

ERRATUM

Open Access



# Erratum to: Genome sequencing of the *Trichoderma reesei* QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype

Alexander Lichius<sup>1†</sup>, Frédérique Bidard<sup>2†</sup>, Franziska Buchholz<sup>1</sup>, Stéphane Le Crom<sup>3</sup>, Joel Martin<sup>4</sup>, Wendy Schackwitz<sup>4</sup>, Tina Austerlitz<sup>1</sup>, Igor V. Grigoriev<sup>4</sup>, Scott E. Baker<sup>5</sup>, Antoine Margeot<sup>2</sup>, Bernhard Seiboth<sup>1\*</sup> and Christian P. Kubicek<sup>1</sup>

Erratum to: *BMC Genomics* doi 10.1186/s12864-015-1526-0

Following the publication of our recent article in *BMC Genomics* [1] we wish to bring the following corrigendum to your attention. In the above paper, we wrote in the discussion on page 13: "These are V756F in XlnR (corresponding to V801 in XYR1) and A804V (based on our analysis; not A824V as stated by the authors) in XYR1". Our analysis of the XYR1 sequence was based on the available *Trichoderma reesei* QM6a XYR1 sequences deposited in the NCBI database [Protein Accession Number XP\_006966092.1 and EGR48040.1]. Recently, Derntl *et al.* [2] identified that the second intron in *xyr1* is in fact not spliced thus giving rise to a protein that, while maintaining the reading frame, is 20 amino acids longer. Consequently, the position A824V given by Derntl *et al.* [2] is correct, and the numbering of amino acids in our paper after G319 has to be increased by 20.

A corrected version of our statement would read: "These are V756F in XlnR of *A. niger* which corresponds to V821 in *T. reesei* XYR1, as well as A824V in XYR1 of *T. reesei* [35, 42]".

We apologize for this mistake, but would like to stress that none of the results or conclusions in our paper are affected by this change.

#### Author details

<sup>1</sup>Research Division Biotechnology and Microbiology, Institute of Chemical Engineering, Vienna University of Technology, A-1060 Vienna, Austria. <sup>2</sup>IFP Energies Nouvelles, 1-4 Avenue de Bois-Préau, 92852 Rueil-Malmaison, France. <sup>3</sup>Sorbonne Universités, UPMC Université Paris 06, Institut de Biologie Paris Seine (IBPS), FR 3631, Département des Plateforme, F-75005, Paris,

\* Correspondence: bernhard.seiboth@tuwien.ac.at

†Equal contributors

<sup>1</sup>Research Division Biotechnology and Microbiology, Institute of Chemical Engineering, Vienna University of Technology, A-1060 Vienna, Austria

France. <sup>4</sup>US Department of Energy Joint Genome Institute, 2800 Mitchell Avenue, Walnut Creek, CA 94598, USA. <sup>5</sup>Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA 99354, USA.

Received: 10 September 2015 Accepted: 10 September 2015

Published online: 22 September 2015

#### References

1. Lichius A, Bidard F, Buchholz F, Le Crom S, Martin J, Schackwitz W, et al. Genome sequencing of the *Trichoderma reesei* QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. *BMC Genomics*. 2015;16:326.
2. Derntl C, Gudynaite-Savitch L, Calixte S, White T, Mach RL, Mach-Aigner AR. Mutation of the xylanase regulator 1 causes a glucose blind hydrolase expressing phenotype in industrially used *Trichoderma* strains. *Biotechnol Biofuels*. 2013;6:62.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)

