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Original Scientific Article

CAMPYLOBACTERS IN BROILER FLOCKS IN BOSNIA AND HERZEGOVINA: PREVALENCE AND GENETIC DIVERSITY

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Summary: Campylobacters are the most commonly reported bacterial gastrointestinal pathogens in humans. In the EU, the number of reported and confirmed human campylobacteriosis cases was 48.6 per 100,000 population in 2010. Poultry is considered to be the main reservoir of *Campylobacter* because they persist in the gastrointestinal tract of birds in industrial poultry flocks; *Campylobacter*-contaminated poultry meat and meat products are an important risk factor for campylobacteriosis in humans. The aim of this study was to establish the prevalence, genetic diversity and geographical relationships of *Campylobacter* isolates from an assortment of broiler flocks in Bosnia and Herzegovina. The calculated *Campylobacter* prevalence in faecal samples, based on isolation of *Campylobacter* spp. from selected broiler farms in the period from October 2009 to June 2010, was 62.0 %. At slaughter line, skin/carcass samples were positive in 18 out of 31 *Campylobacter*-positive farms (58.1 %). A total of 44 isolates (35 *Campylobacter jejuni* and nine *Campylobacter coli*) from caecal contents (n=31) and skin/carcasses (n=13) of chicken were genotyped by pulsed-field gel electrophoresis (PFGE) using *Sma* I. In general, the obtained *C. jejuni* and *C. coli* isolates exhibited limited genetic diversity. Only isolates with identical or very similar profiles were found on individual *Campylobacter*-positive farms. In addition, skin/carcass isolates showed the same or very similar profiles to campylobacters isolated from pooled caecal content originating from the same broiler batch. Accordingly, carcass cross contamination could not be observed in slaughter line samples.

Key words: *Campylobacter*; poultry; Bosnia and Herzegovina; PFGE; caecal contents; skin; carcass

Introduction

Bacteria from the genus *Campylobacter* have long been known as a causative agent of diarrhoea in cattle and septic abortion in cattle and sheep, but were only recognized as an important cause of human illness in the mid-1970s when *Campylobacter jejuni* was found to be responsible for infectious diarrhoea in man for the first time (1). Campylobacters preferentially inhabit the intestines of birds, including chickens, turkeys, quails, ducks, wild birds and even ostriches (2). Epidemiological studies have revealed a firm association between *Campylobacter* infections in humans and the handling and consumption of raw or undercooked poultry meat; this has been confirmed in many cases (3-8). It is commonly assumed that contamination of poultry meat with campylobacters occurs during slaughterhouse processing and that campylobacters survive throughout the food chain, posing a major risk to public health (4,9). In addition to poultry products, outbreaks of campylobacteriosis have been associated with the consumption of some other animal products, e.g., raw milk (10).

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In 2010, campylobacters continued to be the most commonly reported gastrointestinal pathogens in humans with a notification rate increasing from 45.6 per 100,000 population in 2009 to 48.6 per 100,000 population in 2010 (11). A typical seasonal pattern is often exhibited, especially in northern countries, with peaks during the warm summer months (11,12). The most commonly reported *Campylobacter* species in the EU is *C. jejuni*, accounting for 93.4 % of the confirmed human cases characterized at the species level in 2010 (11). Among the Member States, the prevalence of both the *Campylobacter* colonization in broiler batches (>72 %) and of the *Campylobacter* contamination of fresh poultry meat sampled at slaughter, processing or at retail (>70 %) can be extremely high; however, the prevalence greatly varies at the community level (11). Data demonstrate that the percentage of contaminated carcasses roughly reflects the *Campylobacter* prevalence in broiler batches and that the prevalence is much lower in northern than in central and southern European countries, probably due to different climatic conditions over the year (7,11,12). A geographical relationship of some *Campylobacter* genotypes has also been noticed (13,14).

In Bosnia and Herzegovina (BIH), detailed research on *Campylobacter* prevalence in primary poultry production had not been conducted until the present study. However, the prevalence in broiler flocks was partly studied, giving the main information on the extent of *Campylobacter* carcass contamination during the slaughtering process, since research was performed on poultry retail meat samples (6). Encouraged by the 2008 EU Baseline Study (12), the present research was performed as an initial investigation on the topic. Additionally, pulsed-field gel electrophoresis (PFGE) was employed to discover the genetic diversity of campylobacters on broiler farms and perhaps to demonstrate some geographical relationships of broiler farms, since PFGE has been proven to be appropriate for epidemiological studies (15,16) and a useful tool for identification of potential campylobacteriosis outbreaks (17). To date, PFGE has been used to evaluate the genetic diversity of *Campylobacter* isolates originating from poultry retail meat, human isolates and some isolates of live farm chickens (6) but not for *Campylobacter* isolates originating from different stages of broiler breeding.

