

Volume: 02 / Issue: 03 / 2023 - Open Access - Website: <u>www.mijrd.com</u> - ISSN: 2583-0406

Biological Activities of Bacterial Isolates from Adiangao Cave, San Jose Camarines Sur

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Abstract— Considered an extreme environment, caves possessed a unique and poorly studied ecosystem comprising a unique microbial community carrying out various biological activities. This study aimed to isolate, identify, and characterize the biological activities of bacteria isolated from soil samples in Adiangao Cave, San Jose, Camarines Sur. Seventeen bacterial isolates were identified and characterized in terms of enzymatic activity, phosphate solubilizing activity, formaldehyde resistance, and antagonistic activity. Based on 16S rDNA sequencing, the most prevalent isolates obtained were members of the Bacillus genera. Results have shown that 11 isolates exhibited amylase activity, and 12 had cellulase activity, showing its potential for industrial application. Eight isolates were positive for phosphate solubilization, which can be used for plant growth promotion and heavy metal immobilization. It was also shown that 13 isolates could grow under the presence of formaldehyde showing its potential application for the bioremediation of formaldehyde. Isolate CS31, identified as Bacillus paranthracis, is noted to have great potential for the production of antimicrobial compounds that can inhibit pathogenic microorganisms such as Pseudomonas aeruginosa, Escherichia coli, Staphylococcus aureus, and Salmonella typhimurium. The results of this study demonstrated the importance of cave bacteria for the production of valuable bioactive compounds that are commercially important.

Keywords— Adiangao Cave, biological activity, antimicrobial.

I. INTRODUCTION

One of the unique and poorly studied ecosystems on Earth is caves. Considered an extreme environment, caves generally have a low and stable temperature, minimum light, low nutrients, and high humidity (Palmer 1991; Tomczyk-Żak and Zielenkiewicz 2015). The most common caves are karstic caves that are formed through geomorphological and microbiological processes (Engel 2010; Tisato et al., 2015; Bontognali et al., 2016).

Studies have shown that various microorganisms can be isolated from various caves worldwide, including Grampositive bacteria, Gram-negative bacteria, protozoa, and fungi (Gulecal-Pektas, 2016, Yasir, 2018). Due to their unique environmental conditions, caves are composed of unique microbial communities.

Some microbial isolates were identified to be causing rock weathering processes and biomineralization, while some are carrying out various enzymatic activities (Bindschedler S, Cailleau G, Verrecchia E. Role of Fungi in the Biomineralization of Calcite. Minerals. 2016; 6(2):41. https://doi.org/10.3390/min6020041).

These microorganisms are thriving in unfavorable growth conditions with many limiting factors. With the combinations of these different unique conditions, it is expected to harbor novel microorganisms producing unique beneficial chemical compounds with biotechnological benefits.

MIJRD Multidisciplinary International Journal of Research and Development

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One of the identified caves in San Jose Camarines Sur is the Adiangao Cave, located at Barangay Adiangao, San Jose, Camarines Sur. It is popular with locals due to its chain of grottoes, and the numerous stalactites and stalagmites that can be seen along the floor and ceiling of the caves. Bacterial diversity and their biological activities have not yet been studied, hence, this study aims to isolate, identify, and characterize the biological activities of bacteria isolated from soil samples of Adiangao Cave.

II. PROCEDURE FOR PAPER SUBMISSION

A. Isolation and identification of bacterial isolates from soil samples.

Soil samples were collected from Adiangao Cave located in Adiangao, San Jose, Camarines Sur $(13^{\circ}43.376' \text{ N}, 123^{\circ}41.255' \text{ E})$ and were transported in a cooler and immediately processed in the laboratory. Samples were serially diluted using 9ml of 0.1% (w/v) peptone water tubes. Diluted samples were then plated on Nutrient Agar (NA) and were incubated at 37°C for 24 h. Colonies were enumerated, and counts were expressed in log10 CFU/ml.

