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EVALUATIONS OF ANTIBIOTIC RESISTANCE IN PHENOL DEGRADING ISOLATE PSEUDOMONAS AERUGINOSA MTCC 4497

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ABSTRACT

In recent years the worldwide emergence of multidrug-resistant strains of *Pseudomonas aeruginosa* has been studied. This organism shows a remarkable capacity to resist antibiotics. In the present study, phenol degrading *P. aeruginosa* MTCC 4997 showed highest antibiotic resistance in penicillin, followed by antimycin, ampicillin, kanamycin and nystatin. The remarkable ability of *P. aeruginosa* MTCC 4997 to adapt and thrive in wide variety of environments is may be due to its extensive genetic versatility.

INTRODUCTION

Pseudomonas aeruginosa is one of the important bacterial pathogens isolated from various samples. *P. aeruginosa* is an aerobic Gram-negative bacillus considered to be an opportunistic pathogen. It is a highly versatile microorganism able to tolerate low oxygen conditions and grow in temperatures ranging from 4-42°C (Stover *et al*., 2000). It has capacity to adapt easily to change in the environment. It needs a minimal nutritional requirement to grow and rapidly develop resistance to antibiotics (Strateva *et al*., 2010). It is normally inhabits the soil and surfaces in aqueous environments. Its adaptability and high intrinsic antibiotic resistance enable it to survive in a wide range of other natural and artificial settings (Gellatly and Hancock, 2013). Most pseudomonas spp. are naturally resistant to penicillin and majority of related beta-lactum antibiotics, but a number are sensitive to piperacillin, imipenem, tobramycin or ciprofloxacin. Nowadays more and more resistance of *P. aeruginosa* is encountered (Rajat Rakesh *et al*., 2012). *P. aeruginosa* is intrinsically resistant to several antibiotics because of the low permeability of its outer-membrane, the constitutive expression of various efflux pumps, and the production of antibiotic-inactivating enzymes (e.g., cephalosporinases) (Hancock, 1998). Furthermore, it also has a remarkable capacity to develop or acquire new mechanisms of resistance to antibiotics. This may be related to the large size and the versatility of its genome, and to its distribution in aquatic habitats, which could constitute a reservoir for bacteria carrying other resistance genes (Vaisvila *et al*., 2001). *P. aeruginosa* has always been considered to be a difficult target for antimicrobial chemotherapy. However, the complete sequencing of a wild-type *P. aeruginosa* strain, achieved in 2000, has provided a great deal of useful information, concerning not only its pathogenicity, but also its potential for resistance (Stover *et al*., 2000). The main goal of this paper is to determine antibiotic resistance of *Pseudomonas aeruginosa* MTCC 4997 isolated newly from effluent collected from petrochemical industries.

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MATERIALS AND METHODS

The phenol degrading new strain *P. aeuriginosa* MTCC 4997 used in this study was isolated from effluents collected from petrochemical industries by enrichment technique. Antibiotic sensitivity of natural isolate was determined using different antibiotics such as, ampicillin, chloramphanicol, streptomycin, novomycin, nystatin, antimycin, kanamycin and penicillin. To determine the LD_{50} value of different antibiotics, the isolate was grown in Luria Bertani broth mixed with different

