P0300

Paper Poster Session II

Focus: Acinetobacter, Pseudomonas and other nonfermenters

Environmental reservoirs of *Acinetobacter*-producing carbapenem-hydrolysing class D-beta-lactamases in Angola with evidence of human exposure

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Although Acinetobacter baumannii has been the main agent for healthcare infections, recent reports suggest that some Acinetobacter environmental species should be considered as a potential cause of disease. In Angola, an African country with an emerging economy, there are no previous data on Acinetobacter environmental reservoirs and resistance features. We aimed to investigate the occurrence and diversity of Acinetobacter species and the presence of resistance mechanisms in different non-clinical settings in Angola.

Sixty-three samples collected from different sources in Benguela (2013) were included: faeces [healthy volunteers (n=8), wildlife (n=5) and healthy farm animals (n=10)]; water [rivers (n=3), wastewaters (n=5), treated (n=7) and untreated (n=5) drinking water for human/animal, water for farm (n=3) and wildlife (n=2) animals]; animal feed (n=3) and floor/walls farm samples (n=2). Identification was performed by MALDI-TOF MS. Presumptive Acinetobacter isolates were confirmed by rpoB partial gene sequencing. Antimicrobial susceptibility was assessed by disc diffusion/E-test methods. Carbapenemase activity was search by Blue-CARBA. Carbapenemase genes (blaNDM, blaIMP, blaVIM, blaOXA-51, blaOXA-23, blaOXA-58, blaOXA-24, blaOXA48, blaKPC) and their genetic context were investigated by PCR and sequencing. Genetic location for carbapenemase genes was determined by I-CeuI and S1-hybridizations. Clonality was studied by ApaI-PFGE.

Acinetobacter species were detected in 46% of samples and some harbored more than one species: faeces [healthy volunteers (n=8/63; A.baumannii, A.ursingii, A.junii, A.berezinae), healthy farm animals (n=7; A.genospecies 15TU, A.gerneri, A.baumannii, A.pittii, A.soli)], water [rivers (n=3; A.junii, A.towneri, A.johnsonii, A.baumannii, A.pittii, A.soli)], wastewater (n=4; A.junii, A.towneri, A.baumannii, A.pittii), treated drinking water for humans (n=1; A.johnsonii, A.baumannii, A.pittii) and untreated drinking water for humans/animals (n=6; A.junii, A.baumannii, A.pittii)]. Susceptibility to aminoglycosides and quinolones was variable. Eleven isolates had reduced susceptibility to carbapenems but only 4 presented carbapenemase activity: ANG 1-4. ANG1, identified as A.johnsonii, showed resistance to cefotaxime, cefepime and intermediate behaviour to ciprofloxacin, tetracycline, ceftriaxone, ceftazidime, imipenem (MIC=1.5mg/L) and meropenem (MIC=0.75mg/L), presenting blaOXA-58 followed by ISAba3 and associated with a~75 kb plasmid. ANG 2-4 were identified as A.towneri by MALDI-TOF MS but rpoB only confirmed the close relatedness to this species. ANG2-4 had MICs>ECOFF at least to one carbapenem and revealed blaOXA-23 preceded by ISAba1, being epidemiologically unrelated (ApaI-PFGE).

The wide range of environments studied revealed a high diversity of Acinetobacter species. It is of note the frequent detection (36%) of A.baumannii, considered a hospital-adapted species. This work also describes the first environmental OXA-58-producing A.johnsonii isolate (domestic drinking water), and OXA-23-producing A.towneri (river and wastewater). These findings could suggest that human action might drive the spread of antibiotic resistance genes to geographic areas with low selection pressures (carbapenems are not approved in Angola), or that these regions might be at the origin of these genes. In any case, they could act as important reservoirs in the global epidemiological context.