Raju Koorakula

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Summary

6+ years' experience in the fields of microbial genomics, microbiome, resistome, and bioinformatics. Particularly, I have developed extensive skills in the design, execute and analysis of Whole metagenomic and metatranscriptomic projects, including sample processing, library preparation, QC, sequencing, and data analysis.

Work Experience

NGS/Microbiome Scientist

University of Veterinary Medicine Vienna [01/06/2022 – 31/01/2023]
Vienna, Austria

- Design, support and executes NGS/microbiome experiments including wet lab data
- Bioinformatics analysis of DNA/RNA sequence data; QC, mapping, assembly, annotation, gene expression, statistics and visualization
- The study of gut resistome, with main focuses on the expression of ARGs and the role of MGE in the spread of AMR in the livestock gut, to develop effective strategies to reduce the threat of ARGs to human health and the environment
- Identification and characterization of genomic variations in pathogen genomes

Research Associate

FFoQSI GmbH [01/02/2018 – 30/12/2022]
Tulln an der Donau, Austria

- Optimized pipeline for sample collection, stabilization, DNA/RNA isolation, quantification, library preparation and bioinformatic analysis is developed for superior quality sequencing and analysis of gut microbiome in high throughput manner

- Study of dynamics of antibiotics resistance in microbial communities in livestock gut by using whole shotgun metagenome and metatranscriptome sequencing
- Assembly of novel bacterial genomes from chicken colon samples based on PacBio long-read sequencing

Research assistant/Master thesis

Austrian Institute of Technology [01/07/2015 – 31/05/2017]
Tulln an der Donau, Austria

Utilization of indigenous microbial communities in diverse soils with organic amendments as an application for bioremediation of polycyclic aromatic hydrocarbons (PAHs). Methods included DNA isolation and quantification with nanodrop, Qubit, gel electrophoresis and Bioanalyzer. Then a 16S rRNA gene library was prepared, including amplicon PCR, Index PCR, PCR clean-up, library validated with Bioanalyzer, qPCR, and sequenced on the Illumina-MiSeq platform. Raw data was analysed using the QIIME2 pipeline, and statistical analysis was performed in R.

Medical Sales Representative

Piramal Enterprises Limited [01/01/2012 – 31/01/2014]
Hyderabad, India

- Covering Hospitals & Trade, generating sales through demonstrating or presenting products effective coverage of targeted doctors, pharmacies, and key accounts
- Building and maintaining good business relationships with hospital-based healthcare to encourage repeat purchases
- Following up on leads generated by the company
- Carrying out CRM activities as per promo plan
- Managing customer database & to ensure effective coverage for target achievement
- Monitor sales results by customer and product taking corrective measures when necessary
- Attending and organising trade exhibitions, conferences and meetings
- Identifying and establishing new business

Bachelor thesis

MSN labs [04/06/2011 – 30/12/2011]
Hyderabad, India

Preparation and evaluation of methocarbamol and paracetamol bi-layer tablet based on standard operating procedures of various instruments including, HPLC, Atomic absorption spectroscopy, dissolution test, disintegration test, and bursting strength apparatus for quality control of tablets, capsules according to the Indian Pharmacopoeia (IP).

Education

Doctor of Natural Resources and Life Sciences - Dr.nat.techn (PhD)

University of Natural Resources and Life Sciences (BOKU) [01/03/2018 – 03/2023]
Muthgasse 18, 1180 Vienna, Austria
https://boku.ac.at/
Masters in Biomedical Engineering and Sciences

University of Applied Sciences Technikum Wien [05/06/2014 – 11/05/2017]
Höchstädtpl. 6, 1200 Vienna, Austria
https://www.technikum-wien.at/
Bachelors of Pharmacy

Osmania University [12/06/2008 – 10/06/2012]
Hyderabad, India
https://www.osmania.ac.in/

Professional Skills

Bioinformatics:

- NGS data analysis: data preprocessing, quality check, mapping/assembly, functional annotation, gene expression, variant calling etc.
- Hands-on experience in microbiome analysis and tools (Illumina and PacBio HiFi Reads) including functional metagenomic and metatranscriptomic analysis
- Extensive knowledge of 16S rRNA amplicon sequencing data analysis
- Understanding of high-volume statistical data analysis and visualization using R/Bioconductor
- Scientific scripting languages such as bash and R or Python, ability to implement and modify metagenomics pipelines.
- Understands bioinformatics concepts, databases, and tools
- Proficiency in working on high-performance Linux clusters

Molecular Microbiology:

- DNA, RNA isolation from stool, soil, chicken, pigs and human using commercially available kits.
- DNA and RNA purity, integrity and quantification using nanodrop, Qubit, gel electrophoresis and Bioanalyzer.
- RT-qPCR assays were developed/modified to measure the bacterial DNA/RNA extraction efficiency/stability or total bacterial load or host contamination based on 16S rRNA gene,

HKG genes.

- 16S rRNA, metagenomic library preparation, quantification and validation.
- Preparation of various media which are suitable for growth and selective isolation of different microorganisms.
- Performed various biochemical tests and staining methods on microorganisms for identification.

Writing skills:

- Scientific content writing, manuscript writing, presentation preparation, poster content writing and writing for projects and extramural grants.
- Excellent organization, communication skills with an emphasis on strong presentation skills and working in challenging environments.

Research Publications

1. Metatranscriptomic analysis of the chicken gut resistome response to in-feed antibiotics and natural feed additives - accepted
Raju Koorakula, Matteo Schiavinato, Mahdi Ghanbari, Gertrude Wegl, Nikolaus Grabner, Andreas Koestelbauer, Viviana Klose, Juliane C. Dohm, Konrad J. Domig
https://www.frontiersin.org/articles/10.3389/fmicb.2022.833790/full

2. Storage media and RNA extraction approaches substantially influence the recovery and integrity of livestock fecal microbial RNA
Raju Koorakula, Mahdi Ghanbari, Matteo Schiavinato, Juliane C. Dohm and Konrad J. Domig
https://peerj.com/articles/13547/

3. Characterization of the composition and function of the chicken gut microbiome metagenome using long-read sequencing - submitted
Raju Koorakula, Matteo Schiavinato, Juliane C. Dohm and Konrad J. Domig

Conferences / Workshops attended

- Participated in “10th ÖGMBT Annual Meeting” which was held under the title “10 years of life, science and molecules” - 2018 in Vienna.
- Attended “German Conference on Bioinformatics at University of Vienna, 2018.
- Participated in “FFoQSI Annual Assembley” – 2018, 19, 20 in Vienna.

- Attended “Microbiome Data Congress 2021”- online 2021, 2022.

Presentations at Conferences

- **Oral presentation** - "FEED2021 – International Feed Conferences" at **Vienna** - Impact of Feed on Animal Health and Welfare and Feed safety.
- Presentation at “FFoQSI Annual Assembley – 2018, 19, 20 and 2021, Vienna Austria.

Personal Interests

- Playing outdoor games
- Interested in updates about innovations around the world
- Listening to Music
- Being a team player

References

1. Univ.Prof. Dipl.-Ing. Dr.nat.techn. Konrad Domig

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   Muthgasse 18, 1190 Vienna, Austria
   Email: konrad.domig@boku.ac.at
   Tel: +43 1 47654-75453

2. Univ.Prof. Mag. Dr.rer.nat. Himmelbauer Heinz

   Head: Institute of Computational Biology, Dept of Biotechnology, BOKU university
   Muthgasse 18, 1190 Vienna
   Email: Himmelbauer.Heinz@boku.ac.at
   Tel: +43 147654-79155

3. Assoc.Prof.Priv.-Doz.Dr.Juliane Dohm

   Muthgasse 18, 1190 Vienna; Email: Dohm@boku.ac.at Tel: +43 147654-79156