and how many roots grow are very important for plants to survive in salty soil. In other crops, scientists have found some key genes called QTLs-like *DRO1*-that control how roots grow. These genes help roots grow deeper or in certain directions to avoid salty layers in the soil, which helps the plants grow better and produce more even under salt stress (Kitomi et al., 2020). These genes can be used to help breed new salt-tolerant plants. They work by changing how roots grow in shallow or deep soil. For pitaya, there are not many studies yet that locate such QTLs, but it's very possible that similar genes also help control how pitaya roots grow.

Under salt stress, the signaling pathway of growth hormone and cytokinin is important for the regulation of root architecture. In pitaya, ethylene-responsive factors such as *HuERF1* are up-regulated in expression under salt stress and contribute to enhanced salt tolerance, suggesting that hormone-regulated gene networks have a central role in root adaptation to salt stress (Qu et al., 2020). In other model plants, genes involved in growth hormone synthesis, such as *CYP79B2*, as well as the *HKT1* gene, which affects ion transport, have been found to be closely associated with lateral root development and root distribution remodeling, especially under salt stress conditions (Julkowska et al., 2017).

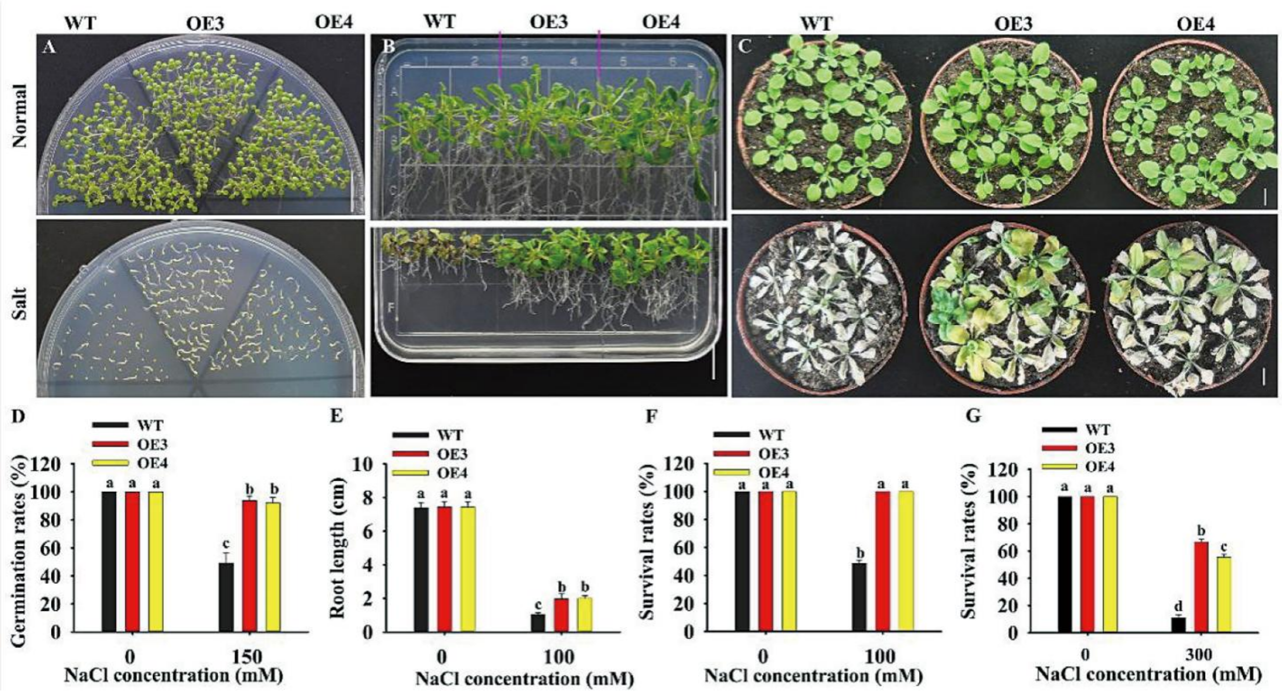

Figure 1 Overexpression of *HuERF1* enhances *Arabidopsis* tolerance to salt stress. (A,D) Overexpression of *HuERF1* improves the seed germination of *Arabidopsis*. Seed germination of *HuERF1*-overexpressing *Arabidopsis* (OE) on MS medium with 0 or 150 mM NaCl for 6 days (A), and germination rates (D) were measured. (B,E,F) Overexpression of *HuERF1* improves the tolerance of *Arabidopsis* growth to salt stress on MS medium. *Arabidopsis* seedlings were grown on MS medium with 0 or 100 mM NaCl for 15 days, root length (E) and survival rates (F) were measured. (C,G) Overexpression of *HuERF1* improves the tolerance of *Arabidopsis* growth to salt stress in pots. The seedlings were grown in pots for 3 weeks with 300 mM NaCl, survival rates (G) were measured. Different letters (D–G) indicate a significant difference at $p < 0.05$, ANOVA followed by Fisher's LSD test. Mean values and SDs of three biological replicates are shown. Bars = 1 cm (Adopted from Qu et al., 2020)

