**SOURCES OF *CAMPYLOBACTER SP.* CONTAMINATION OF PIGLETS IN FARROWING UNITS OF FARROW-TO-FINISH FARMS: FIRST RESULTS**

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**Introduction**

*Campylobacter* sp. is one of the most frequent cause of human enteritis with *Campylobacter jejuni* more commonly implicated than *C. coli*. *Campylobacter* sp. has been isolated from raw beef, pork, lamb, chicken and cooked meats. Campylobacter species are often found in digestive tract of pigs (2, 8, 12, 14, 10, 3, 15, 4, 6). *C. coli* is the large predominant species (12, 14, 6) but *C. jejuni* was also isolated in association with *C. coli* (3, 15, 9). *Campylobacter* colonization of the pigs seems to occur at an early age (3, 13, 15). In France, little information about intestinal carriage of *Campylobacter* sp. in pigs is available. The purpose of the present investigation was to improve our knowledge of the epidemiology of *Campylobacter* in pigs.

**Materials and methods**

**Sampling** (table 1): The samples were collected from 9 pigs farms, randomly selected, situated in the western part of France. The farms were confined farrow-to-finish operations of intensive type and managed using the batch procedure and an all-in/all-out hygiene policy for farrowing, post-weaning and fattening sections. Three batches per farm were tested over a year. For each batch, 10 nursing dams randomly selected and 4 piglets from litters were tested for Campylobacter. Rectal fecal samples were collected once from piglets and the nursing sows. In addition, in 6 farms at each visit, water and piglets feed samples were taken.

**Bacteriological analysis**: All samples were transported to the laboratory at < 10°C. For water and “food” samples, the presence or absence of *Campylobacter* was confirmed as a member of the genus by examining colonies per sample (when present) were plated in duplicate on each following media: Butzler (20°C), Apar (20°C) and Tryptose Soy Agar (TSAB) (37°C), for 5 days in microaerophilic conditions (5% O₂, 10% CO₂, 85 % N₂). The analysis of the gel electrophoresis image was done with Bio 1D++ software (Vilbert Lourmat).

**Results**

*Campylobacter* was not detected from water samples and feed samples. On all the 9 farms, pigs were heavily contaminated by *Campylobacter*. *Campylobacter* was recovered from 75 % of the faecal samples collected from the 1036 piglets and 79 % from the 261 sows. Nevertheless some differences between the 9 farms in the number of pigs tested positive for *Campylobacter* were statistically significant (p < 0.005 SNK test) (fig.1).
The contaminated sows had more contaminated piglets than negative sows (fig. 2). A total of 1,100 isolates were obtained. On the basis of identification with multiplex-PCR, _C. coli_ was the only species recovered from the faecal samples. First results of PCR-RFLP subtyping showed a large diversity of _Campylobacter_ subtypes isolated from the pigs (farm A). Nevertheless piglets and their nursing sows in a same batch often harboured _Campylobacter_ isolates with identical genetic subtyping profiles (fig. 3).

**Discussion**

The high prevalence rates reported in this study agree with other results indicating prevalence of _Campylobacter_ of 85 % amongst piglets (14, 15) and at 75 to 100 % amongst sows (14, 15). Young _et al._ (15) have described a predominant infection of pigs by _C. jejuni_. In our study and in agreement with Nesbakken _et al._ (6), _C. jejuni_ had never been isolated from the faecal samples. These findings suggest that the prevalence of the respective species might differ considerably between breedings companies and countries. An other explanation may be the use of different identification procedures. This study confirms that piglets are already intestinal carriers of _C. coli_ at the age of 25 days on the piggeries. The direct transmission of _C. coli_ from the infected sows to piglets is attested by PCR-RFLP results. The similarities between genetic subtyping profiles of strains isolated from families of pigs (nursing sow and her piglets) and from subsequent groups of pigs housed in a same batch suggest that _C. coli_ strains isolated are more dependent on the origin of contamination (sows) than on the farm (14). Nevertheless, some genetic subtyping profiles are different between sow and her piglets in a same family of a batch (4, 14, and, some piglets were tested positive although their nursing sow was tested negative. This suggests that other sources of piglets contamination by _C. coli_ than the nursing sows exist. Despite negative results in our water and feed samples analysed, the piglets environmental source (other sows of the batch and of the farm, hygienic practices of the farmer …) of contamination by _Campylobacter_ sp. can not be exclude (7). But adoption practices appear to be a major risk factor in the dissemination of _C. coli_ into the farm (3). Contrary to other studies, focused on only 1 or 2 farms (14, 3), our survey reveals that there is a significant distinction between the level of contamination with _Campylobacter_ of the pigs on these farms.

**Conclusion**

Further studies are needed to identify risk factors in the dissemination of _Campylobacter_ sp. in farms and to evaluate the impact of this infection of pigs on the meat and process contamination.

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**References**