

Emergence of integron borne PER-1 mediated extended spectrum cephalosporin resistance among nosocomial isolates of Gram-negative bacilli

Anand Prakash Maurya, Debarati Choudhury*, Anupam Das Talukdar*, Debadatta Dhar (Chanda)**,
Atanu Chakravarty** & Amitabha Bhattacharjee

*Departments of Microbiology, *Life Science & Bioinformatics, Assam University & **Department of Microbiology, Silchar Medical College & Hospital, Silchar, India*

Received August 20, 2013

Background & objectives: *Pseudomonas* extended resistant (PER) enzymes are rare type of extended-spectrum beta lactamases (ESBLs) that confer third generation cephalosporin resistance. These are often integron borne and laterally transmitted. The aim of the present study was to investigate the emergence of integron borne cephalosporin resistant PER-1 gene in diverse incompatibility (Inc) group plasmids among Gram-negative bacteria.

Methods: A total of 613 consecutive, non-duplicate, Gram-negative bacteria of *Enterobacteriaceae* family and non-fermenting Gram-negative bacteria were isolated from different clinical specimens during a period of 18 months. For amplification and detection of *bla*_{PER}, multiplex PCR was done. For understanding the genetic environment of *bla*_{PER-1}, integrase gene PCR and cassette PCR (59 be) was performed. Gene transferability experiment was carried out and PCR based replicon typing was performed for incompatibility group typing of plasmids using 18 pairs of primers. An inhibitor based method was used for phenotypic detection of intrinsic resistance.

Results: Multiplex PCR and sequencing confirmed that 45 isolates were harbouring *bla*_{PER-1}. Both class 1 and class 2 integrons were observed among them. Integrase and cassette PCR (59 be) PCR results confirmed that the resistant determinant was located within class 1 integron. Transformation and conjugation experiments revealed that PER-1 was laterally transferable and disseminated through diverse Inc plasmid type. Efflux pump mediated carbapenem resistance was observed in all isolates. All isolates belonged to heterogenous groups.

Interpretation & conclusions: This study demonstrates the dissemination of cephalosporins resistant, integron borne *bla*_{PER-1} in hospital setting in this part of the country and emphasizes on the rational use of third generation cephalosporins to slow down the expansion of this rare type of ESBL gene.

Key words ESBLs - gene cassette - Gram-negative - Inc group - integron - PER - plasmids

Pseudomonas extended resistant (PER) beta-lactamase belongs to class A extended spectrum beta-lactamase (ESBL), which was first detected in France in *Pseudomonas aeruginosa* isolated from a Turkish patient in 1993¹. The *bla*_{PER-1} gene has been detected in *P. aeruginosa*², *Acinetobacter* spp.³, *Proteus mirabilis*⁴, and in *Salmonella enterica* serovar Typhimurium⁵. It has been reported that the genetic location of *bla*_{PER-1} is either on the chromosome or on the plasmid^{1,6}. Integrons also act as small mobile elements which carry and transfer antibiotics resistant genes. The prevalence of integron borne PER-1 is very high because these carry different antibiotics resistant genes in their gene cassettes⁷⁻¹⁰. This determinant is often carried by transposable elements which are responsible for their lateral spread among diverse group of bacterial pathogens².

This study was carried out to determine the occurrence of cephalosporin resistant, integron borne *bla*_{PER-1} and its transmission dynamics in Gram-negative bacteria.

Material & Methods

Bacterial isolates: A total of 613 consecutive, non-duplicate, Gram-negative bacteria consisting of members of *Enterobacteriaceae* family and non-fermenting Gram-negative bacteria were isolated from different clinical specimens during a period of 18 months (November 2012 to April 2013) from different wards/clinics of Silchar Medical College and Hospital, Assam, India. The work was performed in the department of Microbiology, Assam University, Silchar, Assam. All the organisms were subcultured on MacConkey agar (Hi-Media, Mumbai, India).

Phenotypic detection of ESBL: All isolates were subjected to preliminary screening on Mueller-Hinton (M-H) agar plates containing two antibiotics namely cefotaxime and ceftazidime at 1 µg/ml¹¹. All positive isolates were confirmed by combined disc diffusion method using cefotaxime (30 µg) and ceftazidime (30 µg) alone and in combination with clavulanic acid (10 µg) (Hi-Media, Mumbai, India) as per Clinical and Laboratory Standards Institute (CLSI) recommendation¹¹.

