Contribution of plants to human health and longevity: Utilization of genes for protecting plants against salt stress

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The lifestyle-related illnesses caused by inappropriate intake of nutrients are the most serious for health and longevity in the advanced nations, although food starvation ironically is the gravest in some countries. The green resources in terrestrial parts of the world are necessary for food production, sustainable environment for humans, and alternative fuel production. Soil salinity is a major constraint to food production because it affects plant growth, development and water quality hence reduction in crop yield. Salinity is a worldwide problem and according to the currents estimates, 10-35% of Worlds agricultural land is salt affected. Although careful water management practices can reduce the loss to some extent but improved crop varieties have a vital role to maintain the growth and yield of crops in salt affected area. Therefore to address the aspects of food security and sustainable agriculture it is important to understand the mechanism of stress tolerance and identify new components of stress regulation in plants.

AtbHLH106 recognize GC-box (CACGTG) in promoter regions: Electrophoresis Mobility Shift Assay (EMSA) was performed to identify downstream genes regulated by AtbHLH106. Most of the bHLH proteins recognize CANNTG region in promoter but AtbHLH106 specifically recognized GC-box. In competition assay, AtbHLH106 also interacted with other variants of GC-box however the intensity of interaction was weak. In-silico analysis of promoters of all genes from microarray data produced that a number of genes had GC-box in their promoters. Short probes (24bp) were designed for GC-box regions in promoters and we found that all these promoters also interacted with AtbHLH106. More than 70 genes were found regulated by AtbHLH106 and a few of them are already have established role in abiotic stress tolerance. In addition, knock-out lines of interacting genes have also established some new components of salt stress regulation through AtbHLH106.

Chromatin immunoprecipitation (ChIP) followed by Tilling array (CHIP): ChIP is powerful tool to study interaction of transcription factors with DNA in-vivo. To further confirm our results of EMSA, we have generated and purified antibodies specific to AtBHLH106. Plant samples for ChIP-CHIP have also been fixed and experiment is underway.

Tranformation of wild-type with 35S:AtWBC7: In one of our mutants stc5, a gene responsible for ABC transporter AtWBC7 was activated and its knock-out line was sensitive to salt as well as abscisic acid. Over-expression lines were generated using one of four alternative splice variants of AtWBC7 but expression was not significantly higher. Presently we have been planning over-expression of three other splice variants.

Conclusions: We have presented a new model for identification of abiotic stress regulatory components in plants using activation tagging in dedifferentiated cells. In addition we have also some new components of salt stress regulation in Arabidopsis. Moreover, our results would strengthen ongoing efforts of research as well as food security.