

ASHOK KUMAR SHARMA

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EDUCATION **PhD in Computational Biology** Jan 2013 - May 2018
IISER Bhopal, Madhya Pradesh, India

- Advisor: Dr. Vineet Kumar Sharma
- **Thesis:** Development of Computational Models and Algorithms for Designing of Novel Microbiome-based Therapeutics.

Masters in Pharmacoinformatics July 2010 - June 2012
NIPER Mohali, Punjab, India

- Advisor: Prof. Prasad V. Bharatam
- **Thesis:** Modelling and Designing of Glycogen Synthase Kinase 3 Inhibitors.

Bachelor of Pharmacy Aug 2006 - June 2010
Dr. H. S. Gour University, Sagar, Madhya Pradesh, India

RESEARCH EXPERIENCE **Scientist II, Toxicology** April 2023 - Present
Drug Safety Research Evaluation (DSRE)
Preclinical Translational Sciences (PTS)
Takeda

I am currently engaged in numerous modeling and pipeline development projects, contributing to the creation of safer medicines:

- I provide assistance to project teams in developing advanced computational strategies to support drug safety assessments across DSRE and PTS.
- My primary focus lies in building **AI/ML-based models** for toxicological endpoints, specifically Hepatotoxicity (DILI) and Neurotoxicity - using 3D neural spheroids.
- Additionally, I am involved in pipeline development to streamline ongoing sequencing projects at PTS, encompassing **Bulk RNA-seq, Nanostring**, and other datasets like **sc-RNAseq**.

Postdoctoral Scientist Feb 2021 - Feb 2023
Casero Lab, Cedars-Sinai Medical Center

Advisor: Dr. David Casero, Director, Translational Multiomics, Inflammatory Bowel Immunobiology Research Institute

Co-Advisor: Dr. Suzanne Devkota, Director of Microbiome Research at the F. Widjaja Foundation Inflammatory Bowel and Immunobiology Research Institute

I was deeply involved in the analysis and integration of multi-omics datasets aimed at identifying pathogenic factors in Inflammatory Bowel Disease (IBD). Here is a summary of the specific projects I worked on during that time:

- Quantified **bacterial growth rates from metagenomic datasets** to identify bacterial activities associated with the progression of Crohn's disease.
- Investigated alterations/reprogramming of **cell-specific gene expression** in the host epithelium of Ulcerative Colitis (UC) patients who underwent IPAA surgery and developed pouchitis.
- Conducted an in-depth analysis of **multi-omics datasets** to uncover microbial regulation of immune responses within creeping fat in Crohn's disease.

Postdoctoral Associate
Microbiomics Lab, University of Minnesota
Mentor: Dr. Andres Gomez

March 2018 - Feb 2021

During my tenure as the initial computational team member in the department, my responsibilities included managing and establishing computational pipelines on a high-performance computing facility at UMN. Additionally, I played a pivotal role in the advancement of various projects, which are outlined below:

- Analyzed whole genome sequencing data to comprehend the impact of diet and lifestyle on gut microbial taxonomic and functional compositions across traditional human and nonhuman primate populations.
- Gut microbiome changes in response to consumption of fermented foods and its impact on host health.
- Identified gastrointestinal gene expression patterns in response to functional alterations in the gut microbiome, leveraging meta-transcriptomic data analysis techniques.

Senior Research Fellow (SRF)
MetaBioSys Lab, IISER Bhopal
Mentor: Dr. Vineet Kumar Sharma

June 2015 - March 2018

As a graduate researcher, I contributed to the following projects:

- Developed machine learning-based computational methods for the analysis of complex genomic and metagenomic datasets.
- Conducted high-throughput predictions of gut microbial-mediated drug metabolism and toxicity using chemical structure-centric approaches.
- Identified taxonomic, functional, and metabolic markers associated with colorectal cancer patients in India.

