

**P1515**

**Paper Poster Session**

**Antibacterial resistance: the animal and food production part of one health**

**Intestinal colonization of Brazilian cattle with multidrug-resistant (MDR) non-fermenting Gram-negative bacilli (NFGNB)**

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**Background:** Nonfermenting gram-negative bacilli (NFGNB) have emerged as important healthcare-associated pathogens. Some of them show intrinsic resistance to multiple drugs being responsible for high therapeutic failure in community and hospital infections. *Stenotrophomonas maltophilia* is an emerging MDR pathogen of relevance in the acute healthcare setting. The aim of this study was the detection of MDR gram negative bacilli responsible for intestinal colonization of healthy cattle in Brazil.

**Material/methods:** Selection of the isolates was performed on MacConkey agar with different antibiotics (cefotaxime, ceftazidime, cefepime, meropenem, ertapenem, tetracycline, and ciprofloxacin) in fecal samples previously incubated in TSB overnight. Susceptibility testing was performed by the disk diffusion method according to CLSI guidelines. Presumptive identification was achieved by CHROMagar Orientation. Identification of representative isolates of resistance phenotype patterns was done by ID32GN. Extended-spectrum-beta-lactamase (ESBL) detection was done by the double disk synergy test. Beta-lactamase genes were screened by PCR, using specific primers for *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub> and *bla*<sub>CTX-M</sub>.

**Results:** Three *Stenotrophomonas maltophilia* isolates were selected in three animal samples from two different productions. In addition to the intrinsic resistance to beta-lactam antibiotics, two isolates also showed resistance to ceftazidime due to ESBL production detected by the double disk synergism, but were negative for ESBL gene detection for *bla*<sub>TEM</sub> and *bla*<sub>SHV</sub> and *bla*<sub>CTX-M</sub> and showed amikacin resistance. One isolate showed intermediate resistance to gentamicin and tobramycin. The third isolate was sensitive to ceftazidime and amikacin and showed resistance to chloramphenicol. Five *Pseudomonas aeruginosa* isolates were selected in five samples from three different productions. One isolate showed resistance to cefepime, aztreonam and another showed intermediate resistance to aztreonam and levofloxacin in addition to the intrinsic resistance for the species. The other three isolates showed only intrinsic resistance.

**Conclusions:** Presence of MDR *Stenotrophomonas maltophilia* and *Pseudomonas aeruginosa* in the fecal flora of healthy animals might pose a public health threat in terms of dissemination of these particular opportunistic pathogens. Acquired resistance in some of the selected isolates shows an even more worrying scenario with further diminished therapeutic alternatives to treat these bacteria. One *Stenotrophomonas maltophilia* isolate showed an ESBL and resistance to aminoglycosides, another isolate showed chloramphenicol resistance. *Pseudomonas aeruginosa* showed resistance to cefepime and aztreonam. Important is the fact that these microorganisms are present in stool samples of healthy animals, creating a reservoir of multidrug-resistant microorganisms, which is a relevant

issue for human, animal and environmental health, emphasizing the importance of the One Health approach in terms of antimicrobial resistance dissemination.