

Elucidating potential effectors, pathogenicity and virulence factors expressed by the phytopathogenic fungus *Thecaphora frezii* through analysis of its transcriptome

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and Beltramo, Dante Miguel (2022) *Elucidating potential effectors, pathogenicity and virulence factors expressed by the phytopathogenic fungus *Thecaphora frezii* through analysis of its transcriptome*. European Journal of Plant Pathology. ISSN 0929-1873

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URL Oficial: <https://link.springer.com/article/10.1007/s10658-0...>

Resumen

Thecaphora frezii is a phytopathogenic fungus belonging to the Ustilaginomycetes class, which causes peanut smut disease. In its biological cycle it has three structures, teliospores (is the resistance structure), basidiospores and hyphae. The mycelium is the structure that penetrates the plant's gynophore and initiates the infection. For this action, the expression of effectors, pathogenicity and virulence factor proteins is necessary. The aim of this study was to identify potential *Thecaphora frezii*'s proteins that could exert pathogenicity, virulence and/or effector

functions. Based on the transcriptome of two ontogenetic stages (teliospore and hyphae) of *Thecaphora frezii*, and a series of bioinformatic analyses, 18 potential effectors and 91 factors possibly involved in the level of pathogenicity and virulence were identified. Higher expression levels of candidate effectors were found in the infective stage of the fungus. In the other hand, the major variability observed in pathogenicity and virulence factors expressed between *Ustilago maydis* and *Thecaphora frezii* were the number of virulence factors secreted (higher in *U. maydis*). In the future, when the genome of the fungus will be known, functional studies of these proteins could be carried out to validate their function.

TIPO DE DOCUMENTO: Artículo

DOI: <https://doi.org/10.1007/s10658-022-02562-2>

PALABRAS CLAVE: *Thecaphora frezii*. Patogenicidad. Maní. Virulencia.

TEMAS: [Q Ciencia > Q Ciencia \(General\)](#)

[Q Ciencia > QR Microbiología > QR355 Virología](#)

UNIDAD ACADÉMICA: [Universidad Católica de Córdoba > Facultad de Ciencias Químicas](#)

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