

ORIGINAL RESEARCH ARTICLE

Genetic Analysis of Plastic Degrading Bacterial Strains

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ABSTRACT

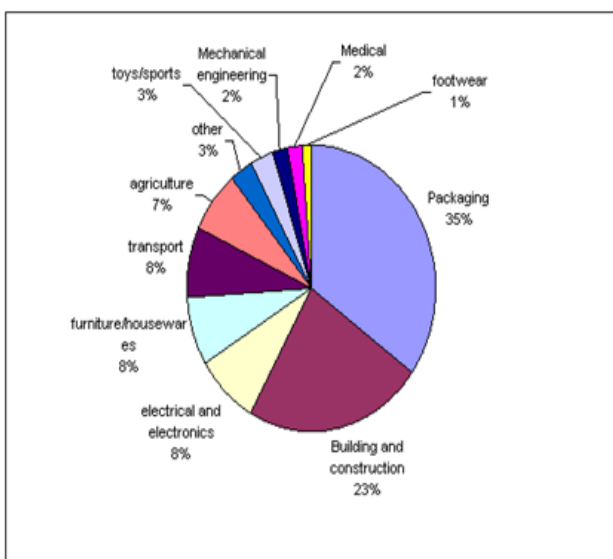
Though plastics have become indigenous, now days, they are very hazardous and should be disposed off, properly. Land filling, incineration and recycling are the most common methods employed for the disposal of plastics and all methods have their own environmental and health hazards. So, biodegradation will be the right choice for the proper disposal of plastic wastes. Soil samples from the compost yard have the rich consortia of biodegrading microbes. These samples were inoculated into mineral salt medium with plastic as the sole carbon source for the isolation of the plastic degrading strains. Characterization of bacterial strains was done based on molecular characterization. To ensure that plastic degradation is plasmid mediated, the plasmid was isolated and purified by the alkaline lysis method from these strains and after plasmid curing they were found to lose this property. Transformed strains showed the ability to degrade plastics.

Key words: Land filling, incineration, recycling, biodegradation, molecular characterization.

INTRODUCTION

Plastics are widely employed in the variety of uses. Out of which, packaging represents the largest single sector of plastics almost in all the nations. The sector accounts 35% of plastics consumption which is the highest, when compared to other usages (APME, 1999). Worldwide Plastics Industry witnessed a steady growth in the year 2007.

USES OF PLASTICS



Asia has been world’s largest plastics consumer for several years, accounting for about 30% of the

global consumption excluding Japan, which has share of about 6.5%. Next to Asia is North America with 26% share, then Western Europe with 23% share in the global market.

Due to the indigenous use of plastics, the plastic waste stream emerges from domestic, industrial and municipal refuse (Jayasekara *et al.*, 2005). The plastic waste is disposed off through land filling, incineration, recycling and degradation (Aamer Ali Shah, 2007). Out of these, first three methods have a number of demerits and hazards.

Microorganisms such as bacteria fungi and actinomycetes are involved in the degradation of both natural and synthetic plastics (Gu *et al*, 2000a).

A wide variety of actinomycetes like *Streptomyces* strains and fungi like *Aspergillus* sp and *Penicillium* sp are reported active against polyethylene(PE) (Zheng *et.al*, 2005).

Curvalaria sp, *Fusarium* sp, *Aureobasidium* sp, *Cladosporium* sp, *Pseudomonas* sp and *Comamonas* sp are found to be effective against polyurethane (Zheng *et.al*, 2005).

Pseudonocardia sp, *Micromonosporaceae* sp, *Thermomonosporaceae* sp (Tokiwa and Jarerat, 2003) *Bacillus* sp, TT96, *Aspergillus* sp and

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Streptomyces sp (Sanchez *et al.* 2000) are effective against PHA.

MATERIALS AND METHODS

PLASTIC FILMS

High density polyethylene (HDPE) and Low density polyethylene (LDPE) which are widely used to manufacture carry bags, milk and oil pouches were used for the study (Gosh *et al.*, 2004).

ENRICHMENT OF PE DEGRADING MICROORGANISMS

Soil samples were collected from a plastic dumpsite inside Madras Christian college campus, Chennai. A total 1g of the soil sample was suspended in 10ml of sterile Milli-Q water and vortexed for 15 minutes. Nearly 100 μ l of suspension was used as inoculums. Erlenmeyer flasks containing 100 ml of mineral salt medium, strips of untreated polyethylene, 0.01 % (w/v) glucose and 1 ml of inoculums were used for maintaining the first pre-culture. Thee later subcultures did not contain glucose but only the polymer as the sole carbon source. After three successive sub-culture, in which microorganisms were grown on Polyethylene (PE) and without glucose, pure cultures were isolated on Nutrient agar plates (Himedia Limited, Mumbai, India) for bacterial isolation (Artham.T& Doble.M, 2008).