Molecular characterization *bla*_{ESBL} genes by multiplex PCR: For amplification and characterization of *bla*_{ESBL} genes, a set of five primers were used namely: *bla*_{TEM}, *bla*_{CTX-M}, *bla*_{SHV}, *bla*_{OXA-2}, and *bla*_{PER}¹². Reactions were

run under the following conditions: initial denaturation at 94°C for five min, 33 cycles of 94 °C for 35 sec, 51°C for one min, 72°C for one min and final extension at 72°C for seven min.

Sequencing of *bla*_{ESBL}: PCR product was purified by Gene Jet PCR purification kit (Thermoscientific, Lithuania). In brief, 30 µl of purified products were used for sequencing along with 20 µl of *bla*_{ESBL} gene primers¹² (10 pmol each primers). Sequence results were analyzed using BLAST suite program of NCBI (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Characterization of integrons by integrase gene PCR: For characterization of class 1 and class 2 integrons, integrase gene PCR assays were performed by using primers Int1F (CAG TGG ACA TAA GCC TGT TC), Int1R (CCC GAG GCA TAG ACT GTA) and Int2F (TTG CGA GTA TCC ATA ACC TG), Int2R (TTA CCT GCA CTG GAT TAA GC)¹³. Reactions were run under the following conditions: initial denaturation at 94°C for five min, 32 cycles of 94 °C for 35 sec, 51°C for one min, 72°C for one min and final extension at 72°C for seven min.

Association of *bla*_{ESBL} with gene cassette: For study of the association of gene cassette with *bla*_{ESBL} gene, 59 gene cassette PCR was performed. Two PCR reactions were performed, one with HS287 and *bla*_{PER} reverse, another with HS286 and *bla*_{PER} forward^{12,14}. The amplified PCR products were further sequenced. PCR amplification was performed using 30 µl of total reaction volume. PCR reactions were run under the following conditions: initial denaturation at 95°C for two min, 30 cycles of 95 °C for 20 sec, 52°C for 45 sec, 72°C for one min and final extension at 72°C for five min.

Plasmid preparation: All ESBL positive bacterial isolates were cultured in Luria-Bertani broth (Hi-Media, Mumbai, India) containing 1µg/ml of cefotaxime. Cultures were incubated on shaker incubator overnight at 37°C. Plasmids were purified by Gene Jet plasmid Miniprep kit (Thermoscientific, Lithuania).

Gene transferability of *bla*_{ESBL} gene by transformation and conjugation: Transformation was carried out using *Escherichia coli* JM107 (Fermentas, USA) as recipient¹⁵. Transformants were selected on cefotaxime (0.5 µg/ml) containing L-B agar plates. L-B agar control plate was used, with and without cefotaxime 0.5 µg/ml.

Conjugation experiments were carried out between clinical isolates as donors and an streptomycin resistant

E. coli recipient strain B (Bangalore Genei, Bengaluru), Overnight culture of the bacteria was diluted in Luria-Bertani broth and was grown at 37 °C till the OD of the recipient and donor culture reached 0.8-0.9 at A₆₀₀. Donor and recipient cells were mixed at 1:5 donor-to-recipient ratios and transconjugants were selected on cefotaxime (0.5 µg/ml) and streptomycin (800 µg/ml) agar plates.

Plasmid profiling and incompatibility (Inc) typing of ESBL producers: For plasmid profiling, 1.5 µl of each transformants was used and analyzed by agarose gel electrophoresis (1% agarose, Hi-Media, Mumbai, India).

For detection of incompatibility group plasmid in all *bla*_{PER} producing strains, PCR based replicon typing was carried out targeting 18 different replicon types, to perform five multiplex and three simplex PCRs to amplify the FIA, FIB, FIC, HI1, HI2, I1-Ig, L/M, N, P, W, T, A/C, K, B/O, X, Y, F and FIIA replicons¹⁶.

