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, 3' tag-seq and single-cell RNA-Seq etc.
- Experience in R, Python and Matlab programming language.
- Comfortable with working in Unix/Linux, HPC computing environment.
- Experience in using command line bioinformatic tools such as bowtie, hisat2, samtools, bedtools, deeptools, HTSeq, Macs2,
- Experience in using various Bioconductor packages such as DESeq2, EdgeR, Rsubread, GOSeq
- Wet laboratory experience in molecular biology, genetics, microscopy and RNA Biology.
- Strong communication and collaboration skills.

Training

Postdoctoral Fellow, 01/2020 – Present
Massachusetts General Hospital, Harvard Medical School
Research Interest: Spatial transcriptomics of normal human liver.
Supervisor: Dr. Alan Mullen

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

Relevant Experience

Postdoctoral Fellow, MGH/Harvard Medical School 01/2020 – Present

- Analyzed of publicly available bulk RNAseq and single cell RNA-Seq (scRNA-Seq) 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).
- Established Matlab based pipeline for designing probe sets for MERFISH.

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

- Analyzed of RNA-Seq and 3' tagSeq 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.
- Performed microscopy to study the impact of ncRNA biogenesis defects on the localization of RNA and associated RNA-binding proteins in yeast.

PhD Candidate, University of Alberta, Canada 09/2013 –12/2019

- Constructed mutant yeast strains (e.g. gene knock-out / protein tagging) to discover relationship between mRNA decay and RNA processing and export.
- Designed and implemented single molecule fluorescent in situ hybridization experiments to identify mRNA export defects in RNA decay mutants.

Research Assistant, University of Regina, Canada 01/2009 – 04/2013

- Investigation of fungal cell wall ultrastructure by Atomic Force Microscopy.

List of publications

1. Ahmed, C. M. S., **Paul, B.,** Cui, Y.; Frie, A., Burr, A., Kamath, R., Chen, J., Nordgren, T., Bahreini, R., Lin, Y., (2021) Integrative analysis of lncRNA-mRNA co-expression in human lung epithelial cells exposed to dimethyl selenide (DMSe)-derived secondary organic aerosols. Chem. Res. Toxicol., 34, 3, 892-900.
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 (* 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.
5. **Paul, B.,** El-Ganiny, A. M., Abbas, M., Kaminskyj, S. G. & Dahms, T. E.S. (2011) Quantifying the importance of galactofuranose in Aspergillus nidulans hyphal wall surface organization by atomic force microscopy. Eukaryotic Cell 10, 646-653.

Invited book Chapters

1. **Paul, B.,** Ma, H., Snook, L. A., Dahms, T. E.S. (2013) High resolution imaging and force spectroscopy of fungal hyphal cells by atomic force microscopy. Laboratory Protocols in Fungal Biology, Eds. V.K. Gupta et al., Springer, USA. ISBN 978-1-4614-2355-3.
2. Bhat S., Jun, D., **Paul, B.** and Dahms E. S. T. (2012) Viscoelasticity in biological systems: A special focus on microbes. Viscoelasticity, INTECH, European Union, ISBN: 980-953-307-335-9.