Image caption: The figure shows that the transgenic plants showed significantly higher seed germination, root length and survival rate under 150 mM NaCl treatment than the wild type, as well as stronger growth advantage under potting salt stress (300 mM NaCl). The results indicated that *HuERF1* overexpression significantly increased the salt tolerance of plants, supporting its positive regulatory effect (Adapted from Qu et al., 2020)

### 5.2 Root transcriptome responses to salt stress in pitaya

Transcriptome analysis of pitaya root system under salt stress conditions revealed large changes in gene expression in different root zones. RNA-Seq studies showed that a total of more than 2,600 transcripts showed changes in expression levels at different time points after salt treatment, reflecting the existence of a dynamic molecular response process in root tissues under stress (Nong et al., 2019).

Among these differentially expressed genes, some of them were consistently up-regulated during salt stress, mainly including related genes involved in glycolysis/glycolysis and antioxidant defense. Changes in the expression of these genes may help root cells maintain metabolic homeostasis and enhance stress tolerance, supporting the sustained growth and functional maintenance of pitaya in saline environments (Nong et al., 2019; Qu et al., 2020).

### 5.3 Root trait heritability and domestication potential in pitaya

In other plant species, studies have documented natural variation in root traits among genotypes under salt stress conditions and confirmed the high heritability of traits such as root angle and lateral root density (Julkowska et al., 2017; Kitomi et al., 2020). Pitaya-related studies are not yet sufficient, but the differences in salt tolerance exhibited among different varieties imply the existence of potential genetic diversity in its root system structure.

The identification of stress-responsive genes and the preliminary validation of the heritability of root traits provide a good basis for breeding pitaya for salt tolerance. By screening varieties with excellent root architecture traits, such as suitable root angle with well-developed lateral root formation capacity, these traits can be integrated into domestication strategies to produce pitaya cultivars that are better adapted to saline environments (Nong et al., 2019; Kitomi et al., 2020; Qu et al., 2020).

## 6 Case Studies

### 6.1 Selection of tolerant genotypes in saline fields

With global climate variability and the expansion of saline areas, screening and breeding salt-tolerant pitaya varieties has become a key direction for germplasm improvement. Studies have shown that red-fleshed pitaya (*H. costaricensis*) is generally more saline-adapted than white-fleshed pitaya (*H. undatus*), especially in terms of seed germination rate, growth potential and biomass accumulation under high salt concentration, pre-osmosis treatments, and organic amendment conditions (Carvalho et al., 2022; Kenanoğlu et al., 2023). This suggests that there are stable salt tolerance differences among pitaya germplasm and provides direction for exploring mechanisms at the molecular level.

Xu et al. (2023) identified 81 CCCH-type zinc finger protein genes through genome mining, among which *HuTZF3* was induced to be expressed under salt and heat stress and was highly expressed in roots and stems (Figure 2). Heterologous expression validation showed that *HuTZF3* enhanced root length and survival in *Arabidopsis* under high salt environment, and improved antioxidant capacity by elevating CAT and POD activities and reducing ROS accumulation. In addition, *HuTZF3* was localized to PBs and SGs particles under stress, suggesting that it is involved in the salt tolerance mechanism by regulating RNA metabolism.

