

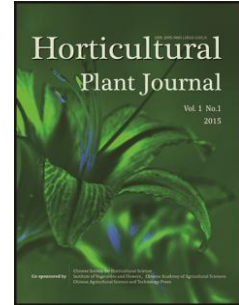
Accepted Manuscript

Title: Genome-Wide Identification of microRNAs That Respond to Drought Stress in Seedlings of Tertiary Relict *Ammopiptanthus Mongolicus*

Author: Liu Shengli, Ni Yanjie, He Qian, Wang Jinyu, Chen Yuzhen, Lu Cunfu

PII: S2468-0141(17)30273-X
DOI: <https://doi.org/doi:10.1016/j.hpj.2017.10.003>
Reference: HPJ 102

To appear in: *Horticultural Plant Journal*



Please cite this article as: Liu Shengli, Ni Yanjie, He Qian, Wang Jinyu, Chen Yuzhen, Lu Cunfu, Genome-Wide Identification of microRNAs That Respond to Drought Stress in Seedlings of Tertiary Relict *Ammopiptanthus Mongolicus*, *Horticultural Plant Journal* (2017), <https://doi.org/doi:10.1016/j.hpj.2017.10.003>.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

1 **Genome-wide Identification of microRNAs that Respond to Drought Stress in Seedlings of**
 2 **Tertiary Relict *Ammopiptanthus mongolicus***

3 **LIU Shengli^{a,1}, NI Yanjie^{a,1}, HE Qian^a, WANG Jinyu^b, CHEN Yuzhen^{a,*}, and LU Cunfu^{a,*}**

4 ^a*Beijing Advanced Innovation Center for Tree Breeding by Molecular Design, College of Biological Sciences*
 5 *and Biotechnology, National Engineering Laboratory for Tree Breeding, Beijing Forestry University, Beijing*
 6 *100083, China*

7 ^b*Analysis and Testing Center, Tsinghua University, Beijing 100083, China*

8 ¹ These authors contributed equally to this work.

9 * Corresponding author. Tel.: +86 10 62338346; Fax: +86 10 62336164

10 E-mail address: chenyzhen@bjfu.edu.cn; lucunfu@bjfu.edu.cn

11 2468-0141 ©2017 Chinese Society for Horticultural Science (CSHS) and Institute of Vegetables and Flowers (IVF), Chinese Academy of Agricultural
 12 Sciences (CAAS)

13 **Abstract**

14 microRNAs (miRNAs) are important post-transcriptional regulators of gene expression in plant abiotic stress responses.
 15 *Ammopiptanthus mongolicus* is a typical evergreen woody xerophyte, which makes it an ideal model system for studying drought
 16 tolerance in woody plants. The response of miRNAs to drought stress is still unknown in this plant. In this research, we obtained
 17 34 695 665 raw reads from two small RNA libraries constructed from control and drought-treated *A. mongolicus* seedlings by the
 18 Illumina deep sequencing technology. Length analysis revealed that reads of 20, 21, and 24 nucleotides accounted for the
 19 majority of the small RNAs in the two libraries. Sequence analyses identified 65 conserved miRNA sequences from 190
 20 members of 31 miRNA families and 20 potential novel miRNAs from 17 families that were differentially expressed between the
 21 two libraries. The expression patterns of 25 of these miRNAs were significantly different in the two libraries, but only am-
 22 miR4a-c was downregulated during drought stress, the other 24 were upregulated. The expression trends determined by the
 23 HiSeq sequencing and by qRT-PCR were similar. Furthermore, 35 target genes for the conserved miRNA were markedly changed
 24 and 52 target genes for the potential novel miRNAs were predicted and their functions were annotated by computational analysis.
 25 Our results provide new molecular evidence for understanding the molecular mechanisms of drought response and tolerance in *A.*
 26 *mongolicus*.

27 *Keywords: Ammopiptanthus mongolicus; drought stress; microRNAs; qRT-PCR*

28 **1. Introduction**

29 microRNAs (miRNAs) are small RNAs that range in length from 20 to 24 nucleotides, and are involved in repressing gene
 30 expression. miRNAs were first discovered in *Caenorhabditis elegans*, where they affect the timing in larval developmental
 31 events (Lee et al., 1993). miRNA genes have been considered that mainly originated from the duplication of preexisting miRNA
 32 genes and protein-coding genes (Nozawa et al., 2012). Through a series of enzymatic processes, pre-miRNAs are cleaved to short
 33 double-stranded mature miRNA/miRNA* duplexes. The miRNA* here is the other complementary or antisense strand (Tomari et
 34 al., 2004). The mature miRNAs are integrated into a RNA-induced silencing complex (RISC), and the mature miRNAs interact
 35 with their target mRNAs by perfect or near-perfect complementarily binding (Aukerman and Sakai, 2003; Bartel, 2004; Voinnet,
 36 2009; Nag and Jack, 2010). miRNAs function by degrading or repressing the translation of the target mRNAs.

37 In plants, miRNAs can regulate the expression of transcription factors, stress response proteins, and other proteins related to
 38 growth, development, and physiology (Voinnet, 2009; Axtell, 2013; Song et al., 2014). miRNAs have been reported to regulate

Download English Version:

<https://daneshyari.com/en/article/8892203>

Download Persian Version:

<https://daneshyari.com/article/8892203>

[Daneshyari.com](https://daneshyari.com)