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Efficacy of Interfectorem as a Novel Antifungal Against the Human Fungal Pathogens, *Candida albicans* and *Candida krusei*

Abstract and Introduction:

Our goal is to identify a novel antifungal that may be of use in the treatment of infections. Dr. J. Dixson has synthesized a compound we have termed Interfectorem. We hypothesize Interfectorem inhibits growth of the human fungal pathogens, *Candida albicans* and *Candida krusei*. Each treatment is tested against each species at various concentrations to determine the minimum inhibitory concentration (MIC), while using the antifungal standard Amphotericin B as a positive control. We determined 80% inhibition of growth to be between 0.75mg/mL and 1.0mg/mL. And 50% was found to be between .5mg/mL and .75mg/mL, for *C.albicans*. 80% inhibition for *C.krusei* was found to be ≤1.25mg/mL, though upon replating this concentration appears almost lethal with the appearance of only several small colonies. 50% inhibition was found to be 0.2mg/mL to 0.25mg/mL.

Bacteria are not the only organisms known to have evolved antibiotic resistances. Human and animal fungal pathogens, such as *Candida albicans* (Fig. A) and *Candida krusei* (Fig. B) as well as other fungi have developed resistance to common drugs used in the treatment of infection. As a result these have become difficult to treat due to the lack of treatment options. Our goal is to identify a novel antifungal agent that may have use in the treatment of fungal infections. In collaboration with Dr. J. Dixson, we are testing the efficacy of a compound he synthesized, which we have termed Interfectorem, as an antifungal agent against the human pathogenic yeasts, *C. albicans* and *C. krusei.* Here we demonstrate that Interfectorem exhibits antifungal activity, determine the MIC range and the concentration at which Interfectorem is fungicidal. After determining the MIC range we then treated both species with concentrations found in our MIC range. Treatments were applied for 24hrs and 2hrs, as well as a control sample, having no treatment. Subsequently, we extracted RNA from the treatments and control of both species for sequencing of the small RNA and the mRNA. The small RNA has been sent for NextGen sequencing. The information gained will be useful in predicting the likelihood that resistance would develop in natural populations of these species