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Title of Entry	: Systematic discovery of novel G protein transcriptional network in response to high salinity
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: High soil salinity imposes both osmotic and ionic toxicity on plants, resulting in the reduction of plant growth and crop yield. Heterotrimeric G protein, composed of G α , G β and G γ subunits, modulates plant morphology, phytohormone responses, and more importantly, various abiotic and biotic stress responses. However, little is known about the G protein gene regulatory network under salt stress. To investigate the role of G protein signaling in salt response, we generated high-resolution comparative transcriptomics data sets from G protein mutants of <i>Oryza sativa</i> and other plant species along the course of salt treatment and combined them with detailed physiological analyses of plants subjected to salt stress. Genotype-specific differentially expressed genes were identified in each species and the changes of those genes were coincided with hyper- or hypo-sensitive phenotypes obtained from the salt treated mutants, suggesting that the G protein signaling network is evolutionarily conserved in response to high salinity in the plant kingdom. We built a gene co-expression network as well as an inferred network by Bayesian network modeling to identify important hub genes. In addition, we further constructed a semi-supervised network for predicting novel G protein functions in abiotic stress tolerance. To experimentally validate the predicted network and function of the hub genes, we performed phenotypic screening on G protein mutants under various abiotic stress and the strong phenotype were shown in previously unreported

stress conditions. Collectively, the data suggest that G proteins rewire complex transcriptional network and their downstream regulatory genes in response to various stresses and that engineering the target genes from the predicted network hold great potential for developing stress tolerant crops

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