REVIEW

IMPORTANT ANALYZING PARAMETERS IN THE ASSESSMENT OF SALT TOLERANCE IN PLANTS

Hoang Thi Lan Xuan1,2,*, Nguyen Phuong Thao1,2

1 Applied Biotechnology for Crop Development Research Unit, School of Biotechnology, International University, Thu Duc City, Ho Chi Minh City, Vietnam
2 Vietnam National University, Ho Chi Minh City, Vietnam

*To whom correspondence should be addressed. E-mail: htlxuan@hcmiu.edu.vn

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SUMMARY

Maximal crop performance potential and land area suitable for cultivation are usually restricted by adverse environmental conditions. Among the abiotic factors, salinity stress is considered as one of the main threats, which causes ionic toxicity, dehydration and oxidative stresses on the plants. Alarminglly, the impact of salinity is predicted to be more severe in the forthcoming years due to global warming. Therefore, development of new cultivars with better salinity resistance with minimized yield penalty under the adverse condition, either by breeding or genetic engineering approach, has attracted a great attention from the scientists. In this review, important parameters used in evaluation of plant resistance ability against salinity stress are discussed, which highlights the necessity to obtain multi-sets of biological data ranging from analyses of morphological alterations to physiological, biochemical and molecular responses, as well as by performing -omics studies to find out network of salinity-responsive pathways. Literature review also demonstrates that the relevance of salinity condition setup in terms of concentration and duration is required in experimental design. Furthermore, recent investigations on genome duplication, activities of non-coding sequence or epigenetics also reveal their regulatory roles in shaping plant response and tolerance degree toward salinity stress. Collection of such data not only contributes to widen scientific understanding of plant response mechanisms and adaptation to this stress factor but also facilitates the identification of important genes associating with plant tolerance to salinity. Therefore, the presented information could be used as a reference for the salinity stress-related studies serving for crop innovation and transgene function characterization.

Keywords: analyzing parameters, gene function characterization, osmotic stress, plant resistance, salinity stress

INTRODUCTION

In addition to drought, salinity has emerged as another major abiotic threat that agriculture production is currently facing with. Presence in high concentration of either sodium bicarbonate NaHCO₃ (i.e. alkaline soil) or sodium chloride NaCl (i.e. saline soil) is the main cause for soil becoming “salinized”, which contains excessive level of Na⁺ ions (Chen et al., 2014). Under effects of climate change and global warming, area of saline soil has been critically expanded due to aggressive intrusion of the sea water onto mainland in recent years (Li et al., 2009). Furthermore, human cultivation activities such as inappropriate water management and fertilizer
usage have worsened the situation (Pessarakli, Huber, 1991; Wanjogu et al., 2001). Excessive salts in soil cause negative effects on growth and productivity of crop plants, which mainly belong to the group glycophyte with the character of low resistance to salinity (Flowers 2004; Munns, Tester, 2008).

Under this adverse condition, plants suffer stunted growth, leaf chlorosis, reduced photosynthesis, cellular water loss, disrupted cellular ionic homeostasis and cell damage due to accumulation of reactive oxygen species (ROS) (Kumar et al., 2013; Golldack et al., 2014) (Figure 1). If the stress is prolonged or too severe, plants even cannot maintain their survival. Following the progress events of salinity stress effects on plants, in the early stage, plants experience with physiological drought (i.e. hyperosmotic stress) due to the difficulties in absorbing water from the soil with high concentrations of ions by the root systems. Following this, accumulation of cellular $\text{Na}^+$ and $\text{Cl}^-$ results in ionic toxicity (i.e. hyperionic stress) to plant cells. Osmotic and ionic stresses can then trigger the oxidative stress with increased production of cellular ROS contents (Gupta, Huang, 2014) (Figure 1). It is noted that apart from direct effects on plants, salinity stress also disturbs the environment in the rhizosphere (i.e. the soil vicinity surrounding the root system), thus preventing the plants from establishment with beneficial microorganisms and uptaking nutrients (Kulkarn et al., 2000; Rao et al., 2002).

In this review, we summarize parameters that the researchers can rely on in evaluating plant resistance capacity to salinity, which will be discussed in connection with current understanding of plant response to this adverse condition and progress in advancement of technologies and methodologies. The information presented here could be used as a reference in designing a relevant and sufficient set of assessment criteria for comparative studies, which serve for the selection or development of salinity-tolerant cultivars and for gene function characterization purpose.

![Salinity Stress Diagram](image)

**Figure 1.** Salinity effects to plant growth, development and productivity.
ANALYZING PARAMETERS ASSOCIATING WITH MORPHOLOGICAL, PHYSIOLOGICAL AND BIOCHEMICAL TRAITS

Evaluate morphological characters and overall plant performance under salinity stress

Examining survival rate upon salinity stress exposure is an indispensable experiment as its results will provide an overall evaluation on the salt tolerance capacity of a plant genotype before its tolerance mechanisms are investigated (Table 1). The assay can be divided into three main stages, which are (i) growing plants under normal condition, (ii) stress application, and (iii) recovery and survival rate calculation. For example, two-week-old Arabidopsis can be treated with 200 mM NaCl solution daily over a three-week-duration, followed by three-day normal irrigation with water prior to calculating the proportion of alive plants (Li et al., 2019). It is noted that the duration and procedure of the stress treatment can be modified depending on plant species, plant age, plant density per container, salt concentration and volume, as well as frequency of the salt solution application (Table 2). In study of Li et al. (2018), four-week-old Arabidopsis seeds were used for application of 300 mM NaCl solution every three days until the stress effects could be visualized. Meanwhile, salt treatment for rice (Oryza sativa) can be set up by exposing the seedlings to ten-day-stress duration using 150 mM NaCl solution (Zhu et al., 2015). Generally, dicot plants have a greater variation in salinity tolerance than the monocot plants (Munns, Tester, 2008). Furthermore, this method can be used to analyze the salt effects on plant productivity by investigating the reproduction-related traits rather than survival rate (Table 1). The agronomic traits are very important in agricultural and economic perspectives in selecting elite cultivars not only with enhanced stress tolerance but also with high productivity (Liang et al., 2016). Singh and others (2015) have demonstrated that among the tolerance indices that can be used to assess the salt resistance associated with plant productivity, mean productivity, geometric mean productivity, and stress tolerance index were more reliable parameters than others such as tolerance index, yield index and yield stability index (read original paper for information of each index calculation).

As salinity stress inhibits early seed development, examination on germination rates as well as shoot- and/or root-associated traits over a range of different salt concentrations is usually conducted (Table 1). For Arabidopsis, the sterilized seeds are placed on half strength Murashige and Skoog (1/2 MS) medium (Murashige, Skoog, 1962) containing NaCl 100 mM under relevant growing condition and the rate of seeds with radicle emergence (i.e. successful germination) can be monitored every 24 hours within five consecutive days since seeding (Li et al., 2019). Germination test using higher salts (e.g. 250 mM) and MS medium has also been reported (Lee et al., 2006). In addition, this test is commonly conducted over a range of different NaCl concentrations. For example, sterilized soybean (Glycine max) seeds can be placed on the medium containing 0, 100, 200 and 300 mM NaCl (Li et al., 2017).

