



Corrigendum: *De novo* assembly of the Japanese lawngrass (*Zoysia japonica* Steud.) root transcriptome and identification of candidate unigenes related to early responses under salt stress

Qi Xie¹, Jun Niu², Xilin Xu³, Lixin Xu¹, Yinbing Zhang¹, Bo Fan¹, Xiaohong Liang¹, Lijuan Zhang⁴, Shuxia Yin^{1*} and Liebao Han^{1*}

OPEN ACCESS

Edited by:

Keqiang Wu, National Taiwan University, Taiwan

Reviewed by:

Ing-Feng Chang, National Taiwan University, Taiwan

*Correspondence:

Shuxia Yin yinsx369@163.com; Liebao Han Hanliebao@163.com

Specialty section:

This article was submitted to Plant Genetics and Genomics, a section of the journal Frontiers in Plant Science

Received: 25 August 2015 Accepted: 17 September 2015 Published: 09 October 2015

Citation:

Xie Q, Niu J, Xu X, Xu L, Zhang Y, Fan B, Liang X, Zhang L, Yin S and Han L (2015) Corrigendum: De novo assembly of the Japanese lawngrass (Zoysia japonica Steud.) root transcriptome and identification of candidate unigenes related to early responses under salt stress. Front. Plant Sci. 6:811. doi: 10.3389/fpls.2015.00811 ¹ Institute of Turfgrass Science, College of Forestry, Beijing Forestry University, Beijing, China, ² Lab of Systematic Evolution and Biogeography of Woody Plants, College of Nature Conservation, Beijing Forestry University, Beijing, China, ³ Bioinformatics, College of Plant Protection, Hunan Agricultural University, Changsha, China, ⁴ Shenzhen Tourism College, Jinan University, Shenzhen, China

Keywords: Zoysia japonica Steud., RNA sequencing (RNA-Seq), salt-stress, transcription factor, simple sequence repeats (SSRs)

A corrigendum on

De novo assembly of the Japanese lawngrass (Zoysia japonica Steud.) root transcriptome and identification of candidate unigenes related to early responses under salt stress by Xie Q, Niu J, Xu X, Xu L, Zhang Y, Fan B, et al. (2015) Front. Plant Sci. 6:610. doi: 10.3389/fpls.2015.00610

Due to an oversight by the authors, data from a different study were incorrectly reported in the Abstract and Conclusion of the manuscript.

The number of unigenes found was 32,849, not the 100,800 originally reported. This has been changed throughout the article. Accordingly, the abstract should read as follows:

We first constructed two sequencing libraries, including control and NaCl-treated samples, and sequenced them using the Illumina $\operatorname{HiSeq^{TM}}$ 2000 platform. Approximately 157.20 million paired-end reads with a total length of 68.68 Mb were obtained. Subsequently, 32,849 unigenes with an N50 length of 1781 bp were assembled using Trinity, among which 70,127 unigenes were functionally annotated (*E*-value \leq 10-5) in the non-redundant protein (NR) database. Furthermore, three public databases, the Kyoto Encyclopedia of Genes and Genomes (KEGG), Swiss-prot, and Clusters of Orthologous Groups (COGs), were used for gene function analysis and enrichment. The annotated genes included 57 Gene Ontology (GO) terms, 120 KEGG pathways, and 24 COGs. Compared with the control, 1455 genes were significantly different (false discovery rate \leq 0.01, $|\log 2Ratio| \geq 1$) in the NaCl-treated samples. These genes were

1

enriched in 10 KEGG pathways and 73 GO terms, and subjected to 25 COG categories.

The conclusion has been modified to remove the text "of which 73,862 produced hits against the NR database" as this was in reference to the incorrect data.

All conclusions were drawn using the correct data and, as such, these are unaffected by the above changes.

The original article was updated.

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2015 Xie, Niu, Xu, Xu, Zhang, Fan, Liang, Zhang, Yin and Han. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.