Indian Biological
Data Centre

IPD Project Details

Project ID: IPD3310

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

Description: The project is aimed at characterizing the effect of deletion of surface associated aspartyl protease(s) on the secretome of of the human opportunistic fungal pathogen Candida glabrata.

Principal Investigator: Dr Rupinder Kaur

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Sample Preparation: The supernatants of YNB medium-grown logarithmic-phase cultures of Cgyps7? and Cgyps2?ypsC? 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

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