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Genomic Stability in the Fungal Pathogen *Candida albicans*: Measuring Mutation Rates under Stressful Conditions

The opportunistic fungal pathogen *Candida albicans* is a commensal organism that most humans carry in the natural microbial flora of their gastrointestinal and genitourinary tracts. However, the organism can become pathogenic when the immune system is compromised. (Berman and Sudbery 2002) Although eukaryotic, *C. albicans* does not undergo meiosis. Nonetheless, it generates genetic diversity that leads to changes such as the acquisition of drug resistance. The organism tolerates many genome changes, including whole chromosome and segmental aneuploidies, translocations (Coste et al 2007), and recombination events that result in loss of heterozygosity (LOH). The focus of this study is to measure rates of loss of heterozygosity as stress (oxidative, temperature, anti-fungal drug) is applied in order to determine mechanisms that lead to genetic changes. The strains used each have the URA3 counter-selectable marker inserted into different chromosomal locations. For each strain, stress was added in different amounts and using fluctuation analysis tests, the LOH of URA3 was determined. Preliminary results suggest that the rate of LOH is higher near the telomeres compared to centromere locations. Further studies will compare LOH rates of different strains to see what affect chromosome length, gene distance from the telomere, and gene distance from the centromere have on chromosome stability under stressful conditions.



Poster Number: Session: