In-silico Approach of Antifungal Properties of Natural Plant Compounds Against *Candida Albicans*

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Abstract

Candida species are opportunistic pathogens responsible for a wide range of infections, from simple mucocutaneous conditions to life-threatening fungemia, particularly in immunocompromised hospitalized individuals. *Candida albicans* is still the most researched yeast and is most commonly linked to fungal infections in humans. When combined with a weakened host immune response, this microorganism's survival and virulence characteristics make infections difficult to control. The rising incidence of resistance to antifungals and the limited availability of effective antifungal agents highlight the urgent need for medications with unique modes of action. However, there are many difficulties with the conventional medication development method, which is costly and time-consuming. Bioinformatics developments have brought in-silico technologies like molecular docking, which can significantly streamline drug discovery by reducing timelines and costs. This review emphasizes the utility of molecular docking in identifying and designing targeted drugs against *C. albicans*. It also explores promising protein targets within *C. albicans* that could serve as the basis for developing innovative antifungal therapies, addressing the growing threat of drug resistance, and improving treatment outcomes for fungal infections.

Keywords: candidiasis, *candida albicans*, drug discovery, phytochemical compounds, Molecular dynamics.

ACKNOWLEDGMENT:

This work is supported by the Alagappa University Research Fund (AURF) Seed Money 2024 [grant sanctioned vide Letter No. AU/SO(P&D)/AURF Seed Money/2024 Alagappa University, Karaikudi, Tamil Nadu, India, Date 11th December 2024], DST-FIST [SR/ FST/LSI-667/2016(C)], DST-PURSE [SR/PURSE Phase 2/38 (G)], UGC-Innovative and MHRD-RUSA-phase 2.0 grant sanctioned vide [F.24-51/2014-U policy (TNMulti–Gen), Dept of Edn. Govt of India Dt, 09.10.2018] for the infrastructure facilities available in the Department of Bioinformatics and Computer Science, Alagappa University.