BIOGRAPHICAL SKETCH

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NAME: PAULAMI CHATTERJEE

eRA COMMONS USER NAME (credential, e.g., agency login): PAULAMI

POSITION TITLE: Postdoctoral Scholar, Division of Pulmonary, Allergy and Critical Care Medicine, Stanford University School of Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Calcutta, India	B.Sc.	05/2010	Microbiology
University of Calcutta, India	M.Sc.	06/2012	Biochemistry
Bose Institute, University of Calcutta, India	Ph.D.	11/2019	Biophysics, Molecular Biology and Bioinformatics

A. Personal Statement

My academic training and diverse research experience in fields ranging from molecular biology, microbiology, biochemistry to bioinformatics and computational biology inspire me in applying a multi-pronged approach to unravel the complexities of human diseases. Investigation of MMP19 functional polymorphism in ovarian cancer was my first foray into academic research during my graduate studies. Later in my doctoral research, I developed computational methods to explore molecular interaction and dynamics of biomarkers in neurodegenerative diseases. In my postdoctoral career, I delved into mycology research under the mentorship of Dr. David A. Stevens, where I investigated bacterial-fungal interaction in cystic fibrosis (CF). With this targeted focus on inter-microbial relationship, I transitioned to Dr. Joe Hsu's lab. I was truly fascinated by his research on the role of microenvironmental changes after tracheal transplant that contribute to *Aspergillus* invasion. I am particularly interested in exploring transcriptomic changes and inferring molecular crosstalk in CF patients who developed ABPA due to Aspergillus induced hypersensitivity. I want to focus my studies on children with ABPA due to the high susceptibility of CF patients to get Aspergillus infections. I plan to implement multi-omic approaches coupled with immunology and molecular biology techniques to identify significant fungal virulent molecules correlated with severe disease outcome. Complete understanding of this interaction and enriched pathways will help us define clinically relevant targets for therapeutic use. Successful endeavors in this field will empower me to mature into an independent and productive researcher.

B. Positions and Honors

Positions:

2020-present Postdoctoral Scholar, Pulmonary, Allergy and Critical Care Medicine, Stanford University School of Medicine

2015-2017 Senior Research Fellow, Bose Institute, University of Calcutta, India

2013-2015 Junior Research Fellow, Bose Institute, University of Calcutta, India

Other Experience and Professional Memberships:

2019-2020 Research Volunteer, Infectious Disease Research Laboratory, California Institute for Medical Research, California, USA

2011 Summer Research Intern, CSIR-Indian Institute of Chemical Biology (CSIR-IICB), Kolkata, India

Honors:

2020 Best Poster Presentation, 9th Advances Against Aspergillosis & Mucormycosis 2020, Lugano, Switzerland

2020 Scholarship for presenting research poster at Advances Against Aspergillosis & Mucormycosis 2020, Lugano, Switzerland

2014 Best poster award at Drug Discovery and Therapy World Congress 2014 (DDTWC 2014), Boston, USA

2013 Best poster award at Frontiers in Modern Biology 2013 (FIMB 2013), Kolkata, India

C. Contributions to Science

1. Investigated the role of *Pseudomonas virulence* factor pyocyanin as an anti-*Aspergillus* molecule

Pseudomonas aeruginosa share the same polymicrobial niche (airways of immunocompromised patients, or individuals with cystic fibrosis) with the opportunistic fungus *Aspergillus fumigatus*. It has been shown that under limiting iron conditions the siderophore pyoverdine is the most effective antifungal *P. aeruginosa* product. Our study provided evidence that under nonlimiting iron conditions *P. aeruginosa* supernatants lack pyoverdine but still possess considerable antifungal activity. Spectrometric analyses of *P. aeruginosa* supernatants revealed the presence of phenazines, such as pyocyanin, only under nonlimiting iron conditions. Supernatants of quorum sensing mutants of strain PA14, defective in phenazine production, as well as supernatants of the *P. aeruginosa* strain PAO1, lacked pyocyanin, and were less inhibitory toward *A. fumigatus* biofilms under nonlimiting iron conditions. When blood as a natural source of iron was present during *P. aeruginosa* supernatant production, pyoverdine was absent, and phenazines, including pyocyanin, appeared, resulting in an antifungal effect on *A. fumigatus* biofilms. In summary, these studies are the first to identify the iron-dependent dual anti-fungal mechanisms of *P. aeruginosa* and indicated that it can switch from iron-denial-based to toxin-based antifungal activity. These findings have implications for the evolution of the microbiome in clinical settings where the two pathogens co-exist. I served as the co-investigator in these studies.

