

ISOLATION AND CHARACTERIZATION OF HEAVY METALS AND ANTIBIOTIC RESISTANT BACTERIA FROM ENVIRONMENTAL SAMPLES

S.M. Gopinath*, Sheetal, Suneetha T.B, Amar Shankar

Department of Biotechnology Engineering, Acharya Institute of Technology, Acharya Institute of Technology, Acharya Dr. Sarvepalli Radhakrishnan Road, Bangalore- 560090
Karnataka, India.

Article Received on
08 July 2015,

Revised on 01 Aug 2015,
Accepted on 25 Aug 2015

***Correspondence for
Author**

S.M Gopinath

Department of
Biotechnology
Engineering, Acharya
Institute of Technology,
Acharya Institute of
Technology, Acharya Dr.
Sarvepalli Radhakrishnan
Road, Bangalore- 560090
Karnataka, India.

ABSTRACT

In current years toxic heavy metal pollution has become one of the most critical environmental problems. In the present study, screening, isolation and characterization of heavy metal and antibiotic resistant bacteria from different environmental samples was carried out. Those bacterial isolates which shows $>512 \mu\text{g/ml}$. minimum inhibitory concentration were examined for antibiotic resistance activity. Antibiotics such as Ciprofloxacin, tetracycline, amoxicillin and erythromycin were taken for antibiotic resistance activity. Concentration of antibiotics were taken >16 to $>64 \mu\text{g/ml}$. Then characterization of selected bacterial isolate was carried out by 16S rDNA technique. The bacteria which has more resistivity towards both heavy metal and antibiotics that was identified by 16S rDNA sequencing as *Pseudomonas aeruginosa* and is the most heavy metal and antibiotic tolerant bacteria found in the environment.

KEYWORDS: Heavy metals, MIC, 16S rDNA.

INTRODUCTION

Heavy metal is a common collective term, which utilizes to the group of metalloids and the metals with their atomic density greater than 4000 Kg/m^3 . Environmental pollution by heavy metal comes from mining application of pesticides containing metal, fertilizer and the disposal of the environmental wastes by several industries.^[1] Heavy metal can collect in biological systems and eventually be introduced into food web via different mechanisms. In

the environment several different forms of heavy metal can originate considerable modifications of their microbial activities and communities.^[9, 14, 17] Industrial wastes cause toxic effects in aquatic organisms especially in fishes. Bioremediation is based on the plants, microorganisms or biological systems provide a cost- effective and their friendly environment for metal clean-up.^[8, 16] Heavy metals are depends on their concentration and availability of metals on the actions of complex processes to regulate by multiple factors. Heavy metal such as chromium (Cr), lead (Pb), zinc (Zn), and copper (Cu) were toxic to aquatic organisms and danger in the environment.^[18] The heavy metal tolerance bacteria has been declared as an indicator of potential toxicity of metals to other form of life. Heavy metals are naturally occurring but toxic levels are very rare. Most common problem are *cationic* metals (metallic elements whose forms in soil are positively charged cations e.g., Pb²⁺) are mercury, cadmium, lead, nickel, copper, zinc, chromium, and manganese. Some aerobic bacteria have been recognized for their degradative abilities such as *Pseudomonas*, *Alcaligenes*, *Sphingomonas*, *Rhodococcus*, and *Mycobacterium*. It has been reported that these microbes have been often used to degrade heavy metals, pesticides and hydrocarbons compounds. Generally, Working or living near an industrial site which utilizes these metals and their compounds increases ones risk of exposure, as does living near a site where these metals have been improperly disposed. Higher risks of exposure can be imposed also due to subsistence lifestyles and health impacts because of hunting and gathering activities. Therefore, the present study was initiated to analyse the heavy metal and antibiotic tolerance of these microorganisms achieved from environmental samples.

MATERIALS AND METHODS

Collection of Environmental samples

Collected soil samples were from various waste disposal sites of the urban environment of Bangalore city such as Contaminated soil (peenya industrial area, Sunkadakatte and Chikkabanavara), Vegetative leaves (coriander, Mint and Palak leaf), Industrial solid waste (Textile, Polymer, and Wood industry), Industrial liquid waste (Textile, paint, and chemical industry).