The aim of our study was to determine the *Campylobacter* prevalence at different stages of the broiler production cycle, to analyze the genetic diversity of isolates from individual broiler flocks and to compare it among different broiler flocks in BIH.

Materials and methods

Samples

From October 2009 to June 2010, 50 broiler flocks originating from 29 municipalities were randomly selected for the isolation and identification of *Campylobacter* species within the scope of a pilot *Campylobacter* surveillance program conducted in BIH (Figure 1). With the highest density of poultry population, central and northern BIH were selected for sampling. Sampling (10 caeca per sample) of farms (Table 1) started with one-day-old chickens on their arrival at the farm (day 1) and was subsequently performed every seventh day until the end of breeding, when the animals were sent to the slaughterhouse (days 7, 14, 21, 28, 35 and 42). After collection, samples were transported to the laboratory within six hours in a cooling box (4-8 °C) and analysed according to recommended and standardized methods (12,18,19). In total, 3500 caeca (350 samples) were investigated. In addition, five skin/carcass samples were collected at the slaughter line from every *Campylobacter*-positive flock (155 samples in total). The first broiler flock that was confirmed as *Campylobacter*-positive was subjected to more intensive sampling, i.e., every

Table 1: Timetable of sampling for all 50 farms

Period of sampling	Farm numbers (1-50)
October 2009	1-4; 41-43
November	15, 16, 38, 45, 46
December	5-8, 17-19
January 2010	39, 40
February	9, 10, 20, 32-34
March	23, 24, 35-37, 48-50
April	11, 21, 22, 44
May	25, 26
June	12-14, 27-31, 47

Note: For farm numbers, see Table 2. For geographical distribution of farms, see Figure 1. Farms selected for PFGE typing are underlined (farms 1-14).

day after confirmation of *Campylobacter* infection until slaughtering (eight samples of 10 caeca each, in addition to the seven regular samples) and at 12 different positions of the slaughter line (seven skin/carcass samples, in addition to the five regular samples).

Campylobacter isolates

Isolation and identification of *Campylobacter* spp. from faecal material was performed according to the EU guidelines prepared for the 2008 Baseline Study on the prevalence of *Campylobacter* in broiler flocks and *Campylobacter*/*Salmonella* in broiler carcasses (18). Isolation and identification from broiler skin/carcasses was performed according to ISO 10272-1:2006 (19). Briefly, one inoculation loop of 10 pooled caecum contents was streaked onto the selective media mCCDA (modified Charcoal Cefoperazone Deoxycholate Agar) and Skirrow agar. Skin/carcass samples were enriched by the use of modified Bolton broth (1:9), incubated at 41.5 °C in a micro-aerobic atmosphere for 24-48 hrs, then streaked onto the mCCDA and Skirrow media and incubated at 41.5 °C in a micro-aerobic atmosphere for 24-48 hrs.

Bacteria from suspected *Campylobacter* colonies were examined for morphology and motility by dark-field microscopy. After sub-culturing on blood agar plates and antibiotic susceptibility disc-diffusion testing in nalidixic acid (30 µg) and cephalotin (30 µg), they were subjected to determination by selected biochemical tests (catalase, oxidase, indoxyl acetate and hippurate hydrolysis) and aerobic growth at 41.5 °C. Isolates identified as *C. jejuni* or *C. coli* were stored at -76 °C in a cryo-protective medium for PFGE genotyping.

PFGE typing

PFGE was conducted for selected *C. jejuni* and *C. coli* isolates, based on their geographical origin and its importance if occurring in major poultry production regions (Figure 1). From frozen beads, isolates were recovered on blood agar medium and subjected to PFGE genotyping employing *Sma*I restriction endonuclease according to the PulseNet standardised one-day protocol (20). The obtained fragments were electrophoretically separated under the following conditions: 18 h at 6 V/cm and 14 °C, with pulse-times from 6.7 s to 35.4 s employing the CHEF-DR II System (BioRad, USA). PFGE profiles (i.e., pulsotypes) were subjected to computer-assisted analysis with BioNumerics software (version 6.6; Applied Maths, Belgium). In brief, normalization was done according to molecular size standard (three lanes per gel), i.e., *Salmonella* serotype Braenderup H9812 (ATCC BAA-664). Similarity matrices were constructed using the band-based Dice coefficient with optimization and band-matching tolerance set to 1.5 %. Cluster analysis was based on the UPGMA algorithm and the cut-off value defining clusters of isolates was 90 % of similarity according to the dendrogram (21).