1. Sass G, Nazik H, **Chatterjee P**, Shrestha P, Christine-Groleau M, Deziel E, Stevens DA. Altered Pseudomonas strategies to inhibit surface Aspergillus colonies. Frontiers in Cellular and Infection Microbiology, ***2021***, (Accepted, In Press).
2. Sass G, Nazik H, **Chatterjee P**, Stevens DA. Under nonlimiting iron conditions pyocyanin is a major antifungal molecule, and differences between prototypic Pseudomonas aeruginosa strains. Med Mycol. ***2020***;myaa066.
3. **Chatterjee P**, Sass G, Swietnicki W, Stevens DA. Review of Potential *Pseudomonas* Weaponry, Relevant to the *Pseudomonas-Aspergillus* Interplay, for the Mycology Community. J Fungi (Basel). ***2020***;6(2):81.

2. Performed system-level study to identify significant molecular markers in neurodegenerative diseases

In my Ph.D. research, I utilized network biological approaches to study biomolecules, their interaction, and dynamics in neurodegenerative diseases, such as Alzheimer's Disease (AD) and Parkinson's Disease (PD) by combining transcriptomic and text mining approaches. We constructed co-expression and regulatory networks from microarray data of PD patients. In this work, inter-regulatory measures were used for the first time to characterize bottleneck hub microRNAs (miRs). In another study, we considered network based topological parameters as well as epigenetic parameters in a single pipeline to predict novel epigenetic genes and miRs for AD. Several network motifs such as Feed-Forward, Feed Back Loops and Multiple Input Modules were identified as the recurrent pattern of AD-specific regulation. Epigenetic regulation of these network motifs in terms of miR associated lncRNAs, histone modification pattern and CpG islands in the miR upstream sequence were also studied. Finally, we performed a system-level comparative study of RNA-Seq data obtained from PD brain and blood samples. Differentially expressed miRs were subjected to generate the Co-expression networks. Highly co-expressed miR clusters led to the identification of biological pathways shared and unique to both the tissue samples. I served as the primary-investigator in these studies.

1. **Chatterjee P**, Roy D, Bhattacharyya M, Bandyopadhyay S. Biological networks in Parkinson's disease: an insight into the epigenetic mechanisms associated with this disease. BMC Genomics. ***2017***;18(1):721.
2. **Chatterjee P**, Roy D. Structural Insight into GRIP1-PDZ6 in Alzheimer's disease: study from protein expression data to molecular dynamics simulations. J Biomol Struct Dyn. ***2017***;35(10):2235-2247
3. **Chatterjee P**, Roy D. Comparative analysis of RNA-Seq data from brain and blood samples of Parkinson's disease. Biochem Biophys Res Commun. ***2017***;484(3):557-564.
4. **Chatterjee P**, Roy D. Insight into the Epigenetics of Alzheimer's Disease: A Computational Study from Human Interactome. Curr Alzheimer Res. ***2016***;13(12):1385-1396.
5. **Chatterjee P**, Bhattacharyya M, Bandyopadhyay S, Roy D. Studying the system-level involvement of microRNAs in Parkinson's disease. PLoS One. ***2014***;9(4):e93751.

3. Development of computational drug repositioning pipeline

Drug repositioning refers to finding new indications of already existing drugs. As part of my Ph.D. research, I developed computational pipelines for drug repositioning in neurodegenerative diseases. Our proposed pipelines identified repositioning candidates suitable as AD epigenetic drugs and identified their targets from extensive human interactome. The proposed repositioning drugs shared targets and miRs with known AD epigenetic targets and miRs. Furthermore, several shared functional categories and enriched pathways were obtained for these drugs with FDA approved epigenetic drugs and known AD drugs. The findings of our work may provide insight into future AD therapeutics. We also developed a bidirectional (Top-down & Bottom up) method that considered the topological significance of drugs in the tripartite Indication-Drug-target network as well as the significance of their targets in the PD specific protein-protein interaction network. To find out the efficiency of the repositioning candidates we introduced a novel parameter called the On-target ratio (OTR). In this way, non-Parkinsonian drugs were proposed as the significant repositioning candidates for PD. I served as the primary or co-investigator in these studies.

1. **Chatterjee P**, Roy D, Rathi N. Epigenetic Drug Repositioning for Alzheimer's Disease Based on Epigenetic Targets in Human Interactome. J Alzheimers Dis. ***2018***;61(1):53-65.
2. Rakshit H, **Chatterjee P**, Roy D. A bidirectional drug repositioning approach for Parkinson's disease through network-based inference. Biochem Biophys Res Commun. ***2015***;457(3):280-7.

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/paulami.chatterjee.2/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance

2012 Selected for Lectureship through CSIR-UGC National Eligibility Test, India