Antimicrobial susceptibility and minimum inhibitory concentrations (MIC): Antimicrobial susceptibility was determined by Kirby Bauer disk diffusion method on M-H agar plates¹⁷. Antibiotics used in this study were listed in Table I. MICs of various antibiotics were also determined on Muller-Hinton agar plates containing 2, 4, 8, 16, 32, 64, 128, 256 µg/ml of antibiotics, by agar dilution method according to CLSI guidelines¹¹.

Table I. Antimicrobial agents used for the study

Antimicrobial agents	Concentration used (µg)
Amikacin	30
Ciprofloxacin	5
Gentamicin	10
Imipenem	10
Meropenem	10
Ertapenem	10
Trimethoprim/sulphomethoxazole	1.25/23.75
Cefopodoxime	10
Cefotaxime	30
Ceftazidime	30
Cefepime	30
Aztreonam	30

Detection of efflux pump activity: Efflux pump activity of the isolates were phenotypically detected by double disc synergy test using meropenem (10 µg) alone and in combination with CCCP (100 mM) (carbonyl cyanide m-chlorophenylhydrazone) (Hi-Media, Mumbai, India) as described earlier¹⁸. MIC reduction assay was performed with imipenem, meropenem and ertapenem alone and in combination with CCCP at a fixed concentration of 20 µg/ml¹⁹.

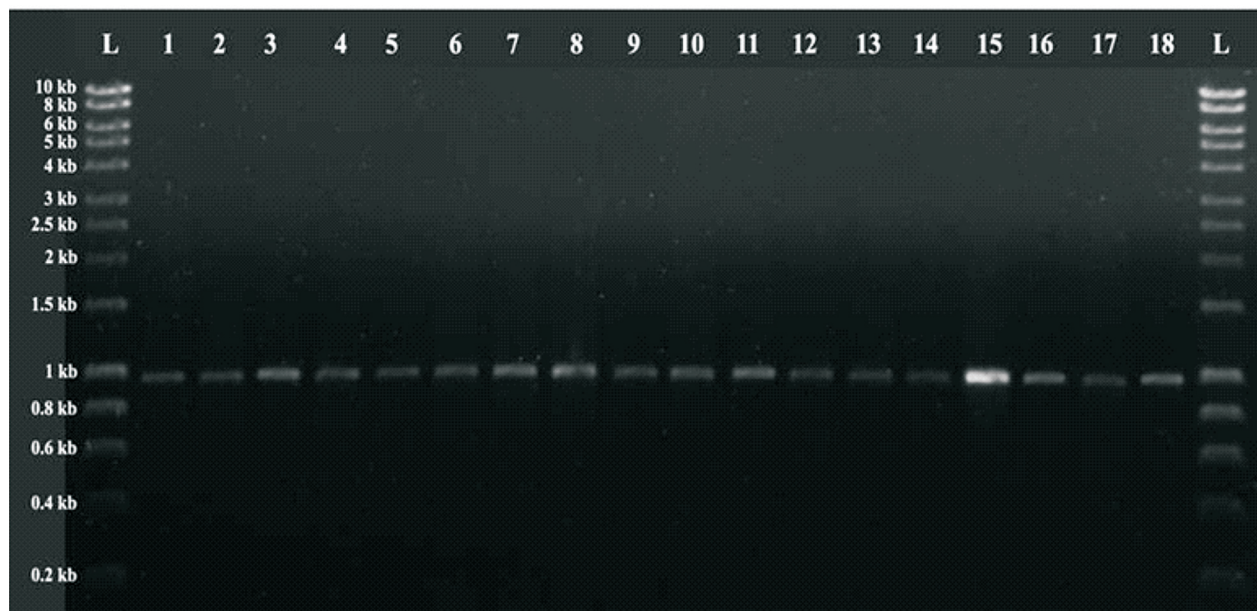


Figure. PCR amplified product of *bla*_{PER-1}. L: Hyper ladder I (Bioline; UK); 1-18: 920 bp PCR amplified product of *bla*_{PER-1}.

