Annals of Plant and Soil Research 26(3): 498-502 (2024) https://doi.org/10.47815/apsr.2024.10390

Exploration and characterisation of protease-producing bacterial strain *klebsiella pneumonia* isolated from soil

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Received, March, 2024; Revised accepted, August, 2024

ABSTRACT

Microbial enzymes are recognized for their significance in today's world. They convert more intricate or complicated molecules into simpler components. The study aims to isolate, screen, and identify soil bacterial strains that exhibit the potential to produce industrially important enzymes, particularly protease. Bacteria capable of producing protease were extracted from polluted soil, assayed for protease production using skim milk agar plates, and the protease production was confirmed by protease assay. Four bacterial strains were collected, and among them, one strain exhibited protease activity. Protease producing bacterial strain PRS3A was selected on the basis of their protease test. Morphological and biochemical assessments were conducted on protease-producing organisms, and their identification through 16S RNA sequencing revealed that the bacterial cultures belong to Klebsiella genus and pneumonia species.

Keywords: Protease, Screening, contaminated soil, Klebseilla sp.

INTRODUCTION

Soil ecosystems, teeming with chemical and biological diversity, serve as an extensive reservoir of micronutrients and novel enzymes (Amritanshu et al., 2023; Pachauri et al., 2023). Microbial enzymes, known for their ability to function in extreme environmental conditions, find a particularly conducive habitat in soil an environment considered highly suitable for microbial growth among various unexplored habitat (Karlen and Stott, 1994). These enzymes from microorganisms play a crucial role globally due to their diverse applications in physiology, pharmaceuticals, and industries. More than 300 enzymes have been recognized, and among them protease and lipase have significant applications in industrial processes (Kumar et al., 1994). Proteases, comprising a significant portion of the top three categories of industrial enzymes, hold substantial share of а approximately 60% in total global enzyme sales (Zhu et al., 1994). Functioning as peptidylpeptide hydrolases, proteases catalyze the hydrolysis of peptide bonds within protein molecules (Palsaniya et al., 2012). Proteases are sorted based on their cleavage sites, classifying them into exoproteases and endoproteases, while their acid-base behaviour categorizes them into acid, neutral, or alkaline proteases (Rao et al., 1998, Sayaniya and Patel 2021, Ramkumar et al., 2018) Their widespread commercial applications span food, leather,

detergent, and pharmaceutical industries (de Castro Bizerra et al., 2024, Gupta et al., 2024, Khatoon et al., 2023).Proteases play pivotal roles in diverse industries. In the food sector, they enhance quality through processes like meat tenderization and cheese production (Ismail et al., 2019). In pharmaceuticals. proteases aid in drug formulation, delivery, and protein purification (Varanko et al., 2020). Within textiles, they enable enzymatic stone washing and bio-polishing (Islam, 2021). In leather, proteases are crucial for cleaner products (Wanyonyi and Mulaa, 2020). Proteases also contribute to enzymatic laundry detergents, optimizing bioremediation, and brewing processes, showcasing their versatility and impact on innovation. efficiency. and sustainability across industries.

This study aims to isolate protease-producing bacteria from contaminated soil samples, contributing not only to the understanding of microbial proteases but also uncovering novel sources with potential applications across diverse fields.

MATERIALS AND METHODS

Soil samples were collected from Vytilla in Ernakulam, Kerala, India. The samples were transported to the laboratory in sterile bottles and stored at 37 ^o C for further analysis.

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Isolation of Bacteria and Screening for Protease Enzyme

The soil sample was serially diluted with sterile diluted water until reaching a 10⁻⁷dilution, and isolation was performed using pour plate method on nutrient agar medium(Tanimu *et al.*, 2022, Abdel-Moniem *et al.*, 2021). Proteases producing bacterial strains were isolated on skim milk agar plates (Mohamed *et al.*, 2023).

Identification of the Protease-producing Bacteria

Morphological identification, including Gram staining; biochemical tests such as motility, indole production, MRVP, citrate utilization, catalase, oxidase, nitrate reduction, urease, starch hydrolysis and casein hydrolysis were employed for bacterial identification

Pour Plate 10⁻¹

following Bergey's Manual of Determinative Bacteriology(Shinde *et al.*, 2023).

16S rRNA Sequence Analysis

The bacterial strain PRS3A is selected for 16S rRNA sequence analysis. The isolated bacterial gene's 16S rRNA underwent PCR amplification with 27F & 1492R forward and reverses primers. The gel-purified amplicon was then processed using NucleoSpin® Tissue Kit (Macherey-Nagel) and sequenced on an ABI 3730 XL cycle sequencer.

Phylogenetic Analysis

Sequence analysis utilized the NCBI database's BLAST tool for comprehensive analysis. Sequences of maximum identity were aligned using ClustalW and a phylogenetic tree was constructed using Neighbor Joining method in MEGA11.

