





Disha Sharma

Postdoctoral Scholar, Cardiovascular Medicine

 NIH Biosketch available Online

 Curriculum Vitae available Online

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BIO

I am currently a Postdoctoral Fellow with Dr. Thomas Quertermous at Stanford University. I have joined the lab with more than 7 years of research experience in the field of computational biology wherein I have worked with multi-omics data for multiple diseases to get a deeper understanding of the disease identification and progression.

My background in engineering and bioinformatics provide an excellent background for the studies proposed in this application, which proposes to investigate the genetics and genomics of smooth muscle cell biology in the context of vascular disease. I first pursued a Bachelor's in Biotechnology program at one of the premier institutes in India, Banasthali Vidyapeeth and received my degree in 2007. After qualifying with the IIT-JAM exam in 2010, I joined the Master's in Science (Biotechnology) program at the prestigious Indian Institute of Technology Roorkee in a program of engineering and technology. After my Master's, I joined Dr. Vinod Scaria's lab at CSIR-IGIB as a Project Fellow. During the tenure as Project fellow from 2012-2014, I had the opportunity to work with different transcriptomics data from model organisms including zebrafish, rat and human cell lines to understand the role of long non-coding RNAs and miRNAs. I also worked on clinical datasets of autoimmune disorders. With one and half years of research experience and a UGC fellowship awarded through the NET-JRF examination, I continued working with Dr. Vinod Scaria to pursue my PhD. My research interest for the degree focused on the identification and characterization of circular RNAs, and this work has now been published in multiple manuscripts listed below. Over the years at CSIR-IGIB, I have had the chance to work on interesting ideas with multiple collaborating groups. One of them was Dr. Sridhar Sivasubbu, with whom I worked to understand the transcript-level interactions between mitochondria and the nucleus, using zebrafish as a model organism.

In view of my interest in the translational aspects of biology, I obtained the opportunity to work as part of the GUARDIAN Consortium with Dr. Vinod Scaria and Dr. Sridhar Sivasubbu at CSIR-IGIB. This pioneering project is the largest network of researchers and clinicians in India pursuing sequencing patient DNAs to identify rare SNVs and structural variants responsible for muscular dystrophy in these patients. In the interest of advancing genomics in clinical and healthcare settings, I was selected as Intel Fellow 2019 to work for the Intel-IGIB collaboration focussing on "Accelerating Clinical Analysis and Interpretation of Genomic Data through advanced tools/libraries". Our project was selected among top 3 from 50 premier research institutes and I was awarded the Intel-India Fellowship for a year to pursue this project. I was also part of the core team of IndiGen (Genomes for Public Health in India). With the spread of COVID-19 around the world, our group contributed by sequencing and analysing COVID19 genomes to get a better understanding of the disease and I had the opportunity to be part of the core team to analyse the viral sequencing datasets and viral assembly.

I am extremely pleased to have joined the Quertermous lab at Stanford to the study of the molecular mechanisms of cardiovascular disease. Work that I am pursuing in this laboratory, and proposed in this application, are directly in line with my personal aspiration to start an independent career in the field of scientific research to work on projects with high translational value and of interest to the public health.

HONORS AND AWARDS

- Postdoctoral Fellow, Stanford University (1-9-2020 to present)

- Intel-India Fellow, CSIR-Institute of Genomics and Integrative Biology and Intel pvt ltd. (2019-2020)
- Senior Research Fellow, CSIR-Institute of Genomics and Integrative Biology (2016-2019)
- Junior Research Fellow, CSIR-Institute of Genomics and Integrative Biology (2014-2016)
- Project Fellow, CSIR-Institute of Genomics and Integrative Biology (2012-2014)

STANFORD ADVISORS

- Thomas Quertermous, Postdoctoral Faculty Sponsor
- Thomas Quertermous, Postdoctoral Research Mentor

