Medium, MSA manitol salt agar (Oxoid), m Enterococcus Agar (Sigma Aldrich). The antibiotic sensitivity patterns (Kirby Bauer) to marbofloxacine, oxytetracycline, eritromycine, amikacyne, ampicilline, enrofloxacin, ciprofloxacin, streptomycin were adapted to CLSI standards. MAR (multiple antibiotic resistance) index for each bacterial genus and strain as well as mean values were calculated and analyzed by Statistica program.

Results: The results suggested a heavy bacterial pollution of both water and sediment. A total of 47 strains (water 21, 44.68%; sediment 26, 55.32%) were isolated, namely each *Enterococcus spp.* and *Staphylococcus spp.*, equally distributed in the water and sediment (47.62% and 52.38%, respectively), while *E. faecalis* (5 strains) was prevalent in the sediment (80%). There were no significant differences between the sensitivity to antibiotics of enterococci from water (w) and sediment (s), but although the latter were less resistant to ampicilline (42.86% versus 100%), their MAR index was higher (0.2±0.072 versus 0.156±0.05) indicating the strains originated from high risk sources. The staphylococci were least sensitive to ampicilline (w 66.67%, s 20%), but resistance to eritromycine, enrofloxacin, ciprofloxacin and streptomycin was present, ranging from 16.4 to 40%. The MAR index was the highest for the strains in the sediment (0.333±0.072).

Conclusion: The results of the study partially supported our hypothesis, indicating a large numbers of enterococcal and staphylococcal isolates, with an increased antibiotic resistance posing a high health risk in the ecosystem. Supported by PNII/61-2012

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19.044

Resistance of nosocomial pathogens in burns unit (Yaroslavl, Russia)

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Purpose: In patients in burn units (BU) with infectious complications are often problems with the appointment of antimicrobial agents, including in relation with a higher level of resistance of pathogens. The aim of our study was to evaluate the resistance of the main problematic pathogens in the BU.

Methods & Materials: Pathogen isolates were collected from patients hospitalized in BU of Yaroslavl Emergency Clinical Hospital in 2015 year. Susceptibility (S) and resistance (R) of *Ps.aeruginosae, Acinetobacter baum., E.coli, Klebsiella pneum. and S.aureus* was interpreted to principal antimicrobial drugs according to current EUCAST standard by disk-diffusion.

Results: In 2015 was isolated from patients in the BU: *S. aureus* - 26, *Acinetobacter baum.* - 9, *Ps. aeruginosae* - 7, *Klebsiella pneum.* - 6 and *E. coli* - 3. The localization of pathogenic material were burn wounds. Of the 26 strains of *S.aureus* only 7 were MRSA. These strains were susceptible to aminoglycosides, rifampicin and fusidin. R of *Ps. aeruginosae* was extremely high for all drugs, including carbapenems (R to imipenem and to meropenem - 28.5% and 42.8%, respectively). High activity (R <25%) maintained: ceftazidime, aztreonam, gentamicin (S for all - 100%), amikacin, tobramycin (S both - 14.3%). *Acinetobacter baum.* showed a higher level of resistance. Activity retained: cefoperazone / sulbactam (R - 0%), ampicillin / sulbactam (R - 11%), imipenem (R - 22.2%), while the level R to other drugs (ceftazidime, meropenem, aztreonam, piperacillin / sulbactam, ciprofloxacin, amikacin, tigecycline) was much higher - 89, 100, 100, 88, 83, 75 and 38% respectively. All strains of *E.coli* were producers beta-lactamases (ESBL (+), AmpC (+)). Pathogens were resistant to carbapenems. At the same time, all strains of E.coli were susceptible to cefoperazone / sulbactam and piperacillin / tazobactam.

Conclusion: Among pathogens from patients in BU there is no clear predominance of Gram (-) or Gram (+) flora. The highest levels of resistance have been reported in Gram (-) pathogens. The spread of strains resistant to carbapenems is a serious problem for practical public health.

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19.045

Prevalence of ESBL-producing *Escherichia coli* from different canine populations in Italy

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Purpose: The increased diffusion of antimicrobial-resistant bacteria, especially extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* in humans, animals, and their surrounding environments is a severe problem of Public Health. Cephalosporins represent one of the few therapeutic options to treat many bacterial infections, so they are defined as critically important drugs for their broad activity. Since the spread of these bacteria implies different transmission routes and reservoirs including pets, the aim of this study was to provide data on the prevalence and characterization of ESBL-producing *E. coli* from dogs of different origins.

Methods & Materials: Faecal samples of 511 dogs (237 from households, 193 from kennels and 81 from public gardens) were plated on MacConkey agar supplemented with cefotaxime and Brilliance-ESBL Agar (Oxoid). Presumptive ESBL-producing *E. coli* were confirmed by combination disk diffusion tests. Susceptibility to the non-beta-lactams was determined by the disk diffusion method according to the CLSI guidelines.

Results: Of the 511 samples, 31 (6%) carried an ESBL-producing *E. coli*. Most of the ESBL-producers (22 strains; 71%) were isolated from kennels, followed by 7 (22.6%) from faeces from public gardens and 2 (6.4%) from household dogs. Most of these isolates were also classified as multidrug-resistant, showing resistance to at least three antimicrobial classes. All the ESBL-producing isolates indeed showed resistance to at least one of the quinolones tested and a range of resistance to carbapenems from 22% in samples from kennels to 50% in samples from households animals and public gardens.

Conclusion: The presence of commensal ESBL-producing *Escherichia coli* in canine faeces confirms the role of pets as potential homely and environmental sources of resistant bacteria to critically important drugs for humans. The high number of pets, their close relationship with humans and the increased attention to their health poses risks of transmission of antimicrobial-resistant bacteria among dogs and humans. Indeed, the spread of resistance due to the use in pets of drugs for treatment of infectious diseases, including compounds of primary importance in the treatment of human infections, should not be underestimated. Therefore, this study highlights the need of monitoring antimicrobial-resistance

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

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19.046

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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19.048

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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