Teesta Naskar
Biographical Sketch

NAME: Teesta Naskar

eRA COMMONS USERNAME: NASKART

POSITION TITLE: Post Doctoral Researcher

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Vidyasagar University, Midnapore, India	Bachelor of Science	08/2003	07/2006	Microbiology
Jiwaji University, Gwalior, India	Master of Science	08/2006	07/2008	Microbiology
University of Calcutta, Kolkata India	Doctor of Philosophy	01/2014	09/2019	Biochemistry, Neuroscience, Genetics
New York University Grossman School of Medicine, New York USA	Post-doctoral researcher	03/2020	04/2022	Genomics, Neuroscience, Bioinformatics
Icahn School of Medicine at Mount Sinai, New York City, New York 10029, USA	Post-doctoral researcher	04/2022	Present	Epigenetics, Neuroscience

A. Personal Statement

I have always been fascinated by the intricate workings of the human brain, particularly how the unique interplay of an individual's genetic blueprint and the dynamic landscape of epigenetic regulation shapes diverse phenotypes and behavioral manifestations. My long-term research interests focus on understanding how environmental exposures influence brain development, particularly in relation to neuropsychiatric conditions and behavioral outcomes.

Throughout my research career, a central direction has been to explore the critical impact of environmental exposures on brain development, functioning, and behavior. Currently, in my postdoctoral work, I am investigating how prenatal and early postnatal cannabinoid exposure influences brain development and behavior. This research has revealed significant effects of cannabis on placental transcriptomics and proteomics, and their subsequent impact on offspring, contributing to the development of neuropsychiatric manifestations.

My first foray into addressing these goals started during my PhD while working on dyslexia. I identified protocadherin gamma gene cluster associated in the evolution of human specific cognitive skill critical to reading, revealing how genetic variations affect neural connectivity.

Looking ahead, I aim to establish myself as an independent neuroscientist, leading research that bridges brain development in critical period with long-term neuropsychiatric health. In long term, my goal is to prevent and treat neuropsychiatric disorders by developing strategies rooted in a deep understanding of their environmental and developmental origins.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2022- Present Post-doctoral researcher, Yasmin Hurd lab, Department of Neuroscience, Icahn School of Medicine at Mount Sinai, New York, USA

2020- 2022 Post-doctoral researcher, Aravinda Chakravarti lab, Centre for Human Genetics and Genomics and Joel Schuman's lab, Department of Ophthalmology , New York University Grossman School of Medicine, New York, USA

2019- 2020 Research Scientist, Artemis Hospital, Gurugram, India

2014- 2019	Senior Research Fellow, Indian Council of Medical Research (ICMR), India; worked at National Brain Research Centre, Manesar, India
2014- 2018	PhD student, University of Calcutta, Kolkata, India & National Brain Research Centre, Manesar, India
2011- 2013	Project Assistant, National Brain Research Centre, Manesar, India
2010- 2011	Project Research Assistant, Manovikas Biomedical research and Diagnostic Centre, Kolkata, India
2009- 2010	Research Trainee, School of Tropical Medicine, Kolkata, India

Selected Awards & Honors

2019	Best poster award in 44th Annual Conference of ISHG (Genomics of Complex Disease) Kalyani, India, 2019.
2018	Best poster award in India| EMBO Symposia (Big Data in biomedicine) New Delhi, India
2016	Scholarship and travel award from SciGenome Research Foundation (SGRF) for NextGen Genomics, Biology, Bioinformatics and Technologies Conference (NGBT), Cochin, India.
2015	Senior Research Fellowship from Indian Council of Medical Research (ICMR), Government of India.
2011	Project Assistant Fellowship at National Brain Research Centre, Department of Biotechnology Government of India.

