Molecular typing of extended spectrum β-lactamase producing *Klebsiella pneumoniae* strains isolated in the university hospital center of Dakar

**Abstract**

*Enterobacteria*, the bacteria most frequently isolated in pathology laboratories, are responsible for the majority of community and nosocomial infections. β-lactam antibiotics are used as the first-line treatment for these infections. However, the emergence of strains resistant to this family of antibiotics, due to the production of extended-spectrum β-lactamases (ESBLs) in particular, considerably decreases their efficacy. In this study, we aimed to detect the ESBLs secreted by *Klebsiella pneumoniae* (*K. pneumoniae*) at Fan Hospital in Dakar, and to characterize them molecularly. We identified 32 isolates producing ESBLs. The molecular characterization of these strains identified genes encoding CTX-M-15 (96.87%) and TEM (78.13%) enzymes. In 75% of isolates, both CTX-M-15 and TEM genes were identified. None of the 32 isolates carried the OXA-1, CTX-M-9 or CTX-M-25 genes.

The CTX-M-15 gene was thus found in 96.87% of the isolates studied was the most frequently detected ESBL gene in this study.

**Keywords:** *Klebsiella pneumoniae*, ESBL, molecular characterization, Senegal

**Introduction**

*Enterobacteriaceae* bacteria are an important bacterial family in human medicine. They are responsible for nosocomial and community infections. β-lactams antibiotics are the basic treatment for enteric infections. These are increasingly resistant to β-lactams by the production of extended spectrum β-lactam (ESBL). The first narrow-spectrum penicillinases (TEM-1/2: Temonere; SHV-1: sulphydryl-variable) were detected in *Escherichia coli* and *K. pneumoniae* (*K. pneumoniae*) in the 1960s. They were followed, in the 1980s, by SHV-2, an enzyme hydrolyzing broad-spectrum cephalosporins produced by *K. pneumoniae*. The activity spectra of these enzymes are continually expanding to include other beta-lactams. Also, new enzymes, not derived from either TEMs or SHVs, have appeared and spread rapidly: CTX-M (cefotaximase-Munich) enzymes.

The overall aim of this study was to detect the production of ESBLs by isolates of *K. pneumoniae* in the Bacteriology Laboratory of Fan University Hospital (CHUF) in Dakar. The specific objective was to use molecular biology tests to characterize the genes encoding these enzymes. This part of the work was carried out at the Bacteriology Laboratory of Pierre et Marie Curie University (Paris VI) in France.

**Materials and methods**

**Materials bacterial isolates**

The isolates studied were obtained from the Bacteriology Laboratory of the CHUF in Dakar. We studied 32 ESBL-producing isolates of *K. pneumoniae*. Their isolation and identification between January 2009 and December 2010, these isolates were stored at -80°C until their molecular characterization.

**Bacteriological media and reagents**

We used the following media: eosin methylene blue (EMB) agar and Mueller-Hinton (MH) agar for strain isolation and determination of the antibiogram. The API 20E-Bio Merieux panel was used for the identification of isolates.

Discs bearing the following antibiotics (from BioRad) were tested: amoxicillin, amoxicillin-clavulanic acid, ticarcillin, piperacillin, cephalothin, ceftriaxone, cefotaxime, cefazidime, aztreonam and imipenem.

**Materials molecular biology reagents**

We used Qiagen minikits, an Applied Biosystems 3730XL capillary sequencer (Applied Biosystems), and the BigDye Terminator v3.1 Cycle sequencing kit. The reaction mixture used for PCR consisted of 5µl of 10X Taq buffer, 5µl of 2MM dNTPs, 0.5µl of forward primer, 0.5µl of reverse primer, 0.2µl of Taq polymerase (5U/µl) and 36.8µl H₂O. We used forward and reverse primers for the TEM, CTX-M-9, CTX-M-15, CTX-M-25 and OXA-1 genes Table 1.

**Methods**

**Isolation and identification of strains**

At the Bacteriology Laboratory of the CHUF in Dakar, isolates obtained from urine, blood, pus and vaginal secretions were identified on the basis of their morphological, culture and biochemical characteristics (API 20E, Biomerieux). Antibiogram analyses were carried out by the disc diffusion method on MH agar. ESBLs were detected in tests of synergy between discs carrying third-generation cephalosporins (CEFtriaxone, cefazidime and cefotaxime) and discs carrying amoxicillin-clavulanic acid. The results were interpreted according to the recommendations of the Comité de l’Antibiogramme de la Société Française de Microbiologie (CA-SFM).

