Persistance of antimicrobial resistance genes from sows to finisher pigs

Antimicrobial resistance in pigs has been under scrutiny for many years. However, many questions remain unanswered, including whether the initial antimicrobial resistance level of a pig will influence the antimicrobial resistance found at slaughter. Faecal samples from finishers pigs from 681 farms and from sows from 82 farms were collected, and levels of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W), were quantified by high-capacity qPCR. There were 40 pairs of observations where the finishers were born in the farms of the sows. The objective of this study was to evaluate whether the levels of AMR genes found in finisher pigs at slaughter were associated with the levels in the farm where the finishers were born, and whether the levels of the AMR genes were equal in the sow and finisher pig populations. We found a significant positive correlation between the levels of AMR genes in finishers and the sows in the farms where the pigs were born for some of the genes (ermB (ρ = 0.47, p-value = 0.002), ermF (ρ = 0.41, p-value = 0.03), and tet(O) (ρ = 0.33, p-value = 0.04)). Furthermore, there were significant differences between AMR gene levels for the sow and finisher populations for ermB, ermF, sulI, sulII, tet(O), and tet(W), though not for tet(M).
Antimicrobial resistance in Danish pigs: A cross sectional study of the association between antimicrobial resistance and geography, exposure to antimicrobials, and trade

Antimicrobial resistance is a worldwide problem of paramount importance for both humans and animals. To combat the emergence of antimicrobial resistance, the problem must be targeted in all major reservoirs as it is assumed that a high level of AMR genes in environmental reservoirs can increase the risk of human pathogens becoming resistant. Pigs might constitute an important reservoir. Therefore, it is important to manage antimicrobial resistance in pigs. Before effective actions can be initiated, it is crucial to know which factors are associated with the levels of antimicrobial resistance in pigs. The Danish pig farm is an ideal place to study AMR, as the pigs are all kept together in a confined space and managed in a similar manner. Furthermore, movements of pigs between farms and the purchase of antimicrobials for use at the farm are registered in national databases, thus facilitating the collection of information on relevant factors. The aim of this PhD project was to study the relationship between the levels of antimicrobial resistance genes and three factors in Danish pig farms: the geographical location of the farm, the exposure to antimicrobials, and the trade patterns. Data collection was necessary in order to fulfill the aim of the project, and early in the project it became evident that a thorough consideration of how the data should be collected was needed. This resulted in three different projects, each contributing to the planning process. Throughout the entire PhD project, the focus was on seven antimicrobial resistance genes - ermB, ermF, sul1, sul2, tet(M), tet(O), and tet(W). The levels of these genes were determined using a quantitative real-time polymerase chain reaction (qPCR). The erm genes confer resistance against macrolides, the sul genes confer resistance against sulfonamides, and the tet genes confer resistance against tetracyclines. It was necessary to determine the minimum number of individual faecal samples that should be pooled together to represent the average level of antimicrobial resistance genes in the farm. It was estimated that a sample pooled from individual samples from five pigs was optimal. The pooling method was optimised, and was found to have strong agreement with previously used pooling methods. Samples were collected from 687 Danish pig farms in February and March 2015. However, 6 farms did not fulfill the criteria for the target population and were excluded. The samples were collected at five abattoirs located on Zealand and in Jutland. The sample material was faeces, and it was collected by squeezing a small amount out of the rectum at the slaughter line. After collection the samples were sent to the laboratory. The samples were pooled into one aliquot per farm and DNA was extracted from the faecal material. The antimicrobial resistance gene levels were then measured using quantitative real-time PCR. As the samples were collected at the abattoir it was not possible to know in advance which farms were available for sampling. Consequently, it was not possible to estimate whether the sampled farms were representative of the target and study populations prior to sampling. However, an evaluation of the representativeness of sampled farms (in terms of farm size and geographical location) was carried out post-sampling. It was found that the sampled farms were larger than nonsampled farms. Furthermore, there was an undersampled area in the western part of Jutland and an oversampled area in the northern part of Jutland. A simulation study showed that the sampling procedure would inevitably result in a bias towards larger farms and with some non-randomness in the spatial distribution. One of the aims of this PhD project was to estimate the quantitative relationship between the antimicrobial resistance gene levels and antimicrobial exposure. Previous studies have indicated that antimicrobial exposure in early periods of a pig’s life can influence the antimicrobial resistance gene levels found later in life. In order to quantify the relationship, an estimate of the antimicrobial exposure throughout the entire lifetime of a slaughter pig was required. An algorithm to estimate the LEA was therefore developed. Previous studies have shown that livestock farms in close proximity share common pathogens. Furthermore, there have been indications that phenotypic antimicrobial resistance can be spatially clustered. Therefore, the spatial pattern of the antimicrobial resistance gene levels was assessed, and both areas with high levels and areas with low levels of some of the genes were found. However, it was concluded that the geographical location of the farm had only a minor effect on the antimicrobial resistance gene levels. Antimicrobial exposure is the most important risk factor for the development of antimicrobial resistance. However, previous studies of the relationship between antimicrobial resistance and antimicrobial exposure have focused on phenotypic antimicrobial resistance in a small number of farms. In this PhD project, the focus was on genotypic antimicrobial resistance. The quantitative relationship between the levels of seven antimicrobial resistance genes and the lifetime exposure of 11 different antimicrobial classes was estimated. It was found that some antimicrobial classes had a positive correlation with the levels of some antimicrobial resistance genes, but a negative correlation with other antimicrobial resistance genes. In conclusion, it was found that even though exposure to antimicrobials was associated with the antimicrobial resistance gene levels, it could only explain 10% - 42% of the variation in the gene levels. The microflora of a pig is established soon after birth. The source of the microflora is bacteria in the environment and from the sow. It has been shown that antimicrobial exposure of the sow will influence the antimicrobial resistance levels in the piglet. Therefore, the correlation between the levels of antimicrobial resistance genes in finisher farms and that of the sow farms with which they had trade connections was assessed. A significant correlation was found for most of the antimicrobial resistance genes with correlation coefficients ranging from 0.06 to 0.47. Of the three factors that were studied in this PhD project, only the antimicrobial exposure and the level of antimicrobial resistance in the sow farm with a trade connection were found to have a considerable effect on the antimicrobial resistance genes. However, it became apparent during the project that many other factors could affect the levels of antimicrobial resistance genes. This could lay the foundation for future studies.
Association between selected antimicrobial resistance genes and antimicrobial exposure in Danish pig farms

