The Reference Genome of the Halophytic Plant Eutrema salsugineum
2013
Posted by : webmaster
Posted on : 2013/5/6 19:10:38

Yang R, Jarvis DE, Chen H, Beilstein MA, Grimwood J, Jenkins J, Shu S, Prochnik S, Xin M, Ma C, Schmutz J, Wing RA, Mitchell-Olts T, Schumaker KS, Wang X.
Source

School of Plant Sciences, University of Arizona Tucson, AZ, USA.

Front Plant Sci. 2013;4:46. doi: 10.3389/fpls.2013.00046. Epub 2013 Mar 21.

Abstract

Halophytes are plants that can naturally tolerate high concentrations of salt in the soil, and their tolerance to salt stress may occur through various evolutionary and molecular mechanisms. Eutrema salsugineum is a halophytic species in the Brassicaceae that can naturally tolerate multiple types of abiotic stresses that typically limit crop productivity, including extreme salinity and cold. It has been widely used as a laboratorial model for stress biology research in plants. Here, we present the reference genome sequence (241?Mb) of E. salsugineum at 8× coverage sequenced using the traditional Sanger sequencing-based approach with comparison to its close relative Arabidopsis thaliana. The E. salsugineum genome contains 26,531 protein-coding genes and 51.4% of its genome is composed of repetitive sequences that mostly reside in pericentromeric regions. Comparative analyses of the genome structures, protein-coding genes, microRNAs, stress-related pathways, and estimated translation efficiency of proteins between E. salsugineum and A. thaliana suggest that halophyte adaptation to environmental stresses may occur via a global network adjustment of multiple regulatory mechanisms. The E. salsugineum genome provides a resource to identify naturally occurring genetic alterations contributing to the adaptation of halophytic plants to salinity and that might be bioengineered in related crop species.

KEYWORDS:

Arabidopsis thaliana, Brassicaceae, Eutrema salsugineum, genome annotation, halophyte, whole-genome sequencing