Publications

PUBLICATIONS

- **ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.** *Circulation*
Cheng, P., Wirka, R. C., Clarke, L. S., Zhao, Q., Kundu, R., Nguyen, T., Nair, S., Sharma, D., Kim, H. J., Shi, H., Assimes, T., Kim, J. B., Kundaje, et al
2022
- **Initial Insights Into the Genetic Epidemiology of SARS-CoV-2 Isolates From Kerala Suggest Local Spread From Limited Introductions** *FRONTIERS IN GENETICS*
Radhakrishnan, C., Divakar, M., Jain, A., Viswanathan, P., Bhoyar, R. C., Jolly, B., Imran, M., Sharma, D., Rophina, M., Ranjan, G., Sehgal, P., Jose, B., Raman, et al
2021; 12: 630542
- **Founder variants and population genomes-Toward precision medicine.** *Advances in genetics*
Jain, A. n., Sharma, D. n., Bajaj, A. n., Gupta, V. n., Scaria, V. n.
2021; 107: 121–52
- **A genome-wide circular RNA transcriptome in rat.** *Biology methods & protocols*
Sharma, D., Sehgal, P., Sivasubbu, S., Scaria, V.
2021; 6 (1): bpab016
- **Genetic epidemiology of autoinflammatory disease variants in Indian population from 1029 whole genomes.** *Journal, genetic engineering & biotechnology*
Jain, A., Bhoyar, R. C., Pandhare, K., Mishra, A., Sharma, D., Imran, M., Senthivel, V., Divakar, M. K., Rophina, M., Jolly, B., Batra, A., Sharma, S., Siwach, et al
2021; 19 (1): 183
- **Functional long non-coding and circular RNAs in zebrafish.** *Briefings in functional genomics*
Ranjan, G. n., Sehgal, P. n., Sharma, D. n., Scaria, V. n., Sivasubbu, S. n.
2021
- **High throughput detection and genetic epidemiology of SARS-CoV-2 using COVIDSeq next-generation sequencing.** *PloS one*
Bhoyar, R. C., Jain, A. n., Sehgal, P. n., Divakar, M. K., Sharma, D. n., Imran, M. n., Jolly, B. n., Ranjan, G. n., Rophina, M. n., Sharma, S. n., Siwach, S. n., Pandhare, K. n., Sahoo, et al
2021; 16 (2): e0247115
- **Asymptomatic reactivation of SARS-CoV-2 in a child with neuroblastoma characterised by whole genome sequencing.** *IDCases*
Yadav, S. P., Thakkar, D. n., Bhoyar, R. C., Jain, A. n., Wadhwa, T. n., Imran, M. n., Jolly, B. n., Divakar, M. K., Kapoor, R. n., Rastogi, N. n., Sharma, D. n., Sehgal, P. n., Ranjan, et al
2021; 23: e01018
- **IndiGenomes: a comprehensive resource of genetic variants from over 1000 Indian genomes.** *Nucleic acids research*
Jain, A. n., Bhoyar, R. C., Pandhare, K. n., Mishra, A. n., Sharma, D. n., Imran, M. n., Senthivel, V. n., Divakar, M. K., Rophina, M. n., Jolly, B. n., Batra, A. n., Sharma, S. n., Siwach, et al
2021; 49 (D1): D1225–D1232
- **Asymptomatic reinfection in two healthcare workers from India with genetically distinct SARS-CoV-2.** *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America*
Gupta, V. n., Bhoyar, R. C., Jain, A. n., Srivastava, S. n., Upadhyay, R. n., Imran, M. n., Jolly, B. n., Divakar, M. K., Sharma, D. n., Sehgal, P. n., Ranjan, G. n., Gupta, R. n., Scaria, et al

2020

- **Circad: a comprehensive manually curated resource of circular RNA associated with diseases.** *Database : the journal of biological databases and curation*
Rophina, M. n., Sharma, D. n., Poojary, M. n., Scaria, V. n.
2020; 2020
- **Saliva microbiome in primary Sjögren's syndrome reveals distinct set of disease-associated microbes.** *Oral diseases*
Sharma, D. n., Sandhya, P. n., Vellarikkal, S. K., Surin, A. K., Jayarajan, R. n., Verma, A. n., Kumar, A. n., Ravi, R. n., Danda, D. n., Sivasubbu, S. n., Scaria, V. n.
2020; 26 (2): 295–301
- **Genomics of rare genetic diseases-experiences from India** *HUMAN GENOMICS*
Sivasubbu, S., Scaria, V., GUARDIAN Consortium
2019; 13 (1): 52
- **A genome-wide map of circular RNAs in adult zebrafish.** *Scientific reports*
Sharma, D. n., Sehgal, P. n., Mathew, S. n., Vellarikkal, S. K., Singh, A. R., Kapoor, S. n., Jayarajan, R. n., Scaria, V. n., Sivasubbu, S. n.
2019; 9 (1): 3432
- **Methods for Annotation and Validation of Circular RNAs from RNaseq Data.** *Methods in molecular biology (Clifton, N.J.)*
Sharma, D. n., Sehgal, P. n., Hariprakash, J. n., Sivasubbu, S. n., Scaria, V. n.
2019; 1912: 55–76
- **Organelle transcriptome sequencing reveals mitochondrial localization of nuclear encoded transcripts.** *Mitochondrion*
Sabharwal, A. n., Sharma, D. n., Vellarikkal, S. K., Jayarajan, R. n., Verma, A. n., Senthivel, V. n., Scaria, V. n., Sivasubbu, S. n.
2019; 46: 59–68
- **Autologous NeoHep Derived from Chronic Hepatitis B Virus Patients' Blood Monocytes by Upregulation of c-MET Signaling.** *Stem cells translational medicine*
Bhattacharjee, J. n., Das, B. n., Sharma, D. n., Sahay, P. n., Jain, K. n., Mishra, A. n., Iyer, S. n., Nagpal, P. n., Scaria, V. n., Nagarajan, P. n., Khanduri, P. n., Mukhopadhyay, A. n., Upadhyay, et al
2017; 6 (1): 174–86
- **Does the buck stop with the bugs?: an overview of microbial dysbiosis in rheumatoid arthritis.** *International journal of rheumatic diseases*
Sandhya, P. n., Danda, D. n., Sharma, D. n., Scaria, V. n.
2016; 19 (1): 8–20