This in vitro assay system (100-125 mM NaCl) can also be used to assess root length and fresh weight of Arabidopsis seedlings that has been grown on medium with salt supplementation for a week (Qin et al., 2017; Li et al., 2019). For studies in tobacco (Nicotiana tabacum), NaCl solution with concentrations of 100-200 mM has been applied for germination and growth assays (Kobayashi et al., 2008; Yang et al., 2017). With bigger plants like soybean, growing plants in hydroponic system using half-strength Hoagland solution can make it easier for salt treatment, simply by adding the desired salt amount into the nutrition solution and immersing the root part into this liquid (Li et al., 2017) (Table 1). In addition, certain measurements can be categorized for specifically ranking the plant tolerance capacity. For example, depending on the visualized damage and necrotic degree that the studied plants can be placed in a five-point
scale, with level 1 for no sign of necrosis and level 5 with the highest score of injured areas (75-100%) (Sabra et al., 2012). Similarly, degree of reduction in relative growth rate under salinity stress condition, of which calculation is based on the dry weight recorded at different time points, can be used to divide plants into groups of salt-tolerant, moderately salt-tolerant, moderately salt-sensitive and salt-sensitive species (Cassaniti et al., 2012).

Table 1. Common parameters used for analyses of morphological, physiological and biochemical traits to evaluate plant resistance capacity to salinity stress.

| Assay name                        | Analyzing parameters                                                                 | References                  |
|-----------------------------------|--------------------------------------------------------------------------------------|-----------------------------|
| Survival rate assay               | post-stress survival rate                                                             | Li et al., 2018; Li et al., 2019 |
| Germination assay                 | germination rate                                                                      | Li et al., 2017             |
| Vegetative growth assay           | root length, shoot length, fresh and dry biomass                                      | Wang et al., 2016; Li et al., 2017 |
| Analysis of reproductive traits   | flowering time, number of flowers/pods/fruits/fruit branches, yield per plant         | Liang et al., 2016; Wang et al., 2017 |
| Analysis of accumulated reactive oxygen species | superoxide anion and hydrogen peroxide contents                                     | Wang et al., 2017             |
| Analysis of membrane damage       | ion leakage and malondialdehyde content                                               | Orellana et al., 2010; Wang et al., 2016 |
| Analysis of antioxidant enzyme activities | superoxide dismutase, peroxidase, catalase and glutathione transferase activities | Li et al., 2017; Wang et al., 2017 |
| Measurement of hormonal contents  | abscisic acid and jasmonic acid                                                      | Yang et al., 2001            |
| Measurement of osmolyte contents  | Proline, trehalose and soluble sugar contents                                      | Wang et al., 2017            |
| Measurement of intracellular ion contents | Na⁺, K⁺ and Cl⁻ contents                                 | Xu et al., 2016; Li et al., 2017             |
| Evaluation of photosynthetic performance | Chlorophyll content, stomata aperture and density                                   | Orellana et al., 2010; Liang et al., 2016; Wang et al., 2017 |

Table 2. Concentrations of sodium chloride that have been applied to different plant species in salinity stress-related studies.

| Plant species | Applied NaCl concentration | Duration | Studied system | Studied parameters | References                  |
|---------------|---------------------------|----------|----------------|-------------------|-----------------------------|
| Arabidopsis thaliana | 250 mM                     | 2 weeks  | Soil and irrigation | Survival rate, chlorophyll content | Cao et al., 2017 |
|                |                           | 4, 10, 12, 14 and 16 days | Fv/Fm values |                   |                             |
|                | 100 and 150 mM            | 7 days   | Half-strength MS | Root length       | He et al., 2019             |
|                | 200 mM                    | 12 days (4-d intervals) | Soil and irrigation | Survival rate, fresh weights, Fv/Fm, MDA, proline and H₂O₂ contents, | |

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| Plant Species          | Treatment | Duration | Cultivation Medium | Assessed Parameters                                                                 |
|-----------------------|-----------|----------|--------------------|-------------------------------------------------------------------------------------|
| *Boehmeria nivea*     | 250 mM    | 7 days   | Half-strength Hoagland | Seed germination, Photosynthesis, relative water content, MDA and proline contents, peroxidase activity |
|                       | 300 mM    | 12 days  | Soil and irrigation | Total plant fresh and dry weights                                                        |
|                       | 350 mM    | 11 days  |                     | Fresh and/or dry weights of shoot/root/bast; transpiration                          |
| *Glycine max* (soybean) | 200, 250 and 300 mM | 7 days | Half-strength MS medium | Germination rate                                                                   |
|                       | 300 mM    | 48 hours | Hydroponic         | Root characters                                                                    |
|                       | 200 and 300 mM | 2 weeks | Soil and irrigation | Growth characters                                                                  |
|                       | 300 mM    | 9 days   |                     | Proline and sugar contents                                                         |
| *Gossypium hirsutum*  | 250 mM    | 7 days   | Hoagland solution   | Fresh and dry weights                                                              |
| (cotton)              |           | 2 weeks  |                    | Proline and MDA contents                                                           |
|                       | 100 and 250 mM | 20 days (5- or 10d-intervals) | Soil and irrigation | Photosynthesis, stomatal conductance and transpiration           |
| *Musa acuminata*      | 100, 200 and 250 mM | 6 days | Salt solution       | Leaf disc assay for chlorophyll content determination | Tak et al., 2017 |
| (banana)              | 250 mM    | 15 days  | Soil and irrigation | MDA, Fv/Fm, proline contents                                                      |
| *Nicotiana tabacum*   | 100 mM    | 30 days  | Half-strength MS medium | Root lengths and weights |
| (tobacco)             |           |          |                    |                                                                                   |
| *Oryza sativa* (Rice) | 150 mM    | 6 days   | Hoagland solution   | Na⁺ content                                                                         |
|                       |           |          | Half-strength MS medium | Shoot height, fresh weight, number of later roots                               |
|                       | 200 mM    | 12 days  | Soil and irrigation | Survival rate                                                                       |
|                       | 100 mM    | 5 days   | Hydroponic          | Fresh weight                                                                        |
|                       |           |          |                    |                                                                                   |
Evaluate physiological and biochemical traits of plants under salinity stress