Table II. Clinical and molecular details of organisms harbouring *bla*_{PER-1}

Strain ID	Age (yr)	Sex	Wards/OPD	Type of specimen	Organisms	Genotype of beta lactamase	Integron	Replicon type
1.	71	M	Medicine	Urine	<i>Escherichia coli</i>	<i>PER-1</i>	Class 1	FrepB, N, FIA, FIB, FIC, P
2.	47	M	ICU	Sputum	<i>Acinetobacter</i> spp.	<i>SHV-148, CTX-M-15, TEM-15, PER-1</i>	Class 1	FrepB, FIA, FIB
3.	32	F	Gynaecology	Urine	<i>Pseudomonas aeruginosa</i>	<i>PER-1</i>	Class 1	Frep B, FIC, Y, P
4.	20	F	Surgery	Pus	<i>E. coli</i>	<i>TEM-1, PER-1</i>	Class 1	FrepB, FIA, FIB
5.	70	F	Female Burn Unit	Urine	<i>E. coli</i>	<i>SHV-148, CTX-M-15, TEM-1, PER-1</i>	Class 2	II/Iγ, FIB, Y, FrepB, B/o
6.	17	M	Surgery	Urine	<i>E. coli</i>	<i>CTX-M-15, TEM-1, PER-1</i>	Class 1	FrepB, FIC
7.	24	M	Medicine	Stool	<i>E. coli</i>	<i>CTX-M-15, PER-1</i>	Class 1	FrepB, FIA, B/o
8.	45	F	Female Burn Unit	Pus	<i>Pseudomonas aeruginosa</i>	<i>CTX-M-15, SHV-148, PER-1</i>	Class 1&2	FrepB, FIC, B/o
9.	70	F	Gynaecology	Urine	<i>Pseudomonas aeruginosa</i>	<i>SHV-148, CTX-M-15, TEM-1, PER-1</i>	Class 1	FrepB
10.	2	M	Paediatrics	Urine	<i>E. coli</i>	<i>CTX-M-15, TEM-1, PER-1</i>	--	FIA, FIC, Y, B/o
11.	3 months	F	Paediatrics	Urine	<i>Pseudomonas aeruginosa</i>	<i>CTX-M-15, TEM-1, PER-1</i>	Class 1	FrepB, FIA, FIB
12.	43	F	Surgery	Pus	<i>E. coli</i>	<i>CTX-M-15, TEM-1, PER-1</i>	Class 1	FrepB, Y, B/o
13.	55	F	Surgery	Pus	<i>E. coli</i>	<i>CTX-M-15, PER-1</i>	Class 1	FIB, FrepB, K, B/o
14.	5	F	ENT	Oral swab	<i>E. coli</i>	<i>SHV-148, CTX-M-15, PER-1</i>	Class 1	FIA, FIC, FrepB
15.	30 months	M	Paediatrics	Urine	<i>Pseudomonas aeruginosa</i>	<i>CTX-M-15, TEM-1, PER-1</i>	Class 1	FIA, FIB, FrepB, B/o
16.	50	F	Surgery	Urine	<i>E. coli</i>	<i>TEM-1, PER-1</i>	Class 1	FIA, FIB, FIC, Y, B/o
17.	34	M	Medicine	Stool	<i>Proteus mirabilis</i>	<i>PER-1</i>	Class 1	FIA, FIB, FIC, Y, K
18.	40	M	Medicine	Urine	<i>E. coli</i>	<i>CTX-M-15, PER-1</i>	Class 1	FIB, FrepB, K
19.	70	F	Surgery	Pus	<i>Pseudomonas aeruginosa</i>	<i>SHV-148, CTX-M-15, TEM-1, PER-1</i>	Class 2	FIA, FrepB
20.	40	F	Gynaecology	Urine	<i>E. coli</i>	<i>SHV-148, CTX-M-15, TEM-1, PER-1</i>	Class 1&2	None with target primers
21.	28	F	Medicine	Urine	<i>Pseudomonas aeruginosa</i>	<i>SHV-148, CTX-M-15, TEM-1, PER-1</i>	Class 1	FIA, B/o
22.	10	F	Paediatrics	Urine	<i>Pseudomonas aeruginosa</i>	<i>CTX-M-15, TEM-1, PER-1</i>	Class 1	FrepB, FIA, FIB, P
23.	19	M	Surgery	Urine	<i>Pseudomonas aeruginosa</i>	<i>CTX-M-15, PER-1</i>	Class 1	FIB, FrepB
24.	48	M	Medicine	Sputum	<i>E. coli</i>	<i>SHV-148, CTX-M-15, PER-1</i>	Class 1	FrepB
25.	30	F	Medicine	Stool	<i>E. coli</i>	<i>CTX-M-15, PER-1</i>	Class 1	FrepB, FIA, FIB, FIC, K

Contd...

