


Expression and localization of tubulin isotypes and its mRNAs during *Thecaphora frezii* developments

Figueroa, Ana Cristina , Díaz, María Soledad , Alasino, Roxana Valeria , Yang, Pablo , Soria, Néstor Walter  and Beltramo, Dante Miguel  (2022) *Expression and localization of tubulin isotypes and its mRNAs during Thecaphora frezii developments*. FEMS Microbiol Ecology, 98 (11). ISSN 1574-6941

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RESUMEN

Thecaphora frezii is a phytopathogenic fungus that infects *Arachys hypogaea* L. and produces peanut smut. It has three ontological stages: teliospores, basidiospores, and hyphae. Microtubules are cellular structures that participate in various important cellular processes. In this work, we analyzed the presence and location of α -tubulin isotypes and enzymes that participate in tyrosination-detyrosination in the three stages of *T. frezii*. Although both tyrosinated and detyrosinated tubulin seem to be associated with a membrane fraction component that gives it a similar behavior to integral proteins, in the soluble cytosolic fraction, only detyrosinated tubulin was detected, not tyrosinated tubulin. The presence of α -tubulin was not detected using the monoclonal antibody DM1A as neither acetylated tubulin. The RNA-Seq analysis showed the presence of α , β , and γ -tubulins and the genes that code for tyrosine-tubulin ligase and cytosolic carboxypeptidase 1, enzymes that are involved in post-translational modification processes. These sequences showed a high percentage of identity and homology with *Ustilago maydis*, *Thecaphora thlaspeos*, and *Anthracoctis flocculosa*. This is the first report for tubulins subpopulations and the cellular distribution in *T. frezii*, which together with the data obtained by RNA-Seq contribute to the knowledge of the pathogen, which will allow the development of control strategies. © The Author(s) 2022. Published by Oxford University Press on behalf of FEMS.

TIPO DE DOCUMENTO: Artículo

DOI: <https://doi.org/10.1093/femsec/fiac121>

**PALABRAS
CLAVE:**

Cytoskeleton. Detyrosinated tubulin. Immunostaining. mRNA
sequence. Peanut smut. Tyrosinated tubulin.

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