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Isolation and Identification of Concrete Environment Bacteria

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Abstract. This paper presents the isolation and molecular method for bacteria identification through PCR and DNA sequencing. Identification of the bacteria species is required in order to fully utilize the bacterium capability for precipitation of calcium carbonate in concrete. This process is to enable the addition of suitable catalyst according to the bacterium enzymatic pathway that is known through the bacteria species used. The objective of this study is to isolate, enriched and identify the bacteria species. The bacteria in this study was isolated from fresh urine and acid mine drainage water, Kota Tinggi, Johor. Enrichment of the isolated bacteria was conducted to ensure the bacteria survivability in concrete. The identification of bacteria species was done through polymerase chain reaction (PCR) and rRDNA sequencing. The isolation and enrichment of the bacteria was done successfully. Whereas, the results for bacteria identification showed that the isolated bacteria strains are \textit{Bacillus sp} and \textit{Enterococcus faecalis}.

Keywords: Bioconcrete, effective microorganism, enrichment, 16S rDNA gene sequencing.

1. Introduction

Bacteria is a living micro-organism that are everywhere. From the smallest grain of soil to the small drop of water. Bacteria can also be found in organic matters such as in live bodies of plants and animals. These living micro-organisms are known to live in harsh environments and thrive in these living conditions [1]. The bacteria species isolated from different parts of the world and different environmet have unique characteristics. The uniqueness of these bacteria are slowly being discovered and used to improve problems of human kind. Some groups of bacteria have capability in improving crops, health, degraded organic contaminants and others. An attempt of bacteria in concrete able to improve concrete properties and healing process. Concrete is an important building material. However, the drawback of this material is the deterioration in which intervention in terms of chemicals are normally used. The chemicals are used to repair cracks, reduce water permeability of concrete, early hardening and many more. [2] had stated in his study that bacteria are able to promote precipitation of calcium carbonate in the form of calcite. The
formation occurs as a by-product of a common microbial metabolic process which help in increasing alkalinity and produce microbial calcite precipitation. Many researchers added bacteria into concrete to allow precipitation of calcium carbonate within the concrete to improve its properties [3,4,5]. The bacteria used by previous researchers were isolated from local sources of temperate countries that different in environmental factors. Therefore, this study aims to isolate, enriched and identify a local source of bacteria which has potential to improve concrete properties.

Bacteria identification based on 16S ribosomal gene rDNA sequencing and polymerase chain reaction (PCR) is a popular technique of bacteria identification method [6,7,8,9,10]. This method for bacteria identification is the preferred method due to its speed in obtaining results and accuracy. The use of 16S rDNA gene sequencing are more commonly being employed in routine laboratory diagnostics particularly after adopting PCR in biomedical science [10].

According to [9], PCR based method is a cheaper and more faster method to identify bacteria, the PCR typing assays is design from genome sequence data which uses the concept of observing variation in gene content of strains within a given species.

2. Experimental Procedure

2.1 Bacteria isolation and enrichment

2.1.1 Isolation

The bacteria used in this study are isolated from fresh urine and acid mine water, Kota Tinggi, Johor, Malaysia. Samples from acid mine water was taken over the dry season to avoid auto dilution on the sample via rainfall. Sample was collected from the discharge point of the mining retention pond. A PTFE bottle was used in order to keep the sample collected. To ensure that the sample collected is maintained at the right condition, the PTFE bottle containing the sample was kept in a box with ice cubes before being transported back to the lab. Upon arriving at the lab, the sample was kept at 4°C until enrichment process. Bacteria isolated from fresh urine was temporarily name *Ureolytic bacteria* while bacteria isolated from acid mine water was named *Sulphate reduction bacteria* (SRB). The isolation process of both *ureolytic* and *sulphate reduction bacteria* (SRB) were conducted following a process of enrichment, serial dilution streaking plate, strain purification and gram staining. Isolation and purification method of bacteria was done according to [11]. All process and media used were autoclave at 121°C for 15 minutes for sterilization.