Strain ID	Age (yr)	Sex	Wards/OPD	Type of specimen	Organisms	Genotype of beta lactamase	Integron	Replicon type
26.	72	M	Medicine	Urine	<i>E. coli</i>	CTX-M-15, PER-1	--	FIB, FIC, K,
27.	45	M	Medicine	Stool	<i>E. coli</i>	PER-1	Class 1	None with target primers
28.	25	M	Medicine	Stool	<i>E. coli</i>	PER-1	Class 2	FIA, FIC, Y, B/o
29.	2 months	M	Paediatrics	Urine	<i>Pseudomonas aeruginosa</i>	SHV-148, CTX-M-15, TEM-1, PER-1	Class 1	None with target primers
30.	25	M	ICU	Sputum	<i>Pseudomonas aeruginosa</i>	SHV-148, CTX-M-15, TEM-1, PER-1	Class 1	FrepB, FIA, FIC, Y, B/o
31.	3	F	Paediatrics	Urine	<i>E. coli</i>	SHV-148, CTX-M-15, PER-1	Class 2	FIA, FIB, FIC, Y, B/o
32.	25	M	Orthopedics	Pus	<i>E. coli</i>	PER-1	Class 1	FrepB, N, FIA, FIB, FIC, Y
33.	23	M	Medicine	Stool	<i>Pseudomonas aeruginosa</i>	CTX-M-15, TEM-1, PER-1	Class 1&2	FrepB, FIA, FIC, Y, B/o
34.	33	F	Medicine	Stool	<i>Pseudomonas aeruginosa</i>	SHV-148, CTX-M-15, TEM-1, PER-1	Class 1	FrepB, FIA, FIC, Y, K, B/o
35.	52	M	Dermatology	Urine	<i>E. coli</i>	PER-1	Class 2	FIB, FIC, Y,
36.	28 months	F	Paediatrics	Urine	<i>E. coli</i>	PER-1	Class 1	FrepB, FIB, FIC, Y
37.	55	F	Surgery	Pus	<i>E. coli</i>	SHV-148, PER-1	Class 1	FIB, K, B/o
38.	10	F	Paediatrics	Urine	<i>Klebsiella pneumoniae</i>	PER-1	Class 1	FrepB, N, FIA, FIB, W, FIC, Y
39.	29	M	Medicine	Urine	<i>E. coli</i>	SHV-148, CTX-M-15, TEM-1, PER-1	Class 2	FrepB, Y, B/o
40.	3	F	Paediatrics	Urine	<i>E. coli</i>	PER-1	--	FrepB, FIA, FIB, FIC
41.	3	M	Paediatrics	Urine	<i>E. coli</i>	PER-1	Class 1	FIA, FIB, FIC, K,
42.	27	F	Gynaecology	Urine	<i>Pseudomonas aeruginosa</i>	PER-1	Class 1	FrepB, K, B/o
43.	30	F	Gynaecology	Pus	<i>E. coli</i>	CTX-M-15, TEM-1, PER-1	--	FrepB, FIA, FIB, FIC, Y, B/o
44.	47	F	Gynaecology	Urine	<i>Pseudomonas aeruginosa</i>	CTX-M-15, PER-1	Class 1	FrepB, FIA, FIB, FIC, Y, B/o
45.	10 months	F	Paediatrics	Urine	<i>E. coli</i>	PER-1	Class 1	FrepB, FIA, Y, K

DNA fingerprinting by enterobacterial repetitive intergenic consensus (ERIC) sequences PCR: Typing of all ESBL producing isolates were done by ERIC-PCR, using two primers: ERIC-F and ERIC-R²⁰.

Results & Discussion

Forty five isolates showed amplification with *bla*_{PER} primers (Figure, Table II) which were further confirmed by sequencing as *bla*_{PER-1}. However, 12 isolates were found to carry only *bla*_{PER}, while in the remaining 33 co-existence of CTX-M-15, SHV-148 and TEM-1 was observed along with *bla*_{PER-1} (Table II).