It has been known that oxidative stress is the secondary stress induced by osmotic and ionic disturbance, with increased production of ROS contents (Gupta, Huang, 2014). Accumulation of species such as superoxide \((O_2^-)\) and hydrogen peroxide \((H_2O_2)\) in plants can cause damage of cellular membrane and molecules, as well as interruption of metabolic activities (Gill, Tuteja, 2010). Knowing accumulation degree of these ROS can be used as indicators for the estimation of cellular oxidative stress level. Detection of ROS in the leaf tissues can be achieved by staining methods using nitro blue tetrazolium (NBT) for \(O_2^-\) (Shi et al., 2010) and 3,3’-diaminobenzidine (DAB) for \(H_2O_2\) (Liu et al., 2014). Although total ROS production in intact cells can be visualized by staining with 2,7-dichlorofluorescin diacetate (H\(_2\)DCF-DA) (Zhang et al., 2011; Yang et al., 2017), this method has been claimed not to be accurate due to non-specificity in substrate binding of the chemical reagent (Jakubowski, Bartosz, 2000; Chen et al., 2010). Apart from these histochemical staining assays, \(H_2O_2\) content can be quantified by spectrophotometric approach (Patterson et al., 1984) (Table 1). In addition, oxidative stress-induced damage of cellular membrane can be estimated based on the measurement of electrolyte leakage or malondialdehyde (MDA) contents (Campos et al., 2003; Li et al., 2015) (Table 1). In some studies, examination on cell death by Evans blue staining is also conducted (Zhang et al., 2011; Qin et al., 2017; Yang et al., 2017). In other papers, measurement of \(Na^+\) and \(K^+\) contents is addressed as the plant growth is negatively affected by the high level of \(Na^+\) in the cytosol but supported by the presence of \(K^+\) (Munns et al., 2006; Chen et al., 2014; Xu et al., 2016; Li et al., 2017) (Table 1). Therefore, under salinity stress conditions, maintaining a low cytosolic \(Na^+/K^+\) ratio is important for normal metabolic activities to take place (Munns et al., 2006; Chen et al., 2014). In certain species that are able to effectively prevent the \(Na^+\) accumulation on leaves, measurement of \(Cl^-\) should be conducted as its concentration might be enhanced to a toxic dose level along with potassium ions (Munns, Tester, 2008).

Plants use both enzymatic and non-enzymatic pathways to protect themselves from oxidative stress effects, mainly by scavenging ROS or by using molecules functioning as antioxidants. Regards to the enzyme-mediated defense, superoxide dismutase (SOD) plays in the first line by converting superoxide into \(H_2O_2\). The generated \(H_2O_2\) will be further detoxified by peroxidase (POD) and catalase (CAT) enzymes. In the non-enzymatic defense pathway, certain molecules such as proline, soluble sugars (e.g. trehalose, glucose and fructose) and glycine betaine will play a role in antioxidative protection (Ashraf, Foolad, 2007; Gupta, Huang, 2014; Qin et al., 2017; Wang et al., 2017). The main functions of these compounds are to enhance water retention capacity by lowering cellular water potential under osmotic stress as well as stabilize cellular environment to maintain

| Solanum lycopersicum (tomato) | 100 mM | 10 days | MS medium | Shoot and root growth measurements | Zhu et al., 2014 |
|-------------------------------|--------|---------|-----------|-----------------------------------|-----------------|
|                               | 400 mM | 4 days  | Salt solution | Leaf disc assay for chlorophyll content determination |                 |
|                               |        | 21 days (72-hour interval) | Soil and irrigation | Growth characters |                 |
| Triticum aestivum (bread wheat) | 2%     | 7 days  | Hoagland solution | Survival rate, fresh and dry weights | Saad et al., 2013 |
metabolic activities (Ashraf, Foolad, 2007). Therefore, analyzing enzymatic activities or contents of these antioxidant/osmoprotectant molecules would provide important information on plant defense capacity to salinity (Li et al., 2018; Li et al., 2019) (Table 1).

As salinity stress also causes adverse effects on photosynthetic molecules and performance, measurement of chlorophyll content is usually included in the study. To do this, in small plants like Arabidopsis, aerial part of different plants can be pooled together for being used as a biological replicate (Li et al., 2018) and in bigger plants, individual leaf samples can be analysed separately (Liang et al., 2016). In addition, investigation of stomata-related traits such as aperture size and density also reveal useful information for evaluation of photosynthetic activity potential (Orellana et al., 2010; Liang et al., 2016; Wang et al., 2017).

Hormone-mediated plant response to salinity stress, including abscisic acid (ABA) and jasmonate acid (JA), has also been well documented (Tuteja, 2007; Zhang et al., 2017). A number of transcription factors regulating plant response to salinity has been found to work in ABA-dependent manner (e.g. tomato (Solanum lycopersicum) JERF1), or in both pathways (e.g. Arabidopsis ERF1 and AtMYC2) (Cheng et al., 2013; Zhao et al., 2014). Therefore, quantification of ABA and JA contents by enzyme-linked immunosorbent assays (ELISAs) can be considered (Yang et al., 2001) (Table 1).

TARGET GENES FOR EXPRESSION ANALYSIS BY QUANTITATIVE REVERSE TRANSCRIPTION PCR (RT-qPCR) METHOD

Over the last decade, RT-qPCR has become a more widely used method than RNA gel blotting in detecting differential gene expression between conditions (e.g. stressed versus normal conditions) or genotypes, from which important gene activities in connection with salt tolerance capacity can be identified. RT-qPCR is also employed to validate the transcriptomic analyses. In addition, gene expression data would provide complementary evidence for supporting the phenotypic, physiological or biochemical results, making the conclusion more reliable. For example, transgenic Arabidopsis ectopically expressing sweet potato (Ipomoea batatas) IbRAP2-12 acquired better salt tolerance, with higher proline content and in consistency with higher expression of pyrroline-5-carboxylate synthase 2 (P5CS2) (Li et al., 2019). This gene encodes the key enzyme in biosynthesis of proline, a molecule functioning as an osmolyte used for osmotic adjustment and as an antioxidant in protecting biomacromolecules and scavenging ROS (Ashraf, Foolad, 2007; Li et al., 2019). In another example, increased trehalose content coupled with up-regulation of genes ThTPSI-3 and ThTPPA encoding the key enzymes 3 trehalose-6-phosphate synthase (TPS) and 1 trehalose-6-phosphate phosphatase (TPP), respectively, in the biosynthetic pathway of trehalose is observed in the transgenic Tamarix hispida overexpressing cytokinin response factor 1 (CRF1) (Qin et al., 2017).

Table 3 presents important pathways and functional groups whose gene expression could be regulated in mediating plant response to salinity stress. In general, expression of genes encoding the enzymes working in the biosynthesis of hormones (e.g. ABA and JA), osmoprotectant (e.g. proline, trehalose), as well as in ROS removal (e.g. CATs and PODs) is induced upon salinity stress challenging. For example, increase in expression of Arabidopsis dehydroascorbate reductase 1-encoding gene (DHAR1) under this adverse condition, was reported (Li et al., 2019). DHAR1 is an enzyme belongs to glutathione S-transferase superfamily and responsible for the regeneration of ascorbate, an antioxidant molecule (Ding et al., 2020). Therefore, activity of this enzyme also plays an important role in plant defense. Dehydrin proteins such as late embryogenesis abundant (LEA) proteins, responsive-to-ABA (RAB) proteins and cold-regulated (COR) proteins are well-known members functioning in
cellular protein protection and membrane stabilization under osmotic stress (Verslues et al., 2006; Jia et al., 2014; Shinde et al., 2019). Therefore, expression study of their corresponding encoding genes is an interest. It is found out that the transgenic tomato (Solanum lycopersicum) overexpressing SlAREB1 had increased expression in two dehydrin encoding genes TAS14 and LE25, suggesting their contribution to the enhanced tolerance of the transgenic tomato under salinity stress (Orellana et al., 2010).

