

Carry-over risks in fattening units for *Campylobacter* spp.

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Abstract

There is a lack of information about the prevalence of the important zoonotic pathogens *Campylobacter* spp. and *Yersinia* spp. at different stages in the pig production chain. The aim of this study was to determine these prevalence in a total of 1040 faecal samples and to gather further information about the sources of infection with *Campylobacter* spp. and their qualitative and quantitative importance in the pig production. During the slaughtering process, 122 pigs and their carcasses respectively, were sampled three times. *Campylobacter* spp. were isolated in sows (33.8%), piglets (80.9%), growing (89.2%) and finishing (64.7%) pigs. *Yersinia* spp. were detected in growing (15.2%) and finishing (13.3%) pigs only. For statistical analysis, bacteriological results for *Campylobacter* spp. were evaluated with questionnaire facts from four farrowing and twelve fattening units. In the production stage farrowing, a significant influence for the factors "number of sows" and "forage store cleaning" was detected by a generalized linear model. In the production stage fattening, following factors had a significant effect on the *Campylobacter* spp. prevalence: "number of fattening places", "mixed farm", "sampling time", "bottom", "forage", "antibacterial" and "anthelmintic prophylaxis".

During lairage, *Campylobacter* spp. were identified from faeces of pigs from all farms whereas *Yersinia* spp. were detected in pigs from just two herds. After twelve hours of chilling neither *Campylobacter* spp. nor *Yersinia* spp. were detected. Common slaughter techniques and hygiene procedures may be effective tools to reduce the risk of contamination and recontamination of meat products.

Introduction

Infections caused by *Campylobacter* spp. (C.) are prevalent worldwide. *Campylobacter* spp. are part of the normal gut microflora in many food-producing animal species, including chickens, turkeys, swine, cattle and sheep (BLASER 1997). Transmission to humans appears to occur primarily through the consumption of contaminated poultry products, unpasteurised milk products and meat products (EFFLER et al. 2001; FRIEDMAN et al. 2004). In addition to the consumption of undercooked meat, cross-contamination to other food products may play a significant role in the number of illnesses observed. The infective dose in humans can be very low as 800 colony-forming units of specific strains can lead to *Campylobacter* infection (BLACK 1988).

The farmer and the participating manufacturing industry in the food production have the main responsibility for food safety. Now and in future, this adds up to the demand for preventive measures in primary production following the principle "from the producer to the consumer". For these reasons, this study was conducted with the aim to determine the prevalence of *Campylobacter* spp. in farrowing and fattening units by the collection of faeces and rectal swabs. Further risk factors for the occurrence of *Campylobacter* spp. in farrowing and fattening units should be observed via environmental and feed samples from the checked herds and questionnaires in the corresponding pig farms.

Material and methods

Four farrowing and twelve fattening farms provided the basis for the present study. The sampling size on every farm was calculated according to the formula from NOORDHUIZEN et al. (1997). In

total, 1,040 faecal or swab samples respectively from pigs of all ages from farrowing and fattening units were analysed. Additionally, 56 environmental and feed samples were collected. Cultural methods were used to test all samples for *Campylobacter* spp., including the differentiation of subspecies. The bacterial detection of *Campylobacter* spp. proceeds from ISO 10272 (1995) with following biochemical differentiation of *C. coli* and *C. jejuni*.

Calculation of the intraherd and animal prevalence and the 95%-confidence intervals within the production stage was performed with the PROC SURVEYMEANS procedure from SAS® (2002). On every farrowing and fattening farm, data collection was carried out with the aid of a questionnaire. Besides the general farm information, detailed data about the housing system, management, state of health and aspects of disease surveillance were acquired. In consideration of the bacteriological results, these data contributed to a hazard analysis to detect the origin and spread of *Campylobacter* spp. infections.

The statistical analysis was performed with a generalised linear model. At first the management-specific parameters were tested respectively with the χ^2 -test regarding the influence on the pathogen prevalence. Every parameter having a value $p < 0.3$ in the χ^2 -test and an adequate distribution was included in the generalised linear model. The GENMOD procedure from the software package SAS® (2002) was reviewed for significance ($p \leq 0.05$). For the estimation, a binomial distribution and a logistic link function (i.e. logistic regression) were assumed. As a result of the small sample size in the farrowing unit, it was not possible to perform a risk analysis which yielded significant conclusions. From the fattening unit, the following fixed effects were considered in the model: sampling time (growing pigs, finishing pigs), herd organisation (number of fattening places, mixed farming), housing system and forage (floor space design, feed origin) and health (antibacterial and anthelmintic treatment). The estimates ($\hat{\theta}$) from the risk factors were transformed into odds ratios ($OR = \exp(\hat{\theta})$) and the 95%-confidence intervals were calculated. A low absolute frequency in the least sub classes from some factors did not allow a statistical analysis with logistic regression. For the factors having a p -value ≤ 0.05 in the χ^2 -test, the odds ratios and 95%-confidence intervals were calculated separately.

Results

Campylobacter (*C.*) spp. were isolated in 33.8% of the sows and in 80.9% of the piglets (Figure 1). Neither pathogen was isolated from the environmental and feed samples.

For the statistical risk factor analysis in the fattening unit, 716 results from the bacteriological examination were evaluated in context with the questionnaire data from the twelve fattening herds. Twenty factors were tested regarding their influence on the prevalence of *Campylobacter*. Significant effects were shown for the following factors: sampling time, number of fattening places, mixed farming, floor space design, feed origin, antibacterial and anthelmintic treatments.

