

CASE REPORT

Open Access



# Case of necrotic enteritis associated with campylobacteriosis and coccidiosis in an adult Indian peacock (*Pavo cristatus*)

Aleksandra Ledwoń<sup>1\*</sup> , Małgorzata Murawska<sup>2</sup>, Izabella Dolka<sup>1</sup>, Dorota Chrobak Chmiel<sup>2</sup> and Piotr Szleszczuk<sup>1</sup>

## Abstract

**Background:** To date, *Campylobacter jejuni* has not been found to be pathogenic to peafowl. The available publications show that out of a total of 44 samples tested from peafowl, this bacterium was isolated only in two cases. *Eimeria pavonina* infestations in the peafowl have been described, but no fatal cases have been reported yet.

**Case presentation:** The four-year-old peacock was presented with chronic diarrhea, emaciation and weakness. Post mortem examination revealed enlarged and pale kidneys, small intestinal mucosal necrosis and thickening of intestinal wall, and pericardial effusion. The histopathological examination revealed necrotic enteritis with marked mononuclear cells infiltration associated with the presence of coccidia, additionally there was histological evidence of septicemia in liver and kidneys. Bacteria identification was based on light microscopy of the small intestine sample, culture, and biochemical tests. Further identification was based on PCR. Antimicrobial susceptibility profile was created by determination of minimal inhibitory concentration (MIC) values for 6 antimicrobial agents from 5 different classes. PCR assays were performed to detect virulence factors genes responsible for motility, cytolethal distending toxin production, adhesion and internalization. Bacteriology of the small intestine sample showed abundant growth almost exclusively of *Campylobacter jejuni*, resistant to ciprofloxacin, gentamycin and ampicillin. Bacteria was sensitive to Amoxicillin + clavulanic acid, tetracycline, and erythromycin. All tested virulence factors genes have been detected. The parasitological examination was performed by microscopic examination of fresh faeces and intestinal content, and revealed the moderate number of *Eimeria pavonina*, *Histomonas meleagridis*, single *Capillaria* spp. eggs as well *Heterakis* spp. like parasites.

**Conclusion:** The above case shows that a virulent isolate of *Campylobacter jejuni* in combination with a parasitic invasion may cause chronic enteritis in peafowl, which most likely led to extreme exhaustion of the host organism and death.

**Keywords:** Peafowl, *Campylobacter jejuni*, *Eimeria pavonina*, Necrotic enteritis

## Background

### Campylobacteriosis

*Campylobacter jejuni* (*C. jejuni*) is relatively often isolated from chickens [1, 2] and is considered as non-pathogenic for these birds, however there are reports of hepatitis in poultry (known as avian vibronic hepatitis - AVH), caused by this bacterium [3] in the presence of risk factors (e.g. stress, immunosuppressive conditions of

\*Correspondence: aledwonn@yahoo.pl

<sup>1</sup> Department of Pathology and Veterinary Diagnostics of the Institute of Veterinary Medicine, Warsaw University of Life Sciences, Nowoursynowska 159c, 02-776 Warsaw, Poland

Full list of author information is available at the end of the article



the host) [2]. The source of *Campylobacter* spp. infection for birds is carrier faeces [4].

*C. jejuni* is of interest to veterinarians mainly due to its zoonotic potential [5].

In humans, this infection is a common cause of bacterial enteritis, but can be associated also with Guillain-Barré syndrome (GBS), reactive arthritis and necrotic enterocolitis in children [6, 7].

In birds the pathogenicity of *C. jejuni* depends on its origin and the age. According to some authors, isolates from humans are more pathogenic, for newly hatched chickens than chicken-origin isolates [8]. Screening studies on healthy 31 Indian peafowl from three Michigan zoos have not shown the presence of *Campylobacter* spp., while a moderate number of coccidia has been found in these birds [9]. In a study conducted by a laboratory in Louisiana, *C. jejuni* was found in one Indian peafowl out of 10 samples tested from these birds [10]. Research by Misawa et al. [11] in zoo animals showed the presence of *C. jejuni* in one of the 3 studied peacocks.