Invited Talk

2023	15th Annual Neuroscience Retreat, Friedman Brain Institute (FBI), Icahn School of Medicine at Mount Sinai, New York, USA

Teaching & Mentoring

2022	Mentored the 'Techniques and Approaches in Neuroscience' course (paid) for the Fall 2022 under the graduate school course BSR2707 at the department of Neuroscience, Icahn School of Medicine at Mount Sinai, New York, USA
2023	Mentored in CEYE Summer Bioinformatics Project – 2023 at Icahn School of Medicine at Mount Sinai, New York, USA

Academic services

2023	Hosted Mount Sinai Neuroscience seminar series (MSNseminars) (February & June, 2024)

Scientific outreach & Media coverage

2024	Science story telling with storycollider (https://www.storycollider.org/tickets/2024/3/7/new-york-ny) on how how "lonely brain" may lead to psychiatric vulnerability & how we can contribute to overcoming it
2018	The research article "Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family" was recommended as important hypothesis in Faculty Opinion (formerly F1000 prime).
2018	The part of the PhD thesis work which was published in *EBioMedicine* (Naskar et al., 2018) was also published in the science news of the Hindu BusinessLine. The weblink is http://m.thehindubusinessline.com/news/science/indian-scientists-identify-gene-linked-to- dyslexia/article10045272.ece.

C. Contributions to Science

<u>1. Postdoctoral Career – Impact of prenatal cannabis exposure on offspring brain and behavior</u>

Cannabis is one of the most commonly used recreational drugs in the United States, with increasing legalization for both medical and recreational purposes across numerous states. Despite this, the safety of cannabis consumption during pregnancy is a growing concern, particularly due to its potential harmful effects on fetal development and the long-term consequences that may extend from infancy through adolescence. In my post-

doctoral training at Dr. Yasmin Hurd lab, I am investigating the impact of prenatal cannabis exposure on fetal brain development and on behavioral outcome. The focus of this project centered on studying whole transcriptomic and proteomics profiling on placental biopsies collected at birth from cannabis-exposed pregnant women and on full-term placental tissues from pregnant female rats exposed to THC-CBD as well as the fetal transcriptomic data from humans and rats.

Manuscripts in preparation and about to be submitted

a) **Naskar T**, Bara A, Hurd YL. (2024) Disturbances in monoamine metabolism evident from placental proteome in response to prenatal cannabis exposure.
b) Bara A, **Naskar A**, Ferland JMF, Hurd YL. (2024) Integrative clinical and preclinical investigation decipher imbalanced lipid metabolism dysregulating interaction of cytokines to T-cell mediated immune responses in cannabis exposed placenta specific to males. (*Bara A and Naskar T served as co-first author)
c) **Naskar T,** Hurd YL (2024). Interplay of miRNAs in modulating TGFbeta signaling pathway due to prenatal cannabis exposure.

2. Postdoctoral Career – Mutational landscape of Hirschsprung disease

Hirschsprung disease (HSCR) arises from an absence of enteric neurons originating from a small group of cells originating in the vagal neural crest, invading the foregut, and migrating in a rostro-caudal direction through the developing gut. At my first post-doctoral training at Dr. Aravinda Chakravarty lab, I have studied the mutational burden of known HSCR genes, by analyzing whole exome sequencing (WES) of closely related HSCR cases from European ancestry to identify the pathogenic variants for HSCR. There, I had also extensively worked on creating HSCR gene mutation repository to update and finalize lists of HSCR genes, biological annotation and cis regulatory elements (CREs) associated with each gene by using publicly available data as well as experimental data generated in Dr. Chakravarty laboratory. The goal for creating this repository was to build a database that would be handful to design experimental validation of gene(s) with specific mutation(s), systemic evaluation of forming Gene Regulatory Network (GRN) for HSCR phenotype and for developing genetic marker in diagnostic purpose in near or far future.

3. Postdoctoral Career – Investigation of genetic determinants for structural eye features of glaucoma and disease progression

In my first post-doctoral tenure at NYU school of Medicine, I was also co-mentored by Dr. Joel Schuman at the department of Ophthalmology. There I worked to investigate inter-individual genetic risk of glaucoma in a multicentric longitudinal study of NEIGHBORHOOD project which includes genotype and phenotype data for approximately 1,000 glaucoma eyes and their age-matched controls. Along with the genotype data I have also analyzed their phenotypic parameters includes ocular measurements, including RNFL thickness, vertical cup-disc ratio (vCDR), and disc area (DA), is complete.