B. Molecular identification of bacterial isolates

One ml of 24 h culture was centrifuged at 4,500 rpm for 5 min. The supernatant was discarded, and the pellet was resuspended in 1 ml of sterile double distilled water. The suspensions were then sent to Kinovett for molecular identification. Macrogen Inc., in South Korea, did the sequencing of 16S rDNA PCR amplicons of the isolates. Partial 16S rDNA sequences were imported, checked for sequencing quality, and trimmed using the Staden Package software (Staden, 1996) after which the consensus sequences were compiled and matched to the reference strains found in the National Center of Biotechnology Information (NCBI) GenBank database through BLASTn (Basic Local Alignment Search Tool) (NCB1, 2013).

C. Biological activities of bacterial isolates

1. Screening for Cellulase and Amylase Activity

Qualitative analysis for cellulase and amylase activity was based on Kim et al., (2014) with minor modifications for amylase activity i.e., instead of carboxymethylcellulose (CMC), 1% soluble starch was used as the sole carbon source, respectively. Pure isolates were point-inoculated on Minimal Salts Agar plates (containing 0.5% CMC, 0.1% NaNO3, 0.1% K2HPO4, 0.05% MgSO4, 0.1% KCl, 0.05% yeast extract, 1.5% agar for cellulose agar plates; and 0.3% beef extract, 1% soluble starch and 1.2% agar for starch agar plates) and incubated at 37°C for 48 h. Following incubation, plates for cellulase activity detection were flooded with 1% Congo red for 15 min. The Congo red solution was then poured off, and plates were further flooded with 1 M NaCl for 15 min. Colonies exhibiting zones of the clearing were taken as positive cellulose-degrading bacterial colonies. Plates for detecting amylase activity were flooded with Gram's iodine for 3 to 5 min and zones of the clearing were observed.

2. Screening for phosphate-solubilizing bacteria

Plate assay was done to determine the ability of the bacterial isolates to solubilize phosphate using Pikovskaya agar. Isolates were point-inoculated in the medium and were incubated for 48 hours at 37°C. After incubation, zones of clearing around colony growth were observed for phosphate solubilizing isolates. Screening for the formaldehyde-resistant bacterium



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Growth of the bacterial isolates was then tested in a modified DM-3 medium (30 g of NaCl, 5 g tryptone, 5 g of yeast extract, 6 g of Na2HPO4, 3 g of KH2PO4, 1 g of NH4Cl, 1.2 g of MgSO4, and 111 mg of CaCl2 in 1 L) with 1% formaldehyde concentration. Plates were incubated at 37°C for 48 h. After incubation, bacterial growth was then assessed.

3. Antagonistic activity against pathogenic microorganisms

Agar well diffusion assay was used to test the ability of bacterial isolates to inhibit pathogenic microorganisms, i.e., E. coli P. aeruginosa, S. aureus, B. cereus, and S. typhimurium. Test organisms were swabbed into Mueller Hinton Agar, MHA, (Sigma-Aldrich) and 5 mm wells were bored on the agar. Bacterial isolates were also grown in Nutrient Broth, NB, and incubated for 24 hours at 37°C. After incubation, cultures were centrifuged at 12,000 rpm for 3 min, and the supernatants were collected. Then, 100 µL of supernatants were added to the respective wells. Plates were incubated for 24 hours at 37°C. Cefuroxime served as the positive control, and sterile distilled water was used as the negative control. Antimicrobial activity was detected by measuring the zone of inhibition that appeared after the incubation period.

III. RESULTS AND FINDINGS

Sampling and Characterization of bacterial isolates from Adiangao Cave

Soil samples were collected at the dark zone of Adiangao Cave (Figure 1). From the cultured plates, seventeen bacterial isolates were obtained and purified using NA.



Figure 1. Adiangao Cave located at Barangay Adiangao, San Jose, Camarines Sur.

