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Short communication

Genetic comparison of *Campylobacter jejuni* isolated from different cattle farms

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Abstract

To compare the genotypes of *Campylobacter jejuni*, isolates of cattle origin were collected from 9 Polish farms and genotyped by ERIC-PCR. We identified 28 genotypes among the 43 *C. jejuni* isolates, and demonstrated high genomic diversity. The highest level of diversity was observed in strains isolated from stanchion-barn animals in opposition to those from the loose-housing system.

Key words: *Campylobacter jejuni*, cattle, genotyping, ERIC-PCR

Introduction

Campylobacter is the most common bacterial cause of gastroenteritis in humans. This pathogen can be isolated from the intestines of many animals, including cattle. The sources and transmission routes of *Campylobacter* in cattle are not fully understood. This confusing epidemiological evidence is partly due to the asymptomatic nature of the infection and high levels of genetic diversity (Allos 2001, Frost 2001). Several molecular typing methods have been used to support studies on the epidemiology of *Campylobacter* infections. Although pulsed-field gel electrophoresis and PCR RFLP flagellin typing are highly standardized, polymerase chain reaction-based methods, like ERIC-PCR, have also been successfully applied for the discrimination of *Campylobacter* sp. (Wojciech et al. 2005, Zorman et al. 2006). In this study we describe a molecular epidemiological investigation using ERIC-PCR.

Materials and Methods

Forty three strains of *Campylobacter jejuni* were isolated from cattle feces (rectal samples) from 2006 to 2007, from a total of 9 farms. In 4 farms (strains number: A1-A5, B1-B5, C1-C5, F1-F5) animals were maintained in stanchion-barns, whereas in farms D, E, G and H, (strains number D1-D5, E1-E5, G1-G4, H1-H5) they were maintained in a loose-housing system. One farm (strains I1-I4) was designed for beef production. These animals grazed on the grass. DNA was extracted using a GenomicMini kit (DNA Gdansk, Poland). PCR was performed using FastStart TaqMan[®] Probe Master (ROX) (Sigma, Germany) and primers synthesized by Oligo, Poland. The ERIC-PCR conditions have been previously described by Wojciech et al. (2005). All amplification products were resolved in 2% agarose gel, and stained with ethidium bromide. The 100bp Ladder (Fermentas, Lithuania) was used as a molecular size marker.

Dendrograms were constructed using the unweighted pair group linkage analysis method (UPGAMA), Quantity One software (Biorad, Great Britain).

Results and Discussion

Figure 1 shows ERIC-PCR profiles obtained for *C. jejuni*. The obtained profiles allowed for grouping of the 43 strains into 28 ERIC-genotypes. The most prevailing genotypes were represented by seven strains (16.3% of all isolates), followed by genotypes composed of 4 isolates (9.3%) and 3 isolates (7.0%), four other genotypes were composed of two strains. Twenty-one isolates (48.8%) belonged to individual genotypes. Earlier investigations also reported an extreme heterogeneity of *C. jejuni* isolated from cattle using stereotyping or varied methods of genotyping (Fitzgerald et al. 2001, Nielsen 2002).

chion-barns. Earlier investigations also reported the heterogeneity of *C. jejuni* isolated from cows belonging to a single farm (Fitzgerald et al. 2001, Nielsen 2002). Such results indicate that cattle may have more exposure due to farming practices than chickens, where colonization is usually limited to one strain (Bull et al. 2006).

Our observations indicate that differences can exist in the infection of cattle farmed using different cattle-housing methods. Investigation shows that there were two or more similar strains isolated from cows farmed using a loose-housing system, in opposition to stanchion-barns, where all isolates from one herd were characterized by different genotypes and the lowest similarity (0% to 18%) of *C. jejuni* strains. In the case of the loose-housing system, greater contact between animals can play a major role in dissemination of infection throughout the farm. It is possible that free stall housing creates a more favorable environment for diseases that are spread by fecal-oral transmission.

