Genes involved in maintenance of plant productivity on salt-accumulating land as required for human subsistence

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Food is crucial for human life, but there is a worldwide deficiency, with 28 people per minute dying of starvation around the world. Plants are a major resource for food and for environmental preservation. Salinity represents a major abiotic stress factor that imposes serious threats on agricultural industries on a world scale. Damaged land comprises almost 6% of total world land area, and among toxic substances, salt interferes the most drastically with plant growth. Salt stress has a negative impact on the growth, production and distribution of crop plants. Therefore, an understanding of salt regulatory systems and engineering for salt tolerance of plants are fundamental and critical fields that require attention. We focused on dedifferentiated calli with fundamental cell functions, the salt tolerance of which had not been investigated. An experimental approach was designed based on activation-tagging without the regeneration of plants for the identification of salt-tolerant mutants of *Arabidopsis*.

Out of 62,000 transformed calli screened, 18 potential mutants were obtained that were resistant to 150 mM NaCl. Thermal asymmetric interlaced (TAIL)-PCR was performed to determine the location of T-DNA integration in the genome and real-time PCR was carried out for the identification of causal genes. In addition, microarray (GeneChip) was carried out for whole genome transcriptomic analysis of candidate lines with or without 150 mM NaCl. In one line, referred to as *salt tolerant callus 1* (*stc1*), expression of the gene for *myo*-inositol-1-P-synthase (AtMIPS) was found to be enhanced more than 10 times on standard callus-inducing medium (CIM), and more than 100 times under 150 mM-NaCl stress conditions. Regenerated plants of this mutant showed tolerance to salt and vital germination under salt stress conditions compared to wild-type plants. Constitutive expression of *AtMIPS* resulted in salt tolerance during seed germination and generally in seedlings, calli and plants via an increase of inositol content. The activation-tagging method established here has demonstrated its usefulness in identifying genes throughout the genome for abiotic stress tolerance at the cellular level.

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