Identification of Bacterial Isolates

All purified isolates were identified based on the 16S rDNA sequence. The obtained consensus sequence of each isolate was matched to the reference strains found in the National Center of Biotechnology Information (NCBI) GenBank database through BLASTn (Basic Local Alignment Search Tool). Analysis of the identified isolates showed that the majority of the isolates were members of the Bacillus genera as presented in Table 2.



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Table 2. Genbank accession number, % identity, and species identity of bacterial isolates from cave soil

| IsolateGenbank Accession NumberIdentity (%)SpeciesCS410N005108.198.98Bacillus cereusCS34CP054831.199.51Staphylococcus saprophyticusCS2MZ950778.198.58Bacillus pseudomycoidesRC2KT900621.199.54Bacillus sp.G30N005108.198.98Bacillus cereusG20N012959.1100Bacillus subtilisCC1MW012643.198.39Bacillus subtilisIC10N000579.199.76Bacillus tropicusSM10N000579.199.76Bacillus tropicusG10N000579.199.76Bacillus tropicusIC50N012959.199.89Bacillus tropicus | samples. | | | | | | |
|--|----------|--------------------------|--------------|------------------------------|--|--|--|
| CS41 ON005108.1 98.98 Bacillus cereus CS34 CP054831.1 99.51 Staphylococcus saprophyticus CS2 MZ950778.1 98.58 Bacillus pseudomycoides RC2 KT900621.1 99.54 Bacillus sp. G3 ON005108.1 98.98 Bacillus cereus G2 ON005108.1 98.98 Bacillus cereus G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis IC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 99.76 Bacillus licheniformis IC5 ON0129591 99.89 Bacillus subtilis | Isolate | Genbank Accession Number | Identity (%) | Species | | | |
| CS34 CP054831.1 99.51 Staphylococcus saprophyticus CS2 MZ950778.1 98.58 Bacillus pseudomycoides RC2 KT900621.1 99.54 Bacillus sp. G3 ON005108.1 98.98 Bacillus cereus G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 99.76 Bacillus tropicus LC5 ON012959.1 99.80 Bacillus licheniformis | CS41 | <u>0N005108.1</u> | 98.98 | Bacillus cereus | | | |
| CS2 MZ950778.1 98.58 Bacillus pseudomycoides RC2 KT900621.1 99.54 Bacillus sp. G3 ON005108.1 98.98 Bacillus cereus G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus LC5 ON012959.1 99.76 Bacillus tropicus | CS34 | <u>CP054831.1</u> | 99.51 | Staphylococcus saprophyticus | | | |
| RC2 KT900621.1 99.54 Bacillus sp. G3 ON005108.1 98.98 Bacillus cereus G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus LC4 KX946197.1 81.50 Bacillus licheniformis | CS2 | <u>MZ950778.1</u> | 98.58 | Bacillus pseudomycoides | | | |
| G3 ON005108.1 98.98 Bacillus cereus G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 81.50 Bacillus licheniformis | RC2 | <u>KT900621.1</u> | 99.54 | Bacillus sp. | | | |
| G2 ON012959.1 100 Bacillus subtilis CC1 MW012643.1 98.39 Bacillus subtilis LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 81.50 Bacillus licheniformis | G3 | <u>0N005108.1</u> | 98.98 | Bacillus cereus | | | |
| CC1MW012643.198.39Bacillus subtilisLC1ON000579.199.76Bacillus tropicusSM1ON000579.199.76Bacillus tropicusG1ON000579.199.76Bacillus tropicusCC4KX946197.181.50Bacillus licheniformisLC5ON012959.199.89Bacillus cubtility | G2 | <u>0N012959.1</u> | 100 | Bacillus subtilis | | | |
| LC1 ON000579.1 99.76 Bacillus tropicus SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 81.50 Bacillus licheniformis LC5 ON0129591 90.89 Bacillus cubtility | CC1 | MW012643.1 | 98.39 | Bacillus subtilis | | | |
| SM1 ON000579.1 99.76 Bacillus tropicus G1 ON000579.1 99.76 Bacillus tropicus CC4 KX946197.1 81.50 Bacillus licheniformis LC5 ON0129591 99.89 Bacillus cubtility | LC1 | <u>ON000579.1</u> | 99.76 | Bacillus tropicus | | | |
| G1ON000579.199.76Bacillus tropicusCC4KX946197.181.50Bacillus licheniformisLC5ON012959.199.89Bacillus cubtility | SM1 | <u>ON000579.1</u> | 99.76 | Bacillus tropicus | | | |
| CC4 KX946197.1 81.50 Bacillus licheniformis LC5 ON012959.1 99.89 Bacillus cubtility | G1 | <u>ON000579.1</u> | 99.76 | Bacillus tropicus | | | |
| LC5 ON0120591 Becillus subtility | CC4 | KX946197.1 | 81.50 | Bacillus licheniformis | | | |
| bcs UNU1273311 97.07 Bachius Suburis | LC5 | <u>ON012959.1</u> | 99.89 | Bacillus subtilis | | | |
| RC4 <u>OP903925.1</u> 96.22 <u>Bacillus cereus</u> | RC4 | <u>0P903925.1</u> | 96.22 | Bacillus cereus | | | |
| CS31 MK508861.1 99.86 Bacillus paranthracis | CS31 | MK508861.1 | 99.86 | Bacillus paranthracis | | | |
| CS33 OP592255.1 99.86 Bacillus paranthracis | CS33 | OP592255.1 | 99.86 | Bacillus paranthracis | | | |
| CS42 MN938501.1 99.86 Bacillus inaquosorum | CS42 | MN938501.1 | 99.86 | Bacillus inaquosorum | | | |
| CS52 MW405872.1 99.71 Bacillus atrophaeus | CS52 | MW405872.1 | 99.71 | Bacillus atrophaeus | | | |
| RC2 KY074395.1 100 Bacillus cereus | RC2 | KY074395.1 | 100 | Bacillus cereus | | | |

