

CRYPTOMICSDB: Revealing the Molecular Landscape of Cryptococcosis

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Abstract: Gene expression databases have become essential tools for advancing biomedical sciences, enabling the integration of large datasets and the identification of molecular mechanisms associated with infectious diseases, cancers, and metabolic disorders (1, 2 and 3). These platforms enhance the reuse of previously published information, promote analytical reproducibility, and facilitate the discovery of novel diagnostic and therapeutic targets. However, most available databases are focused on model organisms, highlighting the lack of equivalent bioinformatic resources for non-model pathogens of medical relevance. Among these pathogens, the genus *Cryptococcus* stands out as the etiological agent of cryptococcosis, a severe systemic mycosis caused by the *Cryptococcus neoformans* and *Cryptococcus gattii* species complexes. This infection represents one of the leading causes of fungal meningitis worldwide, particularly in immunocompromised individuals, and is associated with high mortality rates even under antifungal therapy (4). Despite its clinical and epidemiological importance, cryptococcosis remains classified as a neglected disease, characterized by a scarcity of integrated molecular data and dedicated tools to consolidate existing knowledge. To address this gap, we developed CRYPTOMICSDB (<https://sbcdb.inf.ufrgs.br/research/cryptomicsdb>), an interactive and open-access database designed to organize and integrate molecular information related to *Cryptococcus* infection (1). The database compiles transcriptomic and proteomic data published between 2001 and 2025, collected through a systematic search of international scientific repositories followed by rigorous manual curation. In total, 36 studies met the inclusion criteria. CRYPTOMICSDB provides gene expression data from infection models encompassing both pathogen and host perspectives, allowing integrated analyses of the molecular events underlying disease pathogenesis. The web-based and responsive platform enables searches by species, organism, technique, and expression type. Currently, it contains 5,863 expressed genes from *Cryptococcus* and 39,982 expressed genes from various hosts, including *Homo sapiens*, *Mus musculus*, *Rattus norvegicus* and *Macaca fascicularis*. In addition to data visualization and download options, the system provides direct links to gene ontology and metabolic pathway databases, facilitating functional analyses and cross-validation of experimental results. During database construction, we observed a predominance of studies focusing on *C. neoformans* and a limited number of proteomic approaches, underscoring the need to expand functional and molecular investigations of the genus. To the best of

our knowledge, this is the first database dedicated to the genus *Cryptococcus* that integrates molecular information from both major etiological agents of cryptococcosis and from multiple infected hosts. This comprehensive approach enables a more complete understanding of the diversity and complexity of the molecular mechanisms involved in pathogenesis. In the long term, CRYPTOMICSDB is expected to support meta-analyses, gene network modeling, antifungal target prediction, and the development of more effective diagnostic and therapeutic strategies. By virtue of its scope, originality, and applicability, it establishes itself as a reference tool for molecular mycology, democratizing access to complex datasets and driving new discoveries in the field of neglected fungal diseases.

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