Nomenclature of isolates that were subjected to PFGE typing was based on the scheme CJ (for *C. jejuni*) or CC (for *C. coli*) followed by the farm name (abbreviation) and age of chicken at sampling of their caeca (in days; usually 35 or 42). Where chicken skin/carcass samples were *Campylobacter*-positive at the slaughter line, designation S was added to the isolate name (i.e., 42-S).

Results

Distribution of C. jejuni and C. coli

C. jejuni and/or *C. coli* were isolated from 31 (62.0 %) out of 50 investigated farms. From three of the *Campylobacter*-positive farms, both *C. jejuni* and *C. coli* were isolated (9.7 %), from 23 only *C. jejuni* (74.2 %) and from five only *C. coli* (16.1 %). Skin/carcass samples were *Campylobacter*-positive in 18 out of 31 positive farms (58.1 %). Skin/carcasses originating from 15 out of 26 *C. jejuni*-positive farms were positive for *C. jejuni* at slaughtering (57.7 %) and from three out of eight *C. coli*-positive farms positive for *C. coli* (37.5 %). Detailed results are shown in Table 2.

PFGE typing of C. jejuni

A total of 35 *C. jejuni* (CJ) isolates were subjected to PFGE typing: 22 faecal isolates originating from five municipalities (denoted 1-4, 5-8, 9-10, 11 and 13-14 in Figure 1, corresponding to locations Visoko, Gračanica, Srbac, Gradiška and Sarajevo, respectively) and 13 skin/carcass isolates from two farms (S2 and Sr1) (Table 2).

Table 2: *Campylobacter jejuni* and *Campylobacter coli* distribution and origin in *Campylobacter*-positive farms

Farm			Isolates			PFGE	
No.[1]	Name[2]	Location[3]	Ceaca[4] *Day 35*	*Day 42*	S[5]	Isolate name	
1	V1	Visoko	nd	CC	CC		CC V1-42
2	V2		nd	CJ and CC	nd	CJ V2-42	
3	V4		nd	CJ	nd	CJ V4-42	
4	V5		CC	CC	nd		CC V5-35 CC V5-42
5	G1	Gračanica	nd	CC	CC		CC G1-42
6	G2		CJ	CJ	nd	CJ G2-35 CJ G2-42	
7	G3		CJ	CJ	nd	CJ G3-35 CJ G3-42	
8	G4		CJ	CJ	nd	CJ G4-35 CJ G4-42	
9	Sr1	Srbac	CJ	CJ	CJ	CJ Sr1-35 CJ Sr1-42 CJ Sr1-42-S	
10	Sr2		nd	CJ	nd	CJ Sr2-42	
11	Gr1	Gradiška	CC	CJ and CC	nd	CJ Gr1-42	CC Gr1-35 CC Gr1-42
12	T1	Tarčin	CC	CC	nd		CC T1-35 CC T1-42
13	S1	Sarajevo	nd	CJ	nd	CJ S1-42	
14	S2		*Days 28, 33-42* CJ and CC[6]		CJ[7]	CJ S2-28 CJ S2-33…35 CJ S2-38…42 CJ S2-42-S1…S12	CC S2-37
15	BH1	Begov Han	CC	nd	CC		
16	O1	Orašje	CJ	nd	CJ		
17	Z1	Zenica	CJ	nd	CJ		
18	Te1	Tešanj	nd	CJ	nd		
19	Te2		CJ	nd	CJ		
20	P1	Pale	CJ	nd	CJ		
21	N1	Nemila	nd	CJ	CJ		
22	Kl1	Kladanj	nd	CJ	nd		
23	K1	Kakanj	CJ	nd	CJ		
24	Va1	Vareš	CJ	nd	CJ		
25	Gra1	Gradačac	nd	CJ	nd		
26	Tr1	Travnik	nd	CJ	CJ		
27	DG1	D. Golubinja	CJ	nd	CJ		
28	Ž1	Zepče	nd	CJ	CJ		
29	M1	Maglaj	nd	CJ	CJ		
30	Br1	Breza	CJ	nd	CJ		
31	Po1	Posušje	CJ	nd	CJ		