As saline conditions cause ionic and osmotic imbalance, it is important to study the expression levels of genes encoding transporter proteins in the root tissue. Particularly, attention should be paid to genes coding for Na⁺ transporters [e.g. salt overly sensitive 1 (SOS1), cation/H⁺ exchanger (CHX1) and Na⁺/H⁺ antiporters 1 (NHX1), and K⁺ transporters [e.g. CHX1 and high-affinity potassium transporter 1;4 (HKT1;4)], as well as water channels (known as “aquaporin”) [e.g. plasma membrane intrinsic protein 1;6 (GmPIP1;6)]. SOS1 is a well-known Na⁺/H⁺ antiporter working in the SOS-signaling pathway for regulating cellular Na⁺ efflux (Cellier et al., 2004; Chen et al., 2014; Gupta, Huang, 2014; Qi et al., 2014; Zhou et al., 2014; Li et al., 2017). SOS1 and NHX1 are known to reside on the plasma membrane and tonoplast (vacuole) membrane, respectively, and responsible for the prevention of intracellular Na⁺ accumulation, either by Na⁺ exclusion or compartmentalization (Apse et al., 2003; Shi et al., 2000).

For transgenic studies using transcription factor-encoding genes as the transgenes, analyzing the cis-motifs present in the promoter region of target genes could help compiling the list of potential genes whose expression should be prioritized for investigation. Of course, it is possible that genes without the cis-acting elements for the transcription factor binding are also its downstream target genes, as an outcome of indirect regulation/interaction. Salinity stress-related studies have identified participation of various transcription factors that belong to different families, such as dehydration-responsive-element (DRE)-binding proteins (DREBs), zinc finger proteins (ZFPs), ethylene response factor proteins (ERFs) and myeloblastosis proteins (MYBs) (Xu et al., 2016; Wang et al., 2017). As drought and salinity stresses cause osmotic stress, similar strategies and components are used by plants in response to drought and high salinity conditions (Ashraf, Foolad, 2007; Gill, Tuteja, 2010; Golldack et al., 2014; Li et al., 2017).

Table 3. Main pathways that might be under regulation in mediating plant response to salinity stress, based on studies of transgenic plants with improved salinity tolerance and analyzed by RT-qPCR method. Examples for genes with altered expression in each pathway are included.

| Function                        | Transgenic plants | Transgene          | Responsive genes                                                                 | References        |
|---------------------------------|-------------------|--------------------|----------------------------------------------------------------------------------|-------------------|
| Abscisic acid biosynthesis-related pathway | Arabidopsis        | Ipomoea batatas    | abscisic aldehyde oxidase 3 (AAO3)                                              | Li et al., 2019   |
|                                 | Gossypium hirsutum | Zea mays ABP9      | nine-cis-epoxycarotenoid dioxygenase 2 (GhNCED2)                                | Wang et al., 2017 |
| Jasmonic acid biosynthesis-related pathway | Arabidopsis        | I. batatas         | lipoxygenase 2 (LOX2)                                                            | Li et al., 2019   |
|                                 |                   | lbrAP2-12          | alene oxide synthase (AOS)                                                       |                   |
| Proline biosynthesis-related pathway | Arabidopsis        | Tamarix hispida    | pyrrole-5-carboxylate synthase 1 (P5CS1)                                         | Qin et al., 2017  |

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### Trehalose biosynthesis-related pathway

| Plant      | Gene          | Description                                                                 |
|------------|---------------|-----------------------------------------------------------------------------|
| T. hispida | ThCRF1        | 3 trehalose-6-phosphate synthase (ThTPS1-3); 1 trehalose-6-phosphate phosphatase (ThTPPA) |

### Reactive oxygen species removal

| Plant          | Gene          | Description                                                                 |
|----------------|---------------|-----------------------------------------------------------------------------|
| Arabidopsis    | l. batatas    | Glutathione peroxidase 7 (GPX7), ascorbate peroxidase 1 (APX1), dehydroascorbate reductase 1 (DHAR1), catalase 1 (CAT1) |
| T. hispida     | ThCRF1        | Superoxide dismutase-encoding genes (ThSOD1, ThSOD2, ThSOD3)                |
| G. hirsutum    | Z. mays ABP9  | Superoxide dismutase (GhSOD), catalase (GhCAT), Glutathione-S-transferase (GhGST) |

### Transporter proteins

| Plant          | Gene          | Description                                                                 |
|----------------|---------------|-----------------------------------------------------------------------------|
| Glycine max    | GmFDL19       | Cation/H+ exchanger (GmCHX1), plasma membrane intrinsic protein 1;6 (GmPIP1;6), Na+/H+ antiporters 1 (GmNHX1), GmHKT1;4, salt overly sensitive (GmSOS1) |

### Dehydrin proteins (e.g., LEA, RAB and COR subfamilies)

| Plant          | Gene          | Description                                                                 |
|----------------|---------------|-----------------------------------------------------------------------------|
| Solanum lycopersicum | TAS14, LE25 |                                                                                |
| G. max         | GmFDL19       |                                                                             |

### Transcription factors

| Plant          | Gene          | Description                                                                 |
|----------------|---------------|-----------------------------------------------------------------------------|
| G. max         | GmZIP1,       | GmbZIP1, GmNAC11, GmDERB2A:2, GmERF5, GmMYB174                             |
| G. hirsutum    | Z. mays ABP9  | Dehydration-responsive-element (DRE)-binding protein 2 (GhDBP2), zinc finger protein 1 (GhZFP1), ethylene response factor 1 (GhERF1) |

### RECENT ANALYTIC APPROACHES CONTRIBUTING TO COMPREHENSIVE UNDERSTANDING OF PLANT TOLERANCE TO SALINITY

With rapid progress in developing novel technologies and advanced instruments, in addition to transgenic/mutant-based systems, other approaches can be utilized to comprehensively understand the plant tolerance to salinity. It has been shown that microRNA (miRNA) molecules also play a role in determining the plant tolerance capacity (Genie et al., 2019) (Table 4). For example, increasing transcript abundance of certain miRNAs could make the transgenic rice more vulnerable to salinity stress (Gao et al., 2010; Gao et al., 2011). Other studies have indicated that the salt tolerance of plants can be also affected by epigenetic changes such as post-translational modification via activity of ubiquitin ligases or degree of DNA methylation (Park et al., 2010; Feng et al., 2012) (Table 4). With the reduction in cost and time as well as improved instrument versality, analysis at systemic scale can provide global information for the salinity stress-induced changes in transcript profile, protein profile or metabolite profile (Hernández, 2019). It must be emphasized that genome-wide studies remain as an important approach as the tolerance capacity among different cultivars can be compared and assessed based on genetic variants or polyploidy status (Tu et al., 2014; Ganie et al., 2019).
Furthermore, using molecular markers also contributes to the identification of important salinity-related genes and establishment of QTL (quantitative trait locus) mapping of these genes (Ky et al., 2018; Lang et al., 2019; Le et al., 2021) (Table 4). Previously, an important QTL for salinity tolerance in rice, known as Saltol, is reported (Vu et al., 2012).