### Coccidiosis

Coccidia invasions in peafowl have been reported by several authors in the past. Among others, the following species of coccidia in peafowl have been described in Asian countries and Egypt: *Eimeria pavonina* [12], *Eimeria mandalin* [13], *Eimeria roscoviensis* [14], *Eimeria mayurai* [15], *Eimeria riyadhae*, *Eimeria arabica* [16] and *Eimeria pavaegyptica* [17]. In Pakistan, coccidial oocysts were found in 20–30% of peafowl faecal samples [18]. In peafowl kept in Europe, *Isospora mayuri* and *Eimeria pavonina* (*E. pavonina*) were reported [19, 20].

### *Campylobacter* spp. and *Eimeria* spp. coinfection

Invasion of *Eimeria tenella*, which is closely related to *E. pavonina* [20], has been confirmed to increase *C. jejuni* colonization in the intestines of chickens [21]. To date, no fatal co-infection of *C. jejuni* and *E. pavonina* in the Indian peafowl has been reported.

### Case presentation

In June 2020, a 4-year-old Indian peacock (*Pavo cristatus*) has been brought to the Veterinary Clinic of the Institute of Veterinary Medicine, Warsaw University of Life Sciences due to weakness and chronic diarrhea. The peacock was a private property of a person who had 4 more peahens, that did not show any signs of disease. Peafowl were free range. The bird had atrophy of the pectoral muscles and was unable to move independently. The owner's reported that weakness and diarrhea were observed in this bird 3 months ago and numerous coccidia and *Histomonas meleagridis* were detected at the microscopic examination of the fresh faeces sample.

Transient improvement was obtained after the use of toltrazuril (Baycox 2.5%, Bayer, Germany) at a dose 7 mg / kg of body weight, followed by ronidazole (Trichonidazole, Biovet Puławy, Poland) at a dose of 60 mg / l of drinking water for 7 days. The condition of the peacock, however, gradually began to deteriorate, and bird died.

Necropsy was performed on the same day. Necropsy showed that the peacock was emaciated (Supplementary Fig. 1), the feathers around the cloaca were soiled with diarrheal faeces (Supplementary Fig. 2). Serous fluid in the pericardial sac was found. The testes were inactive and kidneys were moderately enlarged and pale. The mucosa of the small intestine was significantly thickened and covered with pale yellow coating (Fig. 1). The lumen of the caeca was dilated, but mucosa of the caeca was unchanged (Supplementary Figs. 3–5). Only the proximal caecum and rectum were thickened and pale pink in color (Supplementary Fig. 5). Macroscopically, no changes were found in other organs.

### Histopathology

Tissue samples (liver, kidney, and intestines) were fixed in 10% neutral-buffered formalin, dehydrated in increasing gradients of ethyl alcohol and embedded in paraffin. The tissue sample was then cut in the microtome at four micron thickness. Finally, paraffin sections were stained with haematoxylin and eosin (H-E). In the jejunum: massive, diffuse inflammatory infiltrate mainly composed of mononuclear cells (numerous lymphocytes, plasma cells, macrophages), intermixed with coccidian parasites in the increased lamina propria showing marked architectural distortion. Severe destruction of the mucosa: loss of the villi (blunt or flattened), marked epithelial necrosis, and sloughing, the loss or damaged crypts, moderate



**Fig. 1** Mucosal thickening of the jejunum with prominent folds, covered with a pale yellow coating

congestion of the mucosa, and focal small grains structures in blood vessels resemble bacterial clusters were detected (Fig. 2). In addition, perivascular mononuclear cell infiltration in the muscular and serous membranes was present focally. In the liver multifocal necrosis of hepatocytes and microvacuolar fatty degeneration of hepatocytes, disintegrated areas with fibrinoid necrosis of vessels surrounded by inflammatory cells (mainly mononuclear cells), fibrin thrombi, numerous were found (Fig. 3). In the kidneys: perivascular mononuclear inflammatory infiltrate, necrosis of blood vessel walls, and necrosis of tubular epithelial cells, glomerulonephritis, fibrin thrombi in the capillary of the glomerulus were found (Fig. 4).