Biological activities of bacterial isolates

Different biological activities of each isolate were determined to further understand its possible importance for industrial application. Each isolate was screened for its ability to produce enzymes responsible for biomass degradation. The activity of these isolates were summarized in Table 3.



Figure 2. Plate assay screening of cave bacterial isolates: (a) amylase, (b) cellulase. A zone of clearing around bacterial growth indicates a positive result for enzymatic activity.

Multidisciplinary International Journal of Research and Development

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Results showed that 11 out of 17 isolates exhibited amylase activity, and 12 had cellulase activity. Based on these results, it was confirmed that bacterial isolates from cave samples possess enzymatic activities and can be explored for possible industrial use. Bacterial isolates were also screened for their ability to solubilize phosphate. Results have shown that 8 isolates were positive for phosphate solubilization that can be used for plant growth promotion and heavy metal immobilization. The ability of the isolates to grow in a formaldehyde-containing medium was also determined, and results showed that 13 isolates out of 17 were still capable of growing under the presence of formaldehyde. This shows that the isolates can use formaldehyde as a carbon source and has the potential application for the bioremediation of formaldehyde.

| Code | Plate Assays | | | | | | |
|------|---------------|-----------------|------------------|-------------------------------|--|--|--|
| | Amylase Plate | Cellulase Plate | Pikovskaya Plate | Growth in Formaldehyde Medium | | | |
| | Assay | Assay | Assay | | | | |
| CS33 | + | - 15 | | + | | | |
| CS41 | - | + 53 53 | - | | | | |
| CS34 | - | + & 2.4 | + | + | | | |
| CS52 | - | + | - | 14) | | | |
| CS42 | + | M N | IJRD | + | | | |
| CS31 | + | + 0 | | - | | | |
| CS2 | + | | + | - | | | |
| RC2 | - | + | - 2 | + | | | |
| G3 | - | + | + | + | | | |
| G2 | + | + | + | + | | | |
| CC1 | + | + | | | | | |
| LC1 | - | - | + | + | | | |
| SM1 | + | + | + | + | | | |
| G1 | + | + | - | + | | | |
| CC4 | + | + | + | + | | | |
| LC5 | + | + | - | - | | | |
| RC4 | + | - | + | + | | | |

Table 3. Biological activities of bacterial isolates isolated from cave soil samples.

