

# Salt cress genome yields new clues to salt tolerance

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An international team, led by Institute of Genetics and Developmental Biology, Chinese Academy of Science, and BGI, the world's largest genomics organization, has completed the genomic sequence and analysis of salt cress (*Thellungiella salsuginea*), a wild salt-tolerant plant. The salt cress genome serves as a useful tool for exploring mechanisms of adaptive evolution and sheds new lights on understanding the genetic characteristics underlying plant abiotic stress tolerance. The study was published online in *PNAS*.

Salt Cress is a typical halophyte with high resistance to cold, drought, oxidative stresses and salinity. Due to its small plant size, short life cycle, copious seed production, small [genome size](#), and an efficient transformation, salt cress could serve as an important [genetic model](#) system for botanist, geneticists, and breeders to better explore the [genetic mechanisms](#) of abiotic stress tolerance.

In the study, researchers sequenced the genome of salt cress (Shandong ecotype) using the paired-end Solexa sequencing technology. The genomic data yielded a [draft sequence](#) of salt cress with about 134-fold coverage. The final length of the assembled sequences amounted to about 233.7 Mb, covering about 90% of the estimated size (~260 Mb). A total of 28,457 protein-coding regions were predicted in the sequenced salt cress genome. Researchers found that the average exon length of salt cress and *A. thaliana* genes was similar, whereas the average intron length of salt cress was about 30% larger than that of *A. thaliana*.

The evolutionary analysis indicated that salt cress and its close relative- [Arabidopsis thaliana](#)- diverged from approximately 7 -12million years ago. When tracing the differences between salt cress and *A. thaliana*, researchers found salt cress was characterized by a dramatically different lifestyle, a unique gene complement, significant differences in the expression of orthologs, and a larger genome size. Noticeably, the salt cress genome showed a dramatically higher content of transposable elements (TEs) than that of *A. thaliana*, which may be the reason for its enlarged genome size. In common with other higher plants, salt cress genome was consisted of abundance of long terminal repeat (LTR) retrotransposons.

Salt can have drastic effects on the growth and yield of agronomical crops. It is estimated that salinity renders about one-third of the world's irrigated land unsuitable for crop production. In this study, researchers identified many genes in salt cress that contribute to its success in high-salt environments, such as the genes related with cation transport, abscisic acid signaling, and wax production.

Junyi Wang, Director of Science & Technology, Research & Cooperation Center, BGI, said, "Salt cress provides an excellent model and opportunity for researchers to explore plant's mechanisms of abiotic stress tolerance. The completed genomic sequence of salt cress will boost the advancement of [stress tolerance](#) research as well as provide a valuable theoretic instruct and technical support for researchers worldwide to better face the challenges of the soil salinization in irrigation area, the development and utilization of shallow offshore waters and beaches, and food security."

**More information:**

<http://www.pnas.org/content/early/2012/07/05/1209954109.abstract?sid=548ade97-58d5-4c0a-a1e4-e1a43a9c9c21>

Provided by BGI Shenzhen

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