Mechanism of Candid drug resistance in yeast pathogen Cryptococcus neoformans

HYPOTHESIS:

Candid drugs are the new generation antifungal drugs with fungicidal activity for several major fungal pathogens, including Candida species, Aspergillus species, and Fusarium species. However, Cryptococcus as the causative agent of deadly cryptococcal meningitis is naturally resistant to this new class antifungal drug even though the target of this drug (beta-glucan synthase) is present and functional. The mechanism of drug resistance is unknown. We hypothesize that the drug may be fail to reach the drug target because of the unique membrane structure in this pathogen, or the presence of high amount of alpha-glucan. It is also possible that a novel drug resistant mechanism is involved. This project is to understand the molecular basis of the inherited resistance of Cryptococcus to Candid drugs.

PROJECT DESCRIPTION (Include design, methodology, data collection, techniques, data analysis to be employed and evaluation and interpretation methodology)

Study design:
Two approaches will be employed for this project. First, we will use reverse genetics to test our hypothesis. A set of mutants that could not produce polysaccharide capsule or alpha-glucan or with altered membrane structure will be used to test the hypothesis that capsule, alpha-glucan or membrane lipids may play a role in drug resistance. The affectivity of Candid drugs (caspofungin and micafungin) in these mutant backgrounds will be tested in vitro condition using 96-well culture plates. We will also apply the forward genetics to screen a random mutagenesis library for those mutant strains failed to grow in the presence of drugs. Mutants sensitive to 8 ug/ml drugs will be selected and rescreened for their sensitivity with lower drug concentrations. A set of most sensitive mutants will be isolated and genomic DNA prepared. The mutated genes in these mutant strains will be identified by using the inverse-PCR technique. The function of identified genes will be analyzed by using bioinformatic approaches and confirmed by mutagenesis. A model will be developed on why Cryptococcus becomes naturally resistant to this drug class.

Techniques to be employed:
PCR-based diagnostic technique will be routinely used to identify gene mutations. Yeast culture growth assays will be applied to determine mutants that become sensitive to drugs. 96-well plate reader will be used to measure the growth as designed time points. Inverse-PCR technique will be used for identifying target genes of mutant strains that become sensitive to drugs. Microscopic techniques will also be used to score the in vitro phenotype of certain mutants. Data collection methods and analysis techniques: Programs Prism and Microsoft excel will be used for data analysis.
SPONSOR’S MOST RECENT PUBLICATIONS RELEVANT TO THIS RESEARCH:


IS THIS PROJECT SUPPORTED BY EXTRAMURAL FUNDS?  
Yes ☐  or  No ☒
(IF YES, PLEASE SUPPLY THE GRANTING AGENCY’S NAME)

THIS PROJECT IS:  ☒Clinical  ☑Laboratory  ☐ Behavioral  ☐ Other

THIS PROJECT IS CANCER-RELATED ☐
Please explain Cancer relevance

THIS PROJECT IS HEART, LUNG & BLOOD-RELATED ☐
Please explain Heart, Lung, Blood relevance

THIS PROJECT EMPLOYS RADIOISOTOPES ☐

THIS PROJECT INVOLVES THE USE OF ANIMALS ☐
Pending ☐  Approved ☐  IACUC Protocol #

THIS PROJECT INVOLVES THE USE OF HUMAN SUBJECTS ☐
Summer Student Research Program
Project Description

PENDING □    APPROVED □    IRB PROTOCOL # M

THIS PROJECT IS SUITABLE FOR:
UNDERGRADUATE STUDENTS ☑    ENTERING FRESHMAN ☐
SOPHOMORES ☐    ALL STUDENTS ☑

THIS PROJECT IS WORK-STUDY:    Yes ☑    or    No ☐

THIS PROJECT WILL BE POSTED DURING ACADEMIC YEAR
FOR INTERESTED VOLUNTEERS?:    Yes ☑    or    No ☐

WHAT WILL THE STUDENT LEARN FROM THIS EXPERIENCE?

The student will gain hands on experience of laboratory research. The student will learn the basic concept of molecular genetics, medical mycology, as well as drug resistance. The student will learn how to design and execute experiments, as well as time management during experiments.