Nitin Kumar (MSc, PhD)

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Professional Summary

I am a bioinformatics researcher with a passion for biological sciences, especially in the field of infection genomics. I have experience with bioinformatic projects in both academic and commercial environments. I have a track record of conducting, managing, and successfully completing high-quality scientific projects within deadlines. I possess strong interpersonal skills, am detail-oriented, and could work effectively in multi-disciplinary teams.

Technical Expertise – FastQC, MultiQC, Samtools, Trimmomatic, HTSeq, bbtools, Trinity, Busco, CheckM, HISAT2, Stringtie2, Bedtools, Bcftools, Velvet, Spades, Prokka, PGAP, Roary, iTOL, RAxML, sequence alignment tools (BLAST, Muscle, MAFFT), 16S rRNA gene amplicon (Mothur), Shotgun metagenomics tools (Kraken, Bracken, Metaphlan, HUMAnN3), Nextflow, BWA, PicardTools, SnpEff and SnpSift, Porechop, Chopper, Nanoplot, NanoComp, Minimap2, Clair3, Flye

Key Skills

- NGS analysis based on whole genome sequences and bioinformatic tools: Illumina and Minion genome DNA quality control and assembly, Illumina and Minion DNA variant calling analysis, Bulk *De novo* and reference-based RNA-seq analysis.
- Expert in genome analysis: genome quality control, assembly and annotation, phylogeny at different taxonomy level, biosynthetic gene clusters analysis, pangenome, average nucleotide identity analysis (species identification), AMR genes detection and functional enrichment using CDD, KEGG, COG, Interproscan.
- Programming languages: Python (pandas, numpy, matplotlib), R (ggplot2, dplyr, tidyverse), Perl, Shell commands (awk, grep)
- Version control: Github, Gitlab
- HPC clusters: FARM, Slurm and AWS
- Interpersonal communication
- Verbal and written communication

Education

Ph.D.: Biology (spec: Bioinformatics) **2013**
University of York **UK**
Thesis - Are bacterial species really ecotypes?

Brief synopsis: Defining bacterial species based on ecological niche has been widely accepted. In this study, I investigated a local population of *Rhizobium leguminosarum*, known for its genomic diversity and ability to fix nitrogen in legumes. Ecologically, it has been classified into two biovars: viciae and trifolii. Draft genomes of 72 isolates (36 viciae and 36 trifolii) were sequenced using Roche 454 sequencing and compared with the published genome of *R. leguminosarum* 3841 (Rlv 3841). Phylogenetic network analysis of core genes and average nucleotide identity analysis (a robust standard tool for species identification) revealed a high level of variation, indicating the existence of five cryptic genospecies in this population, which do not correspond to the biovars. Additionally, we found that 50% of core genes are affected by recombination, reflecting genetic exchange between and within the cryptic species. Furthermore, phylogenetic networks based on Rlv 3841 plasmids mirror the core gene phylogeny, indicating the presence of stable genes in each replicon. Overall, our results provide direct evidence that bacterial species cannot be defined solely by ecological niche.
Key Achievements – 1 Scholarship fund, 1 Travel grant: SGM Autumn Conference 2012 (UK), 1 peer reviewed publication.

M.Sc.: Bioinformatics **2009**
Jamia Millia Islamia **India**
Core Subjects: PERL, Database Management and Data Mining. Scientific Internships: i) Indian Institute of Technology, India, ii) Open Source Drug Discovery, CSIR- Institute of Genomics and Integrative biology, India.
Key Achievements – 1 peer reviewed publication, 1 best participant award in Connect to Decode Programme, OSDD 2010 (India)

BSc Biochemistry **2007**
Kurukshetra University **India**
Core Subjects – Biochemistry, Zoology, Chemistry

Professional Experience

Bioinformatics Consultant **04/2022 – 02/2024**
General Bioinformatics Ltd **Reading, UK**

- Performed bioinformatics analyses including the biocuration of fungal and bacterial genes using ENSEMBL and BioMart, Bulk RNA-seq analysis related to fungi and human genomes, and comparative genome analysis for detecting species specific biosynthetic gene clusters using 300,000 public bacterial genomes.
- Collaborated with other bioinformaticians to design genomic pipelines, including pipeline for genome assembly using either MinION or Illumina reads, genome quality control and variant calling.

Bioinformatics Consultant **08/2020 – 01/2021**
Microbiotica Ltd **Cambridge, UK**

- Provided comprehensive support and expert advice for bioinformatic analysis.
- Key Achievements – i.) Conducted phylogenetic and functional analyses for gut bacteria. ii.) Provided bioinformatic training to 3 bioinformaticians. iii.) Acquired new technical skills like cloud computing (Amazon Web Services).

Senior Bioinformatician **2018 – 2022**
Lawley Lab, Wellcome Sanger Institute **Cambridge, UK**

- Part of the core team for large scale genomic data analysis using advanced and robust techniques.
- Two leading projects: 1. Explored the evolution of a human gut pathogen (*Clostridium difficile*) in response to human diets and modern healthcare practices. Performed bacterial pangenome analysis and manual curation of sporulation and metabolic pathways. 2. Studied and identified different bacterial species of human gut and bladder and their role in human health.
- Part of a collaborating project for taxonomic and functional analysis of metagenomic data to understand the gut microbiome of IBS patients and CDI patients (shotgun metagenomics), and gut microbiome of infants and CDI patients (16S rRNA gene amplicon).
- Key Achievements – Published a *Nature Genetics* paper as a senior author, 3 Nature paper and 1 Gut paper as a co-author. Trained 5 students pursuing PhD and 4 team members.

