**Biplab Paul**

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**SUMMARY OF QUALIFICATION**

* PhD level cell biologist with experience in bioinformatics.
* Expertise in developing computational pipelines to analyze a wide range of next generation sequencing data such RNA-Seq, Chip-Seq, single-cell RNA-Seq etc.
* Experience in R, and Python programming language.
* Comfortable with working in Unix, Linux, HPC computing platforms.
* Experience in using open source bioinformatic tools such as bowtie, hisat2, samtools, bedtools, deeptools, DESeq2, GO-Seq, Seurat, Scanpy, Squidpy IGV etc.
* Wet laboratory experience in molecular biology, genetics, microscopy and RNA Biology.
* Strong communication and collaboration skills through collaborative work during PhD and Postdoc.

**RELEVANT EXPERIENCE**

**Postdoctoral Fellow, 01/2020 – Present**

**Massachusetts General Hospital, Harvard Medical School**

* Analyzed bulk RNA-Seq, single-cell RNA-Seq (scRNA-Seq) and spatial transcriptomics (MERFISH) data generated from human liver tissue.
* Established wet laboratory methods for preparation of spatial transcriptomics sample from normal human liver using Multiplex Error Robust Fluorescence in situ hybridization (MERFISH).
* Adapted Matlab based pipeline for designing probe sets for MERFISH.

**Visiting Research Scholar, University of California, Davis 09/2016 – 12/2019**

* Analyzed RNA-Seq data to identify mutation-specific effects on yeast transcriptomes, including custom analysis of NGS data to identify RNA processing defects using shell scripting, R and Python programming.
* Generated pipeline for analysis of Chip-Seq and RNA-Seq data from public database.
* Analyzed of gene expression by single molecule fluorescence in situ hybridization (smFISH).

**EDUCATION**

**Ph.D. in Cell Biology, University of Alberta, Canada 05/2015 – 12/2019**

Thesis: Nuclear accumulation of polyadenylated non-coding RNA leads to a breakdown in nuclear RNA homeostasis.

Supervisor: Dr. Ben Montpetit

**M.Sc. in Biochemistry, University of Regina, Canada 01/2009 – 04/2013**

Thesis: Role of β-galactofuranose and β-glucan in *Aspergillus nidulans* hyphal cell wall ultrastructure and physical properties.

Supervisor: Dr. Tanya Dahms

**B.Sc. in Biotechnology and Genetic Engineering 09/2001­ – 07/2006**

Khulna University, Bangladesh

**SELECTED PUBLICATIONS**

1. Estevez, M., Li, Rui, **Paul, B.,** Daneshvar, k., Mullen, AC., Romerio, F. and Addepalli, B. Identification and mapping of post-transcriptional modifications on the HIV-1 antisense transcript *Ast* in human cells. *RNA* doi:10.1261/rna.079043.121
2. LC Aguilar\* **B Paul\*,** T Reiter, L Gendron, AAN Rajan, R Montpetit, C Trahan, S Pechmann, M Oeffinger, and B Montpetit (2020) Altered rRNA processing disrupts nuclear RNA homeostasis via competition for the poly(A)-binding protein Nab2. *Nucleic Acid Research* 48-20, 11675–11694 **(\* denotes equal contribution)**
3. Milbury, K., **Paul, B.,** Lari A., Fowler C., Montpetit B. & Stirling, C. P. (2019) Exonuclease domain mutants of yeast DIS3 display genome instability. Nucleus, 10-1, 21–32.
4. **Paul, B,** & Montpetit B. (2016) Altered RNA processing and export leads to retention of mRNAs near transcription sites, nuclear pore complexes, or within the nucleolus. Mol Biol Cell. 27:17, 2742-2756.

**PLATFORM PRESENTATIONS**

* Paul, B., Yong, B. and Montpetit, B. (2015) Disruption of the nuclear surveillance pathway causes both mRNA and mRNA processing factors to localize to the nucleolus. Cell Biology Research Day, University of Alberta, Edmonton, AB, Canada.
* Paul, B., Yong, B. Porter, C and Montpetit, B. (2015) Identifying essential genes that function in mRNA export. Western Canada RNA Conference (RiboWest), June18-June21, 2014, University of Lethbridge, AB, Canada.

**POSTER PRESENTATION**

* Paul, B., Aguilar, L., Pechmann, S., Oeffinger, M., Montpetit, B. Stabilization of poly(A)-RNA species by multiple mechanisms leads to improper RNA processing and a general disruption in nuclear homeostasis. Bay Area RNA Club, 2018, UCSF, CA, USA
* Paul B. and Montpetit B. (2016) Altered RNA processing and export lead to retention of mRNAs near transcription sites and nuclear pore complexes or within the nucleolus. Yeast Genetics Meeting, 2015 July13-17, Orlando, FL, USA