# Personal Profile

**Name:** Dr. Vivek Kumar

**Designation:** Assistant Professor

**Department: Botany**

**Highest Qualification: Ph.D (Banaras Hindu University)**

**Exam Qualified: ICAR-NET (2014), ICAR-SRF (2014), CSIR-JRF/NET (2017), ICMR-SRF (2018)**

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**Date of Joining: 02/06/2022**

## Area of specialization:

I am interested in both culture-dependent and culture-independent (metagenomic) approaches to study of bacterial community and finding of novel gene/enzyme(s) from environmental/human samples. Before 20$^{th}$ century, microbial diversity and their potential role from the environmental/human samples was examined by employing culture-dependent approaches which were based on analysis of microbes cultured in artificial growth media under laboratory conditions. It is now well known that majority of the microbes cannot cultivable in laboratory conditions. Notably, based on the size of

population estimated by serial dilution, plating and microscopy, approximately 1-10 % of microorganism can be culture, and most of them are for way to our reach by applying traditional approaches (culture-dependent). The complete coverage is only possible by use of culture-independent approaches. I have molecular biology expertise like PCR amplification of genes including *16S rRNA*, *nifH*, *pqqC*, *ACCD-DR* from soil sample and *blaCTX-M*, *blaTEM*, *blaOXA-1*, *blaDHA*, *blaCIT*, *blaVEB*, *IL-1β-31*, *IL-1β-511*, *IL-1β+3954*, *HSPA1β+1267* and *HSPA1L+2437* from human sample. And also expertise in techniques such as microbial culture, DNA/RNA/protein extraction, enzymatic assay, DNA fingerprinting, multiplex PCR, Sanger and next generation sequencing (NGS), gene cloning, over-expression and purification, SDS-PAGE, Western blotting, 2D gel electrophoresis, quantitative real time PCR, MALDI-TOF MS, GC-MS, HRMS, NMR, FTIR, bioinformatics tools etc.

## Publications:

- **Kumar V**, Singh A, Tyagi MB, Kumar A (2017) Microbial community composition and functions through metagenomics. In: Singh DP, Singh HB, Prabha R (eds) Plant-microbe interactions in agro ecological perspectives. Springer, Singapore p 633-657
- Rani L, **Kumar V**, Pandey RK, Kumar A (2018) Screening of efficient IAA producing endophytic diazotropic bacteria from ethno medicinal rice of Jharkhand. Journal of the Indian Botanical Society. 100:28-38
- **Kumar V** and Kumar A (2021) Analysis of plant growth-promoting genes from metagenomic DNA of rice rhizosphere employing clone-based sequencing and NGS shows marked differences. (Communicated in Applied Microbiology and Biotechnology: AMAB-D-21-00572)

## Workshops and trainings:

- Application of Bioinformatics in Microbial Diversity" organized by Centre for Bioinformatics, School of Biotechnology, Banaras Hindu University, Varanasi, India (2015).
- "Genes to Genomics: The Current Status" organized by Centre for Bioinformatics, School of Biotechnology, Banaras Hindu University, Varanasi, India (2017).
- "Mining of Metagenome for Genes: Cloning and Expression" organized by National Bureau of Agriculturally Important Microorganisms, Mau, India (2019).