PUBLICATIONS

1. Sarode, G.V., Mazi, T.A., Neier, K., Shibata, N.M., Jospin, G., Harder, N.H., Caceres, A., Heffern, M.C., **Sharma, A.K.**, More, S.K. and Dave, M., **2023**. The role of intestine in metabolic dysregulation in murine Wilson disease. **Hepatology Comm**, 7(10).
2. Guse, K., **Sharma, A.K.**, Weyenberg, E., Davison, S., Ma, Y., Choi, Y., Johnson, A.J., Chen, C. and Gomez, A., **2023**. Regular consumption of lacto-fermented vegetables has greater effects on the gut metabolome compared with the microbiome. **Gut Microbiome** , 4, p.e11.
3. Dina G. Moussa, **Sharma, A.K.**, Tamer Mansour, Bruce Witthuhn; Jorge Perdigao; Joel D. Rudney; Conrado Aparicio; Andres Gomez, **2022**. Functional Biomarkers of Ex-vivo Dental Caries Onset. **Journal of oral microbiology**, 14(1), p.2123624.
4. Rosa, F., **Sharma, A.K.**, Gurung, M., Casero, D., Matazel, K., Bode, L., Simecka, C., Elolimy, A.A., Tripp, P., Randolph, C. and Hand, T.W., **2022**. Human Milk Oligosaccharides Impact Cellular and Inflammatory Gene Expression and Immune Response. **Frontiers in Immunology**. 13: 907529. doi: 10.3389/fimmu.
5. Saxena, R., Prasoodanan PK, V., Gupta, S., Gupta, S., Waiker, P., Samaiya, A., **Sharma, A.K.** and Sharma, V.K., **2022**. Assessing the effect of smokeless tobacco-consumption on oral microbiome in healthy and oral cancer patients. **Frontiers in Cellular and Infection Microbiology**, p.331.
6. Omontese, B.O., **Sharma, A.K.**, Davison, S., Jacobson, E., DiConstanzo, A., Webb, M.J. and Gomez, A., **2022**. Microbiome network traits in the rumen predict average daily gain in beef cattle under different backgrounding systems. **Animal Microbiome**, 4(1), pp.1-15.

7. **Sharma, A.K.**, & Sam Davison; Barbora Pafco; Jonathan B. Clayton, Jessica M. Rothman, Matthew R. McLennan, Marie Cibot, Terence Fuh, Roman Vodicka, Carolyn Jost Robinson, Klara Petrzekova, and Andres Gomez, **2022**. The primate gut mycobiome bacteriome interface is impacted by environmental and subsistence factors. **npj Biofilms Microbiomes** 8(1), pp.1-11..
8. Vishnu Prasoodanan P K, & **Ashok K Sharma**, Shruti Mahajan, Darshan B Dhakan, Abhijit Maji, Joy Scaria, Vineet K Sharma, **2021**. Western and non-western gut microbiomes reveal new roles of Prevotella in carbohydrate metabolism and mouth-gut axis. **npj Biofilms Microbiomes**, Oct 7;7(1):77.
9. **Sharma, A.K.**, & Petrzekova, K., Pafco, B., Robinson, C.A.J., Fuh, T., Wilson, B.A., Stumpf, R.M., Torralba, M.G., Blekhman, R., White, B. and Nelson, K.E., Leigh S.R., Gomez A, **2020**. Traditional human and nonhuman primate populations show parallel gut microbiome adaptations to analogous dietary conditions. **mSystems**, 5(6).
10. Gomez, A., **Sharma, A.K.**, Grev, A., Sheaffer, C. and Martinson, K., **2020**. The horse gut microbiome responds in a highly individualized manner to forage lignification. **Journal of Equine Veterinary Science**, 96, p.103306.
11. **Sharma, A.K.**, & Debusk, W.T., Stepanov, I., Gomez, A. and Khariwala, S.S, **2020**. Oral microbiome profiling in smokers with and without head and neck cancer reveals variations between health and disease. **Cancer Prevention Research**, 13(5), pp.463-474.
12. Gupta, A., Dhakan, D.B., Maji, A., Saxena, R., PK, V.P., Mahajan, S., Pulikkan, J., Kurian, J., Gomez, A.M., Scaria, J. and Amato, K.R., **Sharma, A.K.** and Sharma V.K, **2019**, Association of Flavonifractor plautii, a flavonoid degrading bacterium, with the gut microbiome of colorectal cancer patients in India. **mSystems**, 4(6).
13. Gomez, A.* , **Sharma, A.K.***, Mallott, E.K., Petrzekova, K.J., Robinson, C.A.J., Yeoman, C.J., Carbonero, F., Pafco, B., Rothman, J.M., Ulanov, A. and Vlckova, K, **2019**. Plasticity in the human gut microbiome defies evolutionary constraints. **mSphere**, 4(4), pp.e00271-19.
14. **Sharma, A.K.**, Pafčo, B., Vlčková, K., Červená, B., Kreisinger, J., Davison, S., Beeri, K., Fuh, T., Leigh, S.R., Burns, M.B. and Blekhman, R., Gomez, A, **2019**. Mapping gastrointestinal gene expression patterns in wild primates and humans via fecal RNA-seq. **BMC genomics**, 20(1), p.493.
15. Pafčo, B., **Sharma, A.K.**, Petrzeková, K.J., Vlčková, K., Todd, A., Yeoman, C.J., Wilson, B.A., Stumpf, R., White, B.A., Nelson, K.E. and Leigh, S., 2019. Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. **American journal of physical anthropology**, 169(3), pp.575-585.
16. Dhakan, D.B., Maji, A., **Sharma, A.K.**, A.K., Saxena, R., Pulikkan, J., Grace, T., Gomez, A., Scaria, J., Amato, K.R. and Sharma, V.K, **2019**. The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. **GigaScience**, 8(3), p.giz004.
17. Kumar, K., Dhoke, G.V., **Sharma, A.K.**, Jaiswal, S.K. and Sharma, V.K., **2019**. Mechanistic elucidation of amphetamine metabolism by tyramine oxidase from human gut microbiota using molecular dynamics simulations. **Journal of cellular biochemistry**, 120(7), pp.11206-11215.
18. Kumar, K., Jaiswal, S.K., Dhoke, G.V., Srivastava, G.N., **Sharma, A.K.** and Sharma, V.K., **2018**. Mechanistic and structural insight into promiscuity based metabolism of

