**ABSTRACT**

*Pseudomonas aeruginosa* is an important opportunistic nosocomial pathogen. The incidence of multidrug-resistant (MDR) *P. aeruginosa* is on rise in nosocomial settings across the globe. The present study aims at determining the antibiotic susceptibility patterns i.e. multidrug resistant (MDR), extensive drug resistant (XDR), pan drug resistant (PDR) *P. aeruginosa* prevalent in Shimla region of Himachal Pradesh. Besides, it aims at determining the frequency of ESBL (extended spectrum beta-lactamase) genes (*bla*TEM, *bla*SHV, *bla*PER and *bla*CTX-M) in the isolates. A total of 93 isolates out of one hundred obtained from Indira Gandhi Medical College, Shimla were confirmed as *P. aeruginosa*. The susceptibility patterns of the isolates were determined against 12 antibiotics belonging to six different antibiotic classes by disc diffusion method of Kirby Bauer. *P. aeruginosa* strains (39.78%) were resistant for aztreonam and ciprofloxacin followed by imipenem (34.41%) while lower proportions of resistant strains were recorded against piperacillin/tazobactum (9.6%) and levofloxacin (7.53%) in *in vitro* cultural antibiotic sensitive assay. 20.43% isolates were multi drug resistant (MDR), 11.83% were extensive drug resistant (XDR) while only 2.15% were pan drug resistant (PDR).

For the determination of ESBL producing *P. aeruginosa* (*n*=180) in the preliminary screening, third generation cephalosporins were used and the positive isolates were further confirmed by double disc diffusion synergy (DDST) and E tests. The ESBL producing isolates characterized by these phenotypic tests were further studied to determine the occurrence of selective ESBL genes. 171 out of 180 isolates examined (95%) were ESBL producers in the preliminary screening, 56/171 (32.75%) isolates were confirmed as ESBL producers by DDST method. But only 26.67% were ESBL producers by E test also. The mean MIC values as determined by E-test were recorded as >16μg/ml for mix (mixture of ceftazidime, cefotaxime and cefepime) and 0.442μg/ml for mix+ (mixture of ceftazidime, cefotaxime and cefepime plus clavulanic acid and tozobactam) respectively. Of the 56 ESBL positive isolates analyzed by phenotypic tests, the ESBL genes (*bla*TEM, *bla*SHV and *bla*CTX-M) could be amplified in 14 (25%), 1 (1.78%) and 6 (10.71%) isolates respectively. Of these, three isolates had both *bla*TEM and *bla*CTX-M
genes. The data reflect the occurrence of different extended spectrum β-lactamase genes and their co-occurrence in some isolates. $Bla_{TEM-1}$, $bla_{SHV-12}$, $bla_{CTX-M-15}$ variants were detected in this geographic region on the basis of nucleotide sequence homologies of amplicons of these genes to the published gene sequences. The gene $bla_{TEM}$ as a mechanism of resistance was found in five MDR, two XDR and one PDR isolates whereas $bla_{CTX-M}$ gene was found in three MDR and two XDR isolates. The present study thus reveals moderate frequency of ESBL producing $P. aeruginosa$ in the state of Himachal Pradesh which might have implications in treating infections due to this organism. The study might prove useful in the better management of $P. aeruginosa$ infections. Constant monitoring and surveillance of $P. aeruginosa$ strains is therefore, essentially required to contain the infections particularly in nosocomial settings.

**KEYWORDS:** MDR, XDR, PDR, $P.aeruginosa$, ESBL, MIC, β-lactamase, cephalosporins.