Note: S2 was the earliest *Campylobacter*-positive farm and was therefore subjected to more intensive sampling: in addition to days 1, 7, 14, 21, 28, 35 and 42 (*see text*), also at intermediate days 33, 34 and 36-41 and more intensively at slaughtering (12 skin/carcass samples from different positions on the slaughter line). From farm S2, 22 isolates were subjected to PFGE typing (21 *C. jejuni* and one *C. coli*). From all the *Campylobacter*-positive farms, 44 isolates (abbreviations CJ and CC that are underlined in Isolates column) were subjected to PFGE typing, namely 35 *C. jejuni* isolates from 10 farms and nine *C. coli* isolates from six farms.

Legend: CJ, *C. jejuni*; CC, *C. coli*; nd, not detected

[1], Farm numbers (1-31, *Campylobacter*-positive farms shown in Table 2; 32-50, *Campylobacter*-negative farms not shown in Table 2); [2], Abbreviated farm names; [3], Location of farms (for their geographical distribution according to municipalities, see Figure 1); [4], Caecal samples (age of chicken in days); [5], Skin/carcass samples from the slaughter line; [6], From farm S2, *C. jejuni* was isolated at days 28, 33-36 and 38-42, and *C. coli* at day 37; [7], From farm S2, 12 skin/carcass isolates of *C. jejuni* were obtained from 12 positions on the slaughter line