Table 4. Other data for comprehensive understanding on plant tolerance capacity toward salinity.

| Targets                      | Examples                               | Added information value                                                                 | References                                      |
|------------------------------|----------------------------------------|----------------------------------------------------------------------------------------|------------------------------------------------|
| Non-protein-coding genes     | miRNA                                  | Novel mechanism of plant responses to salinity                                         | Gao et al., 2010; Gao et al., 2011             |
| Epigenetics                  | Ubiquitination genes, DNA methylation  | Affecting protein stability and expression degree                                      | Park et al., 2010; Feng et al., 2012           |
| Genome duplication           | Genome-wide analysis                   | To examine polyploidy status in association with salt tolerance capacity               | Tu et al., 2014                                |
| -Omic studies                | Transcriptomic profiling, proteomic profiling, metabolic profiling | To obtain global salt responsive-network and identify important participants            | Ganie et al., 2019; Hernández, 2019           |
| DNA markers                  | Simple sequence repeats, expressed sequence tag markers, SNPs | Locate important salinity-related genes and quantitative trait loci (QTL mapping)      | Ky et al., 2018; Lang et al., 2019; Le et al., 2021 |

SALINITY STRESS TOLERANCE STUDIES IN VIETNAM

In Vietnam, salinity has not been considered a major threat to agricultural production until recent years, when a higher rate of seawater intrusion to the coastal region and river has been observed. Particularly, the rise in sea level due to climate change makes the agricultural production in Mekong River Delta become vulnerable more than ever. To cope with this, various measures have been suggested or deployed, including infrastructural establishment to prevent the invasion of seawater into the mainland, changes in agronomic practices and cropping pattern (Dam et al., 2021). Regarding development of elite salinity-tolerant cultivars, so far this has been an interest for rice only. This is easily understood as Vietnam is one of the main global rice suppliers and its economy heavily depends on the rice productivity. In fact, research on improvement of rice tolerance to salinity has been conducted many years ago using conventional breeding and the application of marker-assisted selection (MAS) has accelerated this breeding process (Lang et al., 2019). Similarly, marker-assisted backcrossing (MABC) is also adopted to speed up the development of salt-tolerant rice varieties in comparison with the traditional backcrossing method (Vu et al., 2012). Following this, introgression lines with improved salt tolerance were generated by introduction of Saltol QTL into BT7, a rice variety carrying certain desired agronomic traits, by crossing this with a salt-tolerant donor variety, FL478-Saltol (Linh et al., 2012).

Other studies focus on evaluating the salinity tolerance of different rice cultivars (Ky et al., 2018; Lang et al., 2019), including the mutant rice lines (Huong et al., 2020). For example, twelve different rice varieties in Tra Vinh have been analyzed for their salinity tolerance capacity to NaCl 6‰ based on three SSR (simple sequence repeat) markers (RM336, RM10793 and RM10825) and ratio of K+/Na+ uptake (Ky et al., 2018). Phenotype-based parameters, including plant height, root length, survival rate and biomass, have been also...
employed to screen for the rice germplasms with higher salt tolerance (Lang et al., 2019). Meanwhile, another study unraveled the salinity tolerance of different rice varieties based on yield-related properties including productivity, amylose and protein contents (Quan, Vo, 2017). Recently, a transcriptomic analysis has been conducted for two rice varieties with contrasting salinity tolerance, in order to identify pathways and genes associating with the plant tolerance (Ky et al., 2021).

In other plant species, the gained information and outcomes remain limited as only a handful studies have been conducted in relation to salinity stress in Vietnam. Among of these studies, it has been demonstrated that exogenous application of salicylic acid and/or calcium can enhance the salinity tolerance of amaranth (Amaranthus tricolor) via promotion of Na⁺ exclusion from roots, accumulation of phenolic and flavonoid compounds as well as increased antioxidant activities (Hoang et al., 2020). Tolerance of various chili pepper genotypes against different concentrations of NaCl or CaCl₂ (ranging from 0-300 mM) has been also explored, which was based on germination rate, plant height, number of leaves, branches and flowers, leaf area, phenolic compound contents and antioxidant activities (Ai et al., 2021). In another research, comparison for suitability of growing soybean versus Sesbania rostrata for saline land improvement purpose was conducted, with the assessment of plant height, root length, biomass, proline content coupled with endogenous Na⁺ accumulation, and SPAD (Soil-Plant Analyses Development) index to estimate the chlorophyll content (Phuong et al., 2018a). Similar investigations have been performed for mustard (Brassica juncea) (Phuong et al., 2018b) and quinoa (Chenopodium quinoa) (Long, 2016). Apparently, with the foreseen increase in frequency and severity of salinity stress, more research efforts should be given, not only for rice but also for vegetable and fruit plants.

CONCLUSION

This review demonstrated complex responses that the plants employ to cope with salinity stress. This also means that there are various potential target pathways or genes for a researcher to manipulate in developing crop varieties with improved salinity stress resistance. Clearly, in-depth understanding of mechanisms and performance of plants under salinity stress conditions requires a combined data set, which is derived from phenotypic, physiological, biochemical and molecular analyses. In terms of economic and agricultural perspectives, productivity ability of a studied genotype should be examined along with its salinity stress resistance potential. In the future, investigation on how salt-resistant plants (i.e. halophytes) can withstand high salinity conditions might beneficially provide new strategies for development of crop cultivars with better salt resistance.

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REFERENCES

Ai TN, Tran TNB, Lam NH, Nguyen MH, Phan CH (2021) Assessment of salinity tolerance of 4 chili pepper genotypes in Vietnam. J Southwest Jiaotong Uni 56: 94-110.
An X, Liao Y, Zhang J, Dai L, Zhang N, Wang B, Liu L, Peng D (2015) Overexpression of rice NAC gene SNAC1 in ramie improves drought and salt tolerance. Plant Growth Regul 76: 211-223.
Apse MP, Sottosanto JB, Blumwald E (2003) Vacuolar cation/H⁺ exchange, ion homeostasis, and leaf development are altered in a T-DNA insertional mutant of AtNHX1, the Arabidopsis vacuolar Na⁺/H⁺ antiporter. Plant J 36: 229-239.
Ashraf M, Foolad M (2007) Roles of glycine betaine and proline in improving plant abiotic stress resistance. Environ Exp Bot 59(2): 206-216.
Campos PS, Quartin V, Ramalho JC, Nunes MA (2003) Electrolyte leakage and lipid degradation
account for cold sensitivity in leaves of Coffea sp. plants. *J Plant Physiol* 160: 283-292.

Cao H, Wang L, Nawaz MA, Niu M, Sun J, Xie J, Kong Q, Huang Y, Cheng F, Bie Z (2017) Ectopic expression of pumpkin NAC transcription factor CmNAC1 improves multiple abiotic stress tolerance in *Arabidopsis*. *Front Plant Sci* 8: 2052.

Cassaniti C, Romano D, Flowers TJ (2012) The response of ornamental plants to saline irrigation water. In Garcia-Garizabal I, ed. *Irrigation water management, pollution and alternative Strategies*. InTech Europe, Rijeka, Croatia: 132-158.

Chen X, Zhong Z, Xu Z, Chen L, Wang Y (2010) 2',7'-Dichlorodihydrofluorescein as a fluorescent probe for reactive oxygen species measurement: forty years of application and controversy. *Free Radic Res* 44(6): 587-506.