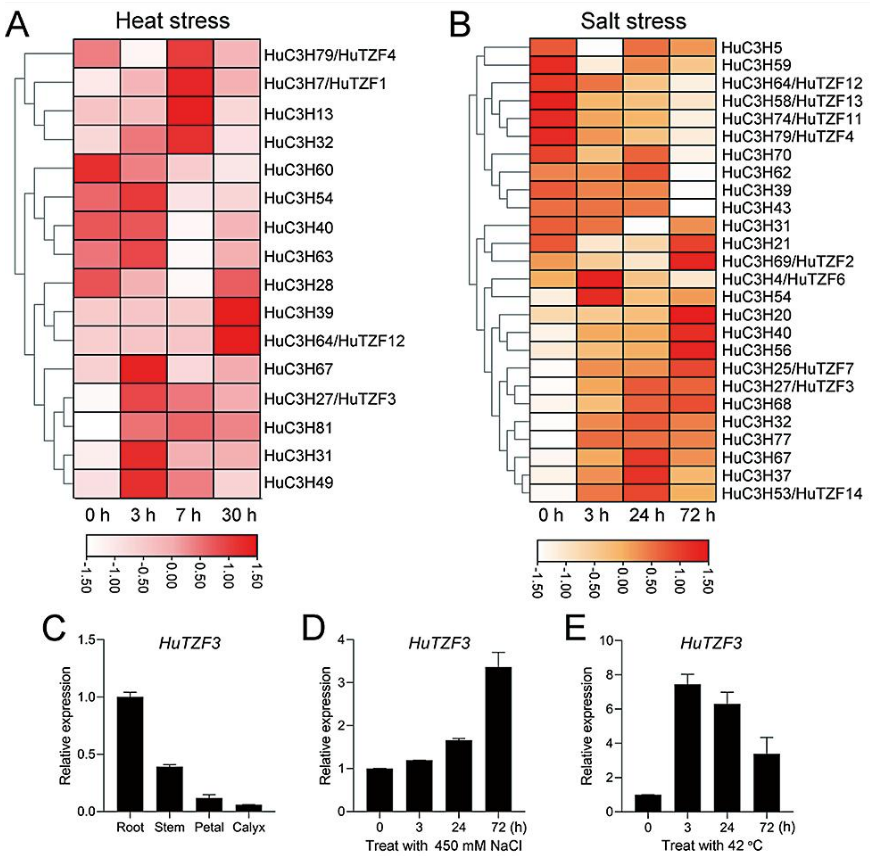

Figure 2 Expression response of pitaya *CCCH* genes to salt and heat stress. (A,B) Heatmap of HuCCCHs response to heat (A) and salt (B) stress. The transcriptomic data cited are from Nong et al. (2019) and Jiao et al. (2021). The three-month-old seedlings grown in a greenhouse, were treated with 450 mM NaCl, or at 42 °C, for different times, then the samples were collected for RNA-seq. (C-E) Expression pattern of HuTZF3 in different tissues of pitaya (C), and in pitaya seedlings under salt (D) and heat (E) treatment. Three-month-old pitaya seedlings were treated with 450 mM NaCl (D) or at 42 °C (E). HuEF1-α was used as the internal reference gene. Values represent means ± SD (n = 3 technical repetitions). All RT-qPCR analyses for gene expression were performed in three biological replicates, with similar results (Adopted Xu et al., 2023)

### 6.2 Melatonin alleviates the combined stress effects of pitaya

With the intensification of climate change, plants are facing an increasing variety of abiotic stresses, such as heavy metal pollution, salinization and drought, which seriously threaten crop yield and quality. As a tropical cash crop, the response mechanism of pitaya to multiple stresses is still unclear, while melatonin, as a plant endogenous signaling molecule, has shown promising applications in adversity mitigation in recent years (Nong et al., 2019; Khokhar et al., 2024).

Khokhar et al. (2024) analyzed the morphological and physiological responses of pitaya by simulating single and combined stresses such as cadmium (Cd), salt (S), and drought (D) and introducing exogenous melatonin (M) treatment. Using a strategy combining morphological observations, measurement of physicochemical indexes and transcriptome sequencing (RNA-seq), it was found that multiple stresses inhibited plant growth, reduced biomass by more than 30%, and stem and stem node development by 40%, while increasing cadmium accumulation (by 50% under single stress, and to 70% under compound stress).

After applying melatonin, the antioxidant capacity of the plants was enhanced, the activities of enzymes such as $H_2O_2$, POD, CAT, APX, and SOD increased, and the accumulation of proline increased, indicating that it plays a key role in regulating stress resistance (Figure 3). The study verified the potential of melatonin in alleviating multiple abiotic stresses and provided a theoretical basis for pitaya stress-resistant cultivation and molecular breeding.

