Chromosome scanning for salt tolerance genes involved in fundamental cell growth of *Arabidopsis* by activation tagging

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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 counties. The green resources in terrestrial parts of the world are necessary for food production, sustainable environment for humans, and alternative fuel production.

Salinity represents a major abiotic stress factor that can adversely limit the production, quality and geographical distribution of crops. In this study we focused on dedifferentiated calli with fundamental cell functions, the salt tolerance of which had not been previously examined. An experimental approach was designed based on activation tagging without regeneration of plants for the identification of salt-tolerant mutants of *Arabidopsis*. Out of 62,000 transformed calli screened, 18 potential mutants resistant to 150 mM NaCl were obtained. Thermal asymmetric interlaced (TAIL)-PCR was performed to determine the location of T-DNA integration in the genome. In one line, referred to as *salt tolerant calli 1* (*stc1*), expression of a gene [AT4G39800: myo-inositol-1-P-synthase (AtMIPS)] was found to be enhanced more than 10-fold on standard callus-inducing medium (CIM), and more than 100-fold under 150 mM-NaCl stress conditions. Regenerated mutant plants showed tolerance and enhanced germination under salt stress conditions compared to wild-type plants. Constitutive expression of AtMIPS results in salt tolerance during seed germination, and generally in seedlings, calli and plants. The activation tagging method established here illustrates its usefulness in identifying genes for abiotic stress tolerance at the cellular level through out the genome.