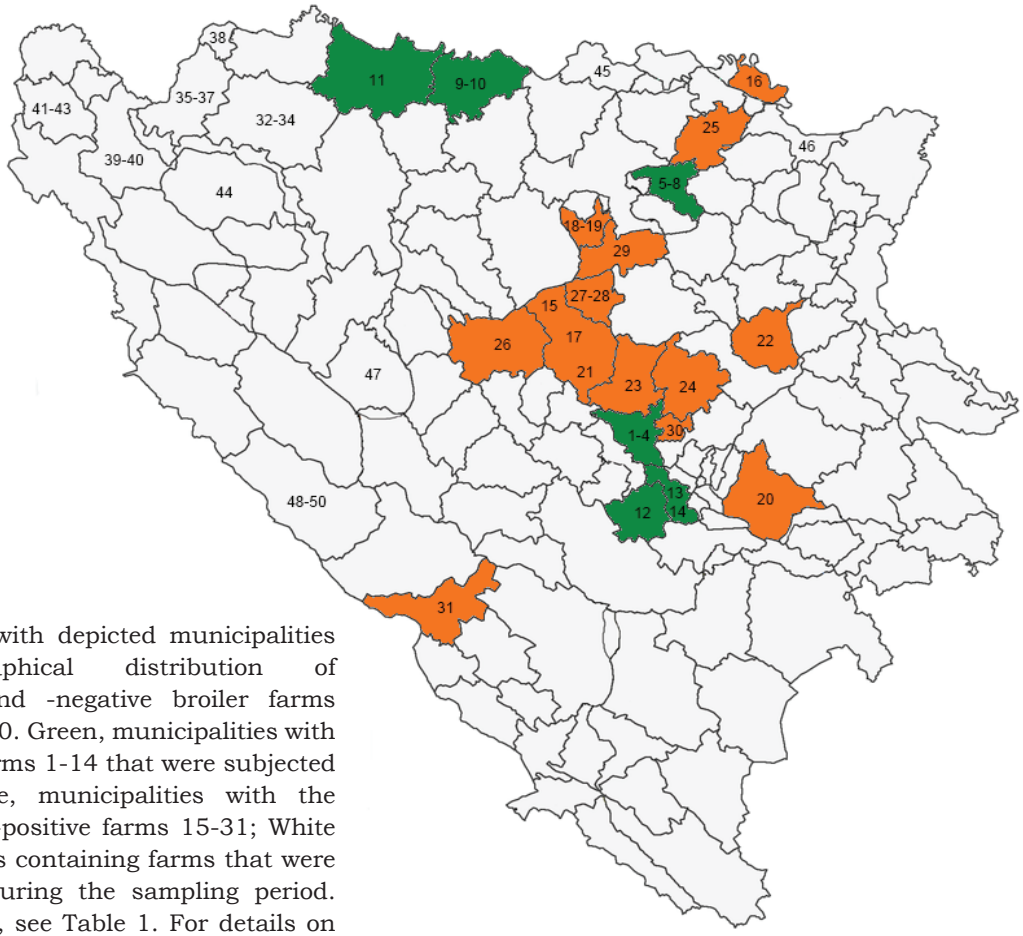

Figure 1: A map of BIH with depicted municipalities showing the geographical distribution of *Campylobacter*-positive and -negative broiler farms denoted with numbers 1-50. Green, municipalities with *Campylobacter*-positive farms 1-14 that were subjected to PFGE typing; Orange, municipalities with the remaining *Campylobacter*-positive farms 15-31; White (numbered), municipalities containing farms that were *Campylobacter*-negative during the sampling period. For timetable of sampling, see Table 1. For details on *Campylobacter*-positive farms 1-31, see Table 2

Pulsotypes revealed five clusters (A1, A2, B, C and D^+) containing 3-4 isolates (farm S2 was subjected to different sampling because of having the earliest *Campylobacter*-positive samples) (Figure 2). Isolates from the farm S2 were assigned to clusters A (A1 and A2), since they showed an 88.9 % similarity due to the difference in position of only one fragment. According to the 90 % cut-off value, cluster D^+ contained three isolates from farms G3 and G4; however, the second isolate from G4 was assigned to the same cluster as it showed a marked similarity of 80 % and did not have other neighbours by similarity in the dendrogram. Four CJ isolates (V4-42, Sr2-42, Gr1-42 and V2-42) with more distinct profiles were not assigned to any cluster.

In clusters A1 and A2 (isolates from S2) and C (isolates from Sr1), containing all CJ isolates from the slaughter line (noted as S), identical *C. jejuni* pulsotypes were revealed when caecal and S isolates were compared. Clusters A1 and A2 comprised 21 isolates with identical (cluster A1 or A2) or very similar (cluster A1 vs. A2) profiles, belonging to *C. jejuni* isolates obtained from animals of different age or from different positions on the slaughter line. Cluster D^+ contained four CJ isolates (G4-42, G3-35, G3-42 and G4-35) showing high genetic similarity, from two farms (G3 and G4) located in the same municipality (denoted 5-8 in Figure 1). Similarly, cluster B also contained isolates, namely three CJ isolates (G2-35, S1-42 and G2-42), from two different *Campylobacter*-positive farms (G2 and S1). However, these originated from geographically distant municipalities (denoted 5-8 and 13-14 in Figure 1), were sampled in two different time periods (G2 in December 2009 and S1 in June 2010; Table 1) and the pulsotypes in cluster B differed in one band in terms of number or position. In general, pulsotypes of *C. jejuni* isolates originating from different farms were heterogeneous in comparison with homogeneous pulsotypes of isolates belonging to the same broiler flock, with the exception of farms G2/S1 and G3/G4; however, the latter two shared the geographical area.

