

## XIII Argentine Congress of Bioinformatics and Computational Biology (XIII CAB2C)

XIII International Conference of the Iberoamerican Society of Bioinformatics (XIII SolBio)

III Annual Meeting of the Ibero-American Artificial Intelligence Network for Big BioData (III RiaBio)





RiaB





bioinformatica\_ar

RiaBioNet





## ID# 058

## Wickerhamomyces anomalus, a Biotechnological Yeast... an Opportunistic Pathogen?

Garolera B<sup>1</sup>, Pajot H. P<sup>1,2</sup>, Fernández P. M<sup>1,2</sup>

<sup>1</sup>PROIMI-CONICET (Planta Piloto de Procesos Industriales Microbiológicos, Consejo Nacional de Investigaciones Científicas y Técnicas)

<sup>2</sup>FACEN-UNCA (Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Catamarca)

## Abstract

Wickerhamomyces anomalus is a yeast with significant biotechnological potential, utilized in the production of fermented beverages and ethanol, as well as in the biocontrol of postharvest diseases, bioremediation of metals and organic contaminants, and surfactant production, among other applications. Its utility arises from its capacity to thrive on various carbon sources, tolerate a wide range of pH values, and survive temperatures ranging from 20 to 40°C. Nevertheless, documented cases of fungal infections in immunocompromised patients, including infants and adults, suggest its potential as an opportunistic pathogen. In our laboratory, we isolated a strain of Wickerhamomyces anomalus with potential for hexavalent chromium bioremediation. The aim of this study was to in silico assess the presence of virulence factor genes in the Wickerhamomyces anomalus M10 strain, which could confer opportunistic pathogenicity in humans.

Using PHI-base, we identified a total of 65 virulence factors, categorized based on their phenotypic impact in mutations. Loss-of-pathogenicity factors (13) are primarily associated with genes involved in hyphae or pseudohyphae formation, such as Cas5, CDC42, and VMA4, whereas virulence reduction factors (37) are linked to genes related to biofilm formation, like BMH1 and RPS41. Furthermore, we identified genes that may enable the yeast to evade host defenses, such as an alpha-mannosyltransferase (MNN10), all belonging to proteins involved in signaling pathways, transport, and transcription regulation.

In summary, based on this initial bioinformatic analysis of the Wickerhamomyces anomalus genome, we suggest that the yeast possesses genes that could facilitate its invasion and dissemination within the host, along with the ability to evade host defenses, potentially conferring opportunistic pathogenicity. It is crucial to conduct in vivo assays to validate these findings, given the potential risk to human health when used in biotechnological processes.