P1633

Abstract (poster session)

**Prevalence and characterisation of extended-spectrum beta-lactamase (ESBL) and CMY-2 producing Escherichia coli isolates from healthy food-producing animals in Tunisia**

R. Ben Sallem, H. Gharsa, K. Ben Slama, V. Estepa, A. Jouini, B. Rojo-Bezares, Y. Sáenz, A. Boudabous, C. Torres* (Tunis, TN; Logroño, ES)

Objective: To analyse the carriage rate of extended-spectrum beta-lactamase (ESBL)- and /or AmpC-beta-lactamase-producing E. coli isolates from faecal samples of food-producing animals in Tunisia, and to characterize the recovered isolates for the presence of other resistance genes and integrons. Methods 80 animal faecal samples (23 of sheep, 22 poultry, 22 cattle, 6 horses, 5 rabbits and 2 dromedaries) were obtained from 35 different farms in Tunisia during 2011. Samples were inoculated onto MacConkey agar plates supplemented with cefotaxime (2 mg/L) for cefotaxime-resistant (CTXR) E. coli recovery. Characterization of ESBL and AmpC genes, of their genetic environment and of integrons were performed by PCR and sequencing. Detection of associated resistance genes, virulence factors, and phylogroup-typing were performed by PCR. Molecular typing of isolates was determined by MLST and PFGE. Results: CTXR E. coli isolates were detected in 11 of 80 faecal samples (13.75%) and one isolate per sample was further characterized (recovered from 10 poultry samples and one dromedary sample). The 11 CTXR isolates were distributed into the phylogroups: B1 (5 isolates), A (2), D (3) and B2 (1). The following beta-lactamase genes were detected: blaCTX-M-1 (7 isolates), blaCTX-M-1+blaTEM-135 (1 isolate), blaCTX-M-1+blaCMY-2+blaTEM-1b (1 isolate) and blaCMY-2 (2 isolates). The ISEcp1 and orf477 sequences were found upstream and downstream of blaCTX-M-1 gene, respectively, in all blaCTX-M-1-positive isolates. The 9 CTX-M-1 producing strains showed unrelated PFGE-patterns and eight different sequence-types (STs) were identified among them (number isolates/phylogroup/patterns): ST155 (2/B1/P1-P11), ST2255 (1/D/P2), ST57 (1/D/P3), ST2164 (1/A/P5), ST2016 (1/B1/P7), ST58 (1/B1/P8), ST88 (1/B1/P9), and ST10 (1/A/P10). The two blaCMY-2 producing strains were typed each one as ST117/D/P6 and STnew /B2/P4. Seven isolates contained class 1 integrons with four different gene cassettes arrangements: dfrA17-aadA5 (3 isolates), dfrA1-aadA1 (2), dfrA15-aadA1 (1 isolate) and aadA1 (1 isolate). All the isolates showed tetracycline resistance and they contained the genes tet(A) or tet(B). Virulence genes detected were (number isolates): fimA (10), aer (8), papC(2), and papGIII, hly, cnf, and bfp (none). Conclusion: Poultry farms constitute a reservoir of ESBL-producing E. coli isolates that potentially could be transmitted to humans via the food chain or by direct contact with them.