

Full Length Research Paper

Isolation, identification and PCR amplification of merA gene from highly mercury polluted Yamuna river

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Mercury resistant *Escherichia coli* strains have been isolated from different mercury polluted sites of India and their minimum inhibitory concentration (MIC) levels were determined. The zone of inhibition was measured to find the antibiotic sensitivity level. The location of mer operon was determined by transforming the isolated plasmids into mercury sensitive host DH5 α cells. Plasmid isolated from transformed DH5 α cells were also analyzed and compared with the plasmid profile of the wild-type strains. Oligonucleotides primer were designed by comparing the known reported sequences of merA from gram-negative bacteria (*Escherichia coli* R100) and 1695 bp of merA gene was amplified by PCR.

Key words: Mercury resistant, *Escherichia coli*, minimum inhibitory concentration (MIC), mer operon, merA.

INTRODUCTION

Mercury (Hg) pollution of soil and water is a world-wide problem (Dean et al., 1972; Kramer and Chardonnens, 2001). The extent to which Hg is harmful depends on the form of mercury present in the ecosystem. Mercury has been released into environment in substantial quantities through natural events and anthropogenic activities (Kiyono and Pan-Hou, 2006). Mercury and its compounds when released into the environment are highly toxic to living cells because of their strong affinity for the thiol groups of proteins (Hajela et al., 2002). Industrial use of mercury led to the pollution of environment. Consequently, mercury removal is a challenge for environmental management. Microorganisms in contaminated environments have developed resistance to mercury and are playing a major role in natural decontamination. An extensively studied resistance system, based on clustered genes in an operon (mer operon), allows bacteria to detoxify Hg²⁺ into volatile metallic mercury by enzymatic reduction (Komura et al., 1971; Summers, 1986). Mercury-resistance determinants have been found in a wide range of gram-negative and gram-positive bacteria isolated from different environments. They vary in the number and identity of genes involved and is encoded by

meroperons, usually located on plasmids (Summers and Silver, 1972; Misra, 1992; Brown et al., 1986; Griffin et al., 1987) and chromosomes (Wang et al., 1987; Inoue et al., 1991); they are often components of transposons (Misra et al., 1984; Kholodii et al., 1993) and integrons (Liebert et al., 1999). A widely employed mechanism of bacterial resistance to mercurial compounds is the reduction of Hg²⁺ to its volatile metallic form Hg⁰ (Libert et al., 1997). The biotransformation is mediated by mercury reductase, an inducible NADPH-dependent, flavin containing disulfide oxidoreductase enzyme. The gene coding for mercury reductase is merA (Scott et al., 1999). The bacterial mer operon encodes a cluster of genes involved in the detection, mobilization and enzymatic detoxification of mercury. Ionic mercury (Hg²⁺) is transported into the cytoplasm by a set of transport genes, where the merA gene, which encodes mercuric ion reductase, reduces this highly toxic ionic mercury (Hg²⁺) to the much less toxic volatile Hg⁰. Researchers developed bioremediation as one feasible way to accelerate or encourage the degradation of pollutants. Bioremediation can be used to clean unwanted substances from air, soil, water and raw materials from industrial processing. Hyper-accumulation and hyper tolerance of Hg is the characteristic of few plants but they have not shown the ability to detoxify the toxic form of Hg to non-toxic form (Lenka et al., 1990).

For this study, the Yamuna river water samples have

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Table 1. Biochemical identification of mercury resistant *E. coli* strain.

Test	Result
Citrate utilization	+ve
Lysine decarboxylase	-ve
Ornithine decarboxylase	v
Urease	-ve
Phenylalanine deamination	-ve
Nitrate reduction	+ve
H ₂ S production	-ve
Glucose	+ve
Adonitol	-ve
Lactose	+ve
Arabinose	+ve
Sorbitol	+ve

V = Unknown

been specifically preferred over the samples from other sites of India as this river is very highly polluted and people are adversely affected using its water. This study aims to isolate, identify, determine their tolerance range, antibiotic sensitivity and then to amplify *Escherichia coli* mercuric reductase gene by PCR from the very highly contaminated water of this river to achieve a specific band pattern. Further we will try to express this gene in plants without codon optimization to enhance their capacity for phytoremediation.