2.1.2 Enrichment

The enrichment of bacteria was conducted after the bacteria were isolated. The enrichment process is conducted to ensure the bacteria survivability in concrete. The process involves adding bacteria into media composition. A control flask without addition of urine and acid mine water were also prepared for ureolytic and sulphate reduction bacteria respectively. Composition of *sulphate reduction bacteria sample* (SRB) consists of 25 ml (nutrient broth) added with 10 ml (Mg SO₄·7H₂O) and 1 ml (water from Sg pelepah Kota Tinggi). *Ureolytic bacteria* composition including 25 ml (nutrient broth), 10ml (urea 40%) and 1 ml (urine). Two environmental condition namely pH and oxygen concentration were controlled in the isolation process. Realising that concrete environment is a high alkaline environment, the pH value of the isolation flask is maintained in alkaline condition for ensuring self survival of the isolated strains. The high pH value contributes to high urease activity which leads to high carbonate precipitation rate [12]. The pH of each sample were adjusted to an alkaline condition by adding NaOH until the pH value reaches the range of 9-11.

Oxygen concentration in the isolation flask was monitored to be in anaerobic condition. This is to ensure only anaerobic or facultative bacteria will be isolated. Adjustment of the oxygen is needed due to lack of oxygen in concrete material. Nitrogen gas was purged in the enrichment
flask before enrichment started to remove the remaining oxygen in the flask. The concentration of oxygen was monitored with a dissolved oxygen meter to ensure very low oxygen or 0 ppm oxygen. The flask was shaken at room temperature. The adjustment of pH and anaerobic condition were done every day over the enrichment period of 20 days. The set-up of the enrichment flask as shown in Fig. 1.

2.1.3 Dilution and Pure Streaking Plate Method
Along 20 days of enrichment, the flask with sample will turn turbid. Every 10 days 0.1 ml of the culture was taken and added to 9.9 ml of sterile distilled water. The serial dilution process was done for both samples using yeast extract and sulphate API agar which were prepared for \textit{Ureolytic} and \textit{Sulphate reduction} bacteria respectively. Each of the dilution was aseptically plated on yeast extract and sulphate API agar which were appropriately labeled. The plates were incubated at 37°C in the incubator until the desired strain growth. Colonies appeared were picked up and cultured. Fig. 2 illustrates agar with colonies of bacteria.

2.1.4 Strain Purification and gram staining
Purification step was performed until pure strain was obtained. Purification involves a streak plate method was done to ensure only single strain obtained in each plating. Gram staining is used to investigate the major categories of microorganism or examine the morphology. In this study simple stains including crystal violet, iodine and safranin were applied. Two groups of bacteria can be distinguished with gram staining. Using this method, gram positive bacteria cell wall will retain crystal violet while gram negative change.
2.2 Bacteria identification process
2.2.1 Preparation of Lysogeny Broth
The bacteria sample is first inoculated into Lysogeny Broth (LB) and incubated for 18 hours with temperature of 37°C and 400 RPM. The samples were then centrifuged to collect pellet for gDNA extraction.

2.2.2 Genomic DNA isolation of bacteria
The DNA extraction of the bacteria used in this study was done based on modified phenol-chloroform protocol. Based on this method, 1.5ml of bacterial cell suspensions was centrifuged at 13,000 RPM, 4°C for 2 min. The bacterial pellets were resuspended with TEN extraction buffer (0.1M NaCl, 10mM Tris-Cl; pH 8.0, 1mM EDTA; pH 8.0). They were then mixed by gently pipetting up and down till homogenized. RNase (10mg/ml) was added to the tube followed by the addition of lysozyme (50µg/ul). The tubes were gently inverted and incubated at 37°C for 30 min. After that, TENST buffer (0.1M NaCl, 10M Tris-Cl; pH 8.0, 1mM EDTA; pH8.0, 0.12% TritonX-100, 1.6% N-lauryl sarcosine) was added to the tubes followed by further 1 hour incubation at 37°C. Proteinase K (10mg/ml) was later added, followed by incubation at 55°C for 1 hour. The almost clear suspensions were treated with 15% SDS prior to further 30 min incubation at 55°C. An equal volume of phenol/chloroform/isoamyl alcohol (25:24:1) was added and mixed gently followed by centrifugation at 13,000 RPM, 4°C; for 5 min.

