

Fluoroquinolone resistance in *E. coli* in broilers: mapping the spread

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Objective

Although restrictions on the use of fluoroquinolones in livestock have been imposed in Belgium since 2016, high levels of fluoroquinolone (FQ) resistance are still found in commensal *E. coli* in broilers. The purpose of this study was to describe the FQ resistance prevalence in *E. coli* and to investigate the role of day-old chicks and the environment in the dynamics of the spread within different flocks.

Materials and methods

On 29 broiler farms, antibiotic use was monitored and both water and environmental samples were collected prior to arrival of the chicks. Thirty broilers were sampled per farm on days 0 (before entering the stable), 3 and 35 of the production round. In all samples, total *E. coli* and FQ resistant *E. coli* isolates were quantified by plating on MacConkey agar without and with 0.25 µg/ml enrofloxacin (ECOFF). All isolates were identified using MALDI-TOF MS. A selection of the isolates was submitted for whole genome sequencing to investigate their phylogenetic relatedness using core-genome MLST (cgMLST) analysis, and to detect resistance determinants.

Results

Before they entered the stable, the day-old chicks carried FQ resistant *E. coli* in 82.8% of the farms and FQ resistant *E. coli* were found in the environment on boots (10.3%), hygiene locks (24.1%), drinking cups (10.3%), feeding pans (20.7%), and stable floors (24.1%). According to cgMLST, overall there was a large diversity of FQ resistant *E. coli* strains. However, identical FQ resistant isolates were found on day 0 and day 35, suggesting that FQ resistant isolates present in the environment at the start of a production round or in day-old chicks, remained present until slaughter, even though no FQs were used.

Conclusion

The continued presence of FQ resistant *E. coli* in Belgian broiler farms is likely the result of both a historical contamination at the farm level and a continuous influx along the production chain.