



## Assessment and extension of Interaction network of the salinity responsive genes in plants

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**Abstract:** Salinity is one of the most important limiting factor for plant growth and extension. This stress has large effect on many aspects of plant metabolism. A lots of genes govern salt stress resistance and many of them identified until now. According to extension of interaction network of the genes involving in salt stress resistance, 162 gene were identified form PubMed published papers and information about them were collected from NCBI web site. These genes were used as "seed genes" for extension the interaction network via String database [1]. Co-expression, gene neighborhood, protein homology, gene fusions and gene co-occurrence criteria were used to extent interaction network [2, 3]. Subsequently, several Candidate genes were introduced from extented network. According to the results CPGK2, ATTPS6, CAK4, CDKD1;3, EMB2107, PKT3RPN1a, RPT2a, RUXF, SNRK2.2, SNRNP-G, SOS3 genes beside of some gene family such as Jaz family, TPS family, PGK family, LSM family and TPI family were the best candidates responsible for salt stress. Study of Gene ontology (GO) characteristics associated with candidate genes for Salinity stress suggested that these genes play important role (GO:0006950) in response to salt stress. Candidate genes can then be tested using a variety of experimental methods, including RNA interference technology, quantitative RT-PCR, and protein assays.

**Keywords:** Salinity stress; Gene ontology; Interaction network; plant metabolism.

### References

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