Bacterial antimicrobial resistance (AMR) in pigs is an important public health concern due to its possible transfer to humans. We aimed at quantifying the relationship between the lifetime exposure of antimicrobials and seven antimicrobial resistance genes in Danish slaughter pig farms. AMR gene levels were quantified by qPCR of total-community DNA in faecal samples obtained from 681 batches of slaughter pigs. The lifetime exposure to antimicrobials was estimated at batch level for the piglet, weaner, and finisher periods individually for the sampled batches. We showed that the effect of antimicrobial exposure on the levels of AMR genes was complex and unique for each individual gene. Several antimicrobial classes had both negative and positive correlations with the AMR genes. From 10-42% of the variation in AMR gene levels could be explained in the final regression models, indicating that antimicrobial exposure is not the only important determinant of the AMR gene levels.

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Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Græsbøll, K. (Intern), Clasen, J. (Intern), Folkesson, A. (Intern), Toft, N. (Intern)
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Associations between Antibacterial Treatment and the Prevalence of Tail-Biting-Related Sequelae in Danish Finishers at Slaughter

Secondary infections as a result of tail biting cause substantial economic losses in pig production and are a subject of concern for animal welfare. The use of first-choice antibacterial agents in the treatment of tail biting in finishing pigs is hypothesized to be negatively correlated with the development of systemic infection. This would be expected to reduce the prevalence of post-mortem pyemic sequelae (such as osteomyelitis and abscesses) in finishers with tail-bite lesions. We performed a register-based study that included three Danish databases, holding information on the purchase of antibacterials at herd level (VetStat), herd demographics (Central Husbandry Register), and relevant observations at slaughter (meat inspection data). We included all finishers from indoor production finisher herds that met the inclusion criterion of at least one slaughtered finisher with a recorded tail-bite observation during 2015 at the single largest Danish abattoir. The final dataset held 1,070 herds with one or more tail-bite observations, from which 14,411 of 2,906,626 finishers (0.50%) had an individual record of a tail bite. Within this group of finishers with tail-bite observations, the recorded tail-biting-related sequelae included osteomyelitis (8.1%), abscesses in the hindquarters (10.5%), abscesses in the forequarters (2.3%), abscesses in the mid-section of the carcass (2.9%), abscesses in the limbs (2.4%), and chronic arthritis (0.5%). Due to a high-herd prevalence (>25%), osteomyelitis and abscesses in the hindquarters were selected for further analysis. The occurrence of osteomyelitis and hindquarter abscesses in individual finishers with tail-bite observations was described using a generalized linear mixed effects model with binomial response and logit link. Herd was included as a random effect, while herd size and various antibacterial treatments were tested for inclusion in the model as fixed effects. The final models indicated a significant association between herd size and both osteomyelitis (p = 0.014) and hindquarter abscesses (p < 0.001), with larger herds (2,001–12,000 registered finisher pigs) showing a reduced risk. Further, a negative association was found between the occurrence of hindquarter abscesses and the use of oral pleuromutilin (p = 0.022). The significant association with herd size highlights the potential importance of management factors in reducing the occurrence of tail-bite lesions in finishing pigs.

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Bibliographical note
Computational algorithm for lifetime exposure to antimicrobials in pigs using register data − the LEA algorithm

Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for finisher batches, as a lifetime exposure measurement.
Improving institutional memory on challenges and methods for estimation of pig herd antimicrobial exposure based on data from the Danish Veterinary Medicines Statistics Program (VetStat)

