Molecular Characterization And Antimicrobial Resistance Patterns Of *Enterococcus* Species Isolated From Patients Attending Aga Khan Hospital, Nairobi, Kenya.

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ABSTRACT

Increasing resistance to antibiotics among the *Enterococcus* spp., to a point where some clinical isolates are resistant to all standard therapies reduces the choices of antibiotics available to treat infections caused by them. These organisms can cause serious invasive infections including endocarditis, bacteraemia, intra-abdominal and urinary tract infections. *Enterococcus faecalis* causes 80-90 percent of human enterococcal infections while *Enterococcus faecium* accounts for majority of the remainder. The aim of this study was to determine prevalence, antimicrobial resistance patterns and resistance genes in *Enterococcus faecium* and *Enterococcus faecalis* isolates from patients attending the Aga Khan University Hospital (AKUH) Nairobi, Kenya. All consecutive clinically significant enterococcal isolates from patients, collected between March 2008 and February 2009 were used. Species level Identification was done using API 20 STREP kits. Antibiotic susceptibility testing was done using Disk diffusion and Minimum Inhibitory Concentration (MIC). Interpretation of the susceptibility results was done using the Clinical and Laboratory Standards Institute (CLSI) guidelines. Resistance gene analysis using Polymerase Chain Reaction (PCR) was done for tetracycline (*tet M* (696bp)), floroquinolones (gyr a (241bp) and chloramphenicol (cat_{pip501} gene (540bp)) resistant isolates. *Enterococcus faecalis* was found in a greater proportion, where 128/150 (85%) isolates, followed by *Enterococcus faecium* 7/150 (5%), while 15/150 (10%) were not *Enterococcus* spp. and no further tests were done on them. Both species were highly resistant to aminoglycosides and tetracyclines while they were most susceptible to glycopeptides. The *gyrA* gene was present in 75.9% of the *Enterococcus faecalis* isolates and in 100% *of* the *Enterococcus faecium* isolates. The *tet M* gene was present in 61.8%

and 60% of the *Enterococcus faecalis* isolates and *Enterococcus faecium* isolates respectively. The *cat* $_{pIP501}$ gene was present in 63% of the *Enterococcus faecalis* isolates and 100% of *Enterococcus faecium* isolates. There being no resistance to penicillin and vancomycin drugs, the PCR process to identify the genes coding for penicillin resistance (*Pbp5*) and vancomycin (*vanA* and *vanB*) resistance was omitted. With the high levels of *Enterococcus* spp. resistance to aminoglycosides and tetracyclines and emerging resistance to fluoroquinolones, routine susceptibility testing will be required before treatment is instituted using commonly available drugs in the hospital. The isolates that did not code for *tet M* resistance-gene in tetracycline resistant isolates should be tested for the other classes of tetracycline- resistance genes. More studies should be done to determine the resistant genes in the other category of antibiotics.