Heavy metals sources

Lead (Pb) – Lead acetate Pb (C₂H₃O₂)₂

Chromium (Cr) – Potassium dichromate K₂Cr₂O₇

Copper (Cu) – Copper sulphate (CuSO₄)

Zinc (Zn) – Zinc sulphate (ZnSO_4)

Isolation of total viable microflora from waste samples and heavy metal resistant bacteria by Pour plate technique

Microorganisms are isolated by serial dilution technique. Enumeration of total viable colonies bacteria were recorded. The environmental samples were collected in standard sized sterile plastic bags and carry for further bacteriological analysis. Based on total viable count the sample was diluted and inoculated into heavy metals – ZnSO_4 , CuSO_4 , $\text{K}_2\text{Cr}_2\text{O}_7$ and $\text{Pb}(\text{C}_2\text{H}_3\text{O}_2)_2$ (@ 100 PPM concentration) incorporating with nutrient agar by pour plate technique.

Identification of heavy metal and Antibiotic resistant bacteria

a. Determination of MIC (Minimal Inhibitory Concentration) for heavy metals in selected bacteria

MIC is described as the lowest concentration of antimicrobial agent required to inhibit growth of the organism. Heavy metal ion resistance studied was done by 64-512mg/l determining the Minimal Inhibitory Concentration (MIC) of the metals ions in tryptone broth media.

b. Micro broth dilution technique

Test Concentrations

Heavy metal stock solution was incorporated into tryptone broth. The heavy metal were serially diluted in sterile tryptone broth to obtain a final concentration of 64 ppm, 128 ppm, 256 ppm, 512 ppm by twofold dilution. The % inhibition of growth in treated was calculated using the formula given below. The concentration of heavy metal giving 50 % inhibition compared to control is considered as MIC.

$$\% \text{ Inhibition} = (\text{Absorbance control} - \text{Absorbance sample} / \text{Absorbance control}) \times 100.$$

c. Determination of Micro broth dilution technique for Antibiotic resistant bacteria in heavy metal tolerant bacteria

The bacterial isolates whose minimum inhibitory concentration (MIC) were >512 those isolates were taken or selected for antibiotic resistance test. Heavy metal tolerant cultures were tested for antibiotic resistance by micro broth dilution technique.

Preparation of stock solution: Ciprofloxacin, Erythromycin, Tetracycline, Amoxicillin.

By using conventional technique pure bacterial cultures that were sub-cultured were further processed for identification. Gram staining [(Hi-media kit: Gram's Crystal Violet (SO12), Gram's Iodine (SO13), Gram's Decolourizer (SO32), Safranin, 0.5% w/v (SO27)], and various biochemical tests such as Lactose fermentation, motility testing, Catalase, Citrate utilization test, Triple sugar iron, Urease, Oxidase, Carbohydrate fermentation tests were carried out for bacterial identification.

Molecular Characterization of heavy metal and Antibiotic resistant bacteria by 16S rDNA Sequencing

a. Genomic DNA extraction: Genomic DNA was isolated by using the InstaGene™ Matrix Genomic DNA isolation kit (Catalog # 732-6030).

b. PCR amplification of 16S gene: Target gene fragment was amplified using MJ Research PTC-225 Peltier Thermal Cycler. The following universal primers UNI_IL forward primer (5'-GGTGGAGCATGTGGTTTA-3'), UNI_IR reverse primer (5'-CCATTGTAGCACGTGTGT-3') (synthesized at Sigma Aldrich, Bangalore) targeting 16S gene were used.

c. Gene sequencing and phylogenetic tree construction: The PCR amplicons were purified and sent for sequencing at Vimta Labs (Hyderabad, India). The gene sequences obtained were analyzed by using the BLAST search programme and aligned with closest matching gene sequences from Genbank by multiple sequence alignment using the CLUSTAL W Program. The aligned sequences were analyzed by Mega 5 program and phylogenetic tree was constructed.