With the increasing occurrence of antimicrobial resistance, more attention has been directed towards surveillance of both human and veterinary antimicrobial use. Since the early 2000s, several research papers on Danish pig antimicrobial usage have been published, based on data from the Danish Veterinary Medicines Statistics Program (VetStat). VetStat was established in 2000, as a national database containing detailed information on purchases of veterinary medicine. This paper presents a critical set of challenges originating from static system features, which researchers must address when estimating antimicrobial exposure in Danish pig herds. Most challenges presented are followed by at least one robust solution. A set of challenges requiring awareness from the researcher, but for which no immediate solution was available, were also presented. The selection of challenges and solutions was based on a consensus by a cross-institutional group of researchers working in projects using VetStat data. No quantitative data quality evaluations were performed, as the frequency of errors and inconsistencies in a dataset will vary, depending on the period covered in the data. Instead, this paper focuses on clarifying how VetStat data may be translated to an estimation of the antimicrobial exposure at herd level, by suggesting uniform methods of extracting and editing data, in order to obtain reliable and comparable estimates on pig antimicrobial consumption for research purposes.

General information
Sampling pig farms at the abattoir in a cross-sectional study – Evaluation of a sampling method

A cross-sectional study design is relatively inexpensive, fast and easy to conduct when compared to other study designs. Careful planning is essential to obtaining a representative sample of the population, and the recommended approach is to use simple random sampling from an exhaustive list of units in the target population. This approach is rarely feasible in practice, and other sampling procedures must often be adopted. For example, when slaughter pigs are the target population, sampling the pigs on the slaughter line may be an alternative to on-site sampling at a list of farms. However, it is difficult to sample a large number of farms from an exact predefined list, due to the logistics and workflow of an abattoir. Therefore, it is necessary to have a systematic sampling procedure and to evaluate the obtained sample with respect to the study objective. We propose a method for 1) planning, 2) conducting, and 3) evaluating the representativeness and reproducibility of a cross-sectional study when simple random sampling is not possible. We used an example of a cross-sectional study with the aim of quantifying the association of antimicrobial resistance and antimicrobial consumption in Danish slaughter pigs. It was not possible to visit farms within the designated timeframe. Therefore, it was decided to use convenience sampling at the abattoir. Our approach was carried out in three steps: 1) planning: using data from meat inspection to plan at which abattoirs and how many farms to sample; 2) conducting: sampling was carried out at five abattoirs; 3) evaluation: representativeness was evaluated by comparing sampled and non-sampled farms, and the reproducibility of the study was assessed through simulated sampling based on meat inspection data from the period where the actual data collection was carried out. In the cross-sectional study samples were taken from 681 Danish pig farms, during five weeks from February to March 2015. The evaluation showed that the sampling procedure was reproducible with results comparable to the collected sample. However, the sampling procedure favoured sampling of large farms. Furthermore, both under-sampled and over-sampled areas were found using scan statistics. In conclusion, sampling conducted at abattoirs can provide a spatially representative sample. Hence it is a possible cost-effective alternative to simple random sampling. However, it is important to assess the properties of the resulting sample so that any potential selection bias can be addressed when reporting the findings.
Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with
respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulI and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