MATERIALS AND METHODS

Description of water samples and determination of bacterial load

Water samples were collected from different geographical regions of India, namely site-I (Y-I) and site-II (Y-II) of Yamuna river, Delhi; Kalu river, Bombay; Yamuna river near Guru Tegh Bahadur hospital, Delhi; Floodwater, Delhi; Hindon river, Ghaziabad; Kalindi Kunj, Delhi; Hoogly river, Kolkata; Coal industry, Faridabad and the ninth sample collected from Dal Lake (a pristine-type lake), Srinagar, Kashmir, was considered as the control. The counts of bacteria in these sites were also found to be variable. Bacterial population at different sampling sites was found to be 2.37 x 10⁷ (Dal Lake), 3.56 x 10⁹ (Yamuna River), 3.43 x 10⁹ (Kalu River), 2.06 x 10⁷ (GTB Hospital), 2.92 x 10⁷ (Hindon River), 2.86 x 10⁷ (Hoogly River), 3.08 x 10⁷ (Coal Industry) and 1.21 x 10² (Floodwater) per ml. It seems that Yamuna and Kalu rivers are having almost same load of bacteria and thus indicating that these 2 river sites have higher load of microbial population compared to others.

Screening, identification, determination of tolerance range and antibiotic sensitivity test

All samples were subsequently diluted and plated on Luria agar (Hi Media, India). The initial screenings of *E. coli* were performed on Eosin Methyl Blue Agar (EMB) plates. The selected strains were subjected to differential and selective growth media, followed by

various biochemical tests for their identification (Table 1). The determination of resistance was also performed for various antibiotics by disk inhibition test. The zone of inhibition for antibiotic sensitivity was measured and HgCl₂ sensitivity of the strains was tested by determining MIC.

Plasmid isolation and transformation studies

Plasmid DNA was isolated by Birnboim and Doly (1979) and the location of mer operon was determined by transforming of the isolated plasmids into host DH5 α cells as described by Hanahan (1983). The corresponding transformants obtained were grown on Luria Agar plates amended with 100 μ M concentration of mercury. Plasmid from isolated colonies was compared with the plasmid profile of the wild-type strains.

PCR amplification of merA gene

Primers were designed by comparing the known reported sequences of merA from gram-negative bacterial (*E. coli* Tn5075 and *E. coli* R100, retrieved from NCBI database) strains. The merA gene from *E. coli* R100 (special gift from Dr. Summers, UK) that was used as a positive control in this study. Primer combinations of merA-FJ containing BamH1 site at 5' (CGG GAT CCA TGA GCA CTC TCA AAA TCA CC) and merA-RJ having Sma1 at 5' (TCC CCC GGGATC GCA CAC CTC CTT GTC CTC) were used for the amplification of merA gene of size 1695 bp from mercury resistant *E. coli* strain. The reaction mixture contained PCR buffer with 100 mM Tris (pH 9.0), 500 mM KCl, 15 mM MgCl₂ and 0.1% gelatin, 0.2 mM deoxynucleoside triphosphate (dNTPs mix), 50 pmol/ μ l each of forward and reverse primers, 1 unit of Taq DNA polymerase and 40 - 50 ng of plasmid DNA. The reaction condition for PCR included denaturation (95°C) for 1 min, primer annealing (63°C) for 2 min and extension (72°C) for 3 min followed by initial denaturation at 95°C for 5 min and final extension at 72°C for 5 min for the amplification of 1695 bp length of the product for 30 cycles in 50 μ l of reaction volume. An aliquot from the mixture was run on 1% agarose gel to check for the amplification.