RESULTS AND DISCUSSIONS

Table 1: Total viable count by pour plate technique

SOURCE	SAMPLES	TOTAL VIABLE COUNT
A- vegetative leaf	1. Coriander leaf	$490 \times 10^{-3}/g$
	2. Palak leaf	$421 \times 10^{-3}/g$
	3. Mint leaf	$594 \times 10^{-3}/g$
B- Contaminated soil	4. sunkadakatte	$5 \times 10^{-3}/g$
	5. penya	$29 \times 10^{-3}/g$
	6. chikabanawara	$70 \times 10^{-3}/g$
C- Industrial waste(liquid)	7. peenya	$365 \times 10^{-3}/g$
	8. Penya (paint industry)	$150 \times 10^{-1}/g$
	9. Penya(chemicals)	$280 \times 10^{-2}/g$

D- Industrial waste(solid)	10. penya	$9 \times 10^{-3}/g$
	11. polymer	$80 \times 10^{-2}/g$
	12. wood	$545 \times 10^{-1}/g$

Table 2: Total viable count of heavy metal resistant bacteria by pour plate technique

SOURCE	SAMPLES	NO. OF HEAVY METAL RESISTANT BACTERIA			
		Pb	Cu	Kr	Zn
A- vegetative leaf	1. Coriander leaf	32	4	0	23
	2. Palak leaf	3	0	0	0
	3. Mint leaf	76	2	0	42
B- Contaminated soil	4. sunkadakatte	178	42	1	43
	5. peenya	405	-	165	198
C- Industrial waste(liquid)	6. chikkabanawara	295	37	307	252
	7. peenya	24	0	0	2
	8. Peenya(paint industry)	500	60	5	37
	9. Penya(chemicals)	245	50	80	277
D- Industrial waste(solid)	10. peenya	35	60	73	135
	11. polymer	522	26	447	258
	12. wood	820	354	656	395

Above table number 1 and 2 explains that the total viable count of bacterial colonies was done by serial dilution technique and pour plate technique(incl. heavy metal) respectively. That was collected from four different environmental samples e.g. vegetative leaf, contaminated soil, industrial waste (liquid), industrial waste (solid).

Minimum inhibitory concentration

Table 3: Minimum inhibitory concentration of bacteria with Lead acetate.

Isolate no.	Minimum inhibitory concentration($\mu g/mL$)
	Lead acetate
1	512
2	>512
3	>512
4	>512
5	>512
6	>512
7	>512
8	512
9	512
10	256

Table 4: Minimum inhibitory concentration of bacteria with Potassium Di- chromate.

Isolate Number	Minimum Inhibitory Concentration (µg/mL)
	Potassium Di-chromate
11	128
12	512
13	>512
14	>512

Table 5: Minimum inhibitory concentration of bacteria with Copper sulphate.

Isolate Number	Minimum Inhibitory Concentration (µg/mL)
	Copper Sulphate
17	>512
18	>512
19	64
20	128
21	512
22	512
23	128
24	>512

Table 6: Minimum inhibitory concentration of bacteria with Zinc sulphate

Isolate Number	Minimum Inhibitory Concentration (µg/mL)
	Zinc Sulphate
25	512
26	>512
27	>512
28	>512
30	128
31	512
33	64
34	128
35	256

Table 3 explains that among the isolate tolerant to Lead, isolates 2, 3, 4, 5, 6 and 7 show maximum tolerance with MIC of >512 µg/ml. Similarly **Table 4** among the isolates tolerant to chromium, maximum tolerance with MIC of >512 µg/ml was observed in isolates 13 and 14. Than **Table 5** among the isolates 13 and 14 tolerant to copper, maximum tolerance with MIC of >512 µg/ml. After that **Table 6** among the isolates 26, 27 and 28 tolerant to Zinc, maximum tolerance with MIC of >512 µg/ml. The concentration of heavy metal giving 50 % inhibition compared to control is considered as MIC.

