PREVALENCE AND DIVERSITY OF CAMPYLOBACTER IN PIG HERDS WITH AND WITHOUT CATTLE OR POULTRY

Jaap Boes*, Eva Møller Nielsen2, Dorte Lau Baggesen3

*National Committee for Pig Production, Danish Bacon & Meat Council, Vinkelvej 11, DK-8620 Kjellerup, Denmark, Ph: 0045-8771-4046, Email: jbo@danishmeat.dk; 2Statens Serum Institut, Artillerivej 5, DK-2300 Copenhagen, Denmark; 3Danish Institute for Food and Veterinary Research, Bülowsvej 27, DK-1790, Copenhagen, Denmark

Abstract The prevalence and diversity of Campylobacter in 24 pig herds with and without cattle or poultry was investigated. Feces was collected on each farm from 20 pigs and, if present, 20 cattle or poultry, and examined for Campylobacter spp, including speciation, serotyping and PFGE. C. jejuni was found in pigs in 8% of herds, but only in <1% of pigs, while C. coli was isolated from 92% of pigs. In contrast, C. jejuni was very prevalent in cattle (43%) and poultry (32%) in mixed herds. Matching serotypes of C. jejuni were not found in pigs and cattle or pigs and poultry, but PFGE typing confirmed that two C. coli serotypes were indistinguishable between pigs and cattle. The results show that there is no substantial transmission of C. jejuni from cattle or poultry to pigs in mixed production herds.

Introduction Campylobacteriosis is a zoonosis of increasing importance in industrialized countries. In Denmark, Campylobacter is the most common cause of zoonotic human enteritis with an incidence of 66 per 100,000 inhabitants in 2003 (Anonymous, 2004). The majority (90%) of Danish human cases are caused by Campylobacter jejuni, whereas 5% are diagnosed as C. coli. Poultry and cattle are considered to be the main reservoir for C. jejuni, whereas C. coli is predominantly found in pigs. C. jejuni may also be isolated from pigs, but usually at a much lower prevalence.

However, recent reports have stated that C. jejuni prevalences may be as high as 30-50% in pigs and pork (Finlay et al, 1986; Harvey et al, 1999), suggesting that pigs may act as a significant reservoir for C. jejuni. This observation prompted investigations in Denmark of Campylobacter prevalence in pigs. The underlying hypothesis for these studies was, that if C. jejuni was present in pigs, this could be due to transmission from cattle or poultry. The overall objective of the studies was to compare the prevalence and diversity of Campylobacter infections in pigs from farms raising only pigs, and pigs originating from farms also producing cattle or poultry.

The first stage of the study was carried out as an abattoir survey comparing C. jejuni prevalence in finisher pigs from farms with and without cattle or poultry. This showed an overall C. jejuni herd prevalence of 8.5% but no significant differences between herd types (Boes et al, 2005). In the second stage of the study, which is reported here, follow-up investigations were carried out in selected herds and this time pigs, cattle and poultry, if present, were included, to study possible transmission between animal species within farms.

Materials and Methods From the Campylobacter abattoir screening (Boes et al, 2005), 24 pig producing herds were selected: 12 herds in which both C. jejuni and C. coli had been detected in finisher pigs, and 12 herds from which only C. coli had been isolated. Of these 24 pig herds, 8 herds also produced cattle and 4 also produced poultry. Each herd was visited once and fecal samples were collected from 20 pigs and, if present, 20 cattle or 20 hens/broilers.

Fecal samples were stored at ambient temperatures and sent to the Danish Institute for Food and Veterinary Research in Copenhagen for cultivation, species identification and serotyping. Campylobacter was cultured from feces according standard procedures using CCDA plating and isolation on blood agar. Species identification was done using hippurate hydrolysis and serotyping was carried out using the Penner scheme. In addition, if matching serotypes were found in pigs and cattle/poultry within the same farm, a number of isolates were typed using pulse-field gel electrophoresis (PFGE).

Results The overall prevalence of C. coli and C. jejuni in pigs was 92.0% and 0.8%, respectively. Herd prevalence of C. jejuni was 8.3%. No significant differences in C. jejuni or C. coli prevalence in pigs were found between herds with and without previous detection of C. jejuni in pigs at the abattoir. The prevalences of C. jejuni and C. coli in pigs, cattle and poultry in the 24 herds are shown in Table 1. The results clearly show that, in mixed production herds, C. jejuni predominates in cattle and poultry, while C. coli predominates in pigs.
Serotyping of 16 *C. jejuni* isolates from pigs revealed four serotypes: 4-complex, 11, 23, and 35. In comparison, a much higher number of *C. jejuni* isolates could be typed from cattle (51 isolates comprising 8 serotypes) and poultry (20 isolates comprising 7 serotypes). The distribution of *C. jejuni* serotypes in pigs, cattle and poultry is shown in Figure 1. As can be seen from Figure 1, all serotypes found in pigs were also found in cattle. However, matching serotypes within the same herd were not detected. Matching *C. jejuni* serotypes were not detected in pigs and poultry.