Pour Plate 10⁻⁵

Pour Plate 10⁻⁷



Pour Plate 10⁻³





Figure 1: Isolation of protease producing microorganisms by pour plate method

RESULTS AND DISCUSSION

Isolation and Screening of Protease Producing Microorganisms

In this work, soil samples subjected to serial dilution, pour-plated, and then incubated at 37°C for 24 hours on nutrient agar. Four predominant morphologically distinct colonies, designated as PRS1A, PRS3A, PRS5A, and PRS7A, were isolated from the soil sample. (Figure 1).

After isolation the bacterial strains were screened for protease activity on skim milk agar. Only one isolate displayed significant proteolytic activity with a distinct zone of clearance, while the other three isolates exhibited poor proteolytic activity, as shown in Figure:2 and Table:1, respectively. Therefore, the efficient protease producing isolate, PRS3A was chosen for furtherinvestigations and biochemical test. In accordance with Bergey's Manual of Determinative Bacteriology, PRS3A underwent comprehensive morphological and biochemical characterization, with the strain's morphology identified through Gram staining. Table 2 presents PRS3A's identification based on its biochemical characteristics. The table indicates that the bacterial strain PR3SA exhibits a rodshaped morpholoav and is non-motile. However, upon staining, the isolate displayed pink colour, indicating it is gram negative. The isolate is negative for indole, methyl red, and oxidase tests, while being positive for the remaining tests.

Table 1: Protease activity of various bacterial strains

SL No.	Bacterial strains	Protease activity (Qualitative)
1	PR S1A	Negative
2	PR S3A	Positive
3	PR S5A	Negative
4	PR S7A	Negative

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Figure 2: Screening of microorganisms for proteolytic activity in skim milk agar

Table2:MorphologicalandBiochemicalcharacteristics of protease producing isolates

Biochemical Test	Bacterial strain PR S3A
Grams Staining	Negative
Motility	Negative
Indole (I)	Negative
Methyl red (MR)	Negative
Vogues Proskauer's(VP)	Positive
Citrate utilization	Positive
Nitrate reduction	Positive
Urea hydrolysis	Positive
Catalase	Positive
Oxidase	Negative
Casein hydrolysis	Positive

Phylogenetic Analysis

The phylogenetic analysis of the 16S rRNA sequences was conducted using neighbour-

ioining method, leading to the identification of the strain PRS3A as Klebsiella pneumonia, with reference to Figure: 3. In this research, we isolated a bacterial strain capable of producing the industrially significant enzvme. protease. Proteases crucial for commercial applications can be derived from microbial, animal, and plant sources. However, microbial-derived proteases are preferred to their rapid growth, ease of manipulation, and shorter production and purification timelines (Yaoet al., 2023, YUANet al., 2021, Ashrafet al., 2023, North et al., 1982). The presently available proteases are not sufficient to meet industrial demands. Therefore, the on-going quest involves exploring diverse bacterial isolates to discover new proteases exhibiting unique characteristics suitable for industrial applications.



Klebsiella pneumoniae, known for its versatile capabilities, produces enzymes crucial for biotechnological applications, including industrial processes and biofuel production (Li *et al.*, 2023). Its genetic toolkit enables genetic

engineering, and its adaptability makes it suitable for various environmental conditions. Despite its pathogenic nature, certain strains are explored for bioremediation, nitrogen fixation in agriculture, ethanol production, and potential probiotic use (Bai *et al.*, 2023). Additionally, *Klebsiella pneumoniae* is a model organism in genetic studies and has applications in biomedical engineering for biosensor development (Tomulescu *et al.*, 2021).

Isolating this protease-producing bacterial strain from contaminated soil samples not only addresses current concerns but also opens up avenues for exploring its biotechnological potential in the future.

CONCLUSION

This research involved the identification, isolation, and genetic characterization of a novel protease-producing strain of Klebsiella pneumoniae from contaminated soil samples collected in Vytilla (Kochi), Ernakulam district, Kerala. The isolates were obtained through serial dilution and cultured on nutrient agar medium. Following 24 hours of incubation, four distinct bacterial strains were identified and from this, one isolate (PRS3A) showed protease activity on skim milk agar medium. The efficient protease producing isolate PRS3A was chosen for gene sequencing and identification. The morphological and biochemical features

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suggested that the isolate belonged to the category of Gram-negative bacteria possessing encapsulation and lacking motility.16S rRNA compared sequence homology was and phylogenetic tree was constructed and the result indicated that the isolate was Klebsiella pneumoniae. The present study disclosed that, this protease producing strain, PRS3A could be helpful for industrial application. The initial screening report on the diversity of Klebsiella species and their enzyme-producing potential indicates a high taxonomic diversity among the isolated Klebsiella strains, emphasizing the significant biotechnological potential of bacterial isolates from soil samples.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGEMENT

The authors concede Xcellogen Biotech Pvt. Ltd, Thiruvananthapuram for the facilities and technical support rendered on us.

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