3. Results and Discussion
3.1 Bacteria
The bacteria strains were successfully isolated and enrichment process was conducted. The bacteria was purified by conducting serial dilution streaking plate. The pure strain of bacteria obtained was analyze by gram staining. The Gram staining results obtained showed that both bacteria was gram positive. Gram positive bacteria denoted that bacteria remain coloured with gram staining even after washing with alcohol or acetone. The characteristic for Gram positive bacteria is absent of outer membrane, 20-30mm thick cell wall, the wall contains 70-80 % murein and teichoic acids. The Gram-positive lineage of bacteria are species which have a common phylogeny and cell wall structure, among the many Gram positive bacteria are Bacillus, Clostridium, Lactobacillus, Mycoplasma species.

3.2 DNA Quantification of bacteria
DNA quantification was quantified spectrophotometrically using a Nanodrop 2000 spectrophotometer (Fisher Scientific). Absorbance measurements were taken at 260nm and 280nm and used to calculate the DNA purity and concentration. DNA samples were considered free from protein contamination if the A260 to A280 ratio was between 1.8 and 2.0. The result of the quantification is in Table 1.
Table 1. The concentration and the quality of DNA using Nanodrop.

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<td>1</td>
<td>S</td>
<td>165.1 ng/µl</td>
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<tr>
<td>2</td>
<td>U</td>
<td>159.7 ng/µl</td>
<td>ng/µl</td>
<td>1.84</td>
<td>2.12</td>
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3.3 Polymerase Chain Reaction (PCR)

PCR primers have been employed to confirm the presence or absence of microorganisms. Primers which are used in both directions: forward and reverse such as in this study are longer primers. This forward and reverse primers sequence are designed based on the short general primers. The PCR reaction condition was a 10X PCR Buffer, 25 mm MgCl₂, 2.5 mm dNTPs, 10 µmol each primer (27F: 1492R), 5U Taq DNA polymerase. Universal 16SrDNA PCR was performed with forward and reverse primers, which are 27 (forward primer) 5’-AGAGTTTGATCMTGGCTCAG-3’ and 1492 (reverse primer) 5’-GGGTTACCTTGTTACGACTT-3’. After 35 cycles consisting of denaturation at 95°C (30 Seconds), Annealing at 50°C (30 Seconds) and extension at 72°C (1 min and 30 seconds), the PCR product is analyzed on an agarose gel. A band indicating a fragment was shown by agarose gel electrophoresis. A PCR product of about 600 kb in size was successfully amplified from the two samples. The agarose gel product is as shown in Figure 3.

3.4 Molecular Identification

After purification of the PCR product using the Qiagen PCR Purification Kit. Identification of DNA isolated. Analysis of DNA sequencing was performed using the BLASTX software (BLAST), National center for biotechnology information. Both DNA sequences for sulphate reduction and ureolytic bacteria resulted to tree of phylogenetic as presented in Figure 7 and 8. The Figures will result to the most promising strains.

3.5 DNA sequences for bacteria

The DNA sequences for both sulphate reduction bacteria and ureolytic bacteria are provided in 3.5.1 and 3.5.2. The basic unit of DNA structure is nucleotide, composed of phosphate, deoxyribose sugar and a nitrogen base. Each deoxyribose sugar bonds covalently in a repeating pattern with two phosphates. One of the bond is to number 5’ (five primer) another bond is to 3’ carbon on deoxyribose. This specifies the order and direction of each strand. The nitrogen bases, purines and pyrimidines attach by covalent bonds at the 1’ position of the sugar. Pairing of purines and pyrimidines is dictated by the formation of hydrogen bonds. Thus DNA sequence, the purine Adenine (A) pairs with pyrimidine Thymine (T) and the purine Guanine (G) pairs with pyrimidine Cytosine (C) [13]. These the bases that made up a strand of DNA. The DNA sequence is then compared to similar or any other DNA sequences by uploading the sequence to BLAST.
programs, which is a program that is supported by the National Center for Biotechnology Information (NCBI).