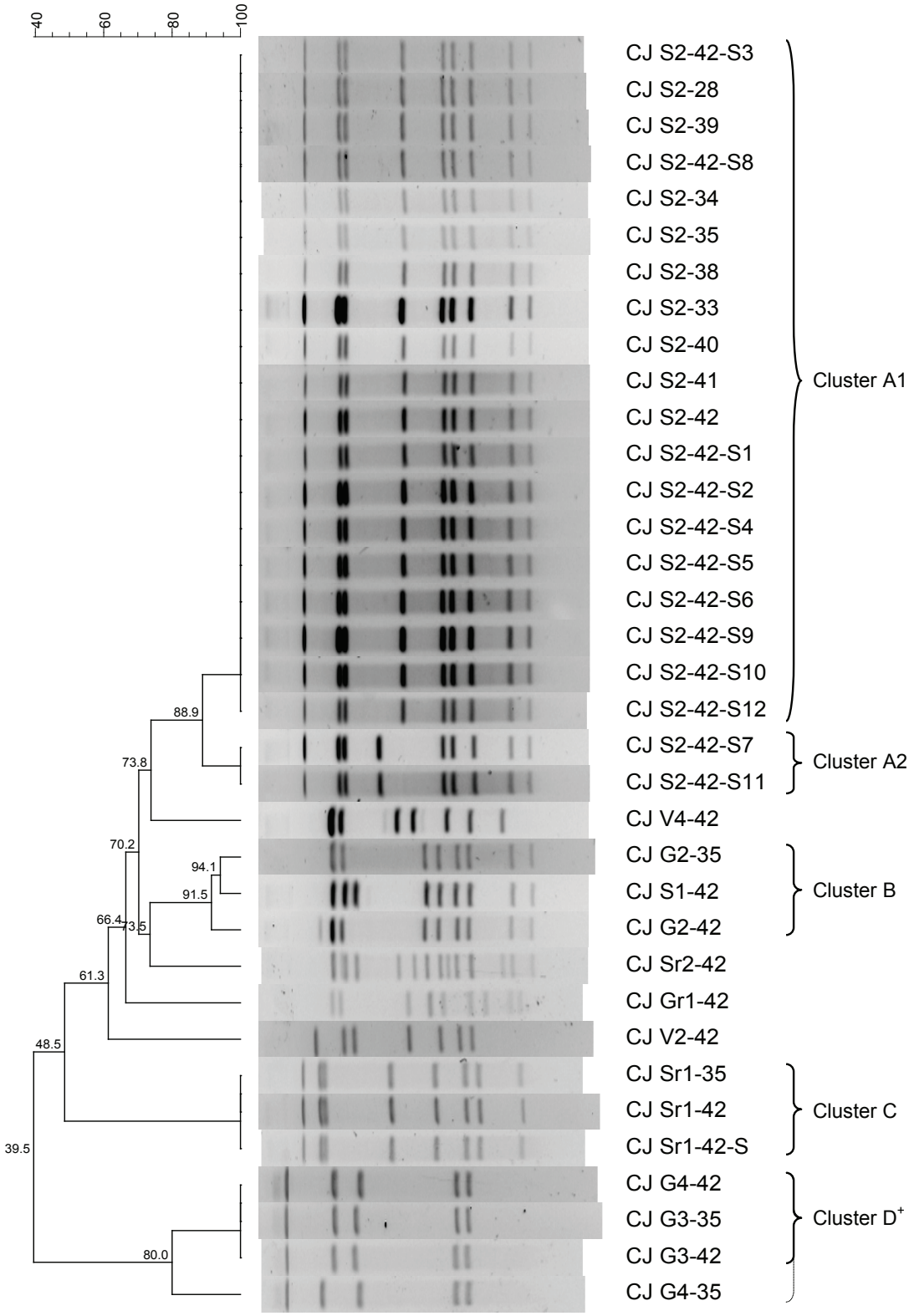

Figure 2: Dendrogram of 35 *Campylobacter jejuni* pulsotypes showing the genetic relatedness of isolates obtained in October 2009 - June 2010 from 10 out of 26 *C. jejuni*-positive broiler farms in BIH. Isolate name consisted of CJ (for *C. jejuni*) followed by the abbreviated farm name (G2, G3, G4, Gr1, S1, S2, Sr1, Sr2, V2 and V4), age of chicken at sampling (35 and 42; for farm S2, also 28, 33, 34 and 38-41) and, when needed for the skin/carcass samples, designation S (42-S; for farm S2, S1-S12 note different positions on the slaughter line). For details, see Table 2

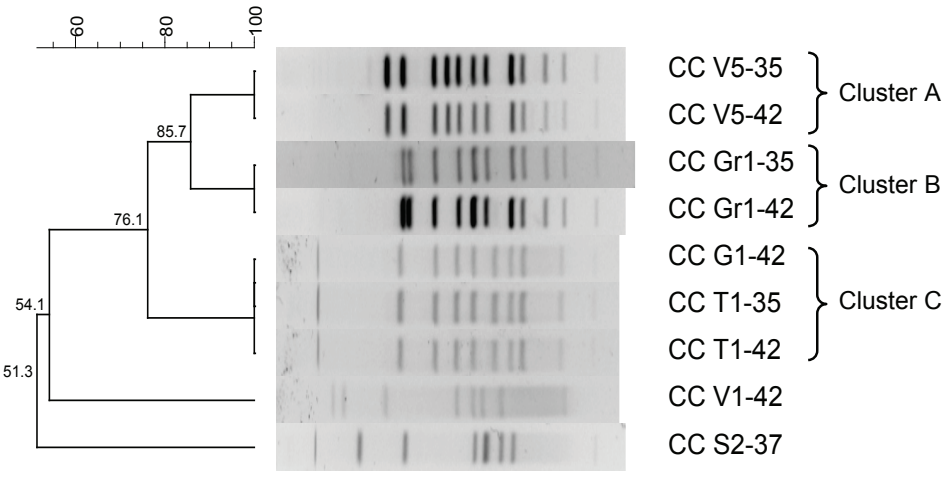

Figure 3: Dendrogram of nine *Campylobacter coli* pulsotypes showing genetic relatedness of isolates obtained in October 2009 - June 2010 from six out of eight *C. coli*-positive broiler farms in BIH. Isolate name consisted of CC (for *C. coli*) followed by the abbreviated farm name (G1, Gr1, S2, T1, V1 and V5) and age of chicken at sampling (35, 37 and 42). For details, see Table 2