4. Research Scientist – Establishment of in-house genetic marker screening strategies and research

As an independent research scientist, I did take the responsibilities of setting up a genetic lab including establishment of several prenatal genetic marker for in-house genetic testing at Artemis Hospital, Gurugram, India.

5. Senior Research Fellow – Genetics of dyslexia and comparative genomics for language and reading

I have investigated genetic underpinning of dyslexia along with a comparative genomic analysis to understand the evolution of cognitive abilities specific to humans such as language and reading at the laboratory of Subrata Sinha, National Brain Research Centre, India as a senior research fellow of Indian Council of Medical Research Centre, India.

6. PhD student – Investigation of the genetic predisposition to dyslexia using a family-based study.

During my doctoral research I have investigated the underlying genetic and molecular mechanism of dyslexia under the co-supervision of Prof. Subrata Sinha, National Brain Research Centre and Prof. Sanghamitra Sengupta, University of Calcutta, India.

Dyslexia impairs reading, a unique ability of humans, with considerable genetic heterogeneity and neurodevelopmental basis. My thesis dealt with the identification of protocadherin gamma (PCDHG) gene cluster in a multiplex family by using whole genome SNP array and whole exome sequencing analysis.
The novelty of this study was not only identification of new genetic loci for dyslexia but also involvement of genes encoding neural adhesion proteins, in particular the presence of the variations in the extracellular domain of Protocadherin gamma (PCDHG), provide an insight of aberrant neural connection prohibiting one's ability to become a skilled reader. Additionally, the presence of lineage specific variations sheds light on the evolution of the human brain for acquisition of this unique skill. The convergence between the findings of genetic underpinning of dyslexia which are critical to neural adhesion, along with an evolutionary significance, underscores the possibility of new avenue of research on the evolution of human specific cognitive skills with integrating neural and molecular mechanism.

Publication

a) **Naskar T**, Faruq M, Banerjee P, Khan M, Midha R, Kumari R, Devasenapathy S, Prajapati B, Sengupta S, Jain D, Mukerji M, Singh NC, Sinha S. Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family. *EBioMedicine*. 2018 Feb; 28: 168-179. doi: 10.1016/j.ebiom.2017.12.031. Epub 2018 Jan 9. PMID: 29409727; PMCID: PMC5835549.

b) Prajapati B, Fatima M, Fatma M, Maddhesiya P, Arora H, **Naskar T**, Devasenapathy S, Seth P, Sinha S. Temporal transcriptome analysis of neuronal commitment reveals the preeminent role of the divergent lncRNA biotype and a critical candidate gene during differentiation. *Cell Death Discov*. 2020 Apr 24; 6: 28. doi: 10.1038/s41420-020-0263-6. PMID: 32351715; PMCID: PMC7181654.

c) Devasenapathy S, Midha R, **Naskar T**, Mehta A, Prajapati B, Ummekulsum M, Sagar R, Singh NC, Sinha S. A pilot Indian family-based association study between dyslexia and Reelin pathway genes, DCDC2 and ROBO1, identifies modest association with a triallelic unit TAT in the gene RELN. *Asian J Psychiatr.* 2018 Oct; 37: 121129. doi: 10.1016/j.ajp.2018.08.020. Epub 2018 Aug 25. PMID: 30199849.