Antibiotic resistance**Table 7: Minimum inhibitory concentration of bacteria with Antibiotic Resistance activity**

Isolate No.	Minimum Inhibitory concentration (µg/mL)				Heavy metal
	Ciproflaxacin	Tetracycline	Erythromyclin	Amoxycilin	
2	16	>64	>64	>64	Pb
3	4	64	64	>64	Pb
4	>16	>64	16	>64	Pb
5	>16	>64	16	>64	Pb
6	>16	>64	16	4	Pb
7	>16	>64	16	4	Pb
13	4	64	64	4	Cr
14	4	64	>64	>64	Cr
17	>16	>64	>64	4	Cu
18	4	>64	>64	4	Cu
24	16	64	>64	64	Cu
26	4	64	4	4	Zn
27	>16	64	64	4	Zn
28	4	64	64	4	Zn

Table 7 explains that among all the selected bacterial isolates, isolate no. 4, 5, 6, 7, 17, and 27 that were carried out for MIC for antibiotic resistance shows maximum Ciproflaxacin tolerance. Similarly, for Tetracycline isolate no. 2, 4, 5, 6, 7, 17, and 18 shows maximum tolerance. For Erythromyclin, isolate no. 2, 14, 17, 18, and 24 shows maximum tolerance and for Amoxycilin isolate no. 2, 3, 4, 5, and 14 shows maximum tolerance.

Identification of bacteria through biochemical test**Table 8: Identification of bacteria through Biochemical test**

isolate no.	Gram	Type	Motility	Lactose	Citrate	H ₂ S	Urease	Catalase	Oxidase	Sucrose	Mannitol	Arabinose	Inositol	Identification
3	-	Bacilli	-	+	+	-	-	-	-	+	+	+	+	<i>Klebsiella</i>
4	-	Bacilli	+	-	+	-	-	+	+	+	+	+	+	<i>Pseudomonas</i>
7	+	Bacilli	-	-	+	-	-	+	-	-	-	-	-	<i>Bacillus</i>
13	-	Bacilli	+	+	+	-	-	+	-	+	+	+	+	<i>Enterobacter</i>
14	+	Cocci	-	-	+	-	-	+	-	+	+	-	-	<i>Staphylococcus</i>
17	+	Cocci	-	-	+	-	-	-	-	+	-	-	-	<i>Streptococci</i>
27	-	Bacilli	+	+	+	-	-	-	-	+	+	+	+	<i>Enterobacter</i>
28	+	Bacilli	+	-	-	-	-	+	-	-	-	-	-	<i>Bacillus</i>

Thus, **Table 8** shows various genres of bacteria that were identified through various biochemical tests. Bacteria such as *Pseudomonas*, *Bacillus*, *Enterobacter*, *Klebsiella*, *Staphylococcus*, *Streptococci*

Molecular Characterization of heavy metal and Antibiotic resistant bacteria by 16S rDNA Sequencing

Heavy metal resistant Isolate was identified by 16S rDNA sequence analysis using universal primers. Identification to the species level was done by Phylogenetic analysis. Genus and Species was identified based on 16S rDNA sequence similarity with that of the published sequence in Gen Bank.

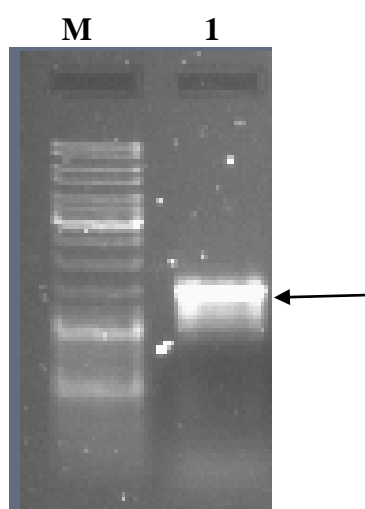


Figure 1: Agarose Gel Electrophoresis image of HMR04 genomic DNA 16S rDNA Amplicon

M: 3000bp ladder (Fermentas), **1-HMR04 amplicon**

Figure 1 arrow indicates that 287bp.

Gene sequencing and phylogenetic tree construction

For determining the nucleotide sequences of 16S rDNA and antibiotic resistance determinants, the PCR amplified products were purified using PCR purification kit (Sigma Aldrich), DNA sequencing of the purified product was performed by dideoxy chain termination method using gene specific primers at the sequencing facility of Vimta Labs (Hyderabad, India). The gene sequences obtained were analyzed by using the BLAST search programme. The sequence of the PCR product was compared with known 16S rRNA gene sequences in the Gene Bank by multiple sequence alignment using the CLUSTAL W Program (Thompson *et al.*, 1994) and the phylogenetic tree was constructed using Mega 5

program.

