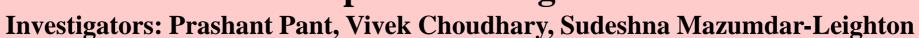




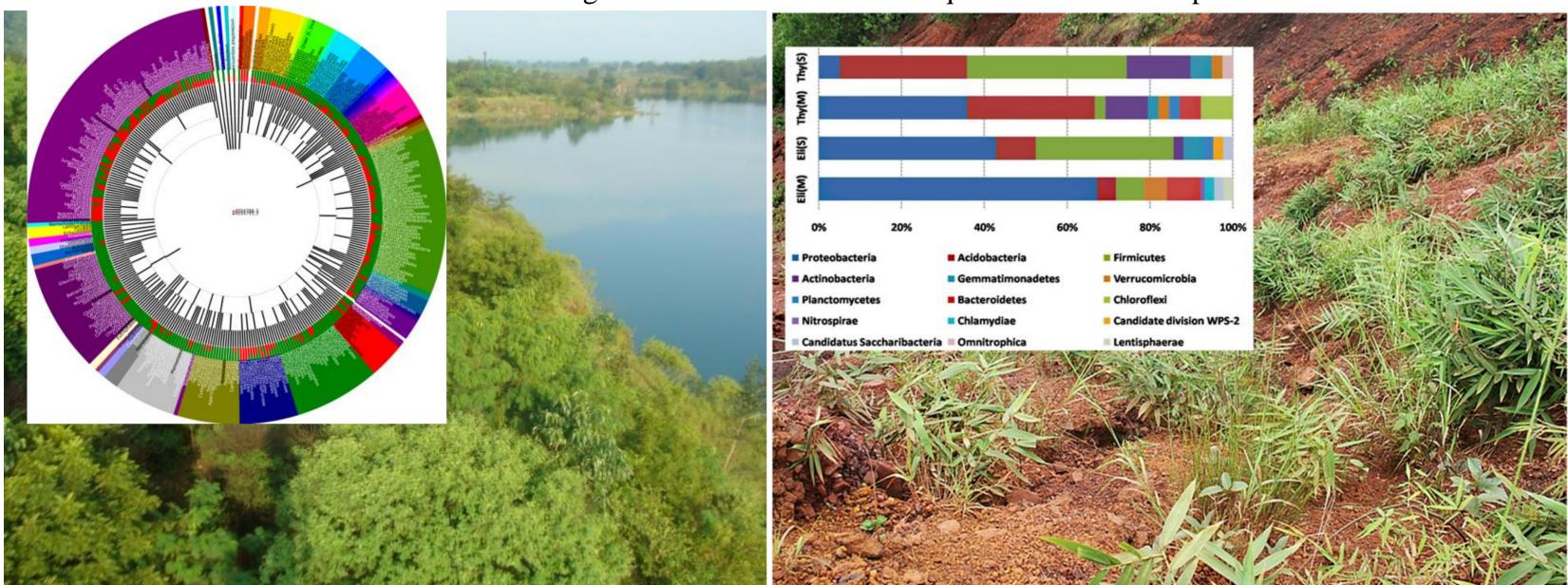
Rhizospheric Metagenomics







Research objective: Identify and characterize microbial communities that enhance plant productivity on degraded soils in Central India. Degraded mined-out study sites in Central India were rendered productive by re-vegetation with native plant species. Plant-associated microbial communities played a crucial role in restoration of degraded ecosystems and improvement in soil health processes. Dynamic microbial communities that enhanced plant productivity on degraded soils undergoing restoration in Central India were identified using Illumina-based NGS techniques with V3-V6 amplicons.



A total of 480 unique rRNA gene sequences were reported from this study. These are submitted to GenBank under the accession number JN604576-JN604667, JN099387- JN099483, HQ318593-HQ318630, FJ816083-FJ816086, EU220251-EU220268, HQ640718-HQ640731.

Project completed:

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Publications:

• Mazumdar-Leighton, S., & Choudhary, V. K. (2017). Metagenomics at grass roots. Resonance, 22(3), 291-301.

Poster Presentations in International Conferences:

- Application and limitations of 28SrRNA gene sequences for monitoring below ground diversity at degraded mine sites understanding eco-restoration at Purnapani, Odisha, India at Annual Meeting of the American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America with the Entomological Society of America, 2015, MN, USA.
- Microbes in changing environments 16S rRNA gene family based microbial typing of rhizospheric communities of a native legume Alysicarpus vaginalis (L.), fam. Fabaceae at Ecology of Soil Microorganisms 2015, Microbes as Important Drivers of Soil Processes, Czech Republic.