**General information**

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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.288 SNIP 1.026 CiteScore 2.19
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BFI (2012): BFI-level 1
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.034 SNIP 1.045
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.053 SNIP 1.192
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Determining the optimal number of individual samples to pool for quantification of average herd levels of antimicrobial resistance genes in Danish pig herds using high-throughput qPCR

The primary objective of this study was to determine the minimum number of individual fecal samples to pool together in order to obtain a representative sample for herd level quantification of antimicrobial resistance (AMR) genes in a Danish pig herd, using a novel high-throughput qPCR assay. The secondary objective was to assess the agreement between different methods of sample pooling. Quantification of AMR was achieved using a high-throughput qPCR method to quantify the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)). A large variation in the levels of AMR genes was found between individual samples. As the number of samples in a pool increased, a decrease in sample variation was observed. It was concluded that the optimal pooling size is five samples, as an almost steady state in the variation was observed when pooling this number of samples. Good agreement between different pooling methods was found and the least time-consuming method of pooling, by transferring feces from each individual sample to a tube using a 10 μl inoculation loop and adding 3.5 ml of PBS, approximating a 10% solution, can therefore be used in future studies.

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Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
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How to pool fecal samples in a cross-sectional study of antimicrobial resistance genes in Danish pig herds

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Spatial patterns of Antimicrobial Resistance Genes in Danish Pig Farms
Samples from 687 Danish pig farms were collected at five finisher slaughterhouses in February and March 2015. Faecal samples from five pigs per farm were collected randomly at the slaughter line and pooled into one sample per farm. DNA was extracted from the pooled samples and the level of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W), was quantified by a high-throughput qPCR. It was evaluated whether the sample method resulted in a study population representative of Danish pig farms with finishers where it was found that the study population was biased towards farms having more finisher and a higher productivity. Spatial cluster analyses were performed in SaTScan®. The results showed significant spatial clusters for ermF, ermB, sulII and tet(W) whereas no significant clusters were found for sulI, tet(M) and tet(O).

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Relations
Activities:

Breeding Restrictions Decrease the Prevalence of Myxomatous Mitral Valve Disease in Cavalier King Charles Spaniels over an 8- to 10-Year Period
BACKGROUND: Cavalier King Charles Spaniels (CKCS) are predisposed to myxomatous mitral valve disease (MMVD). Studies have indicated a strong genetic background. OBJECTIVE: The aim of this study was to evaluate the effect of a breeding scheme involving auscultation and echocardiography. ANIMALS: In the Danish Kennel Club mandatory breeding scheme, 997 purebred CKCS were examined during the period 2002-2011. Each dog was evaluated 1-4 times with a total of 1,380 examinations. METHODS: Auscultation and echocardiography were performed to evaluate mitral regurgitation murmur severity and degree of mitral valve prolapse (MVP). The odds of having mitral regurgitation murmur or MVP > grade 1 in 2010-2011 compared to 2002-2003 were estimated using logistic regression analysis including age and sex as covariates. Odds were estimated for dogs that were products of the breeding scheme (defined as dogs with both parents approved by the breeding scheme before breeding) and non-products of the breeding scheme (defined as dogs with at least 1 parent with unknown cardiac status). RESULTS: In 2010-2011, the odds of having mitral regurgitation murmur were 0.27 if dogs were a product of the breeding scheme compared with dogs in 2002-2003, reflecting a 73% decreased risk (P < .0001). If non-products of the breeding scheme examined in 2010-2011 were compared with dogs in 2002-2003, no difference in odds was found (P = .49). CONCLUSION AND CLINICAL IMPORTANCE: A mandatory breeding scheme
based on auscultation and echocardiography findings significantly decreased the prevalence of MMVD over the 8- to 10-year period. Such a breeding scheme therefore is recommended for CKCS.