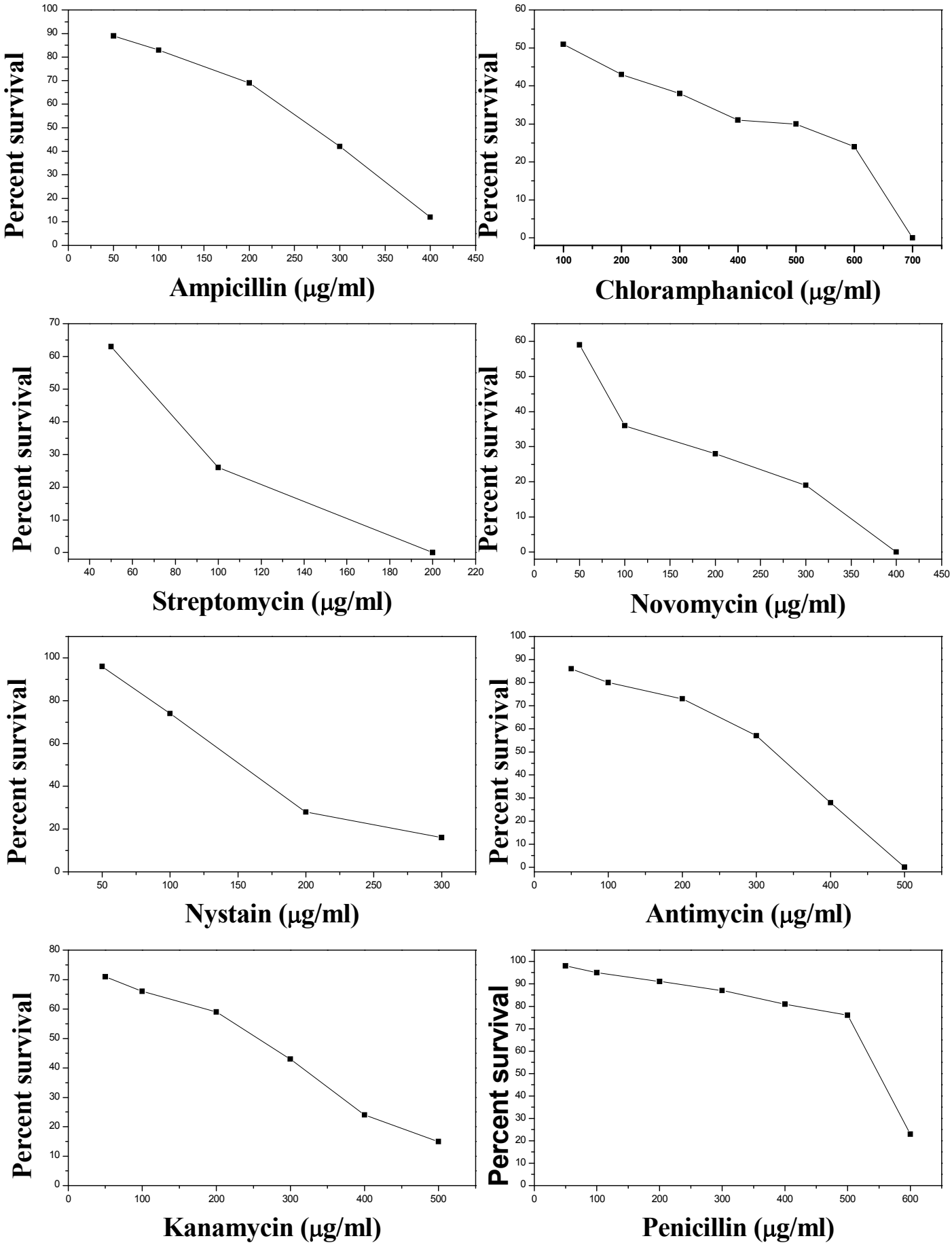

Figure 1. Survival of *Pseudomonas aeruginosa* MTCC 4997 in various concentrations of eight antibiotics

concentrations of selected antibiotics at 37^0C for 24 h and O.D of the culture was recorded at 600 nm. The graph was plotted based on percentage survival of bacterial isolates at different concentrations of antibiotics. The concentration at which the isolate showed 50% survival was considered as LD_{50} value of the isolate.

RESULTS AND DISCUSSION

P. aeruginosa MTCC 4997 was found to be resistant to most of the broad range antibiotics such as chloramphanicol, penicillin, kanamycin, antimycin, ampicillin, novomycin, and nystatin, streptomycin (Figure 1 and Table 1).

Table 1: LD_{50} values of antibiotics for phenol degrading isolate Pseudomonas aeruginosa MTCC 4997.

Sl. No	Antibiotics	LD_{50} (µg/ml)
1	Ampicillin	285
2	Chloramphanicol	110
3	Streptomycin	80
4	Novomycin	90
5	Nystatin	160
6	Antimycin	325
7	Kanamycin	285
8	Penicillin	550

The highest resistance was recorded to penicillin (LD_{50}-550), followed by antimycin (LD_{50}-325), ampicillin (LD_{50}-285) and kanamycin (LD_{50}-285) and nystatin (LD_{50}-160). Wuertz *et al.,* (1991) reported that most of the bacterial isolates, which can resist high level of heavy metals, could also resist high concentration of different antibiotics. Brunis *et al*., (2003), have reported *Pseudomonas pickettii* strain, which is resistant to cadmium as well as some broad range antibiotics. Yomoda *et al*., (2003), have reported *Pseudomonas putida* was resistant to several antibiotics. *Pseudomonas aeruginosa* has been reported to be multi-drug resistant like ampicillin, penicillin, amoxicillin, clavulanic acid, piperacillin, streptomycin, gentamycin, (Sader *et al*., 2002). In the present study, out of eight antibiotics tested, phenol degrading isolate of *P. aeruginosa* MTCC 4997 showed highest resistance to penicillin, antimycin, ampicillin and kanamycin.

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