RESULTS

The water samples collected from the 9 different geographical locations in India had varying physical properties such as pH, temperature, turbidity and concentrations of mercury. The mercury content in these water samples was found to be variable with the Yamuna river, Delhi showing the highest concentration and Guru Tegh Bahadur hospital, Delhi on the other hand having nil. Yamuna river showed mercury content (3.76 ppm) 3 times more than the limit (1 μ g/l) as prescribed by WHO (Javendra, 1995). The order of metal resistance in all of the nine samples showed the following order of incidence of mercury resistant bacteria Dal Lake > Kalu River > Coal Industry > Hoogly River > Hindon River > Floodwater > Yamuna River > Guru Tegh Bahadur Hospital. Our results revealed that the 9 selected strains each from nine different sampling sites used in this study showed significant levels of tolerance to mercuric chloride (HgCl₂). Of the different *E. coli* isolates, Dal Lake sample showed maximum tolerance to HgCl₂, that is, 55 μ g/ml, and the sample collected from the Kalu river tolerated the

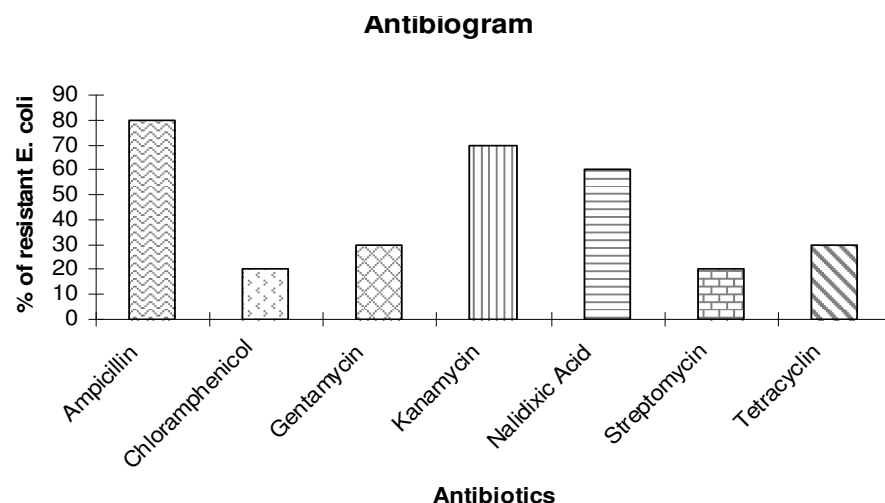


Figure 1. Estimation of the % of the total Hgr *E. coli* population resistant to different antibiotics.

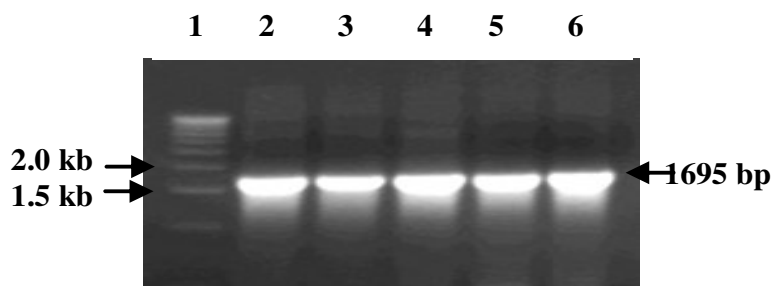


Figure 2. PCR Amplification of *merA* gene from mercury resistant *E. coli* strain.

Lane 1: DNA Ladder, Lane 2 & 5: PCR amplification of *merA* gene from *E. coli* R100 strain (positive control), Lane 3 & 6: PCR amplification of *merA* gene from Yamuna sample site-I (Y-I), Lane 4: PCR amplification of *merA* gene from Yamuna sample site-II (Y-II)