3.5.1 DNA Sequences for Sulphate Reduction bacteria

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GNAGTTGCGGGCGACTATACATGCACTGAGCAATGGATTAAGAGCTTGCTCTTAT
GAAGAAGACGGGCGGGTGGATCTACACATGGACCGGGTGATTTCGAGAA
TGAAGAACGGGCGGGTGGATCTACACATGGACCGGGTGATTTCGAGAA
TGAAGAACGGGCGGGTGGATCTACACATGGACCGGGTGATTTCGAGAA
TGAAGAACGGGCGGGTGGATCTACACATGGACCGGGTGATTTCGAGAA
```
3.5.2 DNA Sequences for Ureolytic bacteria
NNNGANNTNGGGCTGCTATAATGCAGACGCTTCTTTTCTCTCCCGAGTGCTTGCACTCA
ATTGGAAAGGGAGTGGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGG
GGATAAAGCTTTGGAACACAGGGGTGCTAATACCCGATAAACGATTTATGCGGACAGTCATTGCA
GTAAGGGGGCTTTGCCTGGTATGGATGCCGAGGATCTGAGCGACCTGAGAGGGTGACCTGCC
AGGTAACGGCTCACCAAGGCCACGATGCAATGCCGACCTGAGAGGGTGATCGGCCACAC
TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAAT
GGACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAAC
TCTGTTGTTAAGAAGAAACAGGAGCTGTTAATACGGCAAGTGCCTGATCTTAAACC
AGAAAGCCACAGGCTAATACGCGACGGAGCGTTTCTTTAAGCTGCTATGGAAGGACGAC
CCGGGATTTATGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGGAAGGACGAC
GGAAATCCATGTGTAGCGGTGAATGCGTAGATATATGGAGGAACACCAGTGCCGAAAG
CGGCTCTCTGGTCACTAAGCTAGCGCTAGGCTGGAAGGTGGGAGCAAACAGGAGATT
GATACCCCTGTAGTCCACGCCGTTAAGACGTGAGTGTAATGAGTTGGAAGTTTCGCCCT
TCAGTGTCGACAGAACACGATTAAAGCAGTCCGGCTGGGAGATCGACGCGCAAGGTGAA
ACCTAAAGAAGATACCTCAGGCTTTGAGATACCGTCAGGGGACGTTCAGTTACTAACGTCTGGTT
TTCTTTTCTCTTTCTCTTTTCTCTTTTCTCCGTACGCTGCTGCTGTGTTAGCCGTGGCTTT
CTGGTTAGATACCGTCAGGGGACGTTCAGTTACTAACGTCTGGTTTCTCTCTAACAACAA
AGTTTTACGATCCGAAAACTTTCTTCACTCCAGCGGGGGTTGCTCGGGCAAAATTTTCGT
CCATTGGCGAAAAATTCCCTACTGGCTGCCTCCCCGTAAGGAATCTGGGGCCGGGGCTCC
AATCCCAAGTGTGGGCCGAATCACCCCTTCCAAGTGGGGNNTAGGCATCGGGGGCCTTGG
GGAAGCCCGTTACCTCCACCAACTTAGNTTAATGGACNCCGGGGGGTCCTCCATTANGG
GGACCCCGAG

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Figure 4. Phylogenetic position of *Bacillus SP* and closely related taxa (*Sulphate reduction bacteria*).
4. Conclusion
The bacteria in this study was isolated from fresh urine and acid mine drainage water. The isolated bacteria was enriched to suit concrete environment. After enrichment, the bacteria was purified by serial dilution and gram staining was conducted. The Gram staining results revealed that both bacteria was gram positive. The bacteria was identified through PCR and 16S rDNA sequencing as *Bacillus sp* and *Enterococcus faecalis*.

Acknowledgement
This research was supported by Universiti Tun Hussein Onn Malaysia (UTHM) and The Ministry of Higher Education Malaysia through Fundamental Research Grant Scheme (FGRS), Vot 1211.

References