I. Identification of PE degrading bacterial strains

The molecular characterization of the bacterial isolates was done based on 16s rDNA sequencing. Amplification of 16s rDNA fragment of the strains were performed with 125–1, 562 ng of bacterial DNA as template using 0.4 μ M of 8f (AGAGTTTGATCCTGGCTCAG) and 0.4 μ M of 1492r (GGTTACCTTGTTACGACTT) eubacterial universal primers [Mohana,s., et al 2005, Eden, P.A., *et al*, 1991, Weisburg, W.G., *et al*,1991] in a reaction mixture which contained 1.5 mM MgCl₂, 0.3 mM each of dNTPs, and 2.5 U of Taq polymerase (InvitroGene), in a What man Biometra® thermo cycler. The polymerase chain reaction (PCR) program included an initial denaturation of 94°C for 5 min followed by 35 cycles of denaturation at 94°C for 1 min, annealing at 57°C for 1 min, extension at 72°C for 1.5 min, and a final extension at 72°C for 15 min. The amplified product was resolved on 1% (w/v) agarose gel. PCR product elution was carried out with Wizard SV Gel and PCR Cleanup System (Promega). The nucleotide sequence was determined manually using the dideoxynucleotide chain termination method [Thermo Sequenase kit

(Amersham)] or automatically using BigDye® Terminator v3.1 Cycle Sequencing Kit in the ABI PRISM 3100-Avant Genetic Analyzer with universal and reverse primers. DNA sequence analyses were performed using the Blast and Bioedit programs.(Center for Cellular & Molecular Biology, Hyderabad) . The isolates were identified based on the similarity scores and the sequences were submitted to NCBI Gen Bank to get accession number (Soni.R , *et al.*, 2008).

II. Screening and Curing of plasmid from bacterial strains

The bacterial strains used in the study were isolated by the selective enrichment method and maintained in the laboratory (Mashetty *et al.*, 1996). The bacterial capable of degrading PE were initially grown on a mineral salts medium amended with 0.2% (v/v) PE before autoclaving. The flasks were inoculated at 37°C on an orbital shaker at 160rpm for 4-6 days. The PE – grown cells at mid-exponential phase were pelleted by centrifugation and washed with GTE (Glucose-Tris-EDTA) buffer. The pellet was re-suspended in GTE buffer and the plasmid was isolated by the alkali lysis method (Sambrook *et al.*, 1989). The aqueous phase was washed with phenol-chloroform, and the plasmid DNA was precipitated by adding two volumes of ethanol at room temperature. The precipitated DNA was recovered by centrifugation and subjected to electrophoresis after re-dissolving the DNA pellet in TE (10 MM Tris, 1 MM EDTA pH 8.0) on 0.8% agarose gel.

Two methods were tried to cure the plasmid from Bacillus and Pseudomonas sp to check whether the cured organism retain the ability to utilize PE as the sole source of carbon. In the first method, spontaneous loss of the above phenotype was testing by growing the organism on LB agar by up to five or six subculture on agar plates containing 0.2% PE. In the second method, the bacterium was grown in LB broth in the presence of ethidium bromide (Rani *et al.*, 1996).

TRANSFORMATION OF DEGRADATIVE PLASMID

The PE degradative plasmids were transformed in to *E.coli* DH5 α strain by using the procedure of Hanahan (Hanahan *et al.*, 1983).

RESULTS

Identification of plastic degrading bacterial strains:

Plastic degrading bacterial strains were identified as *Pseudomonas mediterranea* strain M2, Accession number (Gen bank) - JQ904748 &

Bacillus megaterium strain B1, Accession number (Gen bank) - JQ904750.The partial 16s Ribosomal RNA gene of *Pseudomonas mediterranea* M2 strain is

