Plant molecular responses to salt stress

Ciarmiello L.F.[1], Carillo P. [1], Woodrow P. [1]
[1]Università della Campania Luigi Vanvitelli, Dipartimento di Scienze e Tecnologie Ambientali, Biologiche e Farmaceutiche *Via Vivaldi, 43 Caserta*
*Corresponding author: lorymail80@libero.it; loredanafilomena.ciarmiello@unicampania.it

Plants are frequently exposed to environmental changes. In fact, abiotic stresses are the most serious factors limiting the productivity of agricultural crops, with adverse effects on germination, plant vigor and crop quality and yield. In particular, salinity stress is a global problem widespread that affects over 800 million ha. In the Mediterranean area, seawater intrusion into freshwater aquifers highly contribute to soil salinisation, resulting in crops productivity decrease. Responses to abiotic stresses are complicated pathways involving the interaction of different signalling molecules to coordinate a specific metabolic pathways. The regulation of these responses involves transcriptional factors, which regulate gene expression by binding to specific DNA promoter sequences. Transcription factors involved in salt stress responses include DRE-related binding factors, leucine zipper DNA binding proteins, putative zinc finger proteins, myb proteins, bZIP/HD-ZIPs, and AP2/EREBP. Particularly, AP2/ERF domain proteins include the DREB or CBF proteins binding to dehydration response elements (DRE) or C-repeats. Transcription factors are powerful targets for genetic engineering in abiotic stress resistance in crops and many studies have been focused on this topic.

Table 1. Consequences of salt stress and plant responses

Stress	Consequences	Plant Responses
Salt stress	High NaCl concentrations affect plant physiology and metabolism at different levels: water deficit, ion toxicity, nutrient imbalance, and oxidative stress (Vinocur & Altman, 2005; Ciarmiello et al., 2011)	Plants adopt two main responses: a rapid protective ones together with a long term adaptation response. During initial exposure to high salt concentrations, plants attempt water stress, which in turn reduces leaf expansion. During long-term exposure to salinity, plants attempt ionic stress, which can lead to premature senescence of adult leaves, and thus a reduction in the photosynthetic area available to growth support (Cramer & Nowak, 1992)

PLANTS ADAPTIVE MECHANISMS AND SIGNALLING PATHWAYS SURING SALT STRESS

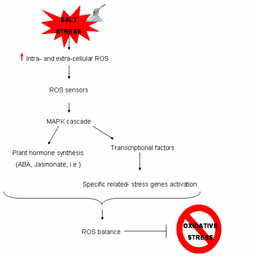

Figure 1. ROS signal transduction pathway under saltinity stress.

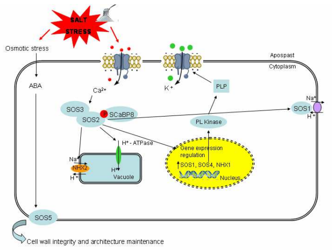

Figure 2. The Ca2+/salt overly sensitive (SOS) cascade. Under salt stress, the SOS pathway is activated by a calcium and SCaBP8 is phosphorylated by SOS2. This latter act on vacuolar H+-ATPase and Na+/H+ exchanger. Vacuolar partitioning of Na+ is mediated by the vacuolar Na+/H+ antiporter (NHX). SOS1 sodium transport requires a proton gradient created by H+-ATPase. SOS2 enhance gene expression.

SOS4 encodes a pyridoxal (PL) kinase involved in pyridoxal-5-phosphate (PLP) biosynthesis, which is associate with AKT1, a potassium channel. SOS5, a putative cell surface adhesion protein, is involved in cell expansion process.

GENE REGULATION AND TRANSCRIPTIONAL FACTOR IN SALINITY STRESS

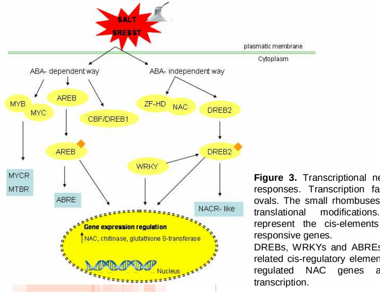

Figure 3. Transcriptional network of salt stress responses. Transcription factors are shown in ovals. The small rhombuses correspond to post-translational modifications. Sky-blue boxes represent the cis-elements present in stress-responsive genes.
DREBs, WRKYs and ABREs TFs bind to stress-related cis-regulatory elements in the promoter of regulated NAC genes and influence their transcription.

EPIGENETIC REGULATION

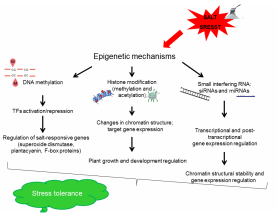

Figure 4. Epigenetic mechanisms such as DNA methylation, histone modification and small interfering RNA can regulate gene expression, playing an important role in plant stress tolerance.

CONCLUSIONS

In the last decade, significant research advances have been made to our understanding of plant salt-tolerance mechanisms in recent years, more studies are required to expand our knowledge, such as the elucidation of salt stress perception and the identification of key components of the salt stress response and development of efficient strategies to improve crop salt tolerance.
The further characterization and in particular functional analysis of transcriptional factors, genes as well as elements with key role in epigenetic control, could help to explain the complex salinity stress regulatory pathways. The ability of TFs and small RNA to induce or repress the expression of stress-responsive genes may be a useful key point to develop improved crop plants resistant or tolerant to salt stress.