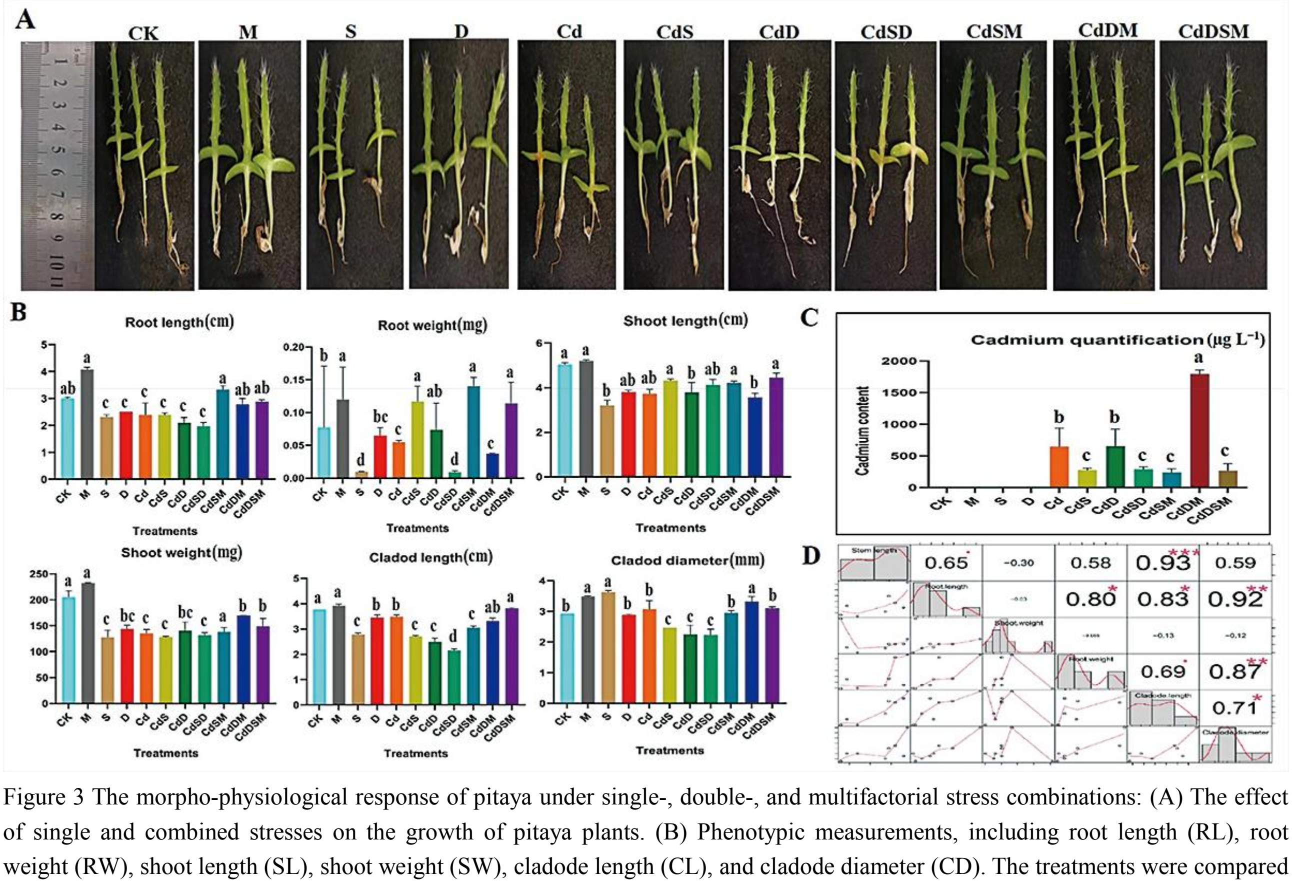

Figure 3 The morpho-physiological response of pitaya under single-, double-, and multifactorial stress combinations: (A) The effect of single and combined stresses on the growth of pitaya plants. (B) Phenotypic measurements, including root length (RL), root weight (RW), shoot length (SL), shoot weight (SW), cladode length (CL), and cladode diameter (CD). The treatments were compared using one-way ANOVA at a 5% ($p \leq 0.05$) probability level, and means were compared using the Duncan test. The different letters display statistically significant differences among cultivars; similar letters depict statistically non-significant values, while bars show standard errors. (C) Cadmium quantification across treatments, with error bars representing standard deviation. (D) A correlation matrix showing significant relationships among RL (cm), RW (g), SL (cm), SW (g), CL (cm), and CD (mm). Significant and highly significant correlations are represented by * ($p<0.05$), ** ($p < 0.01$), *** ($p<0.001$). Abbreviations: control (CK); melatonin (M); salinity (S); drought (D); cadmium (Cd); cadmium + salinity (CdS); cadmium + drought (CdD); cadmium+salinity+drought (CdSD); cadmium+salinity+melatonin (CdSM); cadmium+drought+melatonin (CdDM); cadmium + drought + salinity+melatonin (CdDSM) (Adopted from Khokhar et al., 2024)

