Functional insights into the Indian human microbiomes revealed through multiomics approaches

Dr. Vineet K. Sharma*
MetaBioSys Group, Indian Institute of Science Education and Research,
Bhopal, Madhya Pradesh, India
Email: vineetks@iiserb.ac.in

The Indian human microbiome has several unique aspects such as the human gut that is primarily enriched in Prevotella species with high diversity and compositional variations in both inter-individual and inter-population comparisons. To investigate the composition, diversity, and functional roles of the key driver species in human microbiomes, we carried out a population-wide analysis on healthy samples belonging to western and non-western populations, and generated gut microbiome data for a large Indian cohort. A higher abundance and diversity of *Prevotella copri* species enriched in complex plant polysaccharides metabolizing enzymes, particularly pullulanase containing polysaccharide-utilization-loci (PUL), were found in Indian and non-western populations. A higher diversity of oral inflammations-associated *Prevotella* species and an enrichment of virulence factors and antibiotic resistance genes in the gut microbiome of western populations speculates an existence of a mouth-gut axis. We also included the Inflammatory Bowel Disease samples from western populations to examine the association of Prevotella with inflammatory bowel disease (IBD), including ulcerative colitis and Crohn's disease. The results were further compared with IBD cohorts from US, Netherlands, and Spain. This study provided new insights into the role of diversity, composition, and function of key bacterial species in gut microbiome and their impact on human health. The study also revealed the landscape composition of human gut microbiome and its impact on health in western and non-western populations, particularly in the Indian context. We also examined the differential abundance of Flavanoid Metabolizing Enzymes in the gut microbiomes of healthy and diseased individuals from Western and non-Western populations with distinct dietary habits. Furthermore, using a hybrid of AI, machine learning and chemoinformatics approaches, we have developed novel AIML based computational approaches to predict the metabolic enzymes and bacterial species that can potentially carry out the promiscuous biotransformation of xenobiotic molecules.