Cheng MC, Liao PM, Kuo WW, Lin TP (2013) The *Arabidopsis* ETHYLENE RESPONSE FACTOR 1 regulates abiotic stress-responsive gene expression by binding to different cis-acting elements in response to different stress signals. *Plant Physiol* 162: 1566-1582.

Cellier F, Connéjéro G, Ricaud L, Luu DT, Lepetit M, Costi F, Casse F (2004) Characterization of AtCHX17, a member of the cation/H+ exchangers, CHX family, from *Arabidopsis thaliana* suggests a role in K+ homeostasis. *Plant J* 39: 834-846.

Chen HT, Chen X, Gu HP, Wu BY, Zhang HM, Yuan XX, Cui XY (2014) *GmHKT1;4*, a novel soybean gene regulating Na+/K+ ratio in roots enhances salt tolerance in transgenic plants. *Plant Growth Regul* 73: 299-308.

Dam THT, Tur-Cardona J, Speelman S, Amjath-B TS, Sam AS, Zander P (2021) Incremental and transformative adaptation preferences of rice farmers against increasing soil salinity – Evidence from choice experiments in north central Vietnam. *Agric Sys* 190: 103090.

Ding H, Wang B, Han Y, Li S (2020) The pivotal function of dehydroascorbate reductase in glutathione homeostasis in plants. *J Exp Bot* 71(12): 3045-3046.

Feng Q, Yang C, Lin X, Wang J, Ou X, Zhang C, Chen Y, Liu B (2012) Salt and alkaline stress induced transgenerational alteration in DNA methylation of rice (*Oryza sativa*). *Aust J Crop Sci* 6: 877-883.

Flowers TJ (2004) Improving crop salt tolerance. *J Exp Bot* 55(396): 307-319.

Hoang Thi Lan Xuan & Nguyen Phuong Thao

Ganie SA, Molla KA, Henry RJ, Bhat KV, Mondal TK (2019) Advances in understanding salt tolerance in rice. *Theor Appl Genet* 132: 851-870.

Gao P, Bai X, Yang L, Lv D, Li Y, Cai H, Ji W, Guo D, Zhu Y (2010) Over-expression of *osa-MIR393c* decreases salt and alkali stress tolerance. *Planta* 231: 991-1001.

Gao P, Bai X, Yang L, Lv D, Pan X, Li Y, Cai H, Ji W, Chen Q, Zhu Y (2011) *osaMIR393*: a salinity-and alkaline stress-related microRNA gene. *Mol Biol Rep* 38: 237-242.

Gill SS, Tuteja N (2010) Reactive oxygen species and antioxidant machinery in abiotic stress tolerance in crop plants. *Plant Physiol Biochem* 48: 909-930.

Golddack D, Li C, Mohan H, Probst N (2014) Tolerance to drought and salt stress in plants: unraveling the signaling networks. *Front Plant Sci* 5: 151.

Gupta B, Huang B (2014) Mechanism of salinity tolerance in plants: physiological, biochemical, and molecular characterization. *Int J Genomics* 2014: 701596.

Jakubowski W, Bartosz G (2000) 2',7'-Dichlorodihydrofluorescein oxidation and reactive oxygen species: what does it measure? *Cell Biol Int* 24(10): 757-760.

Jia F, Qi S, Li H, Liu P, Li P, Wu C, Zheng C, Huang J (2014) Overexpression of Late Embryogenesis Abundant 14 enhances *Arabidopsis* salt stress tolerance. *Biochem Biophys Res Commun* 454: 505-511.

Hoang HL, de Guzman CC, Cadiz NM, Hoang TTH, Tran DH, Rehman H (2020) Salicylic acid and calcium signaling induce physiological and phytochemical changes to improve salt tolerance in red amaranth (*Amaranthus tricolor* L.). *J Soil Sci Plant Nutr* 20: 1759-1769.

He K, Zhao X, Chi X, Wang Y, Jia C, Zhang H, Zhou G, Hu R (2019) A novel *Miscanthus* NAC transcription factor *MINAC10* enhances drought and salinity tolerance in transgenic *Arabidopsis*. *J Plant Physiol* 233: 84-93.

Hernández JA (2019) Salinity tolerance in plants: trends and perspectives. *Int J Mol Sci* 20: 2408.

Hong Y, Zhang H, Huang L, Li D, Song F (2016) Overexpression of a stress-responsive NAC
transcription factor gene ONAC022 improves drought and salt tolerance in rice. *Front Plant Sci* 7: 4.

Hu H, Dai M, Yao J, Xiao B, Li X, Zhang Q, Xiong L (2006) Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. *PNAS* 103: 12987-12992.

Huong CT, Anh TTT, Tran H-D, Duong VX, Trung NT, Khanh TD, Xuan TD (2020) Assessing salinity tolerance in rice mutants by phenotypic evaluation alongside simple sequence repeat analysis. *Agriculutre* 10: 191.

Kobayashi F, Maeta E, Terashima A, Takumi S (2008) Positive role of a wheat HvABI5 ortholog in abiotic stress response of seedlings. *Physiol Plant* 134: 74-86.

Kulkarn S, Surange S, Nautiyal CS (2000) Crossing the limits of Rhizobium existence in extreme conditions. *Curr Microbiol* 41: 402-409.

Kumar K, Kumar M, Kim SR, Ryu H, Cho YG (2013) Insights into genomics of salt stress response in rice. *Rice* 6: 27.

Ky H, Giang VQ, Manh NV, Do TI, Tam NT, Khang CTQ, Tung NCT, Hien NL (2021) Transcriptome analysis of Tra Long 2 rice variety under salt stress at seedling stage. *J Vietnam Agric Sci Tech* 1: 40-45.

Ky H, Giang VQ, Tung NCT, Hien NL, Phuc TH (2018) Assessment of 12 potential rice varieties from Tra Vinh province based on SSR markers and their uptake of K+/Na+ ratios. *Can Tho Uni J Sci* 54: 41-46.

Lang NT, Ha PTT, Tra NT, Buu BC (2019) Screening of rice germplasms under salt stress by phenotypic and molecular markers. *Afr J Agric Res* 14: 1154-1162.

Le TD, Gathignol F, Vu HT, Nguyen KL, Tran LH, Vu HTT, Dinh TX, Lazennec F, Pham XH, Very A-A, Gantet P, Hoang GT (2021) Genome-wide association mapping of salinity tolerance at the seedling stage in a panel of Vietnamese landraces reveals new valuable QTLs for salinity stress tolerance breeding in rice. *Plants* 10: 1088.

Lee SC, Choi HW, Hwang IS, Choi DS, Hwang BK (2006) Functional roles of the pepper pathogen-induced bZIP transcription factor, CabZIP1, in enhanced resistance to pathogen infection and environmental stresses. *Planta* 224: 1209-1225.

Li Y, Chen Q, Nan H, Li X, Lu S, Zhao X, Liu B, Guo C, Kong F, Cao D (2017) Overexpression of GmFDL19 enhances tolerance to drought and salt stresses in soybean. *PLoS ONE* 12(6): e0179554.

Li YP, Ye W, Wang M, Yan XD (2009) Climate change and drought: a risk assessment of crop-yield impacts. *Clin Res* 39: 31-46.

