AN ARABIDOPSIS RNA BINDING PROTEIN IS INVOLVED IN TOLERANCE TO DROUGHT AND SALT STRESS

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Soil salinity and drought conditions are environmental stresses that severely limit plant growth and productivity by imposing osmotic stress on plants. The molecular mechanisms underlying osmotic stress response and tolerance are the subject of intense research in plant biology. Previously, we identified and isolated RGGA gene, coding for a glycine-rich RNA-binding protein, whose expression is specifically induced in Solanum tuberosum cells exposed to gradual osmotic stress induced by PolyEthyleneGlycole (PEG 20%).

To confirm the potential role of RGGA gene in plant stress response, we identified the putative RGGA orthologue in Arabidopsis thaliana (AtRGGA, At4g16830) and evaluated the influence of salt and water stress on AtRGGA gene expression in cells and seedlings exposed to high concentrations of NaCl, PEG and abscisic acid (ABA). Interestingly, short-term treatments (24 hour) resulted in a down-regulation of AtRGGA expression, while the gene transcription increased in long-term exposure to the stressors (7 days). A β-glucuronidase (GUS) assay allowed visualization of RGGA promoter activity in different tissues, with strong staining in guard cells and vascular tissues. Through the use of transgenic plants over-expressing a YFP-RGGA fusion protein, was also possible to investigate the protein sub-cellular localization. Fluorescence signal revealed that RGGA is localized in the cytoplasm and the peri-nuclear region. To carry out a functional analysis, a gain- and loss-of-function approach was performed using transgenic Arabidopsis plants over-expressing RGGA and rgga knock-out mutants. Under salt and drought stress conditions, the over-expressing plants showed a higher tolerance both in vitro and in soil and accumulated lower levels of proline, possibly indicating that the intensity of the stress perceived was lower compared to wild-type Col-0. Accordingly, knock-out mutants appeared more sensitive, showing lower seed germination and survival rate than Col-0 when exposed to salt stress. Finally, a global analysis of gene expression using microarrays, followed by qRT-PCR validation, was performed, revealing extensive alterations in the transcriptome of RGGA over-expressing and knock-out plants under salt stress. These evidences indicate that RGGA participates in the modulation of transcript abundance of several key genes involved in abiotic stress response.

Taken together, our results suggest an important role of RGGA in the mechanisms of plant response and adaptation to osmotic stress.