

Construction of a cDNA Library from the Ephemeral Plant *Olimarabidopsis pumila* and Preliminary Analysis of Expressed Sequence Tags

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Z. Naturforsch. **68c**, 499–508 (2013); received March 15/October 23, 2013

Olimarabidopsis pumila is a close relative of the model plant *Arabidopsis thaliana* but, unlike *A. thaliana*, it is a salt-tolerant ephemeral plant that is widely distributed in semi-arid and semi-salinized regions of the Xinjiang region of China, thus providing an ideal candidate plant system for salt tolerance gene mining. A good-quality cDNA library was constructed using cap antibody to enrich full-length cDNA with the gateway technology allowing library construction without traditional methods of cloning by use of restriction enzymes. A preliminary analysis of expressed sequence tags (ESTs) was carried out. The titers of the primary and the normalized cDNA library were $1.6 \cdot 10^6$ cfu/mL and $6.7 \cdot 10^6$ cfu/mL, respectively. A total of 1093 clones were randomly selected from the normalized library for EST sequencing. By sequence analysis, 894 high-quality ESTs were generated and assembled into 736 unique sequences consisting of 72 contigs and 664 singletons. The resulting unigenes were categorized according to the gene ontology (GO) hierarchy. The potential roles of gene products associated with stress-related ESTs are discussed. The 736 unigenes were similar to *A. thaliana*, *A. lyrata*, or *Thellungiella salsuginea*. This research provides an overview of the mRNA expression profile and first-hand information of gene sequence expressed in young leaves of *O. pumila*.

Key words: *Olimarabidopsis*, Comparative Genomics, Gene Expression