Paper ID: 40682
interactive
student

SPACE LIFE SCIENCES SYMPOSIUM (A1)
Interactive Presentations (IP)

Author: Ms. Abby Chiang
Beckman Research Institute of City of Hope, United States

Ms. Adriana Blachowicz
University of Southern California, United States
Dr. Clay Wang
University of Southern California, United States
Ms. Teresa Hong
Beckman Research Institute of City of Hope, United States
Dr. Kasthuri Venkatweswaran
Jet Propulsion Laboratory - California Institute of Technology, United States
Dr. Markus Kalkum
Beckman Research Institute of City of Hope, United States

PROTEIN DYSREGULATION IN FUNGAL ISOLATES FROM THE INTERNATIONAL SPACE STATION BY TANDEM MASS TAG PROTEOMICS

Abstract

Purpose: To identify specific fungal protein expression patterns affected by the conditions of spaceflight. Microorganisms grown during spaceflight have shown increased virulence, antimicrobial resistance, and production of specific secondary metabolites. The molecular mechanisms behind these effects are still largely unknown. Previously, two *Aspergillus fumigatus* strains (IF1SW-F4 and ISSFT-021) isolated from the International Space Station (ISS) showed significantly higher virulence than the clinical strains (Af293 and CEA10). Furthermore, strain ISSFT-021 was viable after 30 minutes of simulated Mars conditions (ISSFT-021-30min). Thus, the objective of this study was to compare the proteomes of ISS strains with those of terrestrial clinical strains to understand their heightened virulence and resistance to extreme environmental conditions. Methods: The *A. fumigatus* strains were cultured separately in liquid potato dextrose (PD) and Czapek-dox media (CD), and on solid glucose minimal medium (GMM). The TMT6plex reagents were used to label digest peptides of proteins from ISS and terrestrial strains, and multidimensional chromatographic mass spectrometric analyses were conducted on an Orbitrap Fusion Tribrid mass spectrometer. Results: Approximately 3800 proteins were identified for *A. fumigatus* strains cultured in the different media. The individual number and identity of proteins that were up or down regulated compared to the mix of proteins from all strains varied between media. However, we discovered that multiple proteins of the Gene Ontology category oxidoreductase were consistently dysregulated in the ISS strains. The protein Asp-hemolysin, a known virulence factor of *A. fumigatus*, and dimethylally tryptophan (DMAT) synthase FtmPT1 were up-regulated in the ISS strains. The latter is responsible for the expression of fumigaclavine A, an antibacterial ergoline alkaloid and secondary metabolite of *Aspergillus*. Conclusions and Future Plans: The quantitative proteomics analysis carried out during this study was powerful when compared with whole genome sequencing to characterize the functional properties of the ISS strains and their earth counterparts. While more in-depth proteomic analyses are required, the preliminary results revealed the molecular basis of the enhanced virulence (Asp-hemolysin), secondary metabolite production (DMAT synthase/fumigaclavine A), and resistance to extreme conditions (oxidoreductase) whereas marked differences were not observed using the SNP approach. We will use the proteomics data to determine which biological pathways are affected by microgravity and enhanced

radiation. Knowledge of such pathways can lead to targeted genetic manipulations for the production of novel compounds and drug candidates. Furthermore, it can guide microbiological practices, astronaut health precautions, and antimicrobial counter measures for future space missions.