Origin

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1  cgggatccag agtttgatcc tggctcagaa cgaacgctgg cggcaggcct aacacatgca
61  agtcgagcgg tagagagggtg cttgcacctc ttgagagcgg cggacgggtg agtaatgcct
121 aggaatctgc ctggtagtgg gggataacgc tcggaaacgg acgctaatac cgcatacgtc
181 ctacgggaga aagcagggga ccttcggggc ttgctgctatc agatgagcct aggtcggatt
241 agctagtggg tgaggtaatg gctcaccaag gcgacgatcc gtaactgggtc tgagaggatg
301 atcagtcaca ctggaactga gacacgggtc agactcctac gggaggcagc agtggggaat
361 attggacaat gggcgaaagc ctgatccagc catgccgcgt gtgtgaagaa ggtcttcgga
421 ttgtaaagca ctttaagtgt ggaggaaggg ccattacctc atactgtgat gttttgacgt
481 taccgacaga ataagcaccg gctaactctg tgccagcagc cgcggtaata cagagggtgc
541 aagcgттаат cgggaattact gggcgtaaag cgcgcgtagg tggttcgтта agttggatgt
601 gaaagccccg ggctcaacct gggaaactgca ttcaaaactg tcgagctaga gtatggtaga
661 gggtggtgga atttctgtgt tagcggtgaa atgcgtagat ataggaagga acaccagtgg
721 cgaaggcgac cacctggact gatactgaca ctgagggtgcg aaagcgtggg gagcaaacag
781 gattagatac cctggtagtc cacgccgtaa acgatgtcaa ctagccgttg ggagccttga
841 gctcttagtg gcgagctaa cgcattaagt tgaccgcctg gggagtacgg ccgcaaggtt
901 aaaactcaaa tgaattgacg ggggcccgca caagcgggtg agcatgtggt ttaattcgaa
961 gcaacgcgaa gaaccttacc aggccttgac atccaatgaa ctttccagag atggattggt
1021 gccttcggga acattgagac aggtgctgca tggctgtcgt cagctcgtgt cgtgagatgt
1081 tgggttaagt cccgtaacga gcgcaaccct tgtccttagt taccagcacg ttatgggtgg
1141 cactctaagg agactgccgg tgacaaaccg gaggaagggtg gggatgacgt caagtcatca
1201 tggcccttac ggctggggct acgcacgtgc tacaatgggtc ggtacagagg gttgccaaagc
1261 cgcgagggtg agctaattcc ataaaaccga tcgtagtccg gatcgcagtc tgcaactcga
1321 ctgctggaag tcggaatcgc tagtaatcgc gaatcagaat gtcgagggtga atactgtccc
1381 gggccttgta cacaccgcc gtcacaccat gggagtgggt tgcaccagaa gtagctagtc
1441 taaccttcgg gggcaggtt accacgggtg gattcatgac tggggtgaag tcgtaacaag
1501 gtaccgtag gatcccg
```

And the *Bacillus megaterium* strain B1 plasmid PE sequence is

Origin

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1  gatcattttg ccgattatgt ttcaatcaga aagttgtggt cgatttcgga cagatatttt
61  gaatatattt attcaactgt taactaaaac tgtctgcaaa ttaatcaatg tctctagtaa
121 aattccgatt ttataccac tctatttttc atcaatagga catgatataa taaaaaagaa
181 cgggatatga ggcctccggt ctcttggttg tacttggtgc aatagtacgt ttatttggtt
241 acgtatatta tagcaagtac tccaacaaaa aatcaatcgt tggaggaatt tagaatgaa
301 tggaaattatc aaaacaataa aaacaacgca atatgctcaa atacataacg cgcattaca
361 aacggacctg gaggacttgc ggtctatcgg tctattaagt catattatga gcttaggtga
421 aggttgagc attaggaaga cccagttaca aaacaaattt tctcgtagaa atgtagacgc
481 tgcttggaag gaattagcta ttaaacaata cgctgtcgggt tttagcgc atgttgacgg
541 aaaaaaagat tatttttacg ccgtatcaga tattccgatt tcgcaagcta atttcgaatt
601 gcttgtcatt gaacaaataa atctcttaca atcgcaaggt aaaaacgtca tgacgttaag
661 cgtgatacaa cattcggcac ttgaaatcac tgaaaaata tctgatgtac aaaatgtaca
721 tcagatacaa aataagcaaa tttcttctga tgtacgttct gtacaacaca gtgtgtacaa
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841 tagtagtagt ccacgtgatt ttattgatga taaattacga gaaaaatata ataatgtacc
901 tttcgacgaa gtgaaaagt aaatgcttaa cgatactgta atcgttgata cgaataagca
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1081 aaatgcagta gcagaagatc ttccagtgaa taatgatttt gaagctgaaa aggaaaaaat