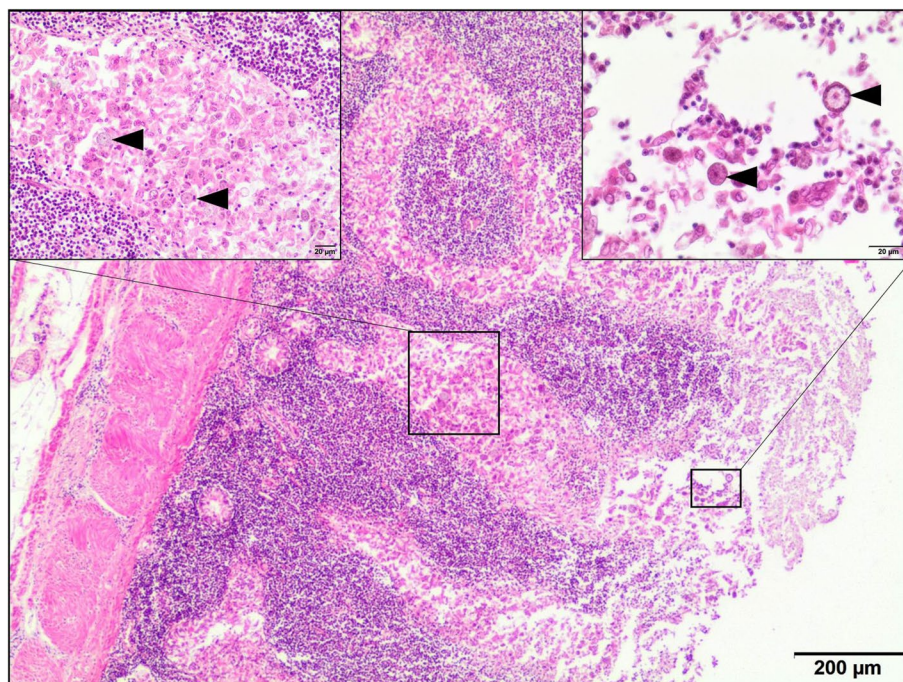
### Parasitology

In order to detect the presence of parasites from the content of the small intestine, caecum and rectum, direct wet mount and stained preparations were made using the Ziehl-Neelsen staining and Hemacolor® rapid staining (Merck, Germany). To determine coccidia species identity, DNA was isolated from the content of the jejunum using the QIAamp DNA Stool Mini Kit (Qiagen GmbH, Germany), following a two-day protocol [22], additionally introducing sample homogenization with glass beads for

10 min on the GeneReady homogenizer (Hangzhou Lifereal Biotechnology Co., Ltd., China). We amplified 767 base pairs of the *cox-1* mitochondrial gene using universal *Eimeria* spp. primer pairs described by Miska et al. [23]. The PCR product was then sequenced. Examination of the rectal and small intestine contents showed an average 4 coccidia oocyst in the high-dry power field (400x magnification), and two eggs of *Capillaria* spp. in the preparation. Examination of the caecal content revealed large, round, mobile flagellates with the morphology of *Histomonas meleagridis* and several nematodes similar to *Heterakis gallinarum*. In the preparation stained with the Ziehl-Neelsen stain, average of 3 coccidia oocysts were found per high-power field (1000x magnification). The presence of *Histomonas meleagridis* was confirmed in a microscopic slide, stained with the Hemacolor® method. Based on the sequencing of the PCR product, the coccidia were identified as *Eimeria pavonina*, and its sequence was uploaded to GenBank and assigned accession number: OM891494.

