Stanford

Varuna Chander

- Postdoctoral Scholar, Genetics
- Temp - Non-Exempt, Office of Technology Licensing (OTL)

Bio

BIO

Dr. Varuna Chander is a postdoctoral researcher specializing in genomics and bioinformatics. She holds a BTech and Masters in Industrial Biotechnology, and has experience in early-stage sequencing product development for 7 years. Dr. Chander earned her PhD in Genetics and Genomics from the Human Genome Sequencing Center at Baylor College of Medicine, where she was awarded the NLM Biomedical Informatics and Data Science Fellowship for three years. Her research focused on investigating the molecular causes of rare diseases and also the relationship between somatic mutations in blood and cardiovascular disease risk. Alongside her research, Dr. Chander collaborated on projects employing computational methods to examine the role of structural variation in genetic diseases. Currently, she works with Michael Snyder to study the genomic basis of complex human diseases using multi-omics and machine learning approaches.

HONORS AND AWARDS

- Charles J. Epstein Trainee Award for Excellence in Human Genetics - Semifinalist, American Society of Human Genetics (ASHG) (2021)
- Three Minute Thesis (3MT) 3rd place winner, Baylor College of Medicine College-wide Competition. (2021)
- National Library of Medicine Fellowship in Biomedical Informatics and Data Science, National Institute of Health (NIH) (2019-2022)
- RFA in Precision Medicine and Population Health Initiative, Baylor College of Medicine President's Circle (2019-2020)
- Merit-based Tuition Scholarship, Department of Biology, Division of Graduate Studies Middle Tennessee State University (2008-2009)

PROFESSIONAL EDUCATION

- Ph.D, Baylor College of Medicine , Genetics and Genomics (2022)
- MS, Middle Tennessee State University , Biotechnology with concentration in Business (PSM) (2009)
- B.Tech, SRM University, India , Industrial Biotechnology (2007)

STANFORD ADVISORS

- Michael Snyder, Postdoctoral Faculty Sponsor

LINKS

- LinkedIn profile: https://www.linkedin.com/in/varunachander/
- Twitter: https://twitter.com/varunamohan

Publications

PUBLICATIONS

- **Long read sequencing and expression studies of AHDC1 deletions in Xia-Gibbs syndrome reveal a novel genetic regulatory mechanism.** *Human mutation*

Chander, V., Mahmoud, M., Hu, J., Dardas, Z., Grochowski, C. M., Dawood, M., Khayat, M. M., Li, H., Li, S., Jhangiani, S., Korchina, V., Shen, H., Weissenberger, et al

2022; 43 (12): 2033-2053

- **Clonal hematopoiesis of indeterminate potential, DNA methylation, and risk for coronary artery disease.** *Nature communications*

  Uddin, M. D., Nguyen, N. Q., Yu, B., Brody, J. A., Pampana, A., Nakao, T., Fornage, M., Bressler, J., Sotoodehnia, N., Weinstock, J. S., Honigberg, M. C., Nachun, D., Bhattacharya, et al

  2022; 13 (1): 5350

- **AHDC1 missense mutations in Xia-Gibbs syndrome** *HUMAN GENETICS AND GENOMICS ADVANCES*

  Khayat, M. M., Hu, J., Jiang, Y., Li, H., Chander, V., Dawood, M., Hansen, A. W., Li, S., Friedman, J., Cross, L., Bijlsma, E. K., Ruivenkamp, C. L., Sansbury, et al

  2021; 2 (4)

- **Genetic testing in ambulatory cardiology clinics reveals high rate of findings with clinical management implications** *GENETICS IN MEDICINE*

  Murdock, D. R., Venner, E., Muzny, D. M., Metcalf, G. A., Murugan, M., Hadley, T. D., Chander, V., de Vries, P. S., Jia, X., Hussain, A., Agha, A. M., Sabo, A., Li, et al

  2021; 23 (12): 2404-2414

- **Phenotypic and protein localization heterogeneity associated with AHDC1 pathogenic protein-truncating alleles in Xia-Gibbs syndrome** *HUMAN MUTATION*

  Khayat, M. M., Li, H., Chander, V., Hu, J., Hansen, A. W., Li, S., Traynelis, J., Shen, H., Weissenberger, G., Stossi, F., Johnson, H. L., Lupski, J. R., Posey, et al

  2021; 42 (5): 577-591

- **Xia-Gibbs Syndrome** *In: GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993. 2021 Dec 9*

  Chander, V., et al

  2021

- **Phenotypic expansion in KIF1A-related dominant disorders: A description of novel variants and review of published cases.** *Human mutation*

  Montenegro-Garreaud, X., Hansen, A. W., Khayat, M. M., Chander, V., Grochowski, C. M., Jiang, Y., Li, H., Mitani, T., Kessler, E., Jayaseelan, J., Shen, H., Gezdirici, A., Pehlivan, et al

  2020; 41 (12): 2094-2104

- **Evaluation of computational genotyping of structural variation for clinical diagnoses** *GIGASCIENCE*

  Chander, V., Gibbs, R. A., Sedlazeck, F. J.

  2019; 8 (9)

- **Targeting Sp1 Transactivation In Waldenstrom's Macroglobulinemia: a Novel Therapeutic Option**

  Fulciniti, M., Amin, S. B., Mohan, V., Yang, G., Nanjappa, P., Tassone, P., Prabhala, R. H., Cheng, L., Anderson, K. C., Treon, S. P., Munshi, N. C.

  AMER SOC HEMATOLOGY.2010: 58-59

- **Biology and Therapeutic Targeting of Sp1 Transactivation In Myeloma**

  Fulciniti, M., Amin, S. B., Nanjappa, P., Rodig, S. J., Hideshima, T., Pal, J., Mohan, V., Lee, K., Shammas, M., Minvielle, S., Prabhala, R., Avet-Loiseau, H., Cheng, et al

  AMER SOC HEMATOLOGY.2010: 64