cardiac drug digoxin by gut microbial enzyme. **Journal of cellular biochemistry**, 119(7), pp.5287-5296.

19. **Sharma, A.K.**, Jaiswal, S.K., Chaudhary, N. and Sharma, V.K., **2017**. A novel approach for the prediction of species-specific biotransformation of xenobiotic/drug molecules by the human gut microbiota. **Scientific reports**, 7(1), pp.1-13.
20. **Sharma, A.K.**, Srivastava, G.N., Roy, A. and Sharma, V.K., **2017**. ToxiM: A toxicity prediction tool for small molecules developed using machine learning and chemoinformatics approaches. **Frontiers in pharmacology**, 8, p.880.
21. Gupta, S., **Sharma, A.K.***, Shastri, V., Madhu, M.K. and Sharma, V.K., **2017**. Prediction of anti-inflammatory proteins/peptides: an insilico approach. **Journal of translational medicine**, 15(1), pp.1-11.
22. Gupta, A., Kumar, S., Prasoodanan, V.P., Harish, K., **Sharma, A.K.** and Sharma, V.K., **2016**. Reconstruction of bacterial and viral genomes from multiple metagenomes. **Frontiers in microbiology**, 7, p.469.
23. Gupta, S., **Sharma, A.K.***, Jaiswal, S.K. and Sharma, V.K., **2016**. Prediction of biofilm inhibiting peptides: an in silico approach. **Frontiers in microbiology**, 7, p.949.
24. **Sharma, A.K.**, Kumar, S., Harish, K., Dhakan, D.B. and Sharma, V.K., **2016**. Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins. **BMC genomics**, 17(1), pp.1-12.
25. Chaudhary, N., **Sharma, A.K.***, Agarwal, P., Gupta, A. and Sharma, V.K., **2015**. 16S classifier: a tool for fast and accurate taxonomic classification of 16S rRNA hypervariable regions in metagenomic datasets. **PLOS One**, 10(2), p.e0116106.

CONFERENCE
PUBLICATIONS

1. **Sharma, A.K.**, Martin, A., Moskowitz, J.E., Bora, S., Legree, K., Dorrestein, P., Underhill, D., Knight, R., Chen, P. and Devkota, S., 2022. 1166: In-patient antibiotic exposure promotes sars-cov-2 persistence in the gi tract in covid-19 admitted patients. **Gastroenterology**, 162(7), pp.S-279].
2. Lahcene, N.L., Moskowitz, J.E., **Sharma, A.K.**, Martin, A., Merchant, A., Fleshner, P. and Devkota, S., 2022. 1059: Spatial characterization of immune cells and bacterial co-localization in crohn's disease's creeping fat. **Gastroenterology**, 162(7), pp.S-241].

BOOK CHAPTER

1. **Sharma, A.K.** and Dubey, V.S., **2021**. Metagenome Assembly for Gut Microbial Functional Diversity Associated with Xenobiotic Degradation. In *Metagenomics and Microbial Ecology* (pp. 79-87). **CRC Press**.