Over the fattening period the *Campylobacter* spp. prevalence decreased. At the beginning the odds ratio increased by a factor of 4.46, the risk factor fattening places per herd was differentiated between farms size under 1000 pigs and alternatively over 1000 pigs. The bacteriological results show that pigs from farms with less than 1000 fattening places had a prevalence of 80.0% and those from larger farms a prevalence of 74.3%. The chance to isolate *Campylobacter* spp. from pigs from smaller herds increased by a factor of 1.44. Housing in separated stalls is another preventive influence. When the animals on mixed farms were kept in separated stalls the chance of a positive bacteriological result decreased ($OR = 0.61$). Pigs which were kept on a plan floor without bedding had the highest prevalence in comparison to the other flooring systems. In this housing system, the chance of obtaining a positive result was highest. An antibacterial treatment at the beginning of the fattening period was implemented on seven herds. The following antibiotics were used for this treatment: Amoxicillin, Tetracycline and Sulfonamide. The chance of a positive finding decreased when the animals were treated with antibacterial substances during this time period ($OR = 0.66$). On four herds, anthelmintics were used at the beginning of fattening period. The appliance of Ivermectin, Flubendazol and Levamisolhydrochlorid was adopted for deworming. The chance of obtaining a positive result rose by a factor of 1.99 when anthelmintics were administered.

Further risk factors "source of piglets", "feed consistency" and "blank dwell time" had an influence on the prevalence of *Campylobacter* spp., too. The chance of obtaining a positive result from the bacteriological investigation was smaller from fattening pigs in a closed herd system ($OR = 0.26$).

Furthermore, the following cases were preventive: feeding meal (OR=0.63) instead of granule or pellets and blank dwell time under 10 days.

Discussion

The results from the present study prove that *Campylobacter* spp. are of increasing importance in farrowing and fattening units: high prevalence of *Campylobacter* spp. were found in suckling, growing and finishing pigs (WEHEBRINK 2006). Other studies also confirm these results (KASIMIR 2005; GAULL 2002).

The occurrence of *Campylobacter* spp. in subsequent samples of pigs and sows was often variable in this analysis. As known from further studies, *Campylobacter* spp. prevalence may vary because the physiological status of the animal and external factors can influence the intestinal flora. The ability of *Campylobacter* spp. to colonise the intestinal tract of pigs is probably subject to the various factors influencing the colonisation resistance of the gut (RUCKEBUSCH et al. 1991). In contrast to recent studies, risk factor analysis in the fattening unit demonstrated a significant influence on the *Campylobacter* spp. detection rate for the "number of fattening places". The chance of obtaining a positive *Campylobacter* spp. result is higher when animals are held in smaller herds (<1000 places). Separating the herds in "mixed farming" is a useful method to decrease pathogen transmission. In contrast to our study, BOES et al. (2005) could not assert this effect: investigation of the occurrence and diversity of *C. jejuni* infections in finisher pigs in herds with combined cattle or poultry production and herds only producing pigs showed no evidence of transmission of *C. jejuni* from cattle or poultry to pigs in mixed production herds. A lower *Campylobacter* spp. detection rate is not promoted by a plan floor without bedding and purchase forage. One reason for the higher prevalence in housing systems with plan floor is the intensive contact of the pigs with their faeces for a longer time. A further result from the questionnaire analysis was that an arranged antibacterial treatment but no anthelmintic treatment was preventive against *Campylobacter* spp. infections. This results must be questioned critically because it is not known first which health status in detail can be found in the different herds and, second, what the antimicrobial resistance of *Campylobacter* spp. is. Further studies will be needed to explain these two risk factors. Despite the fact that forage in granule form is heated during the manufacturing process, the chance of obtaining a positive *Campylobacter* spp. result rose by a factor of 1.23 in this form of forage feeding. SCHUPPERS et al. (2005) detected that important risk factors contributing to the prevalence of resistance strains were shortened tails, lameness, skin lesions, feed without whey, and *ad libitum* feeding. Multiple antimicrobial resistance was more likely in farms which only partially used an all-in-all-out system, or a continuous-flow system compared to a strict all-in-all-out animal-flow. Presence of lameness, ill-thrift, and scratches at the shoulder in the herd also increased the odds for multiple resistance. Thus, the results from SCHUPPERS et al. (2005) showed that on finishing farms which maintained a good herd health status and optimal farm management the prevalence of antimicrobial resistance was also more favourable.

Conclusions

Based on the zoonotic directive (Nr. 2160/2003), a monitoring for *Campylobacter* spp. is mandatory. It should take place at an adequate stage of the food chain. Control has to be directed primarily at the prevention of colonisation of farm animals by means of the implementation of Good Hygienic Practice (GHP), biosecurity measures and husbandry practices incorporating Hazard Analysis Critical Control Point (HACCP) based on risk management systems (WHYTE et al., 2002). Because of this, the objective of this study was to obtain more information about the risk factors influencing the prevalence of this pathogen. As a result of the small sample size in the farrowing unit, it was not possible to perform a risk analysis which yielded significant conclusions. In the fattening unit the attention was focused additionally on risk factors which do not reach the significant limitation of the 5% probability error because of the small sample size. Effects which exceeded the housing and management factors were not acquired in the questionnaire and could not consequently be regarded in the evaluation. Because of this the results should only be regarded as tendencies.

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