

Novel gene for salt tolerance found in wild soybean

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A team of researchers from The Chinese University of Hong Kong, BGI and other institutes have identified a gene of wild soybean linked to salt tolerance, with implication for improving this important crop to grow in saline soil. This study published online in *Nature Communications* provides an effective strategy to unveil novel genomic information for crop improvement.

Soybean is an important crop for the world. Due to domestication and human selection, cultivated soybeans have less genetic diversities than their wild counterparts. Among the lost genes, some may play important roles for the adaptation to different environments. In this study, scientists used wild soybean as a resource for investigating the valuable genes that adapt to certain environmental conditions.

They sequenced and assembled a draft genome of wild soybean W05, and developed a recombinant inbred population for genotyping-by-sequencing and phenotypic analyses to identify multiple QTLs relevant to traits of interest in agriculture. Using the de novo sequencing data from this work and their previous germplasm re-sequencing data, the team discovered a novel ion transporter gene, GmCHX1, and suggested it maybe related with [salt tolerance](#).

During the following rapid gain-of-function tests, the gene GmCHX1 was conferred its function on salt tolerance, and suggested GmCHX1 acted probably through lowering the Na⁺/K⁺ ratio. The authors assumed that the elimination of GmCHX1 in salt-sensitive germplasms may be an

example of negative selection against a stress tolerance gene in unstressed environments. The expression of stress tolerance genes may be an energy burden on the plant if the functions of these genes are not required.

Through this study, researchers developed an efficient strategy using the combination of whole-genome de novo sequencing, high-density-marker QTL mapping by re-sequencing, and functional analyses, which could greatly enhance the efficiency of uncovering QTLs and [genes](#) for beneficial traits in crop breeding.

Provided by BGI Shenzhen

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