Accepted Manuscript

Title: The Hidden Diversity of Flagellated Protists in Soil<!-- RunningTitle>Molecular Techniques Reveal Hidden Diversity of Soil Flagellates</ RunningTitle>-->

Authors: Paul Christiaan Venter, Frank Nitsche, Hartmut Arndt

 PII:
 \$1434-4610(18)30031-2

 DOI:
 https://doi.org/10.1016/j.protis.2018.04.007

 Reference:
 PROTIS 25624

To appear in:

 Received date:
 2-11-2017

 Accepted date:
 17-4-2018

Please cite this article as: Venter, Paul Christiaan, Nitsche, Frank, Arndt, Hartmut, The Hidden Diversity of Flagellated Protists in Soil.Protist https://doi.org/10.1016/j.protis.2018.04.007

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.



ACCEPTED MANUSCRIPT

ORIGINAL PAPER

The Hidden Diversity of Flagellated Protists in Soil

Running title: Molecular Techniques Reveal Hidden Diversity of Soil Flagellates

Paul Christiaan Venter, Frank Nitsche, and Hartmut Arndt¹

University of Cologne, Cologne Biocenter, Institute of Zoology, Department of General Ecology, Zuelpicher Str. 47b, D-50674 Koeln (Cologne), Germany

Submitted November 2, 2017; Accepted April 17, 2018 Monitoring Editor: David Moreira

Corresponding author; fax +49 (0)221 470 5932,

e-mail hartmut.arndt@uni-koeln.de (H. Arndt).

Protists are among the most diverse and abundant eukaryotes in soil. However, gaps between described and sequenced protist morphospecies still present a pending problem when surveying environmental samples for known species using molecular methods. The number of sequences in the molecular PR² database (~130,000) is limited compared to the species richness expected (>1 million protist species) - limiting the recovery rate. This is important, since high throughput sequencing (HTS) methods are used to find associative patterns between functional Download English Version:

https://daneshyari.com/en/article/8392775

Download Persian Version:

https://daneshyari.com/article/8392775

Daneshyari.com