Indian Biological
Data Centre

Indian Proteome Databank

IPD Project Details

Project ID: IPD4304

Project Title: Proteomic profiling of Labeo Rohita; a widely cultivated fish

Description: The aim of this study was to develop a Peptide Atlas repository for Labeo rohita. Using LC-MS/MS, we have performed in-depth proteomics analysis of 19 different sample types, including 17 tissue samples, plasma from female fish and embryo 4-day post fertilization. Whole analysis resulted in the identification of more than 6015 confident canonical proteins along with ~3000 non canonical peoteins corresponding to more than 150 thousands peptides. This proteomic dataset would complement the recently published genome to accelerate further research.

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Sample Preparation: Tg eurea lysis buffer and Benzonse for the endogenous prtienase inhibitors are containg buffer used for the extraction.

Peptide Separation: Fractionated protein bands were performed in-gel digestion using trypsin as protease. Protein digest was extracted from gel pieces using gradient solution of Acetonitrile. Peptides were desalted using c-18 zip tips, vacuum dried and stored till further use for mass spectrometry. For LC-MS/MS, peptides were quantified and around 1 ug of peptides were subjected to mass spectrometry.

Protein Characterization: The DDA-MS data obtained after mass spectrometry was subjected to Trans Proteomic Pipeline (TPP) tool. The raw data (.raw) files were first converted into MzML file using msconvert tool built in TPP. The data was performed comet search against L. rohita protein database (ProteomeID- UP000290572) obtained from unassembled WGS sequence and NCBI protein sequences (Bio project: PRJNA437789) of Labeo rohita. An equal number of decoy sequences generated using “randomize sequences and interleave entries” decoy algorithm and contaminant sequences from common Repository of Adventitious Proteins, cRAP, database. Comet search was followed by other steps in TPP pipeline as peptideProphet, reSpect, iProphet, ProteinProphet. MAYU tool was used for data filtering and finally the ROHU peptide Atlas was developed.

Experiment Type: Shotgun proteomics, Gel-based Experiment

Species: Data in species_details No Data

Tissue: Data in tissue_details No Data

Cell Type: No Data

Disease: Unknown No Data

Instrument Details: Data in instrument_details Data in instrument_details

Protein Modifications: No PTMs

PubMed ID: 34962809