Associations between antimicrobial use and the faecal resistome on broiler farms from nine European countries - DTU Orbit (23/10/2019)

**Objectives**  
To determine associations between farm- and flock-level antimicrobial usage (AMU), farm biosecurity status and the abundance of faecal antimicrobial resistance genes (ARGs) on broiler farms.

**Methods**  
In the cross-sectional pan-European EFFORT study, conventional broiler farms were visited and faeces, AMU information and biosecurity records were collected. The resistomes of pooled faecal samples were determined by metagenomic analysis for 176 farms. A meta-analysis approach was used to relate total and class-specific ARGs (expressed as fragments per kb reference per million bacterial fragments, FPKM) to AMU (treatment incidence per DDD, TIDDDvet) per country and subsequently across all countries. In a similar way, the association between biosecurity status (Biocheck.UGent) and the resistome was explored.

**Results**  
Sixty-six (38%) flocks did not report group treatments but showed a similar resistome composition and roughly similar ARG levels to antimicrobial-treated flocks. Nevertheless, we found significant positive associations between β-lactam, tetracycline, macrolide and lincosamide, trimethoprim and aminoglycoside antimicrobial flock treatments and ARG clusters conferring resistance to the same class. Similar associations were found with purchased products. In gene-level analysis for β-lactams and macrolides, lincosamides and streptogramins, a significant positive association was found with the most abundant gene clusters blaTEM and erm(B). Little evidence was found for associations with biosecurity.

**Conclusions**  
The faecal microbiome in European broilers contains a high diversity of ARGs, even in the absence of current antimicrobial selection pressure. Despite this, the relative abundance of genes and the composition of the resistome is positively related to AMU in European broiler farms for several antimicrobial classes.

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