Emergence of bla\textsubscript{CTX-M} among Enterobacteriaceae isolates in USA Hospitals: Report from the SENTRY Antimicrobial Surveillance Program

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Amplification and sequencing of 16S ribosomal RNA genes (bioMerieux, Hazelwood, MO), when necessary. By standard biochemical tests and the Vitek System package (DNASTAR, Madison, WI). Sequences were analyzed using the Lasergene software (DNASTAR, WI). PCR amplicons were sequenced on both strands and sequences were analyzed using the nucleotide sequences and deduced amino acid sequences. These primers were used, combined with an internal control set of primers for 16S ribosomal RNA gene.

Several types of acquired extended spectrum \(\beta\)-lactamases (ESBLs) other than TEM and SHV types have been described in Enterobacteriaceae, including CTX-M, VEB, and SHV types. Among these, CTX-M-ESBLs are by far the most successful in terms of spread, and their impact is currently comparable or even greater than that previously attributed to TEM- and SHV-enzymes.

\section*{INTRODUCTION}

The \(\beta\)-lactam-resistant phenotype of Enterobacteriaceae is associated with the expression of genes encoding \(\beta\)-lactamase enzymes with extended-spectrum activity, known as \(\beta\)-lactamases of the extended-spectrum class (ESBLs). These enzymes, which are often plasmid-mediated, confer resistance to extended-spectrum \(\beta\)-lactam antibiotics, such as cefotaxime, ceftiraxone, and ceftazidime (1). ESBL-producing Enterobacteriaceae are of great concern because of their widespread dissemination and the potential for cross-resistance to other antimicrobial agents (2,3).

Several types of acquired extended spectrum \(\beta\)-lactamases (ESBLs) other than TEM and SHV types have been described in Enterobacteriaceae, including CTX-M, VEB, and SHV types. Among these, CTX-M-ESBLs are by far the most successful in terms of spread, and their impact is currently comparable or even greater than that previously attributed to TEM- and SHV-enzymes.

\section*{MATERIALS AND METHODS}

\subsection*{Bacterial strains}

A total of 2,843 Enterobacteriaceae isolates were collected from 26 USA hospitals during the 2007 SENTRY Program (2007). One isolate per patient per hospital was selected for analysis. In the study, isolates were collected from bloodstream, respiratory tract and skin infections according to a common protocol. Species identification was confirmed by standard biochemical tests and the Vitek System (bioMerieux, Hazelwood, MO), when necessary.

\subsection*{Antimicrobial susceptibility testing}

All isolates were tested for antimicrobial susceptibility using the broth microdilution method as described by the Clinical and Laboratory Standards Institute (CLSI) document M7-A7, with the following exceptions: strains were tested for the presence of \(\text{bla}\text{CTX-M}\) which was identified in 55 strains, and \(\text{bla}\text{TEM}\) which was identified in 16 of the 26 isolates.

\section*{RESULTS}

Among 206 Enterobacteriaceae isolates displaying the CLSI MIC criteria for ESBLs isolated in USA during 2007, 124 (60.6%) isolates showed positive results for the \(\text{bla}\text{ESBL}\) clavulanate inhibition test at 16\(\mu\)g/ml, which was identified in 55 (68.5%) USA medical centers.

\begin{table}[h]
\centering
\begin{tabular}{|c|c|c|c|c|}
\hline
\textbf{Antimicrobial} & \textbf{MIC (\(\mu\)g/ml)} & \textbf{Isolated (\%)} & \textbf{USA (\%)} & \textbf{Non-USA (\%)} \\
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\text{Ceftazidime} & 16 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
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\text{Cefepime} & 16 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
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\text{Ceftriaxone} & 16 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
\hline
\text{Cephradine} & 16 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
\hline
\text{Ceftazidime} & 64 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
\hline
\text{Cephradine} & 64 & 52 (22.8) & 26 (61.5) & 26 (58.5) \\
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\section*{CONCLUSIONS}

\begin{itemize}
\item CTX-M-14 and CTX-M-15 appear to be rapidly disseminating among USA hospitals.
\item CTX-M-encoded genes were recently found to be more common among isolates of the E. coli ST313 clone. Strains demonstrating a multilocus sequence typing (MLST) profile similar to this clone, however, have been associated with various clinical isolates, and have been shown to have elevated floxacinol MIC values. The correlation among the E. coli ST313, floxacinol resistance, and the presence of CTX-M genes should be further investigated.
\item Overall, this study highlights the increasing prevalence of CTX-M-producing strains that were previously considered rare in the USA. These strains seem to be emerging as an important and prevalent resistance mechanism among Enterobacteriaceae isolates in USA hospitals.
\end{itemize}