Li Z, Tian Y, Xu J, Fu X, G J, Wang B, Han H, Wang L, Peng R, Yao Q (2018) A tomato ERF transcription factor, SiERF84, confers enhanced tolerance to drought and salt stress but negatively regulates immunity against *Pseudomonas syringae* pv. tomato DC3000. *Plant Physiol Biochem* 132: 683-695.

Li Z, Zhu B, Wang B, Gao J, Fu X, Yao Q (2015) Stress responses to trichlorophenol in *Arabidopsis* and integrative analysis of alteration in transcriptional profiling from microarray. *Gene* 555: 159-168.

Liang C, Meng Z, Meng Z, Malik W, Yan R, Lwin KM, Lin F, Wang Y, Sun G, Zhou T, Zhu T, Li J, Jin S, Guo S, Zhang R (2016) GhABF2, a bZIP transcription factor, confers drought and salinity tolerance in cotton (*Gossypium hirsutum* L.). *Sci Rep* 6: 35040.

Linh LH, Linh TH, Xuan TD, Ham LH, Ismail AM, Khanh TD (2012) Molecular breeding to improve salt tolerance of rice (*Oryza sativa* L.) in the Red River Delta of Vietnam. *Int J Plant Genomics* 2012: 949038.

Liu DG, He SZ, Zhai H, Wang LJ, Zhao Y, Wang B, Li R, Liu QC (2014) Overexpression of *IpH5CR* enhances salt tolerance in transgenic sweetpotato. *Plant Cell Tiss Organ Cult* 117: 1-16.

Liu G, Li X, Jin S, Liu X, Zhu L, Nie Y, Zhang X (2014) Overexpression of rice NAC gene *SNAC1* improves drought and salt tolerance by enhancing root development and reducing transpiration rate in transgenic cotton. *PLoS ONE* 9: e86895.

Liu Z-J, Li F, Wang L-G, Liu R-Z, Ma J-J, Fu M-C (2018) Molecular characterization of a stress-induced NAC gene, GhSNAC3, from *Gossypium hirsutum*. *J Genet* 97: 539-548.

Long NV (2016) Effects of salinity stress on growth and yield of quinoa (*Chenopodium quinoa* Willd.) at flower initiation stages. *Vietnam J Agri Sci* 14: 321-327.
Hoang Thi Lan Xuan & Nguyen Phuong Thao

Munns R, James AJ, Läuchli A (2006) Approaches to increasing the salt tolerance of wheat and other cereals. J Exp Bot 57: 1025-1043.

Munns R, Tester M (2008) Mechanisms of salinity tolerance. Annu Rev Plant Biol 59: 651-681.

Murashige T, Skoog F (1962) A revised medium for rapid growth and bioassays with tobacco tissue cultures. Physiol Plant 15: 473-497.

Orellana S, Yañez M, Espinoza A, Verdugo I, González E, Ruiz-Lara S, Casaretto JA (2010) The transcription factor SIAREB1 confers drought, salt stress tolerance and regulates biotic and abiotic stress-related genes in tomato. Plant Cell Environ 33: 2191-2208.

Park GG, Park JJ, Yoon J, Yu SN, An G (2010) A RING finger E3 ligase gene, Oryza sativa Delayed Seed Germination 1 (OsDSG1), controls seed germination and stress responses in rice. Plant Mol Biol 74: 467-478.

Patterson BD, MacRae EA, Ferguson IB (1984) Estimation of hydrogen peroxide in plant extracts using titanium (IV). Anal Biochem 139: 487-492.

Phuong LN, Son DH, Dong NM (2018a) Evaluation of salinity tolerance potential of soybean (Glycine max L.) and sesbania (Sesbania rostrata). J Vietnam Agri Sci Tech 3: 68-71.

Phuong LN, Son DH, Giang NDC, Dong NM (2018b) Evaluation of salinity tolerance potential of soybean (Glycine max L.) and sesbania (Sesbania rostrata). J Vietnam Agri Sci Tech 3: 72-79.

Qi XP, Li MW, Xie M, Liu X, Ni M, Shao GH, Song C, Yim AK-Y, Tao Y, Wong F-L, Isobe S, Wong C-F, Wong K-S, Xu C, Li C, Wang Y, Guan R, Sun F, Fan G, Xiao Z, Zhou F, Phang T-H, Liu X, Tong S-W, Chan T-F, Yiu S-M, Tabata S, Wang J, Xu X, Lam H-M (2014) Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. Nat Commun 5: 4340.

Qin L, Wang L, Guo Y, Li Y, Ümút H, Wang Y (2017) An ERF transcription factor from Tamarix hispida, ThCRF1, can adjust osmotic potential and reactive oxygen species scavenging capability to improve salt tolerance. Plant Sci 265: 154-166.

Quan TAL, Vo CT (2017) Evaluation on the yield of some rice varieties with tolerance to salt stress, a case study. Vietnam J Sci Tech Engineer 59: 32-36.

Rao DLN, Giller KE, Yao AR, Flowers TJ (2002) The effects of salinity and sodicity upon nodulation and nitrogen fixation in Chickpea (Cicer arietinum L.). Ann Bot 89: 563-570.

Saad ASI, Li X, Li H-P, Huang T, Gao C-S, Guo M-W, Cheng W, Zhao G-Z, Liao Y-C (2013) A rice stress-responsive NAC gene enhances tolerance of transgenic wheat to drought and salt stresses. Plant Sci 203-204: 33-40.

Shi HZ, Ishitani M, Kim CS, Zhu JK (2000) The Arabidopsis thaliana salt tolerance gene SOS1 encodes a putative Na+/H+ antiporter. Proc Natl Acad Sci 97: 6896-6901.

Sabra A, Daayf F, Renault S (2012) Differential physiological and biochemical responses of three Echinaceae species to salinity stress. Sci Hort 135: 23-31.

Shi J, Fu X, Peng T, Huang X, Fan Q, Liu J (2010) Spermine pretreatment confers dehydration tolerance of citrus in vitro plants via modulation of antioxidative capacity and stomatal response. Tree Physiol 30: 914-922.

Shinde H, Dudhate A, Tsugama D, Gupta SS, Liu S, Takano T (2019) Pearl millet stress-responsive NAC transcription factor PgNAC21 enhances salinity stress tolerance in Arabidopsis. Plant Physiol Biochem 135: 546-553.

Singh S, Sengar RS, Kulshreshtha N, Datta D, Tomar RS, Rao VP, Garg D, Ojha A (2015) Assessment of multiple tolerance indices for salinity stress in bread wheat (Triticum aestivum L.). J Agric Sci 7: 49-57.

Tak H, Negi S, Ganapathi TR (2017) Banana NAC transcription factor MusaNAC042 is positively associated with drought and salinity tolerance. Protoplasma 254: 803-816.

Tu Y, Jiang A, Gan L, Hossain M, Zhang J, Peng B, Xiong Y, Song Z, Cai D, Xu W, Zhang J, He Y (2014) Genome duplication improves rice root resistance to salt stress. Rice 7: 15.

Tuteja N (2007) Abscisic acid and abiotic stress signaling. Plant Signal Behav 2: 135-138.