## 7 Breeding Strategies for Salt Tolerance in Pitaya

### 7.1 Conventional selection and phenotyping methods

The salt tolerance breeding of pitaya was first carried out by growing it in the field. Field trials are a common method. Different varieties are planted under saline irrigation conditions to directly observe their growth, survival rate and yield performance in a high-salt environment. Although it looks simple, it is very practical. Studies have found that pitaya varieties such as *H. costaricensis* show strong salt tolerance during seed germination and seedling stages (Carvalho et al., 2022; Kenanoğlu et al., 2023), which shows that field screening is still an important way to discover salt-resistant varieties.

In addition to intuitive observation, there is now a relatively standardized quantitative method. For example, germination rate, seedling length, dry weight, and the so-called "stress tolerance index" are all tools used to measure the specific performance of different varieties under salt stress. These indicators have a good correlation and are not difficult to measure, which can improve screening efficiency (Kenanoğlu et al., 2023). Using these quantitative data to assist breeding judgments is much safer than relying solely on experience, and can also more quickly lock in materials worthy of further breeding.

### 7.2 Marker-assisted and genomic selection approaches

With progress in molecular genetics, scientists can now find certain genes and markers, like QTLs and SNPs, that are linked to salt tolerance. In pitaya, studies of the genome and transcriptome have found many genes and areas in the DNA that respond to salt stress (Xu et al., 2023; Khan et al., 2024). These markers can be used in breeding to help pick out the best plants early on. By using these tools, breeders can find salt-tolerant genes faster and more accurately, which makes the whole breeding process quicker and more efficient.

Genomic selection uses DNA markers from across the whole genome to guess how good a plant might be, even before it shows any traits (Pang et al., 2024). By building prediction models that mix transcriptome data and gene network analysis, researchers can find important genes and gene groups linked to salt tolerance. This helps breeders choose the best plants more quickly and accurately, making the breeding process more effective.

### 7.3 Future directions in precision breeding

New gene editing tools like CRISPR let scientists change plant genes with great accuracy (Wang et al., 2021; Han et al., 2022). In pitaya, researchers have found several useful genes through transcriptome and function studies. These include genes that make transcription factors and stress-related proteins (Qu et al., 2020; Xu et al., 2023; Khan et al., 2024). These genes could be good targets for editing to boost salt tolerance. With gene editing, helpful gene versions can be added or changed directly. This helps avoid the long time and low efficiency of traditional breeding.

By putting together data from different sources-like gene studies, detailed plant measurements, and gene editing-scientists hope to design the “ideal” salt-tolerant pitaya. This kind of plant would have better roots, stable ion levels, and strong stress response systems. In the future, breeding will focus on combining several salt-tolerant traits into one plant and making sure the plant fits the local environment. This will help pitaya grow well even in salty soils and support long-term, stable production (Xu et al., 2023; Khan et al., 2024).

## 8 Concluding Remarks

Pitaya’s salt tolerance comes from a well-coordinated system at many levels. It works by keeping the right balance between sodium and potassium ions and using water-control methods to deal with cell water loss. At the same time, the plant also adjusts its root structure to better take in water and nutrients from salty soil. All these actions are guided by special genes and transcription factors that help the plant sense salt stress and respond to it properly.

In recent years, with the development of molecular technology, some important genes, QTLs and molecular markers related to salt tolerance have been identified in pitaya, including genetic elements involved in key links such as ion transport, osmotic regulation and root system construction. These achievements have laid the foundation for subsequent molecular breeding. Marker-assisted selection (MAS), genomic selection (GS) and genetic engineering can be accelerated based on these resources.

But, there are still many problems. At present, there is a lack of high-quality reference genomes, functional verification is also limited, and many key genes cannot be further analyzed in detail. More importantly, most experiments were conducted under controlled conditions, lacking verification of different environments and long-term field data. Next, breeding work should move towards the integration of multi-omics and high-throughput phenotyping, coupled with new technologies such as genome editing, to strive to breed salt-tolerant pitaya varieties suitable for different ecological zones as soon as possible, so that it can truly become a crop that can produce stable and high yields even in saline-alkali land.

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## Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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