BOOK OF ABSTRACTS

8TH MEETING OF YOUNG RESEARCHERS OF UNIVERSITY OF PORTO

U.PORTO

Filling the map for antimicrobial resistance in sub-Saharan Africa: ampicillin resistant enterococci from non-clinical sources of Angola

E. Martins[1], C. Novais[1], AR Freitas[1], A. Dias[1], T. Gonçalves[1], P. Antunes[1,2], L. Peixe[1]
[1] UCIBIO/REQUIMTE, Departamento de Ciências Biológicas, Faculdade de Farmácia. Universidade do Porto. Portugal. [2] Faculdade de Ciências da Nutrição e Alimentação. Universidade do Porto. Portugal

In sub-Saharan Africa (sSA) the antibiotic consumption is rising but surveillance capacity is still minimal. Insufficient antimicrobial resistance (AMR) data impairs a snapshot of true extension of the problem and the application of adequate control measures. *Enterococcus* causes a diversity of human infections in nosocomial and community settings, especially in patients with risk factors (e.g., immunosuppression), abundant in sSA. In a geographical area where other antibiotics, like glycopeptides, are not easily available, beta-lactams are critical for the treatment of enterococcal infections. Ampicillin resistance (AmpR) among *Enterococcus faecium (Efm)* is associated with worldwide nosocomial epidemic clones, being the genetic background of AmpR-*Efm* in sub-Saharan Africa (sSA) still barely known. Among the countries with scarce AMR data from clinical and community sources is Angola, an emergent economy, still with a precarious health system. As part of a surveillance study on the occurrence of Gram-positive and Gram-negative resistant bacteria to key antibiotics used to treat human infections, we searched AmpR-*Efm* in human, animal and environment from Benguela province (June 2013). Samples from healthy humans (faeces n=20), a wild park (faeces from grey monkeys-n=2 and goats of range-n=3, animal drinking water-n=2), farm production animals [faeces from poultry-n=5, veal-n=3, pigs-n=2; facilities walls/floor-n=2; drinking water-n=3], aquatic environment [river-n=3; treated-n=7 and untreated-n=5 human drinking water; residual waters-n=5] were included. They were enriched (1:10) in peptone water supplemented+8mg/l of ampicillin (37ºC/24h) and 0,1ml was plated in Slanetz-Bartley+8mg/l of ampicillin. Resistance to 12 antibiotics was evaluated by disk diffusion/Etest (EUCAST/CLSI). Species identification, search of antibiotic resistance genes [*tet(*MLOSK), *erm*(B), *aad*E, *pbp5*] and virulence factors (*IS16*, *esp*, *hyl, acm*) were searched by PCR/sequencing and clonality was determined by MLST. AmpR was detected in 8 *Efm* from 7 samples (hospital+community residual water, poultry farm facility, poultry and pigs faeces). They were identified within diverse Bayesian Analysis of the Population Structure (BAPS) groups [BAPS 2.3a-ST610; BAPS 2.1b-ST245, ST650, ST971], some described in human infections in sSA. The PBP5 amino acid analysis of 4 AmpR-*Efm* showed 3 different sequences, corresponding mostly to the AmpR consensus region previously described. Two sequences were new but a poultry-*Efm* PBP5 was previously identified in 19 *Efm* (Europe/USA/Israel-bloodstream infections-n=10, unknown origin-n=9) belonging to hospital associated clonal lineages. All, but one AmpR-*Efm,* were multidrug resistant. The *acm* gene was identified in 4 poultry isolates. In conclusion, AmpR-*Efm* carrying diverse antibiotic resistance genes are dispersed in animal and environmental settings of Angola, suggesting a beta-lactams selective pressure. The great number of immunocompromised individuals, the poor hygiene favoring AMR transmission and the non-controlled antibiotics use, justify the monitoring of the emergence and evolution of the clonal lineages of AmpR-*Efm* found, to clarify their impact on public health of Angola and other regions of sSA.