

Biplab Paul

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SUMMARY OF QUALIFICATION

- Ph.D. level cell biologist with experience in bioinformatics.
- Wet laboratory experience in molecular biology, genetics, microscopy, and RNA Biology.
- Experienced in adaptation and optimization of single-molecule FISH and image-based spatial transcriptomics method MERFISH.
- 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 bioinformatics tools such as bowtie, hisat2, samtools, bedtools, deeptools, HTSeq, Macs2,
- Experience in using various Bioconductor packages such as DESeq2, EdgeR, Rsubread, GSeq
- 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 09/2013 – 06/2020
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 – 09/2012
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 – 11/2006
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.
- Adapted and optimized methods for the image-based spatial transcriptomics for the normal human liver using Multiplex Error Robust Fluorescence in situ hybridization (MERFISH).
- Analysis and integration MERFISH and scRNA-Seq data using open source tools.
- 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.

Ph.D. Candidate, University of Alberta, Canada 09/2013 –12/2019

- Constructed mutant yeast strains (e.g. gene knock-out/protein tagging) to discover the 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. 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. 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.

3. 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)
4. 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.
5. **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.
6. **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. (* denotes equal contribution)
7. U Salma, MS Rahman, S Islam, N Haque, M Khatun, TA Jubair, BC Paul. (2008) Mass propagation of *Rauwolfia serpentina* L. Benth. *Pakistan Journal of Biological Sciences: PJBS* 11 (9), 1273-1277

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.

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.
- Paul, B., Yong, B. Porter, C and Montpetit, B. (2015) Identifying essential genes that function in mRNA export. Cell Biology Research Day, Loon Lake Cell Biology Retreat, May 2-4, 2014, BC, Canada.
- Paul B., El-Ganiny M.A., Abbas M. Kaminskj G.W.S., Dhams E.S.T., The role of β - galactofuranose in the organization of *Aspergillus nidulans*

hyphal wall surfaces. Chemical Biophysics Symposium, April 9-11, 2010, University of Toronto, ON, 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
- Paul, B., El-Ganiny, A. M., Abbas, M., Kaminskyj, S. G. & Dahms, T. E.S. The role of β -galactofuranose in cell wall surface structure and elasticity of *Aspergillus nidulans*. Biophysical society 55th annual Meeting, March 5-9, Baltimore, USA.
- Paul B., El-Ganiny M.A., Abbas M. Kaminskyj G.W.S., Dhams E.S.T., The role of β - galactofuranose in the organization of *Aspergillus nidulans* hyphal wall surfaces. Chemical Biophysics Symposium, April9-11, 2010, University of Toronto. Canada. Poster No-8.

Scholarships and awards

- FGSR Graduate Travel Award (2016) Faculty of Graduate Study and Research, University of Alberta.
- 75th Anniversary ward (2015-2016), Faculty of Medicine and Dentistry, University of Alberta.
- University of Alberta Doctoral Recruitment Scholarship (2013-2014), University of Alberta.
- Faculty of Graduate Study and Research Scholarship (2012-2013), University of Regina.
- Graduate student association travel award (2011) – University of Regina.
- International graduate student scholarships (2010) - University of Regina.
- Travel award (2010) – Chemical Biophysics Symposium held at University of Toronto.