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Screening of Brevundimonas Terrae for Production of Amylase

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Abstract: Brevundimonas terrae is a lesser-known but ecologically significant bacterium found in various terrestrial environments. This study explores its morphological, physiological, and biochemical characteristics. By analyzing its growth conditions and potential applications, we aim to contribute to the understanding of this microorganism's role in environmental and industrial settings. Additionally, we performed 16S rRNA sequencing, BLAST analysis, and phylogenetic tree construction to determine its taxonomic position and evolutionary relationships.

I. INTRODUCTION

Brevundimonas terrae belongs to the *Brevundimonas* genus within the *Alphaproteobacteria* class. It is commonly found in soil, water, and extreme environments, demonstrating remarkable adaptability. Given its ability to degrade pollutants and interact with plants, studying *Brevundimonas terrae* can offer insights into bioremediation and agricultural benefits. Despite its environmental significance, limited research exists on its genetic and functional attributes. This study aims to bridge this gap by incorporating molecular analysis through 16S rRNA sequencing and phylogenetic assessment. Brevundimonas species are aerobic Gram-negative, oxidase and catalase positive, non-fermenting rods 1 to 4 µm in length and 0.5 µm in width, belonging to the Alphaproteobacteria class and Caulobacteraceae family with a DNA G + C content of 65% to 68% [15]. Motility is provided by one short polar flagellum. The species Brevundimonas terrae is distinguished by its ability to grow at a wide range of temperatures (15-37°C) and pH levels (5.5-8.5). It is also capable of utilizing various carbon sources, including glucose, sucrose, and maltose. Phylogenetic analysis of the 16S rRNA gene sequence has revealed that Brevundimonas terrae is closely related to other species within the genus Brevundimonas, including Brevundimonas alba and Brevundimonasdiminuta. However, it can be differentiated from these species based on its unique fatty acid profile and biochemical characteristics.

II. AIMS AND OBJECTIVES

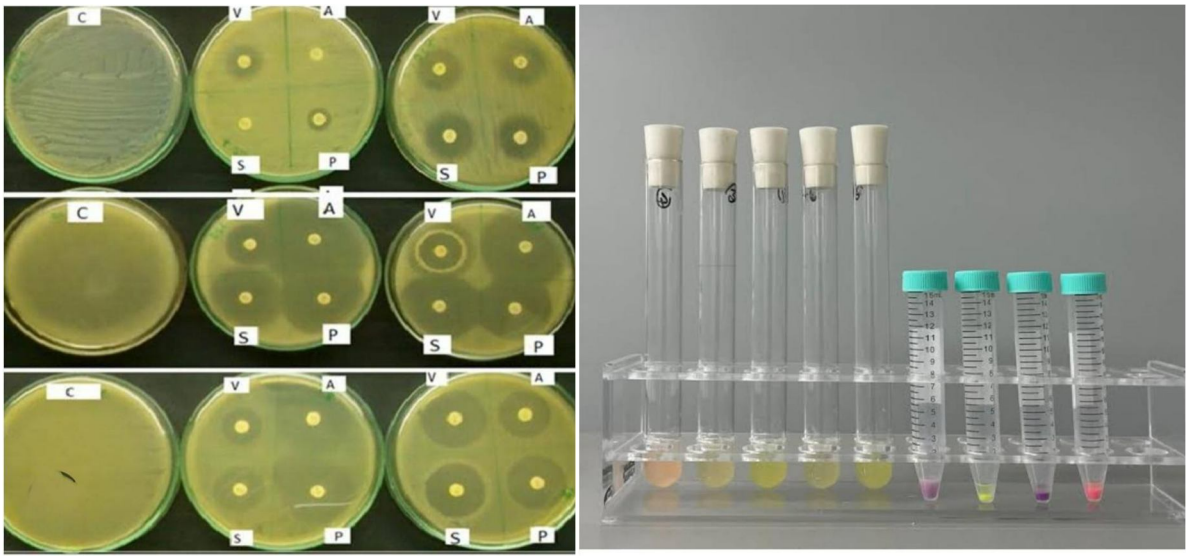
1) To study the morphological and biochemical characteristics of *Brevundimonas terrae*.
2) To determine the optimal growth conditions for the bacterium.
3) To assess its potential applications in environmental and industrial microbiology.
4) To perform 16S rRNA sequencing for accurate identification and phylogenetic analysis.
5) To conduct BLAST analysis for sequence comparison and evolutionary study.
6) To construct a phylogenetic tree to determine its taxonomic position.