PFGE typing of C. coli

A total of nine *C. coli* isolates obtained from the caecal contents of chickens were PFGE typed. Pulsotypes revealed three clusters (A-C; Figure 3) with 2-3 isolates exhibiting identical profiles and belonging to the same farm (V5 or Gr1; cluster A or B) or two separate farms (G1 and T1; cluster C) from two geographically distant municipalities (denoted 5-8 and 12, respectively, in Figure 1, that were, as shown in Table 1, sampled in two different time periods). In addition, two isolates from two different farms (V1 and S2) originating from two neighbouring municipalities (denoted 1-4 and 13-14, respectively, in Figure 1) exhibited distinct profiles.

In general, five pulsotypes (representing clusters A-C and two separate isolates) were observed, belonging to six locations from five municipalities (denoted 1-4, 5-8, 11, 12 and 13-14 in Figure 1) from three different geographical areas. However, clusters A and B (farm V5 and farm Gr1) contained isolates with similar profiles and cluster C (farms G1 and T1) isolates with identical profiles, although obtained over an extended time period and originating from poultry flocks in markedly different geographical areas.

Discussion

Bacteria of the genus *Campylobacter* remain the most frequently reported cause of human gastrointestinal disease in the EU (11,22). Poultry has often been associated with campylobacteriosis (23-28). To date, there have not been sufficient studies estimating the prevalence of *Campylobacter* spp. in primary poultry production in BIH. Bearing in mind the high prevalence of campylobacters in most European countries (11,22), the aim of our study was to carry out a more detailed research on *Campylobacter* prevalence at farm level. The obtained results can confirm the presence of *Campylobacter* spp. in BIH and also reveal their genetic diversity.

Our research showed that broilers in BIH are frequently colonised with *Campylobacter* spp. at farms and at slaughtering; contamination of carcasses, poultry meat and meat products consequently occurs, as has been confirmed by previous studies (6-8). During October 2009 and June 2010, the prevalence of campylobacters in the investigated farms was 62.0 %, which is in accordance with data from other countries, e.g., Germany 48.9 %, UK 75.0 %, France 76.0 %, Slovenia 78.2 % (12,22) and in some previously released publications (23,24,29,30). Given that the sampling period was predominantly during the colder period of the year and that campylobacters show a seasonal pattern (11,12,31-33), the actual prevalence could probably be expected to be even higher. Our results suggest that colonisation of caecum with campylobacters begins around the 28th day during poultry breeding, although it has been suggested that colonisation could occur much earlier (2,34). In our study, *C. jejuni* was more frequently isolated than *C. coli*, namely *C. jejuni* from 74.2 % and *C. coli* from 16.1 % of the *Campylobacter*-positive farms, which is consistent with other publications (11,12,22,31,35). In three cases, both *C. jejuni* and *C. coli* were isolated from the same farm in our study (9.7 %), also consistent with some previously released publications on

the presence of both *Campylobacter* species in a broiler flock (36,37).

The obtained PFGE results indicate a limited variability of pulsotypes belonging to *Campylobacter* isolates at farm level. Other publications suggest a greater genetic diversity of *Campylobacter* isolates, both within a farm and within geographical areas (37,38). Despite difficulties in the epidemiological research of *Campylobacter* bacteria caused by their diversity, our results suggest that a persistent and dominant type of *Campylobacter* strain could occur within a flock and, consequently, at the slaughter line. On the other hand, identical or very similar *C. jejuni* genotypes were obtained from two neighbouring farms (G3 and G4), although that could be a result of many circumstances, such as the presence of house flies (39), rodents, wild birds, flies or humans (e.g., transmission by protective clothing) as vectors (40). It was also revealed that certain *C. jejuni* and *C. coli* isolates obtained from farms in different geographical areas, and over extended time periods, showed marked genetic similarity. Vertical transmission of campylobacters could be suspected, especially if it was proven that both farms obtain animals from the same parent flock. Since evidence of vertical transmission of *Campylobacter* strains in chickens is lacking from publications (41,42), a more detailed sampling program must be performed in parent flocks and hatcheries. In addition, it can be concluded that certain genotypes can persist over time, revealing *C. jejuni* or *C. coli* isolates obtained in different time periods but showing very similar or identical genetic fingerprints.

