



Corrigendum: Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle

Peng Liang^{1,2,3}, Songyu Liu⁴, Feng Xu³, Shuqin Jiang³, Jun Yan³, Qiguang He^{1,2}, Wenbo Liu^{1,2}, Chunhua Lin^{1,2}, Fucong Zheng^{1,2}, Xiangfeng Wang^{3*} and Weiguo Miao^{1,2*}

¹ College of Plant Protection, Hainan University, Haikou, China, ² Key Laboratory of Green Prevention and Control of Tropical Plant Diseases and Pests (Hainan University), Ministry of Education, Haikou, China, ³ Department of Crop Genomics and Bioinformatics, College of Agronomy and Biotechnology, National Maize Improvement Center of China, China Agricultural University, Beijing, China, ⁴ State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, China

OPEN ACCESS

Approved by:

Frontiers in Microbiology
Editorial Office,
Frontiers Media SA, Switzerland

*Correspondence:

Weiguo Miao
miao@hainu.edu.cn
Xiangfeng Wang
sysbio@cau.edu.cn

Specialty section:

This article was submitted to
Plant Microbe Interactions,
a section of the journal
Frontiers in Microbiology

Received: 18 December 2018

Accepted: 02 January 2019

Published: 23 January 2019

Citation:

Liang P, Liu S, Xu F, Jiang S, Yan J, He Q, Liu W, Lin C, Zheng F, Wang X and Miao W (2019) Corrigendum: Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. *Front. Microbiol.* 10:1. doi: 10.3389/fmicb.2019.00001

Keywords: *Erysiphales*, *Oidium heveae*, genome, gene family contraction, fatty acids, CSEPs, positive selection, adaptive evolution

A Corrigendum on

Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle

by Liang, P., Liu, S., Xu, F., Jiang, S., Yan, J., He, Q., et al. (2018). *Front. Microbiol.* 9:3160. doi: 10.3389/fmicb.2018.03160

The order of correspondence authors was incorrectly provided as “Xiangfeng Wang, sysbio@cau.edu.cn” and “Weiguo Miao, miao@hainu.edu.cn” in the Correspondence section. The correct order should be “Weiguo Miao, miao@hainu.edu.cn” and “Xiangfeng Wang, sysbio@cau.edu.cn.”

Also, in the published article, the RNA-seq sequence number SRP158299 was removed by mistake from the “Accession Numbers” section. The correct Accession Numbers statement should read as follows:

“The *O. heveae* genome and RNA-seq sequences have been deposited in GenBank/DDBJ/EMBL under the accession codes of QVIK00000000 and SRP158299, respectively.”

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

Copyright © 2019 Liang, Liu, Xu, Jiang, Yan, He, Liu, Lin, Zheng, Wang and Miao. 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) and the copyright owner(s) 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.