Letters to the Editor

Emergence of Extended-Spectrum β-Lactamase PER-1 in Proteus vulgaris and Providencia stuartii Isolates from Algiers, Algeria

PER β-lactamases are one of the rarer extended-spectrum β-lactamase (ESBL) families; however, their prevalence is increasing more and more. Two PER types have been described previously (1, 3–7). In addition, sequences for PER-3, -4, and -5 from Aeromonas punctata, Proteus vulgaris, and Acinetobacter baumannii are available in the GenBank database (accession no. AY740681, EU748544, and EU687473); however, no data are published. PER-1 was mainly detected in Europe and was particularly widespread in Turkey (5) and Asia (3), while PER-2 occurred in South America, mostly in Argentina (7). Data on the diffusion of this ESBL gene in Africa are virtually nonexistent. Furthermore, the host genera of the PER types do not match those of PER-1. Herein, we report the first description of PER-1 in clinical isolates from an Algerian public hospital.

Five isolates of P. vulgaris (n = 4) and P. stuartii (n = 1) were collected in 2007 by the bacteriology laboratory of Beni Mesous hospital from urine and blood specimens and identified by the API 20E system (bioMérieux, Marcy l’Etoile, France). Antimicrobial susceptibility testing by the disk diffusion method and Etest (AB Biodisk, Solna, Sweden) showed that the five isolates were resistant to ceftazidime (MIC ≥ 256 μg/ml). Intermediate resistance to piperacillin, cefotaxime, and cefepime (MIC = 8 to 32 μg/ml) were also observed. All isolates tested were susceptible to imipenem (Table 1). Finally, a marked synergistic effect between clavulanic acid and ceftazidime, indicative of the production of an ESBL, was observed. PCR analysis using primers previously described (5) and sequencing revealed the presence of blaPER-1. Enterobacterial repetitive intergenic consensus-PCR typing was performed as described previously (2) for the four ESBL producers belonging to the P. vulgaris species. Similar enterobacterial repetitive intergenic consensus-PCR patterns were observed, suggesting clearly that the P. vulgaris isolates are genetically related; thus, clonal expansion is probable.

Conjugation studies, with ceftazidime selection (10 g/ml) and Escherichia coli J53 (rifampin resistant) as the recipient, showed that the blaPER-1 gene was transferable and located on a 100-kb plasmid, which also conferred resistance to trimethoprim, trimethoprim-sulfamethoxazole, and kanamycin for the four P. vulgaris isolates but only trimethoprim for the P. stuartii isolate. Regarding the genetic environment, PCRs were performed according to the schematic map described previously (5). The upstream region of blaPER-1 was explored using primers PER.D and PER.ext.A designed in that study. We observed that ISP12 was present in the five isolates of our study and genetically linked to blaPER-1. However, PCRs failed to identify ISP13 in all of our isolates.

The epidemiological data regarding ESBLs available for Algeria report the presence of only CTX-M-3, CTX-M-15, SHV-12, and VEB-1 in various species of gram-negative bacteria (2). This first report of PER-1 in two enterobacterial species from Algiers indicates that the blaPER-1 gene has spread south of the Mediterranean and perhaps even to Africa.

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REFERENCES


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*Tc, transconjugant; PIP, piperacillin; CTX, cephotaxime; CAZ, ceftazidime; FEP, cefepime; IPM, imipenem; K, kanamycin; TMP, trimethoprim; SXT, trimethoprim-sulfamethoxazole; CS, colistin; TE, tetracycline; GM, gentamicin; TM, tobramycin; C, chloramphenicol.


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