

03. Bacterial susceptibility & resistance

3b. Resistance surveillance & epidemiology: Gram-negatives

Second topic

03. Bacterial susceptibility & resistance / 3g. Spread of resistance incl reservoirs, ecology, mobile elements (excl nosocomial transmission)

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Background *Escherichia coli* is a commensal intestinal bacteria of animals and humans and also an opportunistic pathogen. The aim of the study was to characterize the phenotypes-genotypes of antimicrobial resistance, including extended-spectrum-beta-lactamases (ESBL), molecular typing and integron characterization in environmental *E. coli* isolates of a broiler farm.

Methods 111 *E. coli* isolates recovered from air (n=54) and manure (n=57) from a broiler farm were analyzed. Susceptibility to 12 antibiotics and ESBL-screening was studied by disc-diffusion method. The presence of 18 antimicrobial resistance genes were determined by PCR-sequencing. Class 1 integrons were analyzed and their variable-region were also characterized. Multilocus-Sequence-Typing (MLST) and phylogenetic groups were performed.

Results 96 out of 111 *E. coli* isolates (86.5%) showed resistance to at least one antibiotic and 51 isolates were multidrug-resistant (MDR). High rates of resistance to ampicillin, trimethoprim-sulfamethoxazole (SXT), tetracycline, ciprofloxacin and chloramphenicol (range 30%-80%) and lower rates of resistance to amoxicillin-clavulanate, gentamicin, and cefoxitin (range 1%-15%) were detected, with no resistance to imipenem. Twenty-three ESBL-positive isolates were detected (20.7%), all of them carrying the blaSHV-12 gene (from air and manure); one of the ESBL-positive isolates also contained the blaCMY-2 gene, encoding an acquired-AmpC beta-lactamase (aAmpC). The ESBL-positive isolates belonged to four genetic lineages (sequence-type/phylogenetic group/number of isolates): ST770/E-B2/12, ST117/B2-F-D/4, ST10992/A-C-E/4 and ST68/E/3. Representative ESBL-negative isolates belonged to five genetic lines (sequence-type/phylogenetic group/number of isolates): ST57/B2-E/2, ST/10992/A-C-E/6, ST5766/A/3, ST4512/E/1 and ST115/E/1. The following resistance genes were detected among antibiotic-resistant *E. coli* isolates of the study: beta-lactams (blaTEM, blaSHV-12, blaCMY-2), tetracycline (tetA, tetB), SXT (sul1/sul2/sul3, dfrA1, dfrA12), aminoglycosides (aac(3)-II, aac(6)-Ib-cr, aadA1/aadA2) and chloramphenicol (cmIA). None isolate carried catA, floR or mcr1 genes. The int1 gene, encoding the integrase of class 1 integrons, was detected in 45 SXTR isolates, and three types of gene-cassettes-arrays were found: 2) two linked to sul1: dfrA1-aadA1 (n=5), and dfrA12-aadA2 (n=1); B) one linked to sul3: dfrA12-orfF-aadA2-cmIA (n=1).

Conclusions Antimicrobial resistant *E. coli*, including ESBL- and aAmpC-producers, were frequently detected in environmental samples of a broiler farm. Thus, the farm environment is a

source of a wide variety of resistance genes and integrons structures, so the potential ways of dissemination should be evaluated.

Keyword 1

Escherichia coli

Keyword 2

ESBL

Keyword 3

broiler farm

Conflicts of interest

Other support (please specify)

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