Pulsotypes of *C. coli* showed somewhat higher homogeneity than those of *C. jejuni*; when a strain of *C. coli* was isolated more than once from a broiler flock, it showed an identical genotype profile (e.g., farms Gr1, T1 and V5). In addition, PFGE results revealed that cross-contamination of carcasses at the slaughter line is probably not present; although *C. jejuni* pulsotypes belonging to farm S2 were not identical (cluster A1 vs. A2 in Figure 2), the two pulsotypes that differed in the position of only one band (cluster A2) were very similar to others belonging to skin/carcass isolates from the same farm (cluster A1) and no similar pulsotypes could be observed belonging to samples from other poultry flocks.

Our results revealed and confirmed that different strains of *C. jejuni* and *C. coli* are present in different farms and geographical areas. In view of the considerable number of isolates, the results also indicated that a dominant *Campylobacter* strain may be present in a broiler flock and, consequently, at the slaughter line, consistent with other studies (43). If this hypothesis proves to be correct, it would enable epidemiological research and prevention of campylobacteriosis by linking a particular strain to its source and checking sources and transmission routs in a flock and poultry retail products. Prevention of *Campylobacter* contamination at the farm level would therefore be much more efficient if the critical points were highlighted and strict bio-security measures taken. For better understanding of the epidemiology of *Campylobacter* bacteria in a flock, it is necessary to design successful prevention programs at the farm level. With this in mind, an extensive surveillance program in BIH will be conducted during 2012 in order to gain more knowledge on the genetic diversity of campylobacters.

We believe that the obtained results have scientific value, especially since previous research of this kind in primary poultry production has not given enough data on the prevalence and diversity of specific *Campylobacter* strains. The obtained knowledge brings new possibilities to the epidemiological research of campylobacters and indicates the importance of cooperation between veterinary and public health laboratories.

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KAMPILOBAKTRI V REJAH PITOVNIH PIŠČANCEV V BOSNI IN HERCEGOVINI: PREVALENCA IN GENETSKA RAZNOLIKOST

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Povzetek: Bakterije iz rodu *Campylobacter* so najpogosteje prijavljeni bakterijski povzročitelji prebavnih obolenjih ljudi. V letu 2010 je bilo v Evropski uniji na 100.000 ljudi prijavljenih in potrjenih 48,6 primerov kampilobakterioz. Ker kampilobaktri naseljujejo prebavni trakt živali v industrijskih perutninskih rejah, je perutnina njihov glavni rezervoar; s kampilobaktri okuženo perutninsko meso in mesni izdelki predstavljajo pomemben dejavnik tveganja za kampilobakteriozo pri ljudeh. Namen našega dela je bil ugotoviti prevalenco, genetsko raznolikost in geografsko povezanost izolatov *Campylobacter* iz nabora rej pitovnih piščancev v Bosni in Hercegovini. Na podlagi izolacije bakterij iz rodu *Campylobacter* iz izbranih rej pitovnih piščancev v obdobju od oktobra 2009 do junija 2010 je bila izračunana prevalenca v vzorcih fecesa 62,0 %. Na klavni liniji so bili vzorci kože ali trupov pozitivni v 18 od 31 primerov rej, ki so bile pozitivne na kampilobaktre (58,1 %). Z metodo pulzne gelske elektroforeze (PFGE) smo z encimom SmaI genotipizirali 44 izolatov (35 *Campylobacter jejuni* in 9 *Campylobacter coli*) iz vsebine slepega črevesa (n=31) in kože ali trupov (n=13) piščancev. Pridobljeni sevi *C. jejuni* in *C. coli* so v splošnem izražali omejeno genetsko pestrost. V posameznih rejah, ki so bile pozitivne na kampilobaktre, smo našli samo seve z enakimi ali zelo podobnimi profili. Izolati iz kože ali trupov so imeli enake ali zelo podobne profile kot kampilobaktri, ki smo jih izolirali iz združene vsebine cekuma iz iste reje pitovnih piščancev, torej navzkrižnega okuževanja med vzorci na klavni liniji nismo opazili.

Ključne besede: *Campylobacter*; perutnina; Bosna in Hercegovina; PFGE; vsebina slepega črevesa; koža; trup