



HAL
open science

Correction: Pujic et al. The Proteogenome of Symbiotic Frankia alni in Alnus glutinosa Nodules.

Microorganisms 2022, 10, 651

Petar Pujic, Nicole Alloisio, Guylaine Miotello, Jean Armengaud, Danis Abrouk, Pascale Fournier, Philippe Normand

► **To cite this version:**

Petar Pujic, Nicole Alloisio, Guylaine Miotello, Jean Armengaud, Danis Abrouk, et al.. Correction: Pujic et al. The Proteogenome of Symbiotic Frankia alni in Alnus glutinosa Nodules. *Microorganisms* 2022, 10, 651. *Microorganisms*, 2022, 10 (11), pp.2229. 10.3390/microorganisms10112229 . hal-04459947

HAL Id: hal-04459947

<https://hal.inrae.fr/hal-04459947>

Submitted on 15 Feb 2024

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 destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Correction

Correction: Pujic et al. The Proteogenome of Symbiotic *Frankia alni* in *Alnus glutinosa* Nodules. *Microorganisms* 2022, 10, 651

Petar Pujic ^{1,*} , Nicole Alloisio ¹, Guylaine Miotello ², Jean Armengaud ² , Danis Abrouk ¹ , Pascale Fournier ¹ and Philippe Normand ^{1,*}

¹ Ecologie Microbienne, CNRS, UMR5557, Université Lyon 1, Université de Lyon; INRA, UMR1418, 7330 Villeurbanne, France

² Département Médicaments et Technologies pour la Santé (DMTS), CEA, INRAE, Université Paris-Saclay, SPI, 30200 Bagnols sur Cèze, France

* Correspondence: petar.pujic@univ-lyon1.fr (P.P.); philippe.normand@univ-lyon1.fr (P.N.)

The authors wish to make the following corrections to this paper [1].

Text Correction

The original version of this article contained an error on the control of the proteogenomic experiment, which was not nitrogen-fixing BAP—grown culture (without NH_4^+), but a nitrogen-replete BAP+ (containing 5 mM NH_4^+) culture. We corrected this error by replacing “N-fixing” by “N-replete” throughout the text.

Examples of corrections are given below:

In the **Abstract**:

A proteogenomic analysis of symbiotic *Frankia alni* was done by comparing those proteins more and less abundant in *Alnus glutinosa* nodules relative to N-replete pure cultures with propionate as the carbon source and ammonium as the nitrogen-source. There were 250 proteins that were significantly overabundant in nodules at a fold change (FC) ≥ 2 threshold, and 1429 with the same characteristics in in vitro nitrogen-replete pure culture.

In the **Materials and Methods**:

As a reference, *F. alni* cells were inoculated after syringing with a series of needles (21G, 23G, 25G, 27G) and grown for 10 days (corresponding to the end of the exponential phase) in 250 mL of BAP medium with ammonium (5 mM) in agitated 500 mL Erlenmeyer flasks [25] buffered to pH 6.5. No vesicles could be found.

As here in the **Results**:

The three biological replicates of symbiotic *Frankia alni* overproduced at a fold change of ≥ 2250 proteins (Supplementary Table S1) using a nitrogen-replete propionate-fed pure culture as reference, of which 100 had an FC ≥ 4.38 (Table 1).

And here:

Among *F. alni* proteins, the nitrogenase proteins were the most overabundant with 7 among the 10 highest using as reference a nitrogen-replete pure culture.

As here in the **Legend to Figure 1**:

Figure 1. Circular map of the genome of *Frankia alni* with the proteins over-abundant in nodules relative to a nitrogen-replete pure-culture (FC ≥ 2) positioned along the genome.

As here in the **Title** of Supplementary Materials Table S1:

Table S1: List of *Frankia* proteins identified in nodules and in a nitrogen-replete pure culture and their spectral counts.

And as here in the **Acknowledgments**:

Thanks are expressed to Elise Lacroix for Greenhouse management (Université de Lyon) and to Aude Herrera-Belaroussi (Université de Lyon) for the nitrogen-replete *Frankia* cells.



Citation: Pujic, P.; Alloisio, N.; Miotello, G.; Armengaud, J.; Abrouk, D.; Fournier, P.; Normand, P. Correction: Pujic et al. The Proteogenome of Symbiotic *Frankia alni* in *Alnus glutinosa* Nodules. *Microorganisms* 2022, 10, 651. *Microorganisms* 2022, 10, 2229. <https://doi.org/10.3390/microorganisms10112229>

Received: 11 October 2022

Accepted: 24 October 2022

Published: 11 November 2022

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Reference

Furthermore, reference Clavijo et al. (2015) had been truncated, it should be as:

- 11 Clavijo, F.; Diedhiou, I.; Vaissayre, V.; Brottier, L.; Acolatse, J.; Moukouanga, D.; Crabos, A.; Auguy, F.; Franche, C.; Gherbi, H.; et al. The *Casuarina* NIN gene is transcriptionally activated throughout *Frankia* root infection as well as in response to bacterial diffusible signals. *New Phytol.* **2015**, *208*, 887–903.

The authors state that the scientific conclusions are unaffected. This correction was approved by the Academic Editor. The original publication has also been updated.

Reference

1. Pujic, P.; Alloisio, N.; Miotello, G.; Armengaud, J.; Abrouk, D.; Fournier, P.; Normand, P. The Proteogenome of Symbiotic *Frankia alni* in *Alnus glutinosa* Nodules. *Microorganisms* **2022**, *10*, 651. [[CrossRef](#)] [[PubMed](#)]