Abstract

Campylobacter coli strains from 56 organic and 58 conventional pig colon contents were characterized to evaluate impact of these two productions on antibiotic resistance, genetic diversity and virulence of these strains. 76.8% of organic pigs and 74.0% of conventional pigs were positive in Campylobacter. A total of 262 strains were tested for their resistance to 7 antibiotics. Significant differences were observed for 4 antibiotics (tetracycline, erythromycin, nalidixic acid, ciprofloxacin) between the two productions with higher resistance for conventional pig Campylobacter. Multiresistance was more frequently observed for conventional pig strains (54.8%) than for organic pig strains (26.8%). Strains were typed by PFGE (262 strains) and MLST (120 strains). Genetic diversity was very high for both productions with both typing methods. Strains were distributed in 60 PFGE genotypes and in 51 Sequence Types. Ten PFGE clusters (34% of the strains) and nine ST (41.6% of the strains) were common between the two productions. Presence of 9 virulence genes was checked (120 strains) by PCR. All the strains carried the \textit{ceuE}, \textit{iam}, \textit{ciaB} and \textit{flaA} genes and more than 95% of the strains carried the \textit{casf} and \textit{cdtABC} genes. The \textit{virb11} gene on plasmid was detected only for 13 organic pig strains. Capacity of adhesion and invasion of 61 strains were tested on Caco-2 cells. No link between virulence profile and strain origin was observed. However strains with the \textit{virb11} gene had higher invasive capacity. In conclusion, no impact of the type of production was observed on the genetic diversity and virulence of \textit{Campylobacter} strains. The lower level of antibiotic resistance and multiresistance of \textit{C. coli} strains for organic pigs may be related to the restricted use of antibiotics in this production and / or colonization of organic pigs with susceptible environmental strains.

Introduction

Most studies interested in organic animal production focuses on antibiotic resistance of bacteria. Indeed, antibiotic resistance is considered one of the major global threats for the future and the use of antimicrobials in animal production is contributing to the growing problem with resistant bacteria. Within organic animal production there is generally a more restricted usage of antimicrobials, which likely influences the level of antimicrobial resistance in these herds (Young et al., 2009). Moreover, animals from organic production have access to an open area leading opportunity to encounter wild type \textit{Campylobacter} strains. Such situations, restricted usage of antimicrobials and access to an open area, offer the possibility that organic pigs are colonized by another population of \textit{Campylobacter} that of conventional pigs. These campylobacters can come from wild animals or pets (Mohan, 2015). It was thus interesting to characterize more precisely these \textit{Campylobacter} strains to see if the management of the pig herds, organic / conventional, could influence the type of strains found in pigs. In addition to antibiotic resistance; we looked at the genetic diversity of the strains and their virulence.

Material and Methods

\textbf{Sampling and Campylobacter collection}

Colon contents of 56 organic and 58 conventional pigs were sampled from April to October 2012 at slaughterhouse. They were streaked on Karmali plate. After 48h at 37°C in a microaerobic atmosphere, typical colonies were sub-cultured on blood agar plates for 24h at 37°C for phenotypic and genotypic characterization as described after. A total of 262 strains were kept; 138 from organic pigs and 124 for conventional pigs. All the \textit{Campylobacter} were \textit{Campylobacter coli}.
Pulsed-field gel electrophoresis (PFGE)

The strains (262) were genotyped by PFGE. DNA preparation, Kpn1 restriction endonuclease digestion and PFGE were carried out as described by the Campynet protocol. Electrophoretic patterns were compared using BioNumerics® and strains were clustered by the unweighted pair-group method using the arithmetic mean (UPGMA) (Struelens et al., 1996). The Simpson's index was calculated (Hunter, 1990) to assess the genetic diversity of the Campylobacter populations.

Multi-Locus Sequence Typing (MLST)

Strains (58 from conventional pigs and 62 from organic pigs) were genotyped by MLST as described by Miller et al., (2005). Amplification and sequencing of 7 housekeeping genes: aspA (aspartase A), glnA (glutamine synthetase), glnT (citrate synthase), glnA (serine hydroxymethyltransferase), pgm (phosphoglucosemutase), ttk (transketolase) and uncA (ATP synthase) were achieved. Each sequence was submitted to the MLST website (http://pubmlst.org) in order to have the allele number of the 7 genes for each strain. A sequence type (ST) and clonal complex (CC) were then determined according to the allelic profile.

Antimicrobial susceptibility testing

Minimal inhibitory concentrations of antimicrobials were determined for all strains using the broth dilution method according to Clinical and Laboratory Standards Institute (CLSI) document M31-A3 with Sensititre® plates (Biocentric, Bandol, France) and were interpreted according to the cut-off values recommended by the EU Reference Laboratory for Antimicrobial Resistance. The antimicrobials tested included gentamicin (GEN), streptomycin (STR), ciprofloxacin (CIP), nalidixic acid (NAL), tetracycline (TET), erythromycin (ERY) and chloramphenicol (CHL). All cut-off values used in the interpretation of the Campylobacter MIC results have been developed by EUCAST (www.eucast.org).