III. MATERIALS AND METHODS

1) *Sample Collection*: Soil samples were collected from different Garden soil.
2) *Isolation and Cultivation*: Standard microbiological techniques, including serial dilution and plating on Nutrient agar, were used.
3) *Morphological Identification*: Gram staining and colony characterization were performed.
4) *Biochemical Tests*: Oxidase, catalase, starch hydrolysis and carbohydrate fermentation tests were conducted.
5) *Growth Optimization*: Temperature, pH, and nutrient preferences were analyzed.
6) *16S rRNA Sequencing*: Genomic DNA was extracted, and the 16S rRNA gene was amplified using PCR.
7) *BLAST Analysis*: The obtained sequence was compared with existing sequences in the NCBI database using the BLAST tool.
8) *Phylogenetic Tree Construction*: A phylogenetic tree was generated using MEGA software to analyze evolutionary relationships with related bacterial species.

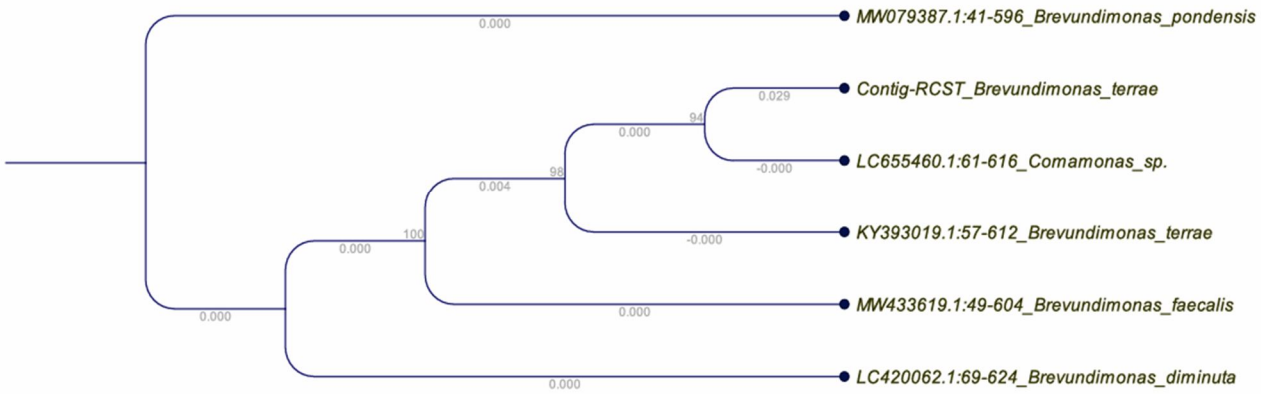
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Amylase Enzyme Diagram Biochemical test:



IV. RESULTS AND DISCUSSION:

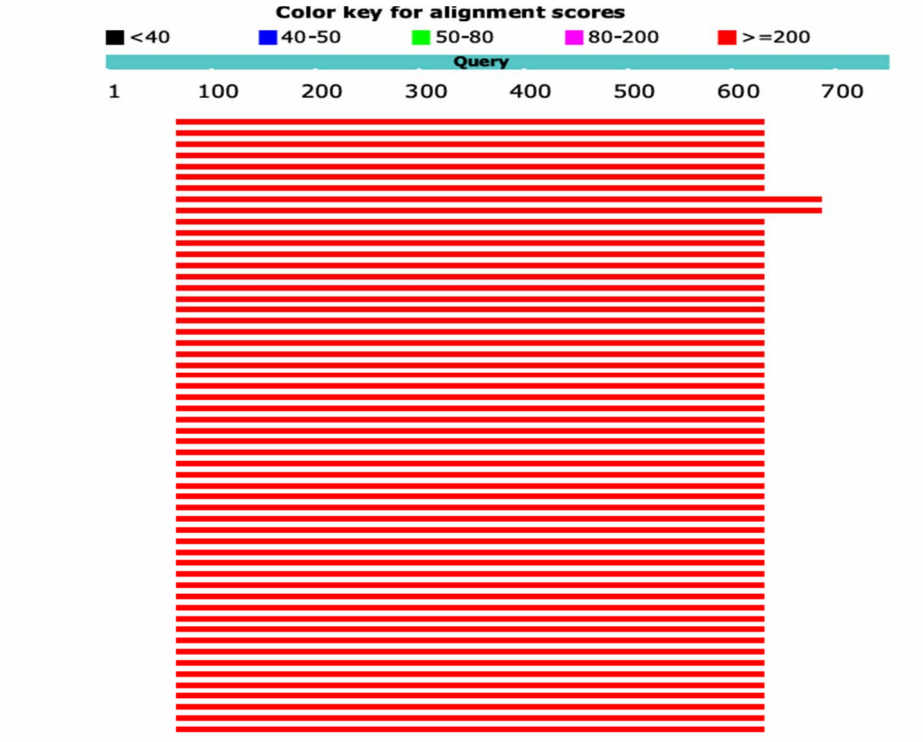
Brevundimonas terrae exhibited small, yellow-pigmented colonies on Nutrient agar. It was Gram-negative, rod-shaped, and motile. Biochemical tests confirmed its oxidative metabolism and ability to utilize various carbon sources. The growth has been studied in relation to both temperature and pH. The bacterium demonstrated optimal growth at 28-30°C and pH 7. These findings align with previous studies indicating its environmental adaptability



The 16S rRNA sequence analysis confirmed its identity, with BLAST results showing high similarity to other *Brevundimonas* species. The phylogenetic tree placed *Brevundimonas terrae* within the *Brevundimonas* cluster, closely related to *Brevundimonassubvibrioides.* This molecular approach strengthens its taxonomic classification and highlights its evolutionary significance.

Potential applications include bioremediation due to its ability to degrade hydrocarbons and other pollutants. Further studies are necessary to explore its full genetic potential and industrial applications.

A. Distribution of top 103 Blast Hits on 100 subject sequences



V. CONCLUSION

This study provides a foundational understanding of *Brevundimonas terrae*, emphasizing its adaptability and potential industrial applications. The inclusion of 16S rRNA sequencing, BLAST analysis, and phylogenetic studies enhances the accuracy of its classification. Future research should focus on its genetic characterization and practical applications in biotechnology, industry and environmental management.

GGGGTGCTGGGGAAGCGCTAAACAATGCAAGTCGTAACAAGGTAGCCGTATTATTGTCGTTACGGCATGAGTAACGC
GTGGGAACGTGCCTTTAGGTGCGGAATAGCTCCTGGAAACGGGTGGTAATGCCGAATGTGCCCTTCGGGGGAAAGAT
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TCGCAACTGCCTTTGATACTGGCGATCTTGAGTGTGTGAGAGGGATGTGGGAACTCCGAGTGTTGTAGGTGAAGATTC
GTGAGATATTTTGGAGGGAAGACCCAGGGGACAAAAAGACGACACTACTTGGCGTCGTTAGCTGAAAGACTGAGTG
CTCGGCGAGCGGGGGAGGACCCCAGCAGGAATTTAAGAT