Verslues PE, Agarwal M, Katiyar-Agarwal S, Zhu J, Zhu JK (2006) Methods and concepts in quantifying resistance to drought, salt and freezing, abiotic
stresses that affect plant water status. *Plant J* 45: 523-539.

Vu HTT, Le DD, Ismail AM, Le HH (2012) Marker-assisted backcrossing (MABC) for improved salinity tolerance in rice (*Oryza sativa* L.) to cope with climate change in Vietnam. *Aust J Crop Sci* 6: 1649-1654.

Wang C, Lu G, Hao Y, Guo H, Guo Y, Zhao J, Cheng H (2017) ABP9, a maize bZIP transcription factor, enhances tolerance to salt and drought in transgenic cotton. *Planta* 246: 453-469.

Wanjogu SN, Muya EM, Gicheru PT, Waruru BK (2001) Soil degradation: management and rehabilitation in Kenya. In: Proceedings of the FAO/ISCW expert consultation on management of degraded soil in Southern and Eastern Africa (MADS-SEA) 2nd networking meeting, Pretoria, South Africa PR: 102-113.

Xu ZL, Ali Z, Xu L, He XL, Huang YH, Yi JX, Shao HB, Ma HX, Zhang D (2016) The nuclear protein *GmZIP110* has transcription activation activity and plays important roles in the response of sweet potato to salt stress. *Sci Rep* 7: 40819.

Zhang X-x, Tang Y-j, Ma Q-b, Yang C-y, Mu Y-h, Suo H-c, Luo L-h, Nian H (2013) *OsDREB2A*, a rice transcription factor, significantly affects salt tolerance in transgenic soybean. *PLoS ONE* 8: e83011.

Zhao Y, Dong W, Zhang N, Ai X, Wang M, Huang Z, Xiao L, Xia G (2014) A wheat allene oxide cyclase gene enhances salinity tolerance via jasmonate signaling. *Plant Physiol* 164: 1068-1076.

Zhu L, Wang C, Liu RF, Han Q, Vandeleur RK, Du J, Tyerman S, Shou H (2014) Constitutive overexpression of soybean plasma membrane intrinsic protein *GmPIP1;6* confers salt tolerance. *BMC Plant Biol* 14: 181.

Zhu M, Chen G, Zhang J, Zhang Y, Xie Q, Zhao Z, Pan Y, Hu Z (2014) The abiotic stress-responsive NAC-type transcription factor SINAC4 regulates salt and drought tolerance and stress-related genes in tomato (*Solanum lycopersicum*). *Plant Cell Rep* 33: 1851-1863.

Zhu N, Nian H (2013) Transcript profile analysis reveals important roles of jasmonic acid signalling pathway in the response of sweet potato to salt stress. *Sci Rep* 7: 40819.

Yang JC, Zhang JH, Wang ZQ, Zhu QS, Wang W (2001) Hormonal changes in the grains of rice subjected to water stress during grain filling. *Plant Physiol* 127: 315-323.

Zhang H, Zhang Q, Zhai H, Li Y, Wang XF, Liu QC, He SZ (2017) Transcript profile analysis reveals important roles of jasmonic acid signalling pathway in the response of sweet potato to salt stress. *Sci Rep* 7: 40819.

Wang C, Lu G, Hao Y, Guo H, Guo Y, Zhao J, Cheng H (2017) ABP9, a maize bZIP transcription factor, enhances tolerance to salt and drought in transgenic cotton. *Planta* 246: 453-469.

Wanjogu SN, Muya EM, Gicheru PT, Waruru BK (2001) Soil degradation: management and rehabilitation in Kenya. In: Proceedings of the FAO/ISCW expert consultation on management of degraded soil in Southern and Eastern Africa (MADS-SEA) 2nd networking meeting, Pretoria, South Africa PR: 102-113.

Xu ZL, Ali Z, Xu L, He XL, Huang YH, Yi JX, Shao HB, Ma HX, Zhang D (2016) The nuclear protein *GmZIP110* has transcription activation activity and plays important roles in the response to salinity stress in soybean. *Sci Rep* 6: 20366.

Yang G, Yu L, Zhang K, Zhao Y, Guo Y, Gao C (2017) A ThDREB gene from *Tamarix hispida* improved the salt and drought tolerance of transgenic tobacco and *T. hispida*. *Plant Physiol Biochem* 113: 187-197.

**CÁC CHỈ SÓ PHÂN TÍCH QUAN TRỌNG DỤNG TRONG NGHIỆN CỦA DÂNH GIÀ KHÁ NĂNG CHỦ MẠN Ở THỰC VẬT**

Hoàng Thị Lan Xuân1,2, Nguyễn Phượng Thảo1,2

1Phòng thí nghiệm Üng dụng Công nghệ Sinh học trong Phát triển giống cây trồng, Khoa Công nghệ Sinh học, Trường Đại học Quốc tế, Thành phố Thủ Đức, Thành phố Hồ Chí Minh, Việt Nam

2Đại học Quốc gia, Thành phố Hồ Chí Minh, Việt Nam

TÓM TÀT

Tiềm năng sản lượng tối đa của cây trồng và diện tích đất phù hợp cho trồng tốt thường bị hạn chế bởi các yếu tố bất lợi từ môi trường. Trong số các nhân tố stress phi sinh học, stress mặn là một trong những mối đe dọa chính, gây ra đe dọa ion nói bao, stress mặt nước và stress ôxy hóa. Tác động
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của stress mận được dự báo là ngày càng nghiêm trọng hơn do biến đổi khí hậu. Việc phát triển các giống cây trồng mới có khả năng chịu mận tốt hơn bằng phương pháp lai tạo truyền thống hay bằng kỹ thuật di truyền luôn là mối quan tâm của các nhà khoa học. Trong bài viết này, chúng tôi luôn luôn những chỉ số quan trọng trong việc đánh giá về khả năng chịu mận của cây để thu thập bộ dữ liệu đầy đủ liên quan đến thay đổi hình thái và điều chỉnh sinh lý, sinh hoá và phân tử; hoặc từ các phân tích ở quy mô -omics để có cái nhìn tổng quan về mạng lưới các con đường tham gia đáp ứng mận. Các nghiên cứu cũng cho thấy rằng việc thiếu lập điều kiện stress mận phù hợp về mặt nông dỗ và thời gian là rất cần thiết trong thí nghiệm. Hơn nữa, các nghiên cứu gần đây cũng chứng minh rằng số lượng gen trong genome, hoạt động từ các phân tử không mã hóa protein và điều hòa ngoại gen cũng ảnh hưởng đến khả năng chống chịu của cây. Tập hợp các thông tin này không chỉ mở rộng mức độ hiểu biết khoa học về các cơ chế đáp ứng tham thọ của thực vật mà còn giúp tìm ra các gen quan trọng trong đáp ứng stress mận. Do đó, bài viết này có thể đưa đến tham khảo trong các nghiên cứu về stress mận phục vụ công tác cải tạo giống và phân tích chức năng gen.

Từ khóa: các chỉ số phân tích, khả năng chống chịu stress của thực vật, phân tích chức năng gen, stress mận, stress thảm thấu