

P1232

Abstract (poster session)

Community-acquired urinary tract infections due to beta-lactamase-producing bacteria isolated in Madeira Island primary health care units

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Objectives: Community-acquired urinary tract infections due to beta-lactamase-producing bacteria are an emerging public health cause of concern. The main aim of this study was to characterize beta-lactamase-producing Gram negative isolates isolated from urocultures in Madeira Island primary health care units and evaluate its impact on treatment strategy. **Methods:** In this study, 33 community-acquired Gram negative isolates were selected based on their resistance to amoxicillin, cefotaxime and/or ceftazidime, obtained from an automatic system (VITEK). Antibiotic susceptibility testing (TSA) against different classes of antibiotics was performed by disk diffusion method. PCR and sequencing were used to screen and identify genes coding for extended-spectrum beta-lactamase (ESBL), ampC, as well as carbapenemases from classes A, B and D. Environment context of blaCTX-M genes was also analyzed by PCR, searching for related insertion sequences. Genetic relatedness of *Acinetobacter baumannii*, *Escherichia coli*, and *Klebsiella pneumoniae* was examined by MLST. **Results:** We detected reduced susceptibility to several beta-lactam antibiotics, suggesting the production of different beta-lactamases; 75.8% of the isolates were multidrug-resistant. Several beta-lactamase-encoding genes were identified: 23 parental (TEM-1, SHV-1, SHV-83, OXA-1-type), 16 ESBL (CTX-M-1, CTX-M-14, CTX-M-15, SHV-27), 10 AmpC (DHA-1, MIR-1) and 3 carbapenemases (OXA-50, VIM-2, OXA-120, the last here firstly described). The most common enzymes detected were CTX-M-15 (39.4%), OXA-1 (33.3%) and both TEM-1 and DHA-1 (24.2%). Insertion sequences in *E. coli* and *K. pneumoniae* isolates, upstream and/or downstream blaCTX-M gene were also detected (15 ISEcp1, 18 IS26 and 1 IS903), supporting the spread of beta-lactamase-mediated resistance intra- and inter-species. The sequence types ST976 and ST401 were here firstly reported in *K. pneumoniae* and *A. baumannii*, respectively. *E. coli* (ST131, ST602, ST617, ST641, ST1406, ST2279, ST2433, ST3027) and *K. pneumoniae* (ST15, ST29, ST35, ST101, ST976) isolates revealed a considerably genetic diversity, with the ST131 being identified in 5 isolates, which has being internationally disseminated, namely in different environments. **Conclusion:** Beta-lactamase-producing Gram negative bacteria appear to be widespread in Madeira's Island community patients, which may represent a threat to the treatment of urinary tract infections.