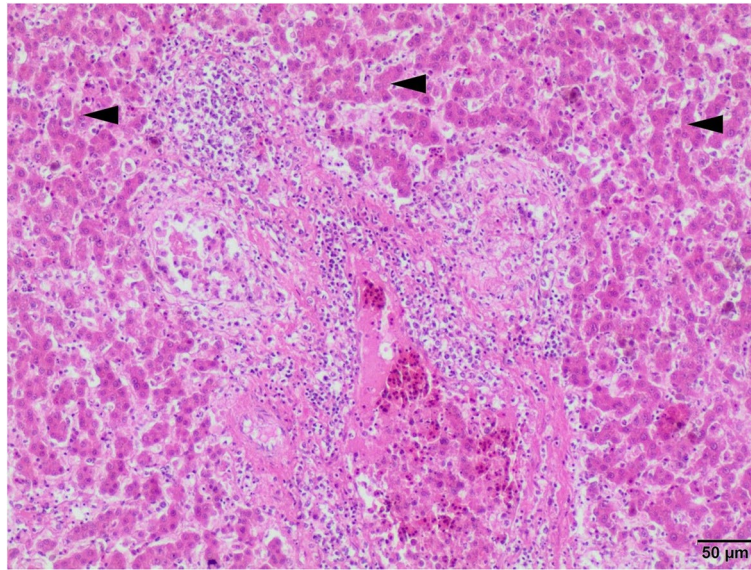
### Bacteriology

**Isolation and identification** A fragment of the jejunum taken aseptically was used for direct microscopic

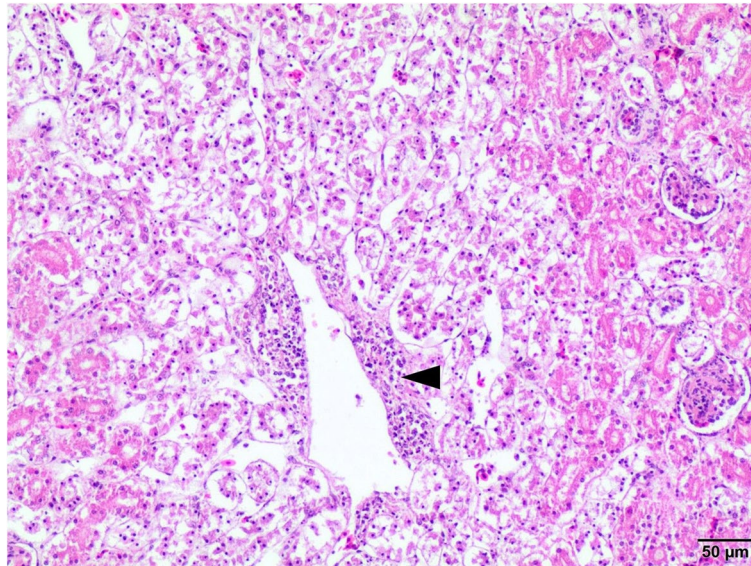


**Fig. 2** Intestine. Necrotic enteritis. Marked inflammation mainly consisted of mononuclear cells in the lamina propria of the mucosa; perivascular inflammation in the muscular membrane. Villus atrophy, crypt epithelial cell proliferation and necrosis, congestion. H-E, 40x. Left insert: Destroyed enterocytes of the intestinal crypt due to invasion of coccidia (arrowheads), 200x. Right insert: free coccidian parasites (arrowheads) intermixed with exfoliated epithelial cells on the destroyed luminal surface of the villi. 400x.\*





**Fig. 3** Liver. Massive inflammation of the portal triad. Liver parenchyma displays necrotic and degenerated hepatocytes (microvacuolar fatty change; arrowheads), venous thrombi, and congestion. H-E, 100x



**Fig. 4** Kidney. Massive perivascular inflammation (arrowhead), proliferative glomerulopathy, necrosis of renal epithelial cells both in the cortex and medulla. H-E, 100x

examination and for culturing. A direct microscope slide was stained using Gram-staining method. After the analysis of direct microscopic slide collected clinical material was streaked on Columbia Agar plates with 5% sheep blood (CBA; GRASO Biotech, Poland) and on modified charcoal-cefoperazone-deoxycholate agar plates (mCCDA; GRASO Biotech, Poland), followed by the

streak plate method was performed. Another 2 fragments of the small intestine were placed in the sterile tubes containing 5 mL of Preston Broth with Preston Modified Supplement (BIOCORP, France) and 5% defibrinated sheep blood (GRASO Biotech, Poland). Agar plates were incubated at 42 °C under microaerophilic conditions created by GasPak Campy Container System (BD, USA) for

48 h. Preston's broth/s were incubated as described above but with shaking (120 RPM) and after pre-propagation 100 µL of the liquid media was streaked on the CBA and mCCDA plates and incubated as described above, without shaking. Obtained colonies were streaked eventually on the CBA plates and incubated as described above. Preliminary identification was based on colony morphology, both on Columbia Agar and mCCDA plates, Gram staining, motility, microscopic morphology, catalase and oxidase tests. Further identification, to the species level, was conducted by PCR [24]. Briefly, genomic DNA was extracted using Genomic Mini isolation kit (A&A Biotechnology, Poland), following the manufacturer's protocol with minor modifications.

For the identification of *Campylobacter jejuni* (mapAF, mapAR for mapA target – 604 bp amplicon) and *Campylobacter coli* (Mu3, Mu for Random target – 364 bp amplicon) species using the PCR method, two pairs of species-specific primers [24] and also, genomic DNA's of standard strains (*C. jejuni* 81–176 and *C. coli* 605) and sterile, deionized water were used as positive and negative controls respectively.