ORAL/POSTER
PRESENTATIONS

- **Selected speaker, 2022** — 'In-Patient Antibiotic Exposure Promotes SARS-CoV-2 Persistence in the GI Tract in COVID-19 Admitted Patients' at *Digestive Disease Week (DDW) 2022*, at San Diego, CA.
- **Delivered a lecture, 2020** — 'Emergence of microbiome in therapeutics – Ongoing efforts, challenges, and future opportunities' at *Department of Pharmaceutical Sciences*, Dr. Hari Singh Gaur University Sagar, India.
- **Selected as one of the finalist's, 2019** in the Novartis – Academia Hackathon event held on event to be held August 12th – 23rd, 2019 on the Novartis Campus in Cambridge, MA, USA.

- **Selected speaker, 2018** — 'Mapping gastrointestinal gene expression patterns from fecal RNA-seq' at EpiQ (Quantitative Epidemiology) seminar series, UMN Seminar.
- **Selected speaker, 2016/2017** — 'Oral presentation on "Prediction of peptidoglycan hydrolases- a new class of antibacterial proteins" in 3rd and 4th Annual Biology meeting at IISER Bhopal, India.
- **Invited speaker, 2015** — 'Demonstration of R-software in data analysis' in *National Workshop at Barkatullah University Bhopal*.
- **Selected speaker 2015** — 'Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets using 16S Classifier' in *The Human Microbiome conference, at EMBL, Heidelberg, Germany*.

EDITOR/REVIEWER
FOR JOURNALS

- **Associate Editor** for *Frontiers in Microbiology - Systems Microbiology*; **Guest Associate Editor** for *Frontiers in Microbiology - Microbiome in Health and Disease*; **Review Editor** for *Frontiers in Microbiology - Gastrointestinal Microbes*

TEACHING
EXPERIENCE

- **BIOL 1961, Foundations of Biology Lab I for Biological Sciences Majors (BIOL):** — Teaching basics of microbiome to computational microbiology students (16 contact hours/week, from July 2018).
- **BIOL 3004, Foundations of Biology for Biological Sciences Majors, Part II Laboratory:** — Leading various groups of computational microbiology students for bioinformatics analysis of 16S rRNA data from published microbiome studies (16 contact hours/week, from July 2018).

ACHIEVEMENTS

- **International Travel Grant, 2019** — Received \$1000 grant to present my work at Keystone Symposium on "Microbiome: Therapeutic Implications (T1)" in *October 2019 at Ireland*.
- **PBC Postdoctoral Fellowship, 2018** — Received a Israel government fellowship for three years to pursue postdoctoral research at *Bar-Ilan University, Israel*.
- **DST Travel Award, 2017** — Received travel award from Department of Science and Technology, India to present my doctoral research in *Symposium: NextGen Immunology at Rehovot, Israel*.
- **EMBL Grant, 2015** — Received €1000 grant to present my work in *The Human Microbiome Conference" at EMBL Germany*.
- **CSIR NET, 2013** — Qualified *CSIR-NET Lectureship Exam* conducted by Council for Scientific and Industrial Research (CSIR).
- **GATE, 2012** — Secured 376 All India Rank in *Graduate Aptitude Test in Engineering for Life Sciences* conducted by IIT Delhi
- **GAPT, 2010** — Secured 456 All India Rank in *Graduate Pharmacy Aptitude test* conducted by M.S. University Vadodara.

SELECTED SKILLS

- **Programming:** Proficient in languages such as Perl, R and Python
- **Shell scripting:** Unix/Linux
- **Bioinformatics libraries:** Galaxy, Bioconductor, Ingenuity Pathways, Nextflow, Sankemake, SciPy, etc.
- **Multi-omics data processing:** 7+ years of experience in the Statistical Analysis and integration of Genomics (Bulk and Single-cell), Metagenomics and Metabolomics datasets, and 1+ analysis of Proteomics, and Imaging Mass Cytometry (IMC) data
- **Statistical analysis:** Data mining, Multivariate statistics, Linear Mixed models, and Machine Learning/Deep Learning for pattern identification from large-scale biological data sets, Predictive Modeling, and Target/Biomarker identification
- **Tools and databases:** Experience in the installation/maintenance, development and implementation of Bioinformatics tools, Pipelines, and Databases at local and High-performance computing environment
- **Cloud platforms:** High-performance computing/AWS ecosystem