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Letters to the Editor

Detection of CTX-M-1, CTX-M-15, and CTX-M-2 in Clinical Isolates of *Enterobacteriaceae* in Bogotá, Colombia

This is the first report regarding the detection of $bla_{\text{CTX-M}}$ genes encoding CTX-M-1, CTX-M-15, and CTX-M-2 cefotaximases in clinical isolates of enterobacteria collected in hospitals in Bogotá, Colombia.

During a period of 4 months in 2005, 117 isolates of enterobacteria having extended spectrum beta-lactamase (ESBL) phenotype were collected from nine third-level hospitals in Bogotá, Colombia. Beta-lactamase-producing $bla_{\text{CTX-M}}$ genes were detected in 56 of them (47.9%) by PCR, having isoelectric points of 8.0, 8.7, and 8.9. CTX-M-1 group genes were detected in 89.3% of these isolates; the rest were from the CTX-M-2 group. No other $bla_{\text{CTX-M}}$ genes were detected. Amplified product sequences showed 100% similarity with the $bla_{\text{CTX-M-12}}$ gene in 56 isolates (60.7%), with $bla_{\text{CTX-M-1}}$ (16.1%), with $bla_{\text{CTX-M-15}}$ (12.5%), and with $bla_{\text{CTX-M-2}}$ (10.7%). Seven isolates obtained from nonhospitalized patients associated with infections acquired in the community were included in this study; the $bla_{\text{CTX-M-1}}$ gene was found in one of them, $bla_{\text{CTX-M-15}}$ in three, and $bla_{\text{CTX-M-2}}$ in the other three.

Group one cefotaximases characterized by greater hydrolytic activity against cefotaxime and ceftriaxone than against ceftazidime have been reported from different parts of the world, initially in Europe, Asia (1), and Africa (5) and recently in North America (6). Group 1 CTX-M enzyme variants manifesting greater activity against ceftazidime, such as CTX-M-15, reported in European countries (2, 3, 4), and especially in Great Britain, have been associated with the appearance of epidemic outbreaks (9). The presence of group 1 $bla_{\text{CTX-M}}$ genes was observed in a study carried out in Colombia with nosocomial enterobacteria (8). Likewise, a high prevalence of CTX-M-1 group cefotaximases was found by our group in a study using isolates collected in 2004 in four hospitals in Bogotá (J. R. Mantilla Anaya, E. M. Valenzuela de Silva, E. B. González Mejía, A. M. Méndez, and A. L. Leal, IV Encuentro Nacional de Investigación en Enfermedades Infecciosas, abstr. 16, Infectio **8:**143, 2004). Six enterobacteria carrying the $bla_{\text{CTX-M-2}}$ gene were also found in this study. The $bla_{\text{CTX-M-12}}$ gene was identified in both studies.

The isolates included in this study presented coresistance to cefepime in 79% of cases, to cefoxitin in 18.3%, to aztreonam in 65.3%, to ciprofloxacin in 30.6%, to gentamicin in 30.6%, to amikacin in 47%, and to sulfamethoxazole in 61.2%. All the isolates studied were susceptible to imipenem. The increase in cefepime resistance with respect to the 20% reported in 2002 (8) is worth noting.

All *Escherichia coli* transconjugants showed resistance to cefotaxime, since they had acquired the $bla_{\text{CTX-M}}$ genes previously detected in parental isolates. In no case was simultaneous transfer of bla_{SHV} genes observed, while simultaneous transfer of bla_{TEM} genes was observed in some cases. No transfer of resistance to other groups of antibiotics being evaluated was observed. This could indicate that resistance to aminoglycosides presented by some parental isolates is encoded by another plasmid, one different from the one which was transferred, contrary to what previously has been reported by several authors. Two $bla_{\text{CTX-M-15}}$ carrier isolates and two $bla_{\text{CTX-M-2}}$ carriers from the community transferred *bla* genes by conjugation, contrary to what was reported in another study with cefotaximases (10). The facility of these genes' transfer by conjugation has become a cause for alarm due to the implications for public health of these microorganisms' dissemination in the community (2, 9).

CTX-M-2 cefotaximase is the ESBL having the greatest prevalence in Argentina, where it recently was reported for the first time (7). It has since become disseminated in several countries in South America (7) and is also endemic in Asian countries (1). $bla_{\text{CTX-M-2}}$ genes were detected in isolates from both hospitalized and nonhospitalized patients in the present study.

Similar to what has been reported from other countries, *Klebsiella pneumoniae* has been found with greater frequency among isolates associated with intrahospital infection, while *E. coli* has been found to predominate in isolates from the community (2, 4, 9).

The dissemination of the $bla_{\text{CTX-M-12}}$ gene was observed to be continuing in hospitals in Bogotá in this study. As the populations in these hospitals were eminently polyclonal, it was presumed that this dissemination was due to the transmission of extrachromosomal elements. Other genes ($bla_{\text{CTX-M-2}}$, $bla_{\text{CTX-M-15}}$, and $bla_{\text{CTX-M-1}}$) were also identified in hospital isolates and in those from the community.

The dissemination and appearance of different types of cefotaximases in our setting reveals the need for evaluating and controlling possible selection mechanisms which have favored this phenomenon.

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