16S rRNA gene sequencing and phylogenetic analysis

The 16S rRNA gene base sequences of the HMR04 were blasted and phylogenetic tree was constructed with closely matched aligned sequence. The phylogenetic tree reveals that isolate closely relates to *P.aeruginosa* strains – SRP2696 and 2604 sequences. The phylogenetic tree of 16S rRNA gene of isolate is presented in Figure 2. The phylogenetic tree confirmed the isolate as *P. aeruginosa*.

HMR04_16S Raw Sequence(273 bp)

```
>GCGCCTAACACTTACCTGGCCTTGACATGCTGAGAACTTTCCAGAGATGGATTG
GTGCCTTCGGGAACTCAGACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGT
GAGATGTTGGGTAAAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCA
CCTCGGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGG
ATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACACACGTGCTACAATG
GAA
```

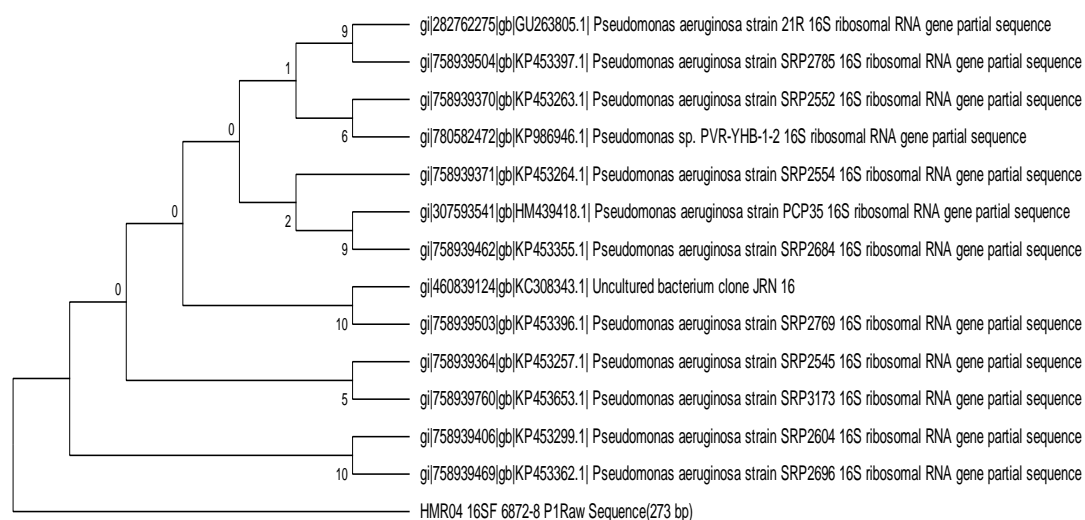


Figure 2. Phylogenetic Tree of HMR04 Isolate

CONCLUSION

Pollution of environment is a serious problem of the modern world. In this current review, an attempt was made to study the heavy metal tolerant bacteria isolated from the industrial effluents (solid, liquid), vegetative leaf, and contaminated soil of urban environment of Bangalore city. Then Enumeration, isolation, identification, characterisation of bacteria was done by which heavy metal tolerant bacteria were identified. Different types of bacteria were

identified which are specially present in environment. and common bacteria found were *Pseudomonas*, *Bacillus*, *Enterobacter*, *Klebsiella*, *Staphylococcus*, *Streptococci*. Minimum inhibitory concentration of heavy metals in selected bacteria was done and heavy metal tolerant cultures were tested for antibiotic resistance by micro broth dilution technique. Antibiotics resistance was determined on Mueller Hinton agar plates (Hi Media, India). The concentration of heavy metal giving 50 % inhibition compared to control is considered as MIC.

Isolates which shows heavy metal resistance will be selected and it's morphological, biochemical and molecular characterization 16S Rdna will be done. Heavy metal resistant Isolate was identified by 16S Rdna sequence analysis using universal primers. Identification to the species level was done by Phylogenetic analysis. Genus and Species was identified based on 16S Rdna sequence similarity of 99% respectively with that of the published sequence in GenBank. The phylogenetic tree reveals that isolate closely relates to *P.aeruginosa* strains – SRP2696 and 2604 sequences. These isolates can further be used for bioremediation of heavy metals from industrial effluent/ wastes.

