"Creating a Candida albicans genome-wide CRISPR interference library for large-scale genetic analysis"

*Candida albicans* is an opportunistic fungal pathogen that also exists as a commensal member of the human microbiota. Infections caused by *C. albicans* can be severe and life-threatening, especially in immunocompromised individuals. Treating *C. albicans* infections is notoriously challenging due to limited availability of safe and efficacious antifungal drugs. The emergence of drug-resistant *C. albicans* strains further complicates treatment options. Thus, it is imperative that we study this pathogen to better understand the fundamental molecular mechanisms that underpin both antifungal drug resistance and how the pathogen interacts with its host to establish infection. Previous work in the Shapiro lab has validated the use of a transcriptional repression system, known as CRISPR interference (CRISPRi), to study gene function in *C. albicans*. We propose scaling this technology up to a genome-wide level to identify previously uncharacterized genes with roles in antifungal drug resistance and host-pathogen interactions. We aim to generate a pooled CRISPRi repression library representing all ~6,100 genes in the *C. albicans* genome. This pooled library will be screened in the presence of antifungal drugs to identify genes that, when repressed, influence antifungal drug susceptibility. The pool will also be screened using a *C. albicans*-macrophage infection model to identify genes that influence phagocytosis of *C. albicans* by macrophages. Genes of interest from these screens will be subject to follow-up analysis to study their function more comprehensively. This research will help to deepen our understanding of how *C. albicans* develops resistance to antifungal drugs and fungal biology altogether.