The quantitative effect of lifetime antimicrobial usage on the abundance of antimicrobial resistance genes in batches of finishing pigs - DTU Orbit (06/08/2019)

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Spread of antimicrobial resistant bacteria caused by use of antimicrobials is one of the most harmful threats to global health. Considering that the antimicrobial usage in animals also contributes to the burden of antimicrobial resistant bacteria among humans, several initiatives have been launched targeting antimicrobial usage in livestock.

The overall aim of the project wherein this PhD thesis/project was performed was to develop a model capable of predicting the change in the abundance of antimicrobial resistance genes in pigs slaughtered in Denmark, based on different intervention scenarios. The predictive model is meant to support authorities in assessments of the effects on antimicrobial resistance of interventions targeted antimicrobial usage in pigs. This thesis provided the parameters for the model. First, a method to estimate the lifetime antimicrobial usage in slaughter pigs based on register-based data was developed and validated. The use of register-data was chosen, in order to be able to calculate lifetime antimicrobial usage at farm level for the majority of pigs slaughtered in Denmark. The method showed that the entire rearing period from the birth of a piglet to the time of slaughter has to be taken into account independent of rearing occurring in one or several farms. Linear regression models were applied to obtain effect estimates of the lifetime antimicrobial usage of slaughter pigs on the abundance of different groups of antimicrobial resistance genes in their gut microbiota close to slaughter. It was found that increased lifetime antimicrobial usage of one or several antimicrobial-classes at dispensing-type level had an increasing effect on the abundance of resistance genes against aminoglycosides, beta-lactams, lincosamides, macrolides, MLSb, sulfonamides and tetracyclines. Thereby, the results demonstrate that the abundance of antimicrobial resistance was significantly connected with the quantitative antimicrobial usage during the pigs' entire life.

Overall, the thesis provided validated significant effect estimates for the predictive model. In turn, the model provides a framework for further development, which may assist in reducing antimicrobial resistance and safeguard antimicrobials for the future.

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