Postdoctoral Research Scientist **2014 – 2018**
Lawley Lab, Wellcome Sanger Institute **Cambridge, UK**

- Leading project with main activity to track transmission of *C. difficile* 027/ST1 lineage between symptomatic patients of a hospital.
- Demonstrated organizational and multitasking skills by managing 3 scientific projects, coordinating with editors and reviewers, resulting in 3 manuscripts. Actively engaged with project team members to solve scientific problems. Liaised with scientists around the world for scientific advancement.
- Key Achievements – i) Published 4-first author papers including a paper in Clin Infect Dis and a Nature paper as a co-author, ii) Presented scientific work in India, UK and Netherlands, iii) Travel grant - ECCMID 2016 (Netherlands).

Publications

Peer-reviewed journal article: First authorships – 7; Total – 22

1. Vervier K, Moss S, **Kumar N**, Adoum A, Barne M, Browne H, et al. Two microbiota subtypes identified in irritable bowel syndrome with distinct responses to the low FODMAP diet. Gut. 2021.
2. Fitzpatrick Z, Frazer G, Ferro A, Clare S, Bouladoux N, Ferdinand J, **Kumar N**, et al. Gut-educated IgA plasma cells defend the meningeal venous sinuses. Nature. 2020;587(7834):472-6.
3. Shao Y, Forster SC, Tsaliki E, Vervier K, Strang A, Simpson N, **Kumar N**, Stares MD, Rodger A, Brocklehurst P et al: Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. Nature 2019, 574(7776):117-121.
4. **Kumar N***, Browne HP et al: Adaptation of host transmission cycle during clostridium difficile speciation. Nature Genetics 2019 (*co-corresponding author).
5. Forster SC*, **Kumar N*** et al: A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology 2019, 37(2):186-192. (*co-first author)
6. Thomas-White K*, Forster SC*, **Kumar N***: Culturing of female bladder bacteria reveals an interconnected urogenital microbiota. Nature Communications 2018, 9(1):1557. (*co-first author)
7. Sharma C, Kumar R, **Kumar N** et al: Investigation of multiple resistance mechanisms in voriconazole resistant Aspergillus flavus clinical isolates from a chest hospital surveillance in Delhi, India. Antimicrob Agents Chemother 2018.
8. Pike LJ, Viciani E, **Kumar N**: Genome watch: Microbial diversity knows no borders. Nat Rev Microbiol 2018, 16(2):66.
9. Fleurbaaij F, Henneman AA, Corver J, Knetsch CW, Smits WK, Nauta ST, Giera M, Dragan I, **Kumar N**, Lawley TD et al: Proteomic identification of Axc, a novel beta-lactamase with carbapenemase activity in a meropenem-resistant clinical isolate of Achromobacter xylosoxidans. Sci Rep 2018, 8(1):8181.
10. **Kumar N**, Forster SC: Genome watch: Microbiota shuns the modern world. Nat Rev Microbiol 2017, 15(12):710.
11. Knetsch CW*, **Kumar N*** et al: Zoonotic transfer of Clostridium difficile harboring antimicrobial resistance between farm animals and humans. J Clin Microbiol 2017. (*co-first author)
12. Iraola G, Forster SC, **Kumar N** et al: Distinct Campylobacter fetus lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. Nat Commun 2017, 8(1):1367.

13. Howell KJ, Kraiczy J, Nayak KM, Gasparetto M, Ross A, Lee C, Mak TN, Koo BK, **Kumar N**, Lawley T et al: DNA Methylation and Transcription Patterns in Intestinal Epithelial Cells From Pediatric Patients With Inflammatory Bowel Diseases Differentiate Disease Subtypes and Associate With Outcome. Gastroenterology 2017.
14. Sharma C, **Kumar N**, Pandey R, Meis JF, Chowdhary A: Whole genome sequencing of emerging multidrug resistant Candida auris isolates in India demonstrates low genetic variation. New Microbes New Infect 2016, 13:77-82.
15. **Kumar N**, Miyajima F, He M et al: Genome-Based Infection Tracking Reveals Dynamics of Clostridium difficile Transmission and Disease Recurrence. Clin Infect Dis 2016, 62(6):746-752.
16. Fung TC, Bessman NJ, Hepworth MR, **Kumar N** et al: Lymphoid-Tissue-Resident Commensal Bacteria Promote Members of the IL-10 Cytokine Family to Establish Mutualism. Immunity 2016, 44(3):634-646.
17. Forster SC, Browne HP, **Kumar N**, Hunt M, Denise H, Mitchell A, Finn RD, Lawley TD: HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. Nucleic Acids Res 2016, 44(D1):D604-609.
18. Browne HP, Forster SC, Anonye BO, **Kumar N**, Neville BA, Stares MD, Goulding D, Lawley TD: Culturing of 'unculturable' human microbiota reveals novel taxa and extensive sporulation. Nature 2016, 533(7604):543-546.
19. Sharma C, **Kumar N**, Meis JF, Pandey R, Chowdhary A: Draft Genome Sequence of a Fluconazole-Resistant Candida auris Strain from a Candidemia Patient in India. Genome Announc 2015, 3(4).
20. **Kumar N**, Lad G, Giuntini E, Kaye ME, Udomwong P, Shamsani NJ, Young JP, Bailly X: Bacterial genospecies that are not ecologically coherent: population genomics of Rhizobium leguminosarum. Open Biol 2015, 5(1):140133.
21. Bailly X, Giuntini E, Sexton MC, Lower RP, Harrison PW, **Kumar N**, Young JP: Population genomics of Sinorhizobium medicae based on low-coverage sequencing of sympatric isolates. ISME J 2011, 5(11):1722-1734.
22. Bhardwaj A, Bhartiya D, **Kumar N**, Open Source Drug Discovery C, Scaria V: TBrowse: an integrative genomics map of Mycobacterium tuberculosis. Tuberculosis (Edinb) 2009, 89(5):386-387.