Uncovering the Microbial Biodiversity in the Ballona Wetlands Through eDNA Analysis

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Abstract

California is a global biodiversity hotspot that has lost nearly 70% of its natural habitat to urban development [2]. This exploratory study sequenced soil samples from the Ballona Wetlands to characterize microbial diversity, successfully identifying distinct bacterial taxa. Comparing this eDNA data with existing distribution maps, this research helps to build a comprehensive inventory of California's species across diverse habitats and seasons.

Hypothesis

This eDNA data will establish a precise baseline for California's current biodiversity and provide a scalable framework for long-term species tracking.

Methods



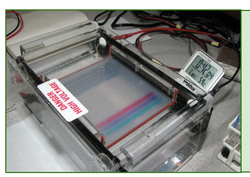
1. Collecting Soil Samples

Multiple soil samples were collected from distinct locations in the Ballona Wetlands utilizing sterile tools and later stored in labeled tubes for eDNA extraction.

2. eDNA Extraction & PCR

eDNA was extracted from soil samples utilizing the Qiagen Soil Kit, and the bacterial 16S rRNA gene (~300 bp) was amplified using specific primers via PCR [3].





3. Gel Electrophoresis

PCR products were run on an agarose gel medium utilizing gel electrophoresis to determine relative length and abundance of eDNA.

4. Sample Barcoding & Pooling

Unique 20-bp barcode sequences were attached to each 16S amplicon to label individual samples, which were then pooled to prevent a single sample from dominating results.





5. Sequencing & Taxonomy

Pooled 16S amplicons were sequenced with Oxford Nanopore Technologies and matched to the NCBI database to identify species distribution.

Results

Table 1: Numbers of classified and unclassified 16s proteins in both samples.

Sample #	# Unclassified	# Classified	Total
2	3,714,832	3,034,822	6,749,654
18	2,831,751	1,825,461	4,657,212

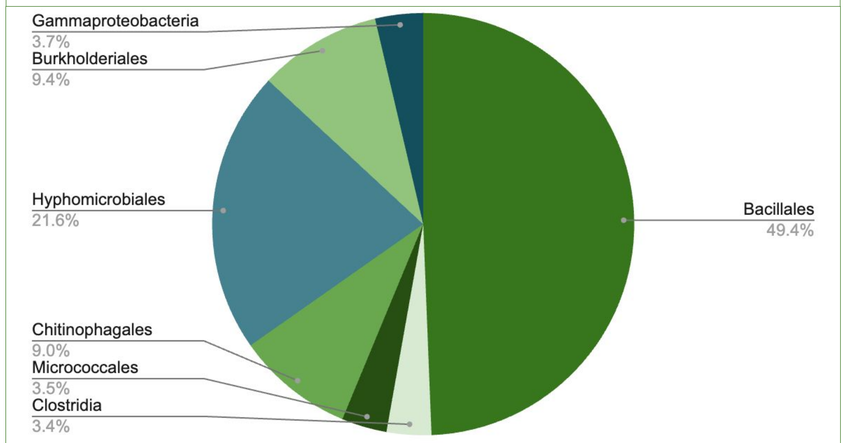


Figure 1: Order Level Biodiversity of Classified Bacteria in Sample 2

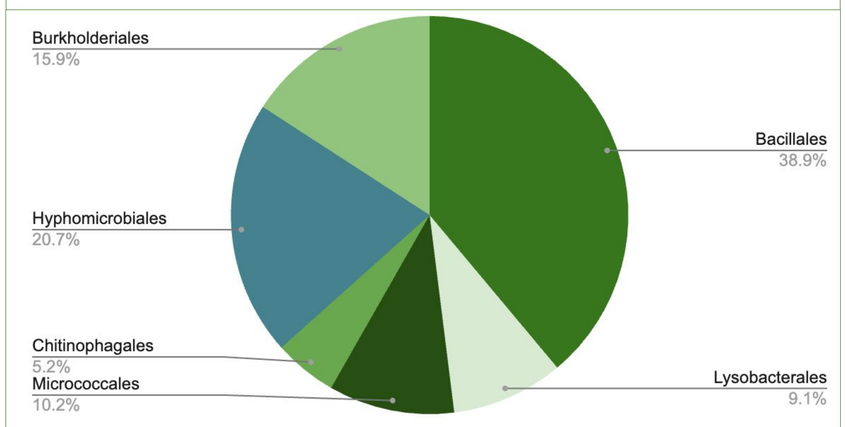


Figure 2: Order Level Biodiversity of Classified Bacteria in Sample 18

Discussion

Our results indicate that the Ballona Wetlands harbor a substantial and still largely unresolved microbial community, underscoring the value of (eDNA) for detecting biodiversity that traditional observation methods may overlook. This supports previous studies showing that eDNA is an efficient and scalable method for biodiversity monitoring, with strong detection power even when other surveys miss cryptic organisms. We identified sequences associated with cable bacteria, filamentous multicellular microorganisms of particular interest for their ability to perform long-distance electron transport. In freshwater sediments, cable bacteria couple sulfide oxidation in deeper sediment layers to oxygen or nitrate reduction near the sediment surface, linking spatially separated redox reactions and contributing to the geochemical functioning of sediment ecosystems [1]. So, the Ballona Wetlands may harbor microbial groups with importance extending beyond biodiversity alone, into sediment biogeochemistry, redox cycling, and naturally conductive microbial systems.

Future Directions

Ongoing sampling of these sediments will classify more sequences and further clarify the ecological and scientific importance of taxa in California wetland environments.

Acknowledgements

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References

[1] Yang, Tingting, et al. *Long-distance electron transport in multicellular freshwater cable bacteria*. https://elifesciences.org/articles/91097#:~:text=Identification%20of%20cable%20bacteria%20sampling.in%20the%20bottom%20surface%20sediment

[2] Butler, Rhett. *An inventory of life in California*, Mongabay, 6 Jan. 2026 news.mongabay.com/2026/01/an-inventory-of-life-in-california/.

[3] Clarridge, Jill E. *Impact of 16S rRNA Gene Sequence Analysis for Identification of Bacteria on Clinical Microbiology and Infectious Diseases*, National Library of Medicine pmc.ncbi.nlm.nih.gov/articles/PMC523561/#:~:text=16S%20rRNA%20gene%20sequence%20analysis%20can%20better%20identify%20poorly%20described,novel%20pathogens%20and%20noncultured%20bacteria.