



HAL
open science

Corrigendum: the comparison of expressed candidate secreted proteins from two arbuscular mycorrhizal fungi unravels common and specific molecular tools to invade different host plants

Laurent Kamel, Nianwu Tang, Mathilde Malbreil, H el ene San Clemente, Morgane Le Marquer, Christophe Roux, Nicolas Frei Dit Frey

► To cite this version:

Laurent Kamel, Nianwu Tang, Mathilde Malbreil, H el ene San Clemente, Morgane Le Marquer, et al.. Corrigendum: the comparison of expressed candidate secreted proteins from two arbuscular mycorrhizal fungi unravels common and specific molecular tools to invade different host plants. *Frontiers in Plant Science*, 2017, 8, <10.3389/fpls.2017.02065>. <hal-04788588>

HAL Id: hal-04788588

<https://hal.science/hal-04788588v1>

Submitted on 2 Jun 2025

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire HAL, est destin ee au d ep ot et  a la diffusion de documents scientifiques de niveau recherche, publi es ou non,  emanant des  tablissements d'enseignement et de recherche fran ais ou  trangers, des laboratoires publics ou priv es.



Distributed under a Creative Commons CC BY 4.0 - Attribution - International License



Corrigendum: The Comparison of Expressed Candidate Secreted Proteins from Two Arbuscular Mycorrhizal Fungi Unravels Common and Specific Molecular Tools to Invade Different Host Plants

Laurent Kamel^{1,2}, Nianwu Tang^{1†}, Mathilde Malbreil¹, H el ene San Clemente¹, Morgane Le Marquer¹, Christophe Roux^{1*} and Nicolas Frei dit Frey^{1*}

¹ Laboratoire de Recherche en Sciences V eg etales, Universit e Paul Sabatier - Universit e de Toulouse, Centre National de la Recherche Scientifique, Castanet-Tolosan, France, ² Agronutrition, Laboratoire de Biotechnologies, Labege, France

OPEN ACCESS

Edited and reviewed by:

Andrea Genre,
Universit a degli Studi di Torino, Italy

*Correspondence:

Christophe Roux
roux@lrsv.ups-tlse.fr
Nicolas Frei dit Frey
frei-dit-frey@lrsv.ups-tlse.fr

† Present Address:

Nianwu Tang,
Key Laboratory for Plant Diversity and
Biogeography of East Asia, Kunming
Institute of Botany, Chinese Academy
of Sciences, Heilongtan, Kunming,
China

Specialty section:

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

Received: 08 November 2017

Accepted: 17 November 2017

Published: 08 December 2017

Citation:

Kamel L, Tang N, Malbreil M, San
Clemente H, Le Marquer M, Roux C
and Frei dit Frey N (2017)
Corrigendum: The Comparison of
Expressed Candidate Secreted
Proteins from Two Arbuscular
Mycorrhizal Fungi Unravels Common
and Specific Molecular Tools to Invade
Different Host Plants.
Front. Plant Sci. 8:2065.
doi: 10.3389/fpls.2017.02065

Keywords: Glomeromycota, secretome, comparative transcriptomics, effectors, symbiosis

A corrigendum on

The Comparison of Expressed Candidate Secreted Proteins from Two Arbuscular Mycorrhizal Fungi Unravels Common and Specific Molecular Tools to Invade Different Host Plants
by Kamel, L., Tang, N., Malbreil, M., San Clemente, H., Le Marquer, M., Roux, C., et al. (2017). *Front. Plant Sci.* 8:124. doi: 10.3389/fpls.2017.00124

In the original article, there was an error in **Table S1A concerning Rhizophagus irregularis in planta RNAseq libraries.**

The corrected **Table S1A** has been published as Supplementary material.

Accordingly, an addendum has been made to **Materials and Methods section, RNA Production and Sequencing, first paragraph:**

“Total RNA extraction and sequencing were performed according to Tisserant et al. (2013) for *R. irregularis* and Tang et al. (2016) for *G. rosea*. Apart from ERM of *G. rosea* where short paired- end sequencing reads were obtained from Illumina Miseq1000 protocols (2 × 151 bp), all libraries were obtained from Illumina Hiseq2000 protocols (2 × 101 bp). Library constructions and sequencing were performed on the GeT-PlaGe facility (Toulouse, France), according to standard Illumina protocols. Data are available at NCBI GEO portal (GSE67906 and GSE67911) for *G. rosea*, and at NCBI Sequence Read Archive (SRR1027885) and at NCBI GEO portal (GSE67926) (—see details on libraries in Table S1A) for *R. irregularis*. Number of reads per libraries, representativeness of fungal reads in symbiotic tissues and variability of data are presented in Tables S1A, S5A for *R. irregularis* and *G. rosea* respectively.”

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way.

The original article has been 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   2017 Kamel, Tang, Malbreil, San Clemente, Le Marquer, Roux and Frei dit Frey. 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.