

**P1511**

**Paper Poster Session**

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

**Multidrug-resistant (MDR) extended-spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae* in intestinal colonization of Portuguese sheep**

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**Background:** Bacterial resistance in farm animals is currently one of the main targets of investigation by the scientific community, because of their relevance and impact on global public health. In this context, the extended-spectrum beta-lactamases (ESBL) are important enzymes view of their ability to degrade oximino-beta-lactam antibiotics. Among the animal production, sheep stand out from the point of view of not only the food chain, but also for being important in other sectors, such as textiles. Among the microorganisms showing bacterial resistance in farm animals, *Enterobacteriaceae* are relevant considering they are the main facultative anaerobic commensal in animal intestinal flora. This study aimed to evaluate the presence of multidrug resistant *Enterobacteriaceae* in feces of healthy sheep in Portugal.

**Material/methods:** Please Selection of the isolates was performed on MacConkey agar with different antibiotics (cefotaxime, ceftazidime, cefepime, meropenem, ertapenemo, tetracycline, and ciprofloxacin). Samples were previously incubated in Tryptic soy broth (TSB). Susceptibility testing was achieved by disk diffusion method according to CLSI. Presumptive identification was performed with CHROMagar Orientation. Extended-spectrum beta-lactamase (ESBL) producers were screened by the double disk synergy test. ESBL coding genes were screened by PCR with specific primers *bla*<sub>TEM</sub>, *bla*<sub>OXA</sub>, *bla*<sub>SHV</sub> and *bla*<sub>CTX-M</sub>.

**Results:** From 21 sheep fecal samples, 150 isolates of *Enterobacteriaceae* were obtained. They showed resistance to amoxicillin (87,3%), tetracycline (66%), cefotaxime (63,3%), amoxicillin plus clavulanic acid (61,3%), sulfamethoxazole plus trimethoprim (45,3%), ciprofloxacin (25,3%), cefoxitin (22,7%), chloramphenicol (18,7%) and gentamicin (8%). Resistance to antibiotics of other families showed a total of 101 MDR isolates. Sixty two selected isolates (41,3%) were ESBL-producing *Escherichia coli*, showing the following beta-lactamase gene profile: *bla*<sub>CTX-M</sub> Group 1 (G1) and *bla*<sub>TEM</sub> (56,6%); *bla*<sub>CTX-M</sub> G1 (30,6%); *bla*<sub>CTX-M</sub> G1 and *bla*<sub>OXA</sub> (1,6%); *bla*<sub>CTX-M</sub> Group 8 (G8) and *bla*<sub>SHV</sub> (4,8%); *bla*<sub>SHV</sub> (3,2%); *bla*<sub>CTX-M</sub> Group 9 (G9) and *bla*<sub>TEM</sub> (1,6%); and *bla*<sub>CTX-M</sub> G9 (1,6%). Results highlight the prevalence of *bla*<sub>CTX-M</sub> G1 present in 87.2% of ESBL-producing *E. coli*. ESBL producers show different associated resistances to other antibiotic families showing a polyclonal spread of these resistance threats.

**Conclusions:** In this single animal production we can highlight the prevalence of MDR *Enterobacteriaceae* and a diversity of ESBL with predominance of *bla*<sub>CTX-M</sub> G1. CTX-M-15 is the prevalent enzyme of this group and already found in food producing animals. Raw milk cheese production might be influenced by this reality and animals may act as reservoirs of multidrug-resistant microorganisms relevant in terms of public health.