Few different *C. coli* serotypes were found in cattle and poultry, whereas 30 different *C. coli* serotypes were found in pigs. All *C. coli* serotypes found in cattle and poultry were also isolated from pigs. Among these, serotype 5 and 46 were found in pigs and poultry within one farm. Likewise, serotypes 24, 25 and 48 were found in pigs and cattle within the same herds.

PFGE analysis of matching serotypes as well as additional serotypes from herds producing only pigs revealed a high degree of diversity: a total of 15 *C. jejuni* and 55 *C. coli* isolates were typed, resulting in 49 different PFGE profiles. The largest diversity was seen in isolates originating from herds producing only pigs. PFGE typing confirmed that 2 *C. coli* serotypes were indistinguishable between pigs and cattle: serotype 24 in one herd and serotype 48 in another herd.

**Discussion** In accordance with our previous study (Boes *et al*, 2005) we found a high prevalence of *Campylobacter* in Danish pigs. From the majority of pigs examined, only *C. coli* was isolated. The prevalence of *C. jejuni* in pigs (0.8%) was even lower than that in the first survey (2.3%; Boes *et al*, 2005), but herd prevalence was comparable (8.3 vs. 8.5%). These results suggest that, in Denmark, prevalence of *C. jejuni* in pigs is low and therefore of minor importance. This is in accordance with reports from other European countries (Cabrita *et al*, 1992; Anonymous, 2001; Pezotti *et al*, 2003). Possible explanations for the fact that other studies have found very high prevalences of *C. jejuni* in pigs (Finlay *et al*, 1986; Harvey *et al*, 1999) could be differences in culture media (favoring one of the species) or different interpretation of the hippurate test.

Our herd study furthermore showed that there is no substantial transmission of *C. jejuni* from cattle or poultry to pigs in mixed production herds. The prevalence of *C. jejuni* was generally high in cattle and poultry, whereas *C. jejuni* was only detected in a few pigs on two farms, and these were not matching with cattle or poultry isolates as shown by PFGE.

On the other hand, our results suggest that the very high prevalence of *C. coli* in pigs may lead to transmission of *C. coli* to cattle or poultry present in the same herd. Previous Danish studies have revealed absence or low levels of *C. coli* in cattle (Nielsen *et al*, 1997). The average level of 6% *C. coli* in cattle in mixed herds found in our study suggests that pig to cattle transmission cannot be ruled out.

Finally, no apparent association was found between prior *C. jejuni* detection at the abattoir and subsequent *C. jejuni* findings in the herd in pigs or in cattle/poultry. Again this suggests that finding *C. jejuni* in finisher pigs at slaughter is not directly related to the presence of cattle or poultry in their herds of origin.

**Conclusions**

- The prevalence of *C. jejuni* in Danish pigs and pig herds is generally low
- The prevalence of *C. jejuni* in pigs does not differ significantly between herds with mixed production and herds producing only pigs
- There is no substantial transmission of *C. jejuni* from cattle or poultry to pigs in mixed production herds
- Transmission of *C. coli* from pigs to cattle or poultry in mixed production herds cannot be ruled out

<table>
<thead>
<tr>
<th>Herd type</th>
<th>Species</th>
<th># examined</th>
<th>% <em>C. coli</em> positive</th>
<th>% <em>C. jejuni</em> positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pigs + cattle</td>
<td>Pigs</td>
<td>160</td>
<td>88.8</td>
<td>1.3</td>
</tr>
<tr>
<td></td>
<td>Cattle</td>
<td>117</td>
<td>6.8</td>
<td>42.7</td>
</tr>
<tr>
<td>Pigs + poultry</td>
<td>Pigs</td>
<td>80</td>
<td>93.8</td>
<td>2.5</td>
</tr>
<tr>
<td></td>
<td>Poultry</td>
<td>79</td>
<td>3.8</td>
<td>31.6</td>
</tr>
<tr>
<td>Pigs</td>
<td>Pigs</td>
<td>240</td>
<td>94.6</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 1. Percent *Campylobacter* positive animals in herds producing pigs and cattle (8 herds), pigs and poultry (4 herds), or pigs only (12 herds).
References


Figure 1. Distribution of C. jejuni serotypes found in fecal samples from pigs (black bars), cattle (open bars), and poultry (grey bars) in mixed production herds.