Integrase gene PCR results demonstrated that 32 isolates harboured class I, and six isolates carried class II integron. Both class I and class II integrons were found in three isolates (Table II), four isolates were negative for integron. *bla*_{PER-1} was found to be class 1 integron borne that was further confirmed by sequencing.

Transformation experiment established the fact that *bla*_{PER-1} was carried within plasmid and was conjugatively transferable in *E. coli* JM 107. PER-1 could be amplified by PCR in both transformants and tranconjugants. Plasmid incompatibility typing of all *bla*_{PER-1} producers illustrated that there were diverse

Inc groups: N, FIA, FIB, W, Y, P, FIC, F and K were present in all *bla*_{PER-1} positive isolates (Table II).

All isolates were susceptible to tigecycline (100%) followed by imipenem (95.55%), and less susceptible to meropenem (75%). Other antibiotics like amikacin, gentamicin, ciprofloxacin, co-trimoxazole, cefepime, ceftriaxone and ceftiofloxacin showed moderate to lower activity. A high MIC was noticed against all tested cephalosporins (≥ 256 $\mu\text{g/ml}$), and monobactam (≥ 256 $\mu\text{g/ml}$). Efflux pump mediated carbapenem resistance was noticed in all 45 isolates. A reduction in MIC was observed in all 45 isolates against imipenem, ertapenem and meropenem when CCCP was added at a fixed concentration of 20 $\mu\text{g/ml}$. All isolates were clonally non related as observed in ERIC-PCR.

In the current study *bla*_{PER-1} was found to be disseminated among members of *Enterobacteriaceae* and in non-fermenting Gram-negative bacteria that were resistant to multiple groups of antibiotics. In Iran, the prevalence rate of PER-1 was 27.5 per cent in *P. aeruginosa* whereas in *A. baumannii* prevalence rate was 51 per cent due to indiscriminate consumption of antibiotics by patients^{7,8}.

The present study gives an insight in to horizontal transferability of this resistance determinant through integron gene cassettes in Gram-negative bacteria which has also been reported from other parts of the world^{7,9,10}. The most important finding of this study was carriage of *bla*_{PER-1} within different incompatibility (Inc) groups of plasmids which revealed that multiple carrier vehicles were responsible for expansion of this determinant and probably had diverse source of acquisition. To complicate the situation further, carbapenem therapy is restricted due to efflux pump activity, leaving little therapeutic alternatives. The study highlights the presence of this rare type of ESBL in this part of the country and deserves immediate awareness and controlled use of broad spectrum antibiotics to slow down the maintenance and persistence of this resistant determinant within hospital environment.

Acknowledgment

The authors acknowledge the University Grants Commission and Department of Biotechnology, New Delhi for financial assistance; and Assam University Biotech Hub for providing laboratory facility.