lowest concentration of HgCl_2 (25 $\mu\text{g/ml}$). The remaining seven strains showed resistance patterns ranging from 25 to 55 $\mu\text{g/ml}$. The minimum inhibitory concentration (MIC) of HgCl_2 for all the mercury resistant *E. coli* strains used in this study lay in the range of 25 - 55 $\mu\text{g/ml}$. Out of seven antibiotics used in this study, ampicillin resistance was much more frequent than the resistance to all the other 6 antibiotics. The resistance pattern observed in all of the Hgr *E. coli* strains towards seven antibiotics was confirmed by antibiograms (Figure 1). Ampicillin, kanamycin, nalidixic acid, tetracycline, gentamycin, streptomycin and chloramphenicol were found in 80, 67, 58, 30, 28, 18 and 18% of mercury-resistant strains respectively. The mercury resistance genes are clustered in the form of operon, which are associated with plasmid in gram-negative bacteria (especially in case of *E. coli*) and involves inducible mercurial detoxifying enzymes, organomercurial lyase (*merB*) and mercuric reductase (*merA*). All

strains showed the presence of at least one detectable plasmid at a position that corresponded to a size of approximately 24 kb of the $\square\text{DNA}/\text{EcoRI} + \text{HindIII}$ marker (Gupta and Ali, 2004). Transformation of the plasmid DNA isolated from these mercury resistant *E. coli* strains into the competent, plasmid-less, mercury-sensitive (Hgs) *E. coli* DH5 α cells yielded transformants in each case on plates supplemented with different concentrations of HgCl_2 to which the donor strains were resistant. The maximum numbers of transformants were observed in case of water sample collected from Yamuna river near Guru Tegh Bahadur hospital and the lowest numbers were seen in case of sample collected from Kalu river, for the same concentration of plasmid DNA. All the transformants could tolerate the same concentrations of mercury as the wild-type strains. The expected size of 1695 bp of *merA* gene (Figure 2) was amplified from 2 different samples collected from two different sites of Yamuna

River; using a set of gene specific primer.

DISCUSSION

Since the Yamuna River (YR) water sample showed mercury content (3.76 ppm) three times more than the limit (1 μ g/l) as prescribed by WHO (Javendra, 1995), it's water remained no longer safe for human life and needs an immediate attention for some remedial measures (Murtaza et al., 2001; Ali et al., 2002). A comparative analysis of the resistance pattern of the strains to HgCl₂ showed that the strains isolated from the Dal lake could tolerate comparatively higher concentrations of HgCl₂ than the strains from the other sites. This was observed despite the fact that the water samples collected from this site showed an almost negligible amount of mercury content. High number of Hgr *E. coli* isolates, some of them having the highest tolerance towards mercury was observed in the least and almost no polluted site, that is, Dal Lake (Murtaza et al., 2005). These results are contradictory to the earlier reports that suggested high metal tolerance in bacteria facing continued exposure of metals as compared with bacteria having no or less exposure. It is observed that mercury resistant strains also showed multiple antibiotic resistances to a great extent. As the genetic determinants for mercury and antibiotic resistance are mostly plasmid borne (Murtaza et al., 2001; Ali et al., 2002), it may, therefore, be hypothesized that the high incidence of multiple antibiotic resistance observed in mercury resistant strains is due to the selection pressure at their natural site.

We have characterized this gene of mer operon (merA) from environmental *E. coli* strains of 1695 bp which is mainly responsible for environmental mercury detoxification. The gene product will convert the dangerous methylmercury and other organic mercury derivatives to ionic mercury; which can then be reduced to Hg⁰ by merA gene (He et al., 2001). Transgenic tobacco plants with mercuric reductase gene through chloroplast engineering will be an excellent example of bioremediation. Transgenic plants carrying the individual mercury metabolic genes can be crossed to create a universal mercury removing plant for areas where methyl-mercury and ionic mercury pollution is simultaneously present (He et al., 2001). Chloroplast transformation may also have application to other metals that affect chloroplast function (Ruiz et al., 2003). Even though chloroplast engineering is a method of choice for developing transgenics, but transient expression of chloroplast transgenics is more of concern. Expression of merA in transgenic plants might provide an ecologically compatible approach for the remediation of mercury pollution (Rugh et al., 1998).

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