Result: Brevundimonas terrae

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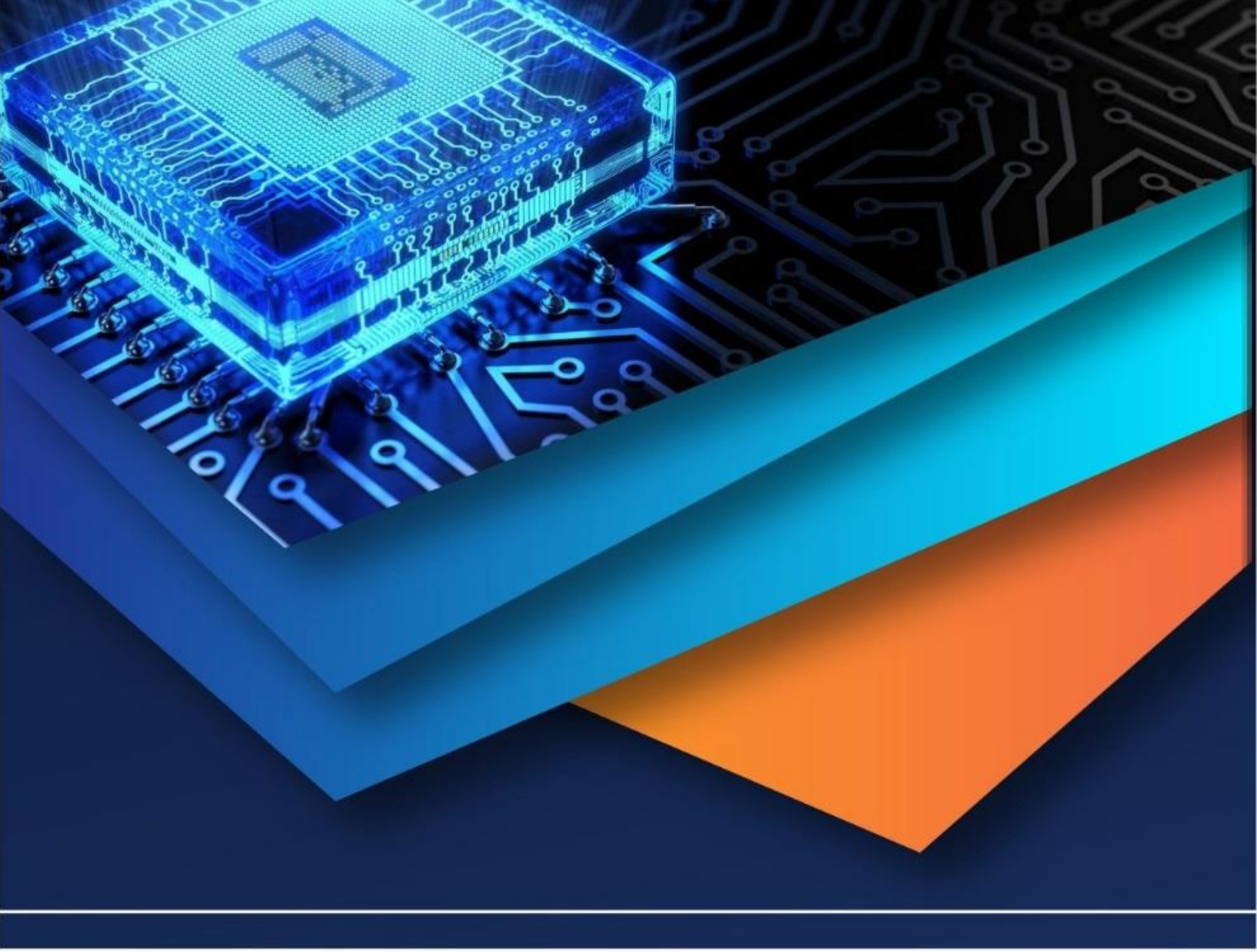
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