

生命科学セミナー

The Genome of an Extremophile, *Thellungiella parvula* (Brassicaceae)

Dong-ha Oh^{1,4}, Maheshi Dassanayake¹, John Cheeseman¹, Dae-Jin Yun^{2,4}, Ray Bressan^{2,3,4}, Jian-Kang Zhu³ and **Hans J. Bohnert**^{1,3,4}

¹University of Illinois at Urbana-Champaign, USA, ²Purdue University, USA, ³KAUST, Saudi Arabia, ⁴Gyeongsang National University and WCU Program, Korea

A close relative of *Arabidopsis thaliana*, *Thellungiella parvula* is adapted to a fundamentally different lifestyle compared to *Arabidopsis*: the plant exemplifies species termed extremophiles. *T. parvula* is extremely salt tolerant, and it is drought and freezing tolerant, while it is equally adapted for life on resource-poor and degenerated soils.

We have determined its genome sequence and stress-dependent transcriptome profiles with the objective of comparing how this plant differs in genome structure and expression characteristics from the model *Arabidopsis*, which does not exhibit any extremophile characters. The genome of *T. parvula* in seven chromosomes is approximately 15% larger than the *Arabidopsis* genome – 138 Mb. Surprisingly little repeat DNA and fewer transposons compared to *Arabidopsis* are present. The transcriptome, in terms of protein-coding as well as non-coding transcribed genes, has expanded by approximately 1,000 units. Examples of genome structure, gene complement and gene expression, and some obvious differences between *T. parvula* and *A. thaliana*, will be discussed.

Our results support the notion that, to a very large degree, all genes that determine the extremophile lifestyle are present in all plants. A major distinction between the two species is the number of and type of gene duplications. Susumo Ohno's 1970 insightful monograph entitled "Evolution by Gene Duplication" is completely justified by our results. This result is in contrast to the "Gene Balance Hypothesis" that argues for preferential retention of "dosage-sensitive genes", whereas other gene duplicates are preferentially lost following a genome duplication event, such as it has happened three times in the Brassicaceae. What characterizes one level of difference seems to be "copy number variation" (CNV) in terms of gene copy numbers as well as in gene expression strength. The second level of differences appears to pertain to protein domain structure and allelic micro-variation by which stress-essential proteins are distinguished from stress-sensitive species by minute alterations, but we have barely touched this aspect. Considering crop breeding in the age of genomics, we point to the importance of selecting extremophile characters in crop species that could be present in or emerge from crosses with wild, stress-adapted species.

4月12日（火） 16:00～17:30

京都大学北部キャンパス農学部総合館

W106 講義室

連絡先 京都大学生命科学研究科全能性統御機構学分野
佐藤文彦 (Fumihiko Sat o) Tel:075-753-6381