

Analyzing the Diversity of Proteobacteria in Baghdara Lake, Udaipur, through 16S rRNA Analysis

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ABSTRACT

Studying bacterial communities in aquatic ecosystems has regained importance due to its impact on ecosystem health and nearby human populations. This research focuses on Badi Lake in the Aravali region, where water samples were taken from ecologically significant sites with varying human influences. Bacterial colonies were isolated and analyzed through 16S rRNA gene sequencing, revealing Proteobacteria as the dominant phylum. This group included diverse classes such as Alphaproteobacteria, Betaproteobacteria, and Gammaproteobacteria, with Alphaproteobacteria being the most diverse. Proteobacteria are crucial for global elemental cycles and interact closely with eukaryotes as both pathogens and symbionts.

Keywords: Bacteria, taxonomy, freshwater, water pollution, diversity

INTRODUCTION

The phylum Proteobacteria, the largest cultured group of Gram-negative bacteria, is categorized into five classes: Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Delta-proteobacteria, and Epsilonproteobacteria (Deák, 2010). This phylum includes notable groups like purple sulfur bacteria within Gammaproteobacteria and non-sulfur bacteria in Alpha and Beta categories. The biological significance of Proteobacteria is underscored by their pathogenicity in

humans, animals and plants, as well as their contributions to the evolutionary origins of eukaryotic cells and organelles (Shin *et al.*, 2015). Their metabolic diversity includes chemoorganotrophic, chemoautotrophic and phototrophic capabilities enhances their relevance across agricultural, medical and industrial domains (Mehta and Satyanarayana, 2013).

The classification of Proteobacteria relies on techniques such as 16S rRNA oligonucleotide catalogues and phylogenetic analyses (Vandamme *et al.*, 1996). Within

the classes, Alphaproteobacteria includes species adapted to nutrient-poor environments while Betaproteobacteria thrives on low nutrient sources, mainly in anaerobic conditions. Gammaproteobacteria is particularly notable for its ecological diversity, comprising 14 orders and 25 families, reflecting a wide range of ecological adaptations and roles (Buee *et al.*, 2009).

MATERIALS AND METHODS

2.1 Study area: Badi Lake, a pristine freshwater body, with nutrients derived from natural sources.

2.2 Sample Collection: Seasonal water samples were taken using sterilized polyethylene bottles, thoroughly cleaned with autoclaved water and 70% alcohol.

2.3 Bacterial isolation: Bacteria were isolated through serial dilution and culturing on nutrient agar. (Zuberer, 1994). This process enabled effective bacterial isolation.

2.4 Bacterial Identification by molecular approach: DNA was extracted and the 16S rRNA gene amplified for sequencing. (Shafi *et al.*, 2021). The samples were later sent for

sequencing to a lab in Delhi, India.

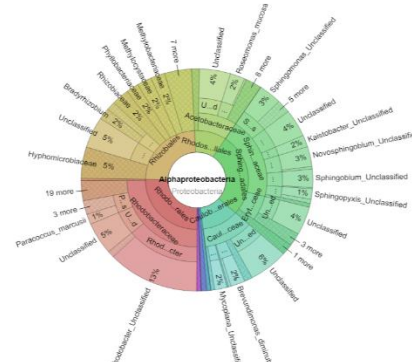


Fig. 1- Class distribution and abundance of Alphaproteobacteria, image generated from Krona

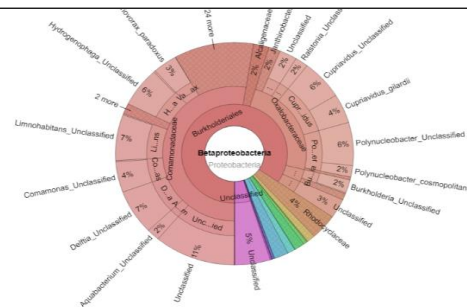


Fig. 2- Class distribution and abundance of Betaproteobacteria, image generated from Krona

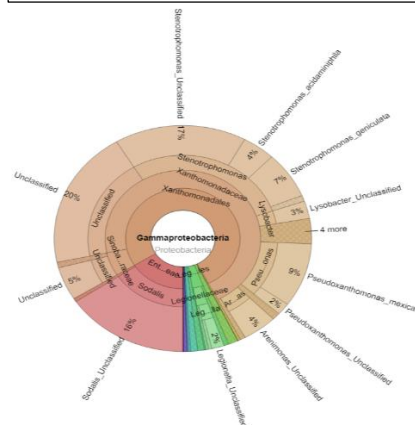


Fig. 3- Class distribution and abundance of Gammaproteobacteria, image generated from Krona

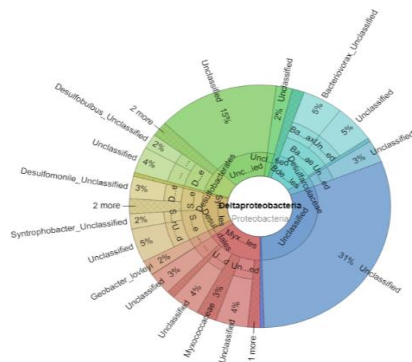


Fig. 4- Class distribution and abundance of Deltaproteobacteria, image generated from Krona

Results

A total of 61 bacterial species from the Proteobacteria phylum were identified in the lake water through molecular techniques, with Alphaproteobacteria showing the highest diversity. Within Alphaproteobacteria, the orders Rhizobiales and Rhodobacterales were prominent, with 16 and 7 species, respectively. Key species from Rhizobiales include *Agrobacterium sullae*, *Methylobacterium komagatae*, *Rhizobium leguminosarum* and *Bradyrhizobium elkanii* while Rhodobacterales featured species like *Rhodobacter sphaeroides* and *Anaerospira hongkongensis*.

Betaproteobacteria was represented by five orders, including Burkholderiales, which had the largest variety with species such as

Acidovorax caeni, *Burkholderia andropogonis* and *Variovorax paradoxus*. Neisseriales contributed four species, including *Neisseria cinerea* and *Aquitalea magnusonii*. Other orders, such as Nitrosomonadales, Methylophilales and Rhodocyclales, each contributed fewer species, with notable representatives like *Nitrosovibrio tenuis* and *Dechloromonas fungiphilus*.

DISCUSSION

The study underscores the phylogenetic diversity within Proteobacteria, emphasizing their ecological roles and interactions with eukaryotes. Specific focus on the ecological roles of Rhizobiales highlights their significance in nitrogen fixation and as pathogens. Members of Betaproteobacteria, particularly *Acidovorax*, show promise for biotechnological applications. (Flórez *et al.*, 2015).

CONCLUSION

This study highlighted the effectiveness of 16S rRNA gene techniques in revealing bacterial diversity in lake ecosystems. It identified specific pathogenic bacteria in the lake water and noted significant anthropogenic impacts, particularly concerning nutrient levels in Baghdara Lake. These findings emphasize the influence of surrounding catchment areas on lake health.

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