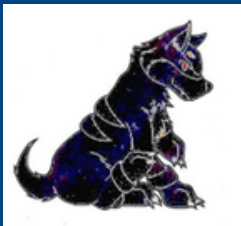


01-03 Nov 2023

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

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

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



Book of Abstracts

 <http://2023.a2b2c.org.ar>

 a2b2c

 bioinformatica_ar

 RiaBioNet



ID# 038

Exploration of heavy metal resistance in the yeast *Wickerhamomyces anomalus*: implications for bioremediation

Garolera B.¹, Pajot H. P.^{1,2}, Fernández P. M.^{1,2}

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

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

Abstract

The inadequate disposal of wastewater containing toxic heavy metals and industrial contaminants has become a critical issue today, posing serious risks to the health of humans, animals, and the environment. Numerous studies have investigated how heavy metals are absorbed, accumulated, and transformed using microorganisms. The yeast strain *Wickerhamomyces anomalus* M10 has demonstrated notable resistance to several heavy metals, showing promising potential for bioremediation.

Therefore, through computational methods (In Silico studies) to investigate metal resistance mechanisms, relevant genes related to this resistance were identified. Specialized databases like BacMet and InterPro were used, compiling genes from bacteria and fungi that enhance survival under environmental stress. These databases categorize resistance genes based on their function and induced phenotypes. Using BacMet, we identified 59 genes, including 11 ABC-type transporters, 10 related to resistance and the efflux of multiple drugs, as well as proteins for copper (5), nickel (10), arsenic (2), mercury (5), and silver (1). These proteins perform functions in binding, reduction, and transport, along with superoxide dismutase proteins, DNA regulation, and repair genes. Additionally, through InterPro, we found 394 genes, including 257 transporters, 25 copper-related proteins, and 23 zinc-related proteins. Fifteen multidrug resistance proteins and other DNA regulation and repair genes (10) were detected.

In summary, our bioinformatics analysis of *Wickerhamomyces anomalus* highlights its potential for bioremediation in metal-contaminated environments. It excels particularly in mitigating nickel and arsenic pollution due to resistance-related genes. However, comprehensive in vivo studies are required to confirm its survival and transformation capabilities against these metals. These findings underline the significant bioremediation potential of yeast strains. The study not only reveals genes that expand the scope of microbial bioremediation but also advances the concept of the substantial role of yeast strains in mitigating environmental pollution challenges