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Drosophila as a host model to investigate toll-mediated innate immune evasion of human pathogenic fungi

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Introduction

Fungal infections represent a substantial and increasing global health burden. Annually, more than 6.5 million individuals develop invasive fungal diseases, leading to approximately 3.8 million deaths, of which around 2.5 million are directly attributable to fungal pathogens (Denning, 2024). In response, the World Health Organization has established the Fungal Priority Pathogens List to guide research and public health strategies by identifying high-impact pathogens with significant unmet needs (WHO, 2022). A major contributor to fungal pathogenicity is the ability of these organisms to evade host immunity through mechanisms that impair immune recognition, suppress defense signaling, and modulate inflammatory responses. Despite their importance, studying fungal immune evasion in mammalian systems remains challenging. These models are associated with high costs, ethical constraints, and regulatory limitations, which restrict experimental scalability and flexibility (Lionakis et al., 2023). In addition, mammalian models are inherently low-throughput due to long generation times, complex physiology, and labor-intensive methodologies, thereby limiting large-scale genetic and pharmacological investigations (Kiani et al., 2022).