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Isolation of responsive genes involved in acquiring salt- and drought-tolerances in tomato Micro-Tom, a new model plant of Solanaceae.

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Summary

Plant cells response to environmental stress by exerting intracellular signaling pathway rapidly, leading to induction of a set of specific genes and then acquiring stress tolerance. Recent progress of whole genomic analysis and reverse genetic approach of *Arabidopsis* clarified that *Arabidopsis* has multiple SNF 1 kinase-related kinase (SRK) families composed of SRK1-, SRK2- and SRK3-subfamilies and that SRK2 has a important role in stress signaling in response to drought, salt stress and ABA. It was also reported that SRK2C-overexpressing *Arabidopsis* plant shows salt- and drought-resistant phenotype.

Now, International Solanaceae Genome project has focused on tomato Micro-Tom as a novel model plant and has started genomic projects. Therefore, tomat genetic resources including EST database (MiBASE, for an example) has come to be broadly available for molecular and genetic research of tomato and Solanaceae-related plants living in various habitats including extremely severe circumstance. Today, we isolated a SRK2 homolog from Tomato MicroTom and analyzed biochemical properties and expression profiles of tomato SRK2 homolog (LeSRK2C). The DNA sequence data of full length cDNA of LeSRK2C indicate that LeSRK2C has a similar domain structure and relatively high similarity of aminoacid sequences in the catalytic domain in the N-terminal domain and the COOH-terminus region to those of AtSRK2C, compared with other SRKs.

We characterized protein kinase activities of recombinant proteins of maltose binding protein fused LeSRK2C expressed in *E.coli* and GST-fused LeSRK2C ectopically and transiently expressed in *Nicotiana benthamiana* leaves by agroinfiltration and DEX-inducible vector system. Our present data by *in vitro* kinase assay and immunoprecipitation assay indicate significant difference between LeSRK2C and AtSRK2C, 1)LeSRK2C phosphorylates myelin basic protein but not histone H1, while AtSRK2C phosphorylates histone H1, 2)LeSRK2C is expressed in photosynthetic organs, floral organs and fruit but not in root, while expression of AtSRK2C is detected in root tips, 3) LeSRK2C is stimulated by chilling stress rather than by NaCl stress, while AtSRK2C is activated by NaCl but not by chilling stress. Detail biochemical mechanism involving activation of LeSRK2C remains to be clarified.

We also focused on expression profiles of candidate genes for trehalose metabolism-related enzymes in tomato under various stress. Semi-quantitative RT-PCR analysis revealed that at least two TPS-/TPP-related candidate genes, Contig15270 and Contig10668 are significantly induced by cold stress and ABA treatment, repectively. Cloning and characterization of full length cDNA of the TPS-related gene Contig15270 are currently in progress.