References

1. Nordmann P, Ronco E, Naas T, Duport C, Michel-Briand Y, Labia R. Characterization of a novel extended-spectrum β -lactamase from *Pseudomonas aeruginosa*. *Antimicrob Agents Chemother* 1993; 37 : 962-9.
2. Ranellou K, Kadlec K, Poulou A, Voulgari E, Vrioni G, Schwarz S, *et al.* Detection of *Pseudomonas aeruginosa* isolates of the international clonal complex 11 carrying the *bla*_{PER-1} extended-spectrum β -lactamase gene in Greece. *J Antimicrob Chemother* 2012; 67 : 357-61.
3. Naas T, Bogaerts P, Bauraing C, Degheldre Y, Glupczynski Y, Nordmann P. Emergence of PER and VEB extended-spectrum β -lactamases in *Acinetobacter baumannii* in Belgium. *J Antimicrob Chemother* 2006; 58 : 178-82.
4. Pagani L, Mantengoli E, Migliavacca R, Nucleo E, Pollini S, Spalla M, *et al.* Multifocal detection of multidrug-resistant *Pseudomonas aeruginosa* producing the PER-1 extended spectrum β -lactamase in northern Italy. *J Clin Microbiol* 2004; 42 : 2523-9.
5. Poirel L, Cabanne L, Vahaboglu H, Nordmann P. Genetic environment and expression of the extended-spectrum β -lactamase *bla*_{PER-1} gene in Gram-negative bacteria. *Antimicrob Agents Chemother* 2005; 49 : 1708-13.
6. Danel F, Hall LM, Gur D, Akalin HE, Livermore DM. Transferable production of PER-1 β -lactamase in *Pseudomonas aeruginosa*. *J Antimicrob Chemother* 1995; 35 : 281-94.
7. Farajnia S, Azhari F, Alikhani MY, Hosseini MK, Peymani A, Sohrabi N. Prevalence of PER and VEB type extended spectrum beta lactamases among multidrug resistant *Acinetobacter baumannii* isolates in North-West of Iran. *Iran J Basic Med Sci* 2013; 16 : 751-5.
8. Akhi MT, Khalili Y, Ghattaslou R, Aghazadeh M, Seroush Bar Haghi MH, Yousefi S. Prevalence of PER-1- type extended-spectrum beta-lactamases in clinical strains of *Pseudomonas aeruginosa* isolated from Tabriz, Iran. *Iran J Basic Med Sci* 2012; 15 : 678-82.
9. Taherikalani M, Maleki A, Sadeghifard N, Mohammadzadeh D, Soroush S, Asadollahi P, *et al.* Dissemination of class 1, 2 and 3 integrons among different multidrug resistant isolates of *Acinetobacter baumannii* in Tehran hospitals, Iran. *Polish J Microbiol* 2011; 60 : 169-74.
10. Libisch B, Poirel L, Lepsanovic Z, Mirovic V, Balogh B, Paszti J, *et al.* Identification of PER-1 extended-spectrum β -lactamase producing *Pseudomonas aeruginosa* clinical isolates of the international clonal complex CC11 from Hungary and Serbia. *FEMS Immunol Med Microbiol* 2008; 54 : 330-8.
11. Clinical and Laboratory Standards Institute (CLSI). *Performance standards for antimicrobial susceptibility testing*; 21st Informational Supplement. M100-S21. Wayne, PA, USA: CLSI; 2011.
12. Lee S, Park YJ, Kim M, Lee HK, Han K, Kang CS, *et al.* Prevalence of Ambler class A and D β -lactamases among clinical isolates of *Pseudomonas aeruginosa* in Korea. *J Antimicrob Chemother* 2005; 56 : 122-7.
13. Koeleman JG, Stoof J, van Der Bijl MW, Vandenbroucke-Grauls CMJE, Savelkoul PH. Identification of epidemic strains of *Acinetobacter baumannii* by integrase Gene PCR. *J Clin Microbiol* 2001; 39 : 8-13.
14. Stokes HW, Holmes AJ, Nield BS, Holley MP, Nevalainen KM, Mabbutt BC, *et al.* Gene cassette PCR: sequence-independent recovery of entire genes from environmental DNA. *Appl Environ Microbiol* 2001; 67 : 5240-6.

15. Sambrook J, Fritsch EF, Maniatis T. *Molecular cloning: a laboratory manual*, 2nd ed. New York: Cold Spring Harbor Laboratory Press; 1989.
16. Carattoli A, Bertini A, Villa L, Falbo V, Hopkins KL, Threlfall EJ. Identification of plasmids by PCR-based replicon typing. *J Microbiol Methods* 2005; 63 : 219-28.
17. Bauer AW, Kirby WM, Sherris JC, Turck M. Antibiotic susceptibility testing by a standardized single disk method. *Am J Clin Pathol* 1966; 45 : 493-6.
18. Quale J, Bratu S, Landman D, Heddurshetti R. Molecular epidemiology and mechanisms of carbapenem resistance in *Acinetobacter baumannii* endemic in New York City. *Clin Infect Dis* 2003; 37 : 214-20.
19. Kriengkauykiat J, Porter E, Lomovskaya O, Wong-Beringer A. Use of an efflux pump inhibitor to determine the prevalence of efflux pump-mediated fluoroquinolone resistance and multidrug resistance in *Pseudomonas aeruginosa*. *Antimicrob Agents Chemother* 2005; 49 : 565-70.
20. Versalovic J, Koeuth T, Lupski JR. Distribution of repetitive DNA sequences in eubacteria and application to fingerprinting of bacterial genomes. *Nucleic Acid Res* 1991; 19 : 6823-31.

Reprint requests: Dr Amitabha Bhattacharjee, Department of Microbiology,
Assam University, Silchar 788 011, Assam, India
e-mail:ab0404@gmail.com