**General information**

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- Web of Science (2016): Indexed yes
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- Web of Science (2014): Indexed yes
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- Scopus rating (2013): SJR 1.529 SNIP 1.681 CiteScore 2.24
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- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 1.301 SNIP 1.524 CiteScore 2.08
- ISI indexed (2012): ISI indexed yes
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- Scopus rating (2011): SJR 1.598 SNIP 1.502 CiteScore 1.98
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- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 1.611 SNIP 1.693
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 1.479 SNIP 1.589
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 1.354 SNIP 1.318
- Scopus rating (2007): SJR 1.528 SNIP 1.672
- Web of Science (2007): Indexed yes
- Scopus rating (2006): SJR 1.093 SNIP 1.514
- Scopus rating (2005): SJR 1.183 SNIP 1.691
- Scopus rating (2004): SJR 0.956 SNIP 1.364
- Scopus rating (2003): SJR 1.304 SNIP 1.991
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Comparison of individual and pooled samples for quantification of antimicrobial resistance genes in swine feces by high-throughput qPCR

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Comparison of individual and pooled samples for quantification of antimicrobial resistance genes in swine feces by high-throughput qPCR

There is a considerable societal interest in the careful monitoring of antimicrobial resistance (AMR) levels in human and animal populations. Sampling and data analysis can be both costly and time consuming. Optimization of sample pooling procedures is therefore important to reduce costs and analysis times. The objective of this study was to estimate how many individual fecal samples are needed to pool to get a representative sample for quantification of AMR-genes in a Danish pig herd. 20 individual fecal samples were collected from one section in a Danish pig herd. One to five rectal fecal samples were taken from each pen with respect to the number of pigs in the pen. A total of 48 pools were made of increasing number of individual samples. The levels of 9 different AMR-genes were quantified using dynamic qPCR arrays on the BioMark HD system (Fluidigm®). DNA was extracted using the Maxwell® 16 Blood DNA Purification Kit (Promega). DNA concentrations were diluted to 40 ng/μl. The efficiency of the primers was determined using standard curves. Obtained results were normalized with 16S ribosomal DNA. There were large variations in the levels of AMR-genes between individual samples. As the number of samples in a pool increased a decrease in sample variation was observed. A steady state in the sample variation was seen when pooling five or more samples. No significant difference was found between pools of five samples and pools of more. There were a significant difference between pools of five or more samples and pools of less (p < 0.0001). In order to quantify the level of AMR-genes pools of five individual samples will give a result representative of the pig herd. The findings of this study could be used in planning of observational studies.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, University of Copenhagen
Authors: Clasen, J. (Intern), Mellerup, A. (Intern), Olsen, J. E. (Ekstern), Angen, Ø. (Intern), Folkesson, S. A. (Intern), Toft, N. (Intern), Birkegård, A. C. (Intern)
Pages: 27-27
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Planning a cross-sectional study of antimicrobial resistance genes in Danish pig farms

General information
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Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
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Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
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Årsrapport for vildtsundhed 2013

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State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology
Authors: Chriél, M. (Intern), Hansen, M. S. (Intern), Larsen, G. (Intern), Holm, E. (Intern), Jensen, T. K. (Intern), Enemark, H. (Intern), Hjulsager, C. K. (Intern), Birkegård, A. C. (Intern), Nielsen, P. K. (Intern)
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Publication: Research - peer-review › Report – Annual report year: 2014

Projects:

Veterinary epidemiology with emphasis on the association between spatial proximity, contact structures, antibiotic consumption and antibiotic resistance
National Veterinary Institute
Period: 01/12/2013 → 20/12/2017
Number of participants: 6
Phd Student:
Birkegård, Anna Camilla (Intern)
Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Main Supervisor:
Toft, Nils (Intern)
Examiner:
Boklund, Anette (Intern)
Dewulf, Jeroen (Ekstern)
Nielsen, Søren Saxmose (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet

Relations
Publications:
Antimicrobial resistance in Danish pigs: A cross sectional study of the association between antimicrobial resistance and geography, exposure to antimicrobials, and trade
Project: PhD

Activities:

SPATIAL PATTERNS OF ANTIMICROBIAL RESISTANCE GENES IN DANISH PIG FARMS
Period: 17 Mar 2016
Anna Camilla Birkegård (Speaker)
National Veterinary Institute
Section for Epidemiology

Related event
SVEPM: Annual Meeting 2016
16/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Talks and presentations › Conference presentations