
**IDENTIFICATION OF ISOLATED ORGANISMS FROM
PETROFIELDS BY GENE SEQUENCING**

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ABSTRACT:

Hydrocarbon degradation can occur with diverse varieties of microbes in nature. Different chemical compounds have shown their susceptibility to the microbial degradation. . Fungal species generally forms carcinogenic trans – diols while bacterial species generally forms cis – diols. Contaminated soil contained significantly higher amount (50 – 75 %) of gram negative bacteria having genotypes enclosing genes compared to pristine soil (0 – 12.5 %). Application of bioinformatics tools like BLAST has identified microorganism1 as *Bacillus cereus*, microorganism2 as *Pseudoxanthomonas mexicana*, microorganism3 as *Halomonas daqingensis* and microorganism4 as *Parapusillimonas granulii*. These microbes were given names accordingly from PS11 to PS14 respectively. They were assigned unique identification numbers starting from KM192258 to KM192261

KEY WORDS : IDENTIFICATION, GENE SEQUENCING, *Bacillus cereus* *Pseudoxanthomonas mexicana*, *Halomonas daqingensis*, *Parapusillimonas granulii*.

INTRODUCTION

. Few microbes show versatility for degradation of various compounds while some microbes can degrade only one or two components. 40 – 80 % of degradation of oil spills is managed by biodegradation process. Marine sediments, soil, estuaries, sea, etc. forms the various habitats for isolation of microbes having hydrocarbon degradation capability. Along with bacteria being the most significant agent for breakdown of hydrocarbons, few of the fungal species like *Candida*, *Fusarium*, *Trichoderma*,

Aspergillus are also known to degrade hydrocarbons. (Adibarata & Achibana 2009; Omotayo *et al.* 2011; Kafilzadeh *et al.* 2010) Amongst bacterial species, few species known for biodegradation of hydrocarbons are *Pseudomonas*, *Acinetobacter*, *Bacillus*, *Alcaligenes*, *Micrococcus*. β – oxidation process is involved in biodegradation of alkanes. (Ting *et al.* 2009; Joo & Kim 2013) Aromatic hydrocarbon rings

are generally hydroxylated to form diols which form cathecols and subsequently give intermediates of the TCA cycle.

Total degradation of aromatic hydrocarbons produces harmless end products like CO₂ and water. Earlier exposure of bacteria to hydrocarbons leads to increased degradation capacity along with the raised population of degrading bacteria at the site of contamination. Bacteria isolated from contaminated sites have greater chances to have plasmid which codes gene responsible for the degradation of hydrocarbon. Few well studies plasmids of *Pseudomonas* are TOL plasmid for toluene degradation, XYL for xylene degradation, CAM for camphor and SAL for salicylate.

MATERIALS AND METHODS

There are several methods are available for identification of microbes. Primary method includes study of colony morphology and gram staining. Both these method will give rough idea about the characteristic of microbes. Various Biochemical test as mentioned in the Bergey's manual and MIDI analysis can provide more information about the microbes but ribosomal small subunit sequencing is one of the most efficient and accurate method for identification of living organism. Since sequences of these subunit is highly conserved hence can be used widely for identification of microbes also.

As compare to the whole genome these region is very small and unique which makes it more potential for identification. However there are other conserved genes also but rarely used for identification. (Thenmozhi et al. 2011; Kumar et al. 2006; Shukla et al. 2010) Here, 16s rRNA sequencing was done as all the microbes were prokaryotes and the sequences obtained were compare with the database available on NCBI.(Singh & Fulekar 2010; Mittal & Singh 2009) All the sequences were submitted to NCBI and given universal identification numbers.

RESULTS

As mentioned earlier ribosomal RNA gene sequencing was used for the identification of microbes. 16s ribosomal gene sequencing is one of the most reliable method for accurate identification of microbes. (Okoh 2006) The following nucleotide sequences were obtained which were further analyzed using bioinformatics tools.