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1201 gaattacacc tacaaaagcg agagcgaacg aggtgaagaa cgtgtcagaa aacgaacgcg
1261 catattggaa tcatgaagta gctgaacaac ttgacatagg tacaagcaca ttaagaaat
1321 ggtgcttaga attggaagag aacgagtacg tgttctctaa aggcgaacaa gaaagccgag
1381 cttttttaa acgtgatatt gatgttttaa tgaacatgaa aaatgaaata cgaaataaga
1441 aaaaatcact caaagatgcy gctaaaatcg cgttagaaaa ggcaagaacg ggggtcgttc
1501 tcgtagaaca agaacaggaa caagcaccce cgttcccgt cgaacaagca cagccgatgt
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1621 gtgagaacga acgagataaa gcactaatgg gtgtcatgcy tgaattacag gatgtaaaaa
1681 aaatgatagc tgcttctcaa gaggtaagta aaaaaaatg gtgggagttt tggaaaacct
1741 aattttttta gaaatcttga gtgcaatata gtttaataca tcttgagcaa cttcaatgga
1801 gtattatcaa caacatgtaa taggttattt cataatacag agaagaagtt ttattaaaaa
1861 atgatacctt caaggtgat cttttttgt agcatggtat atagcatata atattttccc
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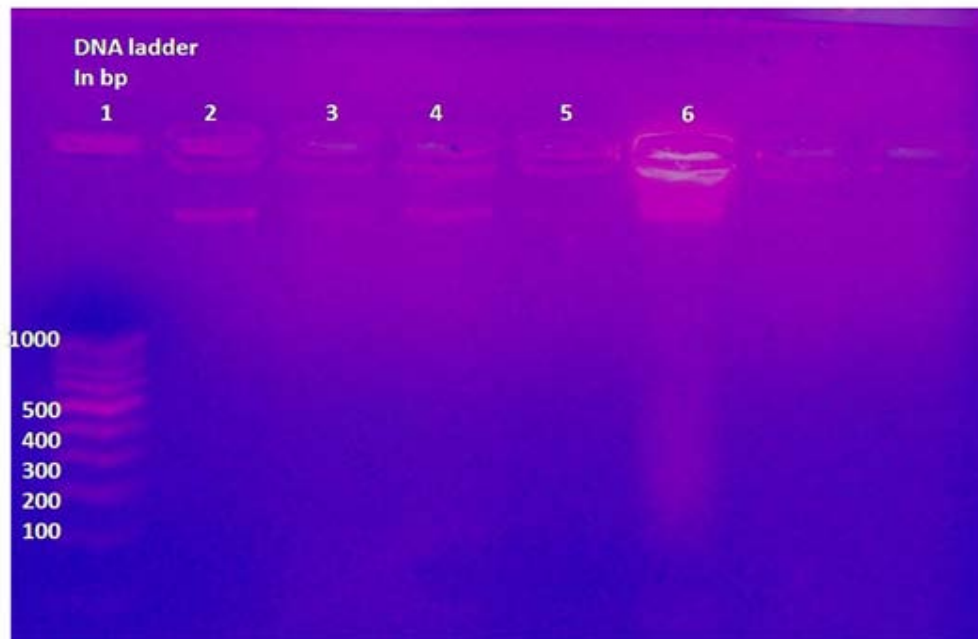
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5401 taaaacgctc atataaggca atatggaa

Plasmid isolation:

Degradative plasmids, which are responsible in degrading HDPE & LDPE were isolated from

both the strains taken from the mineral salt broth (Figure A).

Figure A: Isolation of degrading plasmids



Lane : 1 - Marker DNA

Lane: 2,3 - Plasmids from *Bacillus megaterium*.

Lane: 4,5,6 - Plasmids from *Pseudomonas mediterranea*.

Plasmid curing:

Plasmids were not isolated from both the strains after curing & these strains lost the ability to degrade LDPE & HDPE.

Transformation of plasmid:

Transformed *E.coli* DH5 α strains showed the ability to degrade polyethylene.

DISCUSSION

The 16s rDNA sequences were matched for local-alignment through NCBI-BLAST. Based on the scores and identity percentages, the isolates identified. (Soni.R *et al.*, 2009). Similarly in the present study the isolates identified as *Pseudomonas mediterranea* and *Bacillus megaterium* by molecular characterization. The plasmids were isolated from the culture capable of degrading polyethylene. A similar observation was reported in *Moraxella* sp, where 60-70 kb plasmids encoding phthalate 4,5-dioxygenase and 4,5-dihydro-4,5-dihydroxyphthalate dehydrogenase are involved in *o*-phthalate catabolism (Rani,M. *et al*,1996). Plasmid cured cells lost their ability to grow on Dimethylphthalate (DMP) (Javed Hussain Niazi, *et al*, 2001) and in this present study, 200kb plasmids capable of degrading PE were isolated from the strains and upon plasmid curing they lost that ability. Transfer of plasmids to recipient conferred the characteristics of the donor cells

(Griffith, 1928) upon transformation, the recipient cells gained the ability to degrade PE.

CONCLUSION

Plastic degrading bacterial strains were isolated from compost soil and characterization of these isolates was done by molecular characterization.

To demonstrate that biodegradation of plastics is plasmid mediated, plasmids were isolated from these strains when plasmid curing was done they lost the PE degrading activity.

Transformed *E.coli* DH5 α strain showed the ability to degrade PE.

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