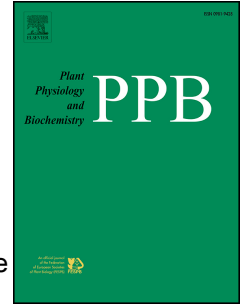


Accepted Manuscript

Co-evolutionary associations between root-associated microbiomes and root transcriptomes in wild and cultivated rice varieties

Lei Tian, Shaohua Shi, Lina Ma, Fahad Nasir, Xiujun Li, Lam-Son Phan Tran, Chunjie Tian



PII: S0981-9428(18)30167-0

DOI: [10.1016/j.plaphy.2018.04.009](https://doi.org/10.1016/j.plaphy.2018.04.009)

Reference: PLAPHY 5214

To appear in: *Plant Physiology and Biochemistry*

Received Date: 8 January 2018

Revised Date: 26 March 2018

Accepted Date: 10 April 2018

Please cite this article as: L. Tian, S. Shi, L. Ma, F. Nasir, X. Li, L.-S. Phan Tran, C. Tian, Co-evolutionary associations between root-associated microbiomes and root transcriptomes in wild and cultivated rice varieties, *Plant Physiology et Biochemistry* (2018), doi: 10.1016/j.plaphy.2018.04.009.

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 **Co-evolutionary associations between root-associated**
2 **microbiomes and root transcriptomes in wild and cultivated**
3 **rice varieties**

4 Lei Tian^{1,2}, Shaohua Shi¹, Lina Ma¹, Fahad Nasir³, Xiujun Li⁴, Lam-Son Phan Tran⁵,
5 ^{6*}, Chunjie Tian^{1*}

6 ¹Key Laboratory of Mollisols Agroecology, Northeast Institute of Geography and
7 Agroecology, Chinese Academy of Sciences, Changchun, Jilin 130102, China;

8 ²University of Chinese Academy of Sciences, Beijing, 100049, China; ³School of Life
9 Sciences, Northeast Normal University, Changchun City, Jilin 130102, China; ⁴Key

10 Laboratory of Wetland Ecology and Environment, Northeast Institute of Geography
11 and Agroecology, Chinese Academy of Sciences, Changchun, Jilin 130102, China;

12 ⁵Institute of Research and Development, Duy Tan University, 03 Quang Trung, Da
13 Nang, Vietnam; and ⁶Signaling Pathway Research Unit, RIKEN Center for

14 Sustainable Resource Science, 1-7-22, Suehiro-cho, Tsurumi, Yokohama 230-0045,
15 Japan

16

17 L. Tian and S. Shi contributed equally in this article.

18

19 **Abstract:** The plant and root-associated microbiomes are closely related. Plant
20 metabolic substances can serve as a nutrient source for the microbiome, and in return,
21 the microbiome can regulate the production of plant metabolic substances. Wild rice
22 (*Oryza rufipogon*), as the ancestor of cultivated rice (*Oryza sativa*), has changed

Abbreviations: OTU, Operational taxonomic unit; ITS, internal transcribed spacer;
IAA, indoleacetic acid; ACC, one-aminocyclopropane-1-carboxylic acid; vs, versus;
DEGs, differentially expressed genes; RDA, Redundancy analysis.

* Corresponding author: *E-mail address:* tiancj@iga.ac.cn (C. Tian) and
son.tran@riken.jp (L.-S.P. Tran)

Download English Version:

<https://daneshyari.com/en/article/8352913>

Download Persian Version:

<https://daneshyari.com/article/8352913>

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