**Detection and characterization of ESBL genes**

This part of the study was carried out at the Bacteriology Laboratory of Pierre et Marie Curie University (Paris VI), France. Total DNA was extracted from the isolates with Qiagen minikits. The DNA was used for PCR to amplify the following genes: TEM, CTX-M-9,
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CTX-M-15, CTX-M-25 and OXA-1. PCR products were subjected to electrophoresis in a 3% agarose gel at 100V for 40minutes.

**Amplicon sequencing**

The PCR products were purified with the ExoSAP-IT enzyme. Their nucleotide sequences were determined by direct Sanger sequencing on an Applied Biosystems 3730XL sequencer, with the Big Dye Terminator v3.1 cycle sequencing kit (Applied Biosystems, Foster City, CA, USA). The nucleotide sequences, which were obtained in Fasta format, were then analyzed and compared with sequences deposited in the GenBank database, via the website of the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov).

**Table 1 Primers used for amplification**

<table>
<thead>
<tr>
<th>Genes</th>
<th>Upper Primer (5′–3′)</th>
<th>Lower Primers (5′–3′)</th>
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<tbody>
<tr>
<td>TEM</td>
<td>ATGAGTATTCACACATTCCG</td>
<td>CCAATGCCTAACGCTATTTTTTA</td>
</tr>
<tr>
<td>OXA-1</td>
<td>TATCAACCTCTGCTATTTTTTA</td>
<td>TTTAGTGTTTGTGAATGTTGA</td>
</tr>
<tr>
<td>CTX-M-9</td>
<td>ATGGTGACAAAGAGTGCA</td>
<td>CTACCTCGGCGATGATTCTC</td>
</tr>
<tr>
<td>CTX-M-15</td>
<td>GGTGAAAATCAGCTGGGC</td>
<td>ATGGTGACACAGGCGATGATTCTC</td>
</tr>
<tr>
<td>CTX-M-25</td>
<td>ATGATGACTCAGACGCTCG</td>
<td>TGGGTACAGGCTTTGCCGCG</td>
</tr>
</tbody>
</table>

**Results**

*K. pneumoniae* isolates were resistant to first and third generation cephaporspins and to aztreonam. However, they remained susceptible to imipenem (100%) and cefoxitin (87.5%) in the standard antibiogram test (disk diffusion in MH agar). A total of 31strains (96.87%) had a champagne cork synergy. This synergy was absent for a single strain that was also resistant to third-generation cephalosporins and aztreonam. PCR amplification identified the following two genes: TEM and CTX-M-15 Figure 1. The CTX-M-15 gene was detected in 31 isolates (96.87%), the TEM gene was detected in 25 isolates (78.13%). We also found that 24 isolates (75%) carried both CTX-M-15 and TEM genes.

**Figure 1 Distribution of genes found in K. pneumoniae**

**Discussion**

Our study is one of the first to report the isolation of *K. pneumoniae* strains carrying the CTX-M-15 gene in Senegal. The CTX-M-15 gene was the most predominant among our strains. It is carried by 96.87% of the isolates. CTX-M-15-type ESBLs have also been found in *K. pneumoniae*, *Salmonella enterica*, *Morganella morgani*, and *K. pneumoniae* in Senegal. It has also been isolated from *K. pneumoniae* strains in Nigeria. In 2004, it was detected in two *K. pneumoniae* strains isolated in Taiwan. In 2004, it was detected in two isolates of *K. pneumoniae* in Taiwan.

In 2004, it was detected in two isolates of *K. pneumoniae* in Taiwan. CTX-M-type ESBLs now make up the majority of ESBLs in all regions of the world, such that their spread can be described as pandemic.

**Conclusion**

Two major ESBL families were found in *K. pneumoniae* at the CHUF in Dakar: CTX-M-15 and TEM. Of these ESBLs, CTX-M-15 was the most frequently detected. The emergence of cross-resistance to several families of antibiotics requires careful surveillance of resistance to prevent therapeutic deadlock situations in the future. Multicenter studies will allow for better characterization of the different types of ESBL produced by *K. pneumoniae* strains circulating in Senegal.

**Acknowledgments**

None.

**Conflicts of interest**

We (the authors) declare that there are no conflicts of interest in relation to this article.

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References