**Antimicrobial susceptibility testing** Antimicrobial susceptibility profile was created by determination of minimal inhibitory concentration (MIC) values, using

ETEST® gradient strips (Biomérieux, France). Six antimicrobial agents from five classes were tested (Tables 1 and 2). Choice of antimicrobial agents was based on their usage in veterinary medicine and the necessity of monitoring resistance of *C. jejuni* to antimicrobials used in human treatment due to zoonotic nature of campylobacteriosis. Interpretation of the obtained results was based on EUCAST [25] or CLSI [26] guidelines Table 1 summarizes information on used antimicrobial agents and criteria of interpretation. Additionally, for ciprofloxacin resistance mechanism determination, a 270 bp fragment of the *gyrA* gene was amplified, according to Chatur et al. [27] and sent for Sanger sequencing to Genomed (Poland) and analyzed for point mutations in our laboratory using DNA Baser Assembler software v. 5.11.3 (Heracle BioSoft SRL, Romania).

**Virulence factors genes detection** PCRs were performed to detect chosen virulence factors genes responsible for: motility (*flaA*, *flaB*), cytolethal distending toxin production (*cdtA*, *cdtB*, *cdtC*), adhesion and invasion to the host's cells (*ciaB*, *pldA*, *cadF*, *flpA*). Assays were performed on genomic DNA of the identified *C. jejuni* isolate (isolation as described in "Isolation and identification" section), using primers and conditions as in reference publications. Used primers along with the amplicons sizes are listed in Table 3.

**Table 1** List of antimicrobial agents, their abbreviations and concentrations used for creating antimicrobial susceptibility profile. Interpretation according to: <sup>a</sup>EUCAST, <sup>b</sup>CLSI

Antimicrobial agent class	Antimicrobial agent	Abbr.	ETEST Concn. [mg/L]	Interpretation		
				S	I	R
<b>β-lactams</b>	Ampicillin <sup>a</sup>	AM	0,016–256	≤2	x	≥8
	Amoxicillin + clavulanic acid <sup>a</sup>	AMC	0,016–256	≤2	x	≥8
<b>Aminoglycosides</b>	Gentamicin <sup>a</sup>	GE	0,016–256	≤0,5	x	≥0,5
<b>Tetracyclines</b>	Tetracycline <sup>b</sup>	TE	0,016–256	≤4	8	≥16
<b>Macrolides</b>	Erythromycin <sup>b</sup>	E	0,016–256	≤8	16	≥32
<b>Fluoroquinolones</b>	Ciprofloxacin <sup>a</sup>	CIP	0,002–32	≤0,5	x	≥0,5

**Table 2** Antimicrobial agents susceptibility profile of *Campylobacter jejuni* isolate

Antimicrobial agent class	Antimicrobial agent	Abbr.	MIC value	Interpretation
<b>β-lactams</b>	Ampicillin	AM	256	R <sup>a</sup>
	Amoxycillin + clavulanic acid	AMC	0,5	S <sup>b</sup>
<b>Aminoglycosides</b>	Gentamicin	GE	0,75	R
<b>Tetracyclines</b>	Tetracycline	TE	0,75	S
<b>Macrolides</b>	Erythromycin	E	1	S
<b>Fluoroquinolones</b>	Ciprofloxacin	CIP	3	R

<sup>a</sup> R-resistant

<sup>b</sup> S- sensitive

**Table 3** Primers used for *C. jejuni* virulence factors genes detection by PCR

Target gene	Primer name	Amplicon size [bp]	Sequence 5' – 3'	Ref.
<i>flaA</i>	flaA-F	1728	GGATTCGTATTAACACAAATGGTGC	[28]
	flaA-R		CTGTAGTAATCTTAAACATTTTG	
<i>flaB</i>	fb1	260	AAGGATTTAAAATGGGTTTTAGAATAAACACC	[29]
	fa2		GCTCATCCATAGCTTTATCTGC	
<i>cdtA</i>	cdtA-f	370	CCTTGTGATGCAAGCAATC	[30]
	cdtA-R		ACACTCCATTTGCTTTCTG	
<i>cdtB</i>	cdtB-F	620	CAGAAAGCAAATGGAGTGTT	[31]
	cdtB-R		AGCTAAAAGCