IPD Project Details

Project ID: IPD8104

Project Title: Secretome analysis of Candida glabrata wild-type and aspartyl protease-deficient strains

Description: The project is aimed at characterizing the secretome of a human opportunistic fungal pathogen Candida glabrata. Additionally, the effect of loss of a family of eleven aspartyl proteases (Cg Yapsins) on the Candida glabrata secretome is studied.

Principal Investigator: Dr Rupinder Kaur

PI Affiliation: Laboratory of Fungal Pathogenesis, Centre for DNA Fingerprinting and Diagnostics (CDFD), Hyderabad, India

Sample Preparation: The supernatants of YNB medium-grown logarithmic-phase cultures of wild-type (wt), Cgyps7?, Cgyps2?ypsC? and Cgyps1-11? strains of C. glabrata cells were collected in duplicates and passed through 0.4 µm membrane or syringe filters to remove the residual cells. The resultant filtrates were concentrated using Amicon Ultra-15 and Ultra-0.5 (10 kDa cutoff) centrifugal filter units. The concentrated secretome fractions were run on a 12% SDS-PAGE and stained with Coomassie Brilliant Blue. The gel lane containing all proteins was sliced into three sections, with each section containing a different size range (<50 kDa, 50-120 kDa and >120 kDa) of proteins.

Peptide Separation: Proteins were identified, after in-gel trypsin digestion, via the microcapillary LC-MS/MS (Liquid chromatography-tandem mass spectrometry) method at the Taplin Biological Mass Spectrometry Facility, Harvard Medical School, Boston, USA using the the LTQ Orbitrap Velos Pro ion-trap mass spectrometer.

Protein Characterization: The acquired fragmentation pattern for each peptide was analysed using the Sequest software, and searches were run against the UniProt C. glabrata reference proteome database. The identified peptides were filtered to 1% false discovery rate.

Experiment Type: Shotgun proteomics

Species: Data in species_details No Data

Tissue: Data in tissue_details No Data

Cell Type: Data in cell_details No Data

Disease: Unknown No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications: dehydrated residue

PubMed ID: 31621333