Virulence

Presence of 9 virulence genes was checked (120 strains) by Real Time PCR SYBR® Green developed for this study using published primers or primers designed for this study. Heights of the genes were localized on the chromosome and one on the plasmid (virB11). The genes are involved in adhesion/invasion of epithelial cell (fsaA, ciaB, cadF, iam, virB11), in the acquisition of iron (ceuE) and in the production of toxine CDT (Cytotothelial Distenting Toxins) (cdtA, cdtB, cdtC).

Capacity of adhesion and invasion of the strains (61 strains) was tested in vitro assays on Caco-2 human intestinal epithelial cells as described by Guyard-Nicodème et al., (2013). The capacity of adhesion and invasion were expressed as percentage of bacteria which adhere to- and invade in- Caco-2 cells from a starting inoculum of 10⁷ UFC Campylobacter.

Results

Genetic diversity of the isolates

Typing by PFGE (262 strains) and MLST (120 strains) allowed to see that genetic diversity was very high for both productions with both typing methods. The index of diversity was slightly higher for organic strains (0.96) but not significantly different from those of conventional strains (0.93). Isolates were distributed in 60 PFGE genotypes and in 51 Sequence Types. 91% of the strains were from Clonal Complex ST-828. Ten PFGE genotypes (34% of the strains) and nine ST (41.6% of the strains) were common between the two productions with a dominant ST854 (18.3% of the strains).

Antimicrobial susceptibility

Only 10 strains (3.8%) among the 262 strains were pansusceptible to the five family of antimicrobials tested. Only 10 strains (3.8%) among the 262 strains were pansusceptible to the five family of antimicrobials tested for both productions with both typing methods. The index of diversity was slightly higher for organic strains (0.96) but not significantly different from those of conventional strains (0.93). Isolates were distributed in 60 PFGE genotypes and in 51 Sequence Types. 91% of the strains were from Clonal Complex ST-828. Ten PFGE genotypes (34% of the strains) and nine ST (41.6% of the strains) were common between the two productions with a dominant ST854 (18.3% of the strains).

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Antimicrobial susceptibility

Only 10 strains (3.8%) among the 262 strains were pansusceptible to the five family of antimicrobials tested (β-lactams, β-lactamase producers, β-lactamase non-producers, aminoglycosides and tetracyclines). None strain was resistant to CHL and only one strain from conventional pig was resistant to GEN. The percentage of strains resistant to STR was high and similar in the two productions; 75.4% of the strains for organic pigs and 73.4% for conventional pigs had this resistance (Figure 1). We observed significant difference for resistance to NAL, CIP, ERY and TET (χ², p<0.05) between the two productions. For these four antibiotics, resistance was higher for Campylobacter isolated from conventional pigs.

Figure 1: percentage of isolates resistant to four antibiotics in organic and conventional pig production

The most frequent resistance profile was resistance to tetracycline with streptomycin; 33.3% of the organic pigs strains and 24.2% of conventional pig strains. Multiresistance (resistance to 3 or more antimicrobial families) were more frequently observed for strains from conventional pig (54.8% of the isolates) than for strains from organic pigs (26.8% of the strains) (χ², p<0.01)

Virulence

All the 120 strains tested carried the ceuE, iam, ciaB and flaA genes and more than 95% of the strains carried the cadF and cadA genes. The virB11 gene on plasmid was detected in 13 strains from organic pigs. There was no significant difference between organic and conventional strains (61 isolates) for adhesion (χ², p=0.523) and for invasion (χ², p=0.590) on Caco-2 cells But strains with the virB11 gene in the chromosome and one on the plasmid (virB11) in the acquisition of iron (ceuE) and in the production of toxin CDT (Cytotoxheal Distenting Toxin) (cdtA, cdtB, cdtC). There was no significant difference between organic and conventional strains (61 isolates) for adhesion (χ², p=0.523) and for invasion (χ², p=0.590) on Caco-2 cells But strains with the virB11 gene in the chromosome and one on the plasmid (virB11) in the acquisition of iron (ceuE) and in the production of toxin CDT (Cytotoxheal Distenting Toxin) (cdtA, cdtB, cdtC).

Figure 2: dispersion of strains according their percentage of adhesion (A) and invasion (B) and the absence or presence of the virB11 gene.