Poster presentation

1. **Teesta Naskar**, Mahammad Farooq, Renu Kumari, Subha Devsenapati, Massarat Khan, Rashi Midha, Bharat Prajapati, Sanghamitra Sengupta, Mitali Mukerji, Nandini Chatterjee Singh, Subrata Sinha. Potential role of Protocadherin gamma gene cluster in human-specific cognitive skill critical to reading. *44th Annual meeting of the Indian Society of Human Genetics*, 2019 Kalyani, India.
2. **Teesta Naskar**, Priyajit Banerjee, Mohammed Faruq, Sanghamitra Sengupta, Deepti Jain, Nandini Chatterjee Singh, Mitali Mukerji, Subrata Sinha. Potential role of protocadherin gamma gene cluster in human-specific cognitive skill critical to reading. *11th Biennial Meeting of the Federation of European Neuroscience Societies (FENS),* 2018 Berlin, Germany.
3. **Teesta Naskar**, Mahammad Farooq, Renu Kumari, Massarat Khan, Rashi Midha, Subha Devsenapati,, Bharat Prajapati, Mitali Mukerji, Nandini Chatterjee Singh and Subrata Sinha. Whole exome sequencing and genome- wide genotyping in a multiplex family identified novel genetic loci on chromosome 5 for dyslexia. *India EMBO symphosium on "Big Data in Biomedicine"*, 2018 New Delhi India.
4. **Teesta Naskar**, Mahammad Farooq, Renu Kumari, Subha Devsenapati, Massarat Khan, Rashi Midha, Bharat Prajapati, Sanghamitra Sengupta, Mitali Mukerji, Nandini Chatterjee Singh, Subrata Sinha. Whole exome sequencing and genome-wide genotyping on a multiplex family identified novel candidate genes for dyslexia encoding neural connectivity proteins. *NextGen Genomics, Biology, Bioinformatics and Technology (NGBT) Conference*, 2016 Cochin India.

7. Project Assistant – Association study of genetic variants in the neuronal migration pathway and behavioral correlates of dyslexia – linking genes and behavior using familial and sporadic cases

As a project assistant at the laboratory of Prof. Subrata Sinha and Prof. Nandini Chatterjee Singh, NBRC, I studied genetic associations across genes that participate in neuronal migration pathway, along with altered cognitive measure using psychometric tests.

8. Project Research Assistant – Genetic association study in the sporadic cases of Autism in Indian population

As a project research assistant at Manovikas Biomedical research and Diagnostic Centre, Kolkata, India, I worked on the genetic association study of sporadic cases of autism particularly for MET gene polymorphism.

D. Self-advancement to serve scientific community

Skills and Expertise

- Working experience in high-performance Linux cluster and cloud computing (such as http://bigpurplews.nyumc.org/wiki/index.php/BigPurple_HPC_Cluster and https://labs.icahn.mssm.edu/minervalab/)
- Proficiency in R
- Experience in Linux shell scripting
- Familiar with Perl, Python, Java
- Strong knowledge of high through put next-generation sequencing (NGS) data analysis pipelines, including alignment, variant calling, and differential expression analysis of whole genome, RNA sequencing (both bulk and single cell), Mass-spectrometry protein data.
- Extensive experience in statistical analysis methods and tools, such as DESeq2, DEqMS, limma, and edgeR, Seurat
- Expertise in network analysis, pathway enrichment, and functional annotation of biological data.
- Tools and software for evolutionary genetics analysis: Proficient in handling MEGA 3.1, Ka/Ks calculator, ParaAT (a Parallel Alignment and back-Translation tool), ClustalW, t-coffee
- Extensive experience with bioinformatics tools and databases, including BLAST, NCBI, Ensembl, and UCSC Genome Browser Allen Brain Atlas, ENSEMBLE, Ancient genome browser, GTEX .
- Molecular Biology (wet lab experience): Library preparation for whole genome, whole exome, RNA sequencing, Immune histochemistry (IHC), confocal microscopy, western blotting, PCR, q-PCR

Note: Please visit https://github.com/TeestaNaskar?tab=repositories to see the entire repository of scripts that I wrote

Workshop

1. **Human and Mammalian Genetics and Genomics: The McKusick Short Course** (Virtual) 2021
2. **Human and Mammalian Genetics and Genomics: The McKusick Short Course** (Virtual) 2020
3. NIBMG-UChicago Workshop on "***Big Data Analysis in BioMedical Genomics"*** 2016, National Institute of Biomedical Genomics (NIBMG), Kalyani, India**.**

Note: Please visit https://teestanaskar.github.io/teesta.profile.github.io/ to see my website