FEB 07, 2019

OPEN ACCESS

DOI:
[dx.doi.org/10.17504/protocols.io.wpdfdi6](https://doi.org/10.17504/protocols.io.wpdfdi6)

External link:
<https://doi.org/10.1371/journal.pone.0211388>

Protocol Citation: Maria P Martin, Thiago Accioly, Julieth O. Sousa, Melanie Roy, Monique Gardes, Iuri G. Baseia 2019. ITS and LSU nrDNA analyses.
protocols.io
<https://dx.doi.org/10.17504/protocols.io.wpdfdi6>

MANUSCRIPT CITATION:
 Accioly T, Sousa JO, Moreau PA, Lécure C, Silva BDB, Roy M, Gardes M, Baseia IG, Martín M.P. Hidden fungal diversity from the Neotropics: *Geastrum hirsutum*, *G. schweinitzii* (Basidiomycota, Geastrales) and their allies. PlosOne (submitted)

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

ITS and LSU nrDNA analyses

Persoonia : Molecular Phylogeny and Evolution of Fungi

Julieth O.
 Maria P Martin¹, Thiago Accioly², Sousa²,
 Monique Iuri G.
 Melanie Roy³, Gardes³, Baseia⁴

¹Departamento de Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2, 28014 Madrid, Spain;

²Programa de Pós-Graduação em Sistemática e Evolução, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.;

³Laboratoire UMR5174 Evolution et Diversité Biologique (EDB), Université Toulouse 3 Paul Sabatier, Toulouse, France;

⁴Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.

Maria P Martin

ABSTRACT

After DNA extraction, the ITS regions were amplified and sequenced using the primer pair ITS1F/ITS4. Part of the LSU was amplified and sequenced using either the primer pair LR0R/LR5. When amplifications were not obtained, nested PCR of ITS and semi-nested PCR of LSU were performed. The samples were sequenced bidirectionally in Macrogen Inc. (Seoul, South Korea).

The molecular dataset of unambiguously aligned ITS sequences was submitted to three types of analyses: maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference. Concatenate ITS/LSU analyses were also carried out through each method, but concatenated datasets included only those specimens which have sequences for both ITS and LSU nrDNA

ATTACHMENTS

[ITS and LSU nrDNA analyses_291218_Martin_et_al.pdf](#)

Created: Dec 30, 2018

Last Modified: Feb 07, 2019

PROTOCOL integer ID:
18885

Keywords: PCR,
amplification, purification,
phylogenetics

1

2

3

4