Discussion

The greatest genetic diversity in organic pigs may be related to the access of pigs to an open area leading the opportunities to encounter Campylobacter from wildlife. Wild animals can excrete Campylobacter and birds play an important role in terms of prevalence and transmission of this bacterium (Greig et al., 2015). Common genotypes between organic and conventional could indicate that these genotypes are adapted to pigs; the other...
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Genotypes corresponding to genotypes specific to the farms of the pigs and not to the type of production. Some of our results on antibiotic resistance are similar those obtained in other studies carrying on organic or antibiotic-free animal production. Thakur and Gebreyes (2005) obtained a lower resistance for TET and ERY for their C. coli in pig production without antibiotic. Moreover, multi-resistance was greater in conventional pig production. Less CIP-resistant Campylobacter jejuni strains were also obtained in antibiotic-free chicken products (Price et al., 2005). Restricted use or absence of antibiotic has therefore an impact on antibiotic resistance of Campylobacter. No difference for the virulence was observed between organic and conventional strains. The high prevalence of virulence genes was already described in other works on C. coli (Wieczorek and Osek, 2013), although clAIP gene was found in only 20% of the C. coli strains of Acik et al., (2013). Only 7% of our strains have the virB11 gene as described before (Acik et al., 2013, Wieczorek & Osek, 2013). This gene is involved in the invasion (Bacon et al. 2002) and we observed that our strains with this gene had a greater invasive capacity than other.

Conclusion
No impact of the type of production was observed on the genetic diversity and virulence of our Campylobacter strains. The lower level of antibiotic resistance was observed in conventional pig strains for organic pigs may be related to the restricted use of antibiotics in this production and / or colonization of organic pigs with susceptible environmental strains. However, although significantly different or not between the two productions, the percentage of strains with resistance in organic pigs remain in some cases relatively high. These pigs are therefore able to bring in the food chain bacteria resistant to antibiotics. The high prevalence of virulence genes and the same pathogenicity capacity, whatever the type of production, suggest that these pig strains have the ability to infect humans.

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Residual contamination detection and serovar distribution of Listeria monocytogenes isolates in pork slaughterhouse and cutting facilities in province of Quebec.


Introduction
L. monocytogenes (L. mono) is recognised as a zoonotic foodborne pathogen. Its control is focused on the “Ready- to Eat” food production level. Recently, Health Canada had reinforced its “Policy on L. mono in Ready-to-Eat Foods”, highlighting environmental surveillance and control of meat processing facilities as important risk reduction tools. The industry wants to improve its management of L. mono risk, taking into account previous steps of meat production. Nowadays, few information are available on the presence, distribution and types of strains in the environments concerning this pathogen in pork slaughterhouses and cutting facilities in Canada. Our objective was to detect and described residual L. mono contamination and analyse serovars distribution in different areas in the pork production continuum and between slaughterhouses and cutting facilities in province of Quebec, during a one year period. Such data are a pre-requisite to achieve the optimization of the management measures by the industries.

Materials and Methods
Sampling: Four main slaughterhouses were involved, representing 60% of the volume of meat produced annually in province of Quebec. A total of 16 exhaustive samplings had been carried out in four different seasons in one year. Each sampling represented a total of 156 samples, they were distributed to characterise the different steps of the slaughter/cutting process: lairage (n=53), slaughter (n=18), carcass dressing (n=23), refrigeration (n=8) and cutting (n=54). A total of 2,496 samples were analyzed in the current study. All samples were performed after sanitation procedures and analysed following a sensitive bacteriological method. All samplings was performed on 900 cm2 surfaces, beginning with brushing, then wiping of target surfaces with O/E neutralizing broth moistened swabs, (DIFCO BD, Sparks, MD.) supplemented by Ferric Ammonium Citrate (Fraser, selective supplement, Lab M, United Kingdom) and were incubated for 48 h at 37°C. Both enrichments were streaked onto specific blood agar plates for confirmation of L. mono colonies. The enriched plates were further confirmed on sheep blood agar to confirm the hemolysis activity (type β+) on sheep blood agar. Finally, biochemical analyses were performed using carbohydrates (xylose, mannitol and rhamnose) use in broths (DIFCO, BD, Sparks, MD.)

Multiplex PCR and agglutination based serotyping: All isolates were subjected to a multiplex PCR assay method to confirm the genus and species by amplification of rps and pfb genes, and at the same time genoserogrouping the strains into five molecular serogroups by amplification of four targeting genes lmo0737, lmo1118, ORF2819, ORF2110. A second PCR assay was conducted in order to detect flaA gene presence as described by Kérouanton et al. in 2010. In addition, commercial O antisera (Denka, Sekien Co., Ltd, Tokyo, Japan) were used according to the manufacturer’s instructions to conclusive identification of strain the serotype.

Results
Mean residual detection after one year survey was 10% (240/2,496 samples analyzed). The prevalence of L. mono over time revealed that, whatever the season considered, the residual contamination detection...