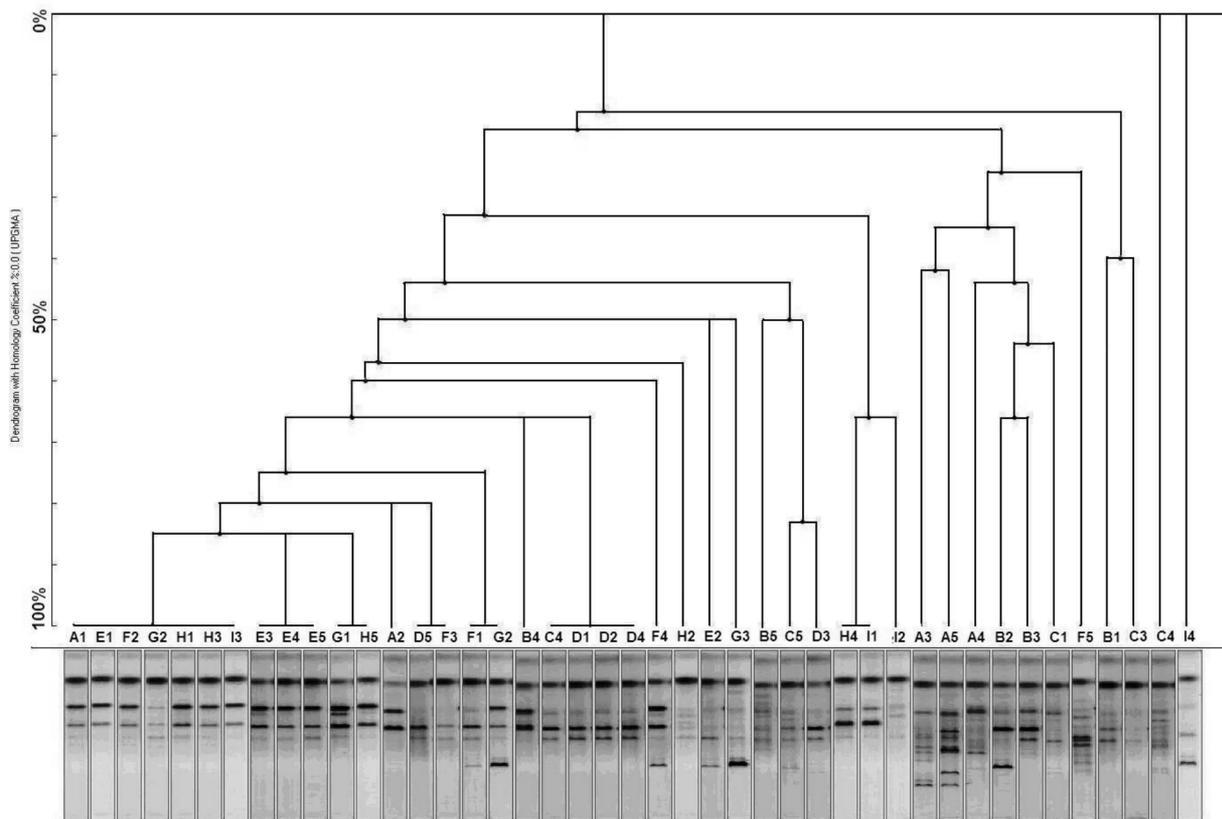


Fig. 1. Dendrogram of ERIC-PCR for *C. jejuni* isolates (n=43).

The results of our study showed an extensive genomic diversity among *C. jejuni* strains isolated from animals belonging to single farms, most notably among *C. jejuni* isolated from farms using stan-

References

- Allos BM (2001) *Campylobacter jejuni* infections: update on emerging issues and trends. Clin Infect Dis 32: 1201-1206.

- Bull SA, Allen VM, Domingue G, Jorgensen F, Frost JA, Ure R, Whyte R, Tinker D, Corry JEL, Gillard-King J, Humphrey TJ (2006) Sources of *Campylobacter* spp. colonizing housed broiler flocks during rearing. *Appl Environ Microbiol* 72: 645-652.
- Fitzgerald C, Stanley K, Andrew S, Jones K (2001) Use of pulsed-field gel electrophoresis and flagellin gene typing in identifying clonal groups of *Campylobacter jejuni* and *Campylobacter coli* in farm and clinical environments. *Appl Environ Microbiol* 67: 1429-1436.
- Frost JA (2001) Current epidemiological issues in human campylobacteriosis. *J Appl Microbiol* 90: 85S-95S.
- Nielsen EM (2002) Occurrence and strain diversity of thermophilic campylobacters in cattle of different age groups in dairy herds. *Lett Appl Microbiol* 35: 85-89.
- Wojciech L, Bednarski M, Wieliczko A, Ugorski M (2005) Genotype analysis of *Campylobacter jejuni* isolated from broilers in Poland. *Pol J Vet Sci* 8: 41-47.
- Zorman T, Heyndrickx M, Uzunovic-Kamberovic S, Smole Mozina S (2006) Genotyping of *Campylobacter coli* and *C. jejuni* from retail chicken meat and humans with campylobacteriosis in Slovenia and Bosnia and Herzegovina. *Int J Food Microbiol* 110: 24-33.