Prevalence and antimicrobial-resistance characterization of vancomycin resistant enterococci (VRE) strains in healthy household dogs in Italy

also in companion animals to have a complete picture of the dynamics of this phenomenon.

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Prevalence and antimicrobial-resistance characterization of vancomycin resistant enterococci (VRE) strains in healthy household dogs in Italy

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Purpose: Enterococci are one of the leading causes of nosocomial infections for humans and the emergence of vancomycin-resistant enterococci (VRE) and high-level aminoglycoside-resistant enterococci (HLRA) caused public health concern because these drugs are often one the few therapeutic alternatives for treatment of multidrug-resistant (MDR) enterococcal infections. The widespread effect of MDR enterococci is partially driven by the selective pressure produced by the use and overuse of drugs in both human and veterinary medical practice. In recent decades, the analyses of their virulence and antimicrobial-resistance traits in hospital-acquired infections have been extensively reported in humans. However, less attention has been given to the role of pets as reservoir of MDR enterococci, despite their relationship with humans. The aim of this study was to evaluate the prevalence and the antimicrobial-resistance traits of VRE from household dogs.

Methods & Materials: Faecal samples of 237 healthy household dogs were tested to detect *Enterococcus* spp. using the classical bacteriological procedure. The species identification was confirmed by PCR assays as previously described. Antimicrobial-resistance to vancomycin was assessed by plating single colonies on Brilliance VRE Agar (Oxoid). The antimicrobial susceptibility to high-level aminoglycosides and to other compounds (together with the confirmation of vancomycin-resistance), was evaluated by the disk diffusion method based on recommendations of the CLSI.

Results: Enterococci were detected in 72% (n=170) 170 of dogs and, in accordance with other studies, the most prevalent *Enterococcus* species were *Enterococcus faecalis* (n=118; 69.4%) and *Enterococcus faecium* (n=50; 29.4%). The 49% of the isolates (n=84) were VRE and 2.4% (n=2) and 21.5% (n=18) of VRE strains showed HLR to gentamycin and streptomycin respectively. Interestingly, most of these isolates were also classified as multidrug-resistant.

Conclusion: These results demonstrate that dogs are commonly colonized by antimicrobial-resistant enterococci and highlight the role of pets as reservoir of last-line drug resistances. Moreover, the close contact with humans confirms the possible transmission of antimicrobial-resistant bacteria from dogs to humans. Therefore, the study stresses the need of surveilling this phenomenon also in companion animals.

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Detection of carbapenemase production by multidrug-resistant acinetobacter baumannii isolates from selected wards in dr george mukhari academic hospital

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Purpose: Carbapenem-resistant *Acinetobacter baumannii* has emerged as an important cause of nosocomial outbreaks worldwide. Detection of carbapenemase production by modified Hodge test using Mueller Hinton agar has been reported to be less sensitive. The objectives of this study were two-fold: i. to compare the performance of MacConkey agar (MA) and Mueller Hinton agar (MHA) for the detection of carbapenemases; ii. to determine the type of carbapenemases that are produced by *A. baumannii* isolates from Dr George Mukhari Academic Hospital (DGM).

Methods & Materials: Twenty four stored carbapenem-resistant and 2 carbapenem-susceptible *A. baumannii* isolates were identified using Vitek 2 automated system (bioMerieux, France). The modified Hodge test (MHT) was done according to CLSI guidelines on MHA (DMP, South Africa) and MA (DMP, South Africa) using *Escherichia coli* ATCC 25922 and meropenem disks. All the plates were incubated at 37^0C overnight. Detection of carbapenem-resistance genes (OXA-23, OXA-40, OXA-58, SIM, VIM-1, VIM-2 AND IMP-like) was done according to published molecular methods.

Results: Of the 24 carbapenem-resistant isolates which were screened, 87.5% (21) and 62.5% (15) were found to be carbapenemase positive by MHT on MA and MHA, respectively. The cloverleaf pattern on MHA appears to be absent for some of the isolates but it is accentuated on MA. Both MHA and MA showed 50% false positive result for the 2 susceptible isolates. Of the 24 resistant isolates which were screened for *bla* genes, 87.5% (21) and 25% (6) were found to have OXA-23 and OXA-40, respectively.

Conclusion: MA may be used in place of MHA for the screening of carbapenem-resistant *A. baumannii* and thus will impact on infection control practices**.** OXA-23 *bla* gene was the most prevalent carbapenemase type at DGM Hospital. Though the numbers were small, the study confirms that phenotypic methods lack specificity and sensitivity, hence their results have to be confirmed by molecular methods.

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