Microorganism Sequence 1

gaaaccgggg ctaataccgg ataacattht gaaccgcat ggttcgaaat tgaaaggcgg cttcggctgt cacttatgga tggaccgcg
tcgattagc tagttggtga ggtaacggct caccaaggca acgatgcgta gccgacctga gagggatgac ggccacactg ggactgagac
acggcccaga ctctacggg aggagcagc agggaaatctt ccgcaatgga cgaaagtctg acggagcaac gcccggtgag tgatgaaggc
tttcgggtcg taaaactctg ttgttaggga agaacaagtg ctagtgaat aagctggcac cttgacggta cctaaccaga aagccacggc
taactacgtg ccagcagccg cggtataacg taggtggcaa gcgttatccg gaattattgg gcgtaaagcg cgcgcagggtg gtttcttaag
tctgatgtga aagcccacgg ctcaaccgtg gagggcatt ggaaactggg agacttgagt gcagaagagg aaagtggaat tccatgtga
gcggtgaaat gcgtagagat atggaggaac accagtggcg aaggcgactt tctggtctgt aactgacact gaggcgcgaa agcgtgggga
gcaaacagga ttagataccc tggtagtcca cgccgtaaac gatgagtgtc aagtgttaga gggttccgc ctttagtgc tgaagttaac
gcattaagca ctccgctgg ggagtagcgc cgcaaggctg aaactcaag gaattgacgg gggcccgcac aagcgggtga gcatgtggtt
taattcgaag caacgcgaag aacctacca ggtcttgaca tctctgaaa acctagaga tagggcttct cttcggggag cagagtgaca
ggtggtgcat ggtgtcgtc agctcgtgc gtgagatgtt gggttaagtc ccgcaacgag cgcaaccctt gatcttagtt gccatcatta
agttgggcac tctaagtgta ctgccggtga caaacgggag gaaggtgggg atgacgtcaa atcatcatgc cccttatgac ctgggtaca
cacgtgtac aatggacggg acaaagagct gcaagaccgc gaggtggagc taatctcata aaaccgttct cagttcggat tgtaggctgc
aactcgccta catgaagctg gaatcgtag taatcgcgga tcagcatgcc gcggtgaata cgttccggg cttgtacac accgccgctc
acaccacgag agtttgaac acccgaagtc ggtgggggta acctttttg ggagccagcc c

Microorganism 2

agtcgggggt aatggcccac caaggcgacg atcggtagct ggtctgagag gatgatcagc cacactggaa ctgagacacg gtccagactc
ctacgggagg cagcagtgagg gaattattgga caatgggagc aagcctgatc cagccatacc gcgtgggtga agaaggcctt cgggtttaa
agccctttt ttgggaaaga aatcctgtc attaatactc ggtggggatg acggtacca aagaataagc accggctaac ttcgtccag
cagccgaggt aatacgaagg gtcaagcgt tactcggat tactgggctg aaagcgtgc taggtggtgg ttaagtctg ctgtgaaagc
cctgggctca acctgggaat tgcatggat actggatcac tagagtgtg tagaggatg cggaattct ggtgtagcag tgaatgcgt
agagatcaga aggaacatcc ttggcgaagg cggcatcctg ggccaacact gacactgagg cacgaaagcg tggggagcaa acaggattag
ataccctggt agtccagcc ctaaagatg cgaactggat gttgggtgca acttggcacc cagtatcga gtaacgcgt taagtccg
gcctggggag tacggtcga agactgaaac tcaaaggaat tgacgggggc ccgcaaacg ggtggagtat tgggttaat tcatgcaac
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gtcgtcagct cgtgtcgtga gatgttgggt taagtccgc aacgagcga accctgtcc ttagtcca gcacgtaatg gtgggaactc
taaggagacc gccggtgaca aaccggagga aggtggggat gacgtcaagt catcatggcc cttacgacca gggctacaca cgtactaca
tggtggggac agagggtgc aaaccgcga gggtgagcca atcccagaaa ccctatctca gtccgattg gactctgca ctcgactcca
tgaagtcgga atcgttagta atcgagatc agcattgctg cggtgaatac gttccgggc cttgtacaca ccgccgta caccatggga
gtttgtgca ccagaagcag gtagctt

Microorganism 3

ggggaaacc aggtaatac gcatacgtc ctacgggaga aagcaggga ctttcgggc ctgctgctat cggatgagcc tatgtcggat
tagctggttg gtgaggaat ggctaccaa ggcgacgat cgtagctggt ctgagaggat gatcagccac atcgggactg agacacggcc
cgaactccta cgggaggcag cagtggggaa tattggacaa tggcgcaag cctgatccag ccatgccgcg tgtgtgaaga aggcctcgg
gttgtaaagc actttcagtg gggaagaaag ctttcgggt aataccggg aggagggaca tcaccacag aagaagcacc ggtaactcc
gtgccagcag ccgcgtaat acggagggtg cgagcgttaa tcggaattac tggcgtaaa gcgcgctag cggcgttgat aagccggtg
tgaaagcccc gggctcaacc tgggaacggc atccggaact gtcaggctag agtgcaggag aggaaggtag aattcccggt gtagcgtga
aatgcgtaga gatcgggagg aataccagtg gcgaaggcgg cttctggac tgactgac gctgagggtc gaaagcgtgg gtagcaaca
ggattagata ccctgtagt ccacccgta aacgatgtcg actagccgtt gggccttcg cggactttgt ggcgagta acgcgataag
tcgaccgct ggggagtacg gcccaaggt taaaactca atgaattgac gggggcccgc acaagcgggt gagcatgtgg ttaattcga
tgcaacgcga agaacttac ctaccctga catcctcga accctcggg gacgaagggg tgccttcggg aacgcagaga caggtgctgc
atggctgctg tcagctcgtg ttgtgaaatg ttgggttaag tcccgaacg agcgaaccc ttgtccat ttgccagca ttggtcggg
aactctaggg agactgccg tgacaaaccg gaggaagggt gggacgacgt caagtcatca tggccttac gggtagggct acacagctc
tacaatggtc agtacaagg gttgcgaact tgcgagagt agccaatccc agaaagtga tctcagtcg gatcggagtc tgcaactga
ctccgtgaag tcggaatcg tagtaatcgt gaatcagaat gtcagggtga atacgttccc gggccttga cacaccgcc gtcacacat
gggagtggac tgcaccagaa gtggttagcc taacctcgg gagggcgatc accacgg