REFERENCES

1. Alloway BJ. Soil Processes and the Behaviour of Metals. In: Alloway BJ ed. Heavy Metals in Soils BJ Blackie & Son Inc., New York, 1990; 7-28.
2. Asha Latha P. and Sandeep Reddy S. Review on Bioremediation- Potential Tool for Removing Environmental Pollution, International Journal of Basic and Applied Chemical Sciences., 2013; 2277- 2073.
3. Bhattacharya, P., Welch, A.H., Stollenwerk, K. G., McLaughlin, M.J., Bundschuh, J. & Panaullah, G. Arsenic in the environment: Biology and Chemistry, *Science of the Total Environment*, 2007; 379: 109–120.
4. Castro-González, M.I. & Méndez-Armenta, M. Heavy metals: Implications associated to fish consumption. *Environmental Toxicology & Pharmacology*, 2008; 26: 263-271.
5. Chakraborti, D., Sengupta, M.K., Rahaman, M.M., Ahamed, S., Chowdhury, U.K. & Hossain M.A. Groundwater arsenic contamination and its health effects in the Ganga–Megna–Brahmaputra Plain. *Journal of Environmental Monitoring*, 2004; 6: 74–83.
6. Chang, F. H. & Broadbent, F. E. Influence of trace metal on carbon dioxide evolution from a yolo soil. *Soil sci.*, 1982; 132: 416-421.

7. De Rore, H., Top, E., Houwe, F., Mergeay, M. & verstraete., W. Evolution of heavy metal resistant transconjugants in a soil environment with a concomitant selective press. FEMS microbial. Ecol., 1994; 14: 263-273
8. Dixon B. Bioremediation is here to stay, ASM News., 1996; 62: 527–528.
9. Doelman, P., Jansen, E., Michels, M. & van Til, M. Effects of heavy metals in soil on microbial diversity and activity as shown by the sensitivity- resistance index an ecologically relevant parameter. Biol. Fertil. Soil., 1994; 17: 177-184
10. Draghici, C., Coman, G., Jelescu, C., Dima, C. & Chirila, E. (2010). Heavy metals determination in environmental and biological samples, In: Environmental Heavy Metal Pollution and Effects on Child Mental Development- Risk Assessment and Prevention Strategies, NATO Advanced Research Workshop, Sofia, Bulgaria, 28 April-1 May 2010.
11. Figueroa, E. Are more restrictive food cadmium standards justifiable health safety measures or opportunistic barriers to trade? An answer from economics and public health. *Science of the Total Environment*, 2008; 389: 1-9.
12. Garbarino JR., Hayes H, Roth D et al. Contaminants in the Mississippi river. U. S. Geological Survey Circular, Virginia, U.S.A., 1995; 1133.
13. Giller K E, Witter E, McGrath SP. Toxicity of heavy metals to microorganisms and microbial processes in agricultural soils: A review. *Soil Biol Biochem*, 1998; 30: 1389– 1414.
14. Guzzo, A., Du Bow, M. & Bauda, P. Identification and characterization of genetically programmed responses to toxic metal exposure in *Escherichia coli*. Metals and microorganisms: relationships and applications. FEMS microbial. Rev., 1994; 14: 369-374
15. Harrison, N. Inorganic contaminants in food, In: Food Chemical Safety Contaminants, Watson, D.H. (Ed.), pp. 148-168, Ltd, first Edition, Woodhead Publishing ISBN 1-85573-462-1, Cambridge., 2001.
16. Haferburg G, Kothe E. Metallomics: lessons for metal liferous soil remediation, *Appl. Microbiol. Biotechnol.*, 2010; 87: 1271–1280.
17. Hiroki, M. Populations of cd-tolerant microorganisms in soil polluted with heavy metals. *Soil sci. plant Nutr.*, 1994; 40: 515-524.
18. Hoffman E, Mills G, Latimer JS, Quinn JG. Urban runoff as a source of polycyclic aromatic hydrocarbons to coastal waters. *Environ Sci Technol.*, 1984; 18: 580–7.