Many of the Bacillus genera are capable of producing these extracellular enzymes that target various macromolecules such as carbohydrates, lignin, organic phosphate, proteins, and sugars (Harirchi et al., 2022). Some of these extracellular enzymes are being used by microorganisms to overcome competition with other microorganisms. Enzymes such as cellulases and amylases are known for their industrial importance. Amylases from Bacillus sp. have many applications in the food, fermentation, textile, and paper industries (de Silveria et al., 2019).

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Antimicrobial activity against pathogenic microorganism

Isolated bacterial isolates were tested for antimicrobial activity against E. coli, P. aeruginosa, S. aureus, B. cereus, and S. typhimurium. Results have shown that isolate CS31, Bacillus paranthracis, demonstrated a significant inhibitory effect against P. aeruginosa, E. coli, S. aureus, and S. typhimurium. On the other hand, isolate G2, Bacillus subtilis, showed the highest inhibitory effect against B. cereus. Based on statistical analysis, the activity of these promising isolates was significantly different compared to other isolates.



Error Bars: +/- 2 SE

Figure 3. Average zone of inhibition of bacterial isolates against selected pathogenic microorganisms.

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Statistical analysis has shown that the activity of the isolates capable of inhibiting P. aeruginosa has no significant difference from each other (P = 0.200). For the activity against S. aureus, it has been shown that the activity of isolate CS31 is significantly high compared to other isolates. The activity of isolates CS31, CS2, CC1, and LC1 is not significantly different from each other. On the other hand, the activity of isolate G2 against B. cereus is significantly different compared to other isolates. And lastly, for the activity against S. typhimurium, isolate CS31 showed significant activity compared to other isolates.

In this study, Bacillus species displayed a promising antagonistic activity against pathogenic organisms. Studies have shown that Bacillus species are well known for their wide range production of pathogen-inhibiting compounds, such as nonribosomal peptides synthetases (NRPs) that exhibit a broad range of activity (Lopes et al., 2018; Miljaković et al., 2020; Hamdache et al., 2013).

Based on the results of this study, it has shown that bacterial isolates isolated from a cave environment can be a good source of bioactive compounds that can have applications in agriculture, pharmaceutical, and other industries.

IV. CONCLUSION AND RECOMMENDATION

Seventeen bacterial isolates were identified and characterized in terms of enzymatic activity, phosphate solubilizing activity, and formaldehyde resistance. Based on 16S rDNA sequencing, the most prevalent isolates obtained were members of the Bacillus genera. Results have shown that 11 out of 17 isolates exhibited amylase activity, and 12 had cellulase activity, showing its potential for industrial application. Eight isolates were positive for phosphate solubilization, which can be used for plant growth promotion and heavy metal immobilization. It was also shown that 13 of 17 isolates could grow under the presence of formaldehyde showing its potential for antimicrobial activity against pathogenic bacteria, specifically the activity of CS31 against P. aeruginosa, E. coli, S. aureus, and S. typhimurium. The results have demonstrated the importance of cave bacteria for the production of valuable bioactive compounds that are commercially important. It is recommended that the quantification of produced secondary metabolites should be performed.

ACKNOWLEDGEMENT

This study was funded by Partido State University through its internal grant for Research and Development. It was also supported by the Department of Science and Technology – Philippine Council for Industry, Energy and Emerging Technology Research and Development (DOST-PCIEERD) through the project entitled "Establishment of ParSU-MTL (Microbiology Testing Laboratory).

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Volume: 02 / Issue: 03 / 2023 - Open Access - Website: <u>www.mijrd.com</u> - ISSN: 2583-0406

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