Microorganism 4

gggggataac tacgcgaaag cgtggtaat accgcatac cctacgggg gaaaggggg gattctcgg aacctctac tattggagc
gccgatatcg gattagctag ttggtgggt aaaggcctac caaggcgac atccgtagct gtttgagag gacgaccagc cacactggga
ctgagacag gccagactc ctacgggagg cagcagtgga gaattttgga caatgggggc aacctgac cagccatccc gcgtgtgca
tgaaggcctt cgggtgtaa agcactttg gcaggaaga aacaggtctg gcgaatact ggactgaat acggtacctg cagaataagc
accgctaac tacgtgccag cagcccggt aatacgtagg gtgcaagct taatcggat tactggcgt aaagcgtcg caggcgttc
ggaaagaagg gtgtgaaatc ccagggctta acctggaat ggcattcta actaccggc tagagtatgt cagagggggg tagaattca
cgtgtagcag tgaatgcgt agagatgtg aggaataccg atggcgaagg cagcccctg ggataatact gacgctcatg cacgaaagc
tggggagca acaggattag ataccctgt agtccagcc ctaaagatg tcaactagct gttggggct tcggcctta gtagcgcagc
taacgcgtga agttgaccg ctggggagta cggcgcgaag attaaaact aaaggaattg acggggacc gcacaagcgg tggatgatg
ggattaattc gatgcaacg gaaaaactt acctaccctt gacatgtctg gaatcccga gagatttgg agtgctcga agagaaccg
aacacaggtg ctgcatggt gtcgtcagct cgtgtcgtga gatgttgggt taagtcccgc aacgagcga acctgtca ttagtgtca
cgaagggca ctctaatgag actgccgtg acaaaccgga ggaagggtgg gatgacgtca agtctcatg gccctatgg gtagggctc
acagtcata caatggtcgg gacagagggt cgccaagccg cgaggcggag ccaatccag aaaccgatc gtagtcgga ttgagctc
caactcgact gcatgaagtc ggaatcgtg gtaatcgcg atcagcatg cgcgtgatac gt

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REFERENCES

Adibarata, T.H. & Achibana, S.T., 2009. Microbial Degradation of Crude Oil by Fungi Pre-Grown on Wood Meal. *Interdisciplinary studies on Environmental Chemistry*, pp.317–322.

Joo, M.H. & Kim, J.Y., 2013. Characteristics of crude oil biodegradation by biosurfatant producing bacterium *Bacillus subtilis* JK-1. *Journal of Korean Society for Applied Biological Chemistry*, 59, pp.193–200.

Kafilzadeh, F., Farhangdoost, M. & Tahery, Y., 2010. Isolation and identification of phenol degrading bacteria from Lake Parishan and their growth kinetic assay. *African journal of Biotechnology*, 9(40), pp.6721–6726.

Mittal, A. & Singh, P., 2009. Isolation of hydrocarbon degrading bacteria from soils contaminated with crude oil spills. *Indian Journal of Experimental Biology*, 47, pp.760–765.

Okoh, A.I., 2006. Biodegradation alternative in the cleanup of petroleum hydrocarbon pollutants. *Biotechnology and Molecular Biology*, 1(2), pp.38–50.

Omotayo, A.E. et al., 2011. Degradation of aviation fuel by microorganisms isolated from tropical polluted soils. *International Journal Of Biological and Chemical Sciences*, 5(2), pp.698–708.

Shukla, K.P., Singh, N.K. & Sharma, S., 2010. Bioremediation : Developments , Current Practices and Perspectives. Genetic Engineering and Biotechnology Journal, pp.1–20.

Singh, D. & Fulekar, M.H., 2010. Benzene bioremediation using cow dung microflora in two phase partitioning bioreactor. Journal of hazardous materials, 175, pp.336–343.

Ting, S.Y., Tan, H.C. & Aw, C.S., 2009. Hydrocarbon-degradation by isolate *Pseudomonas lundensis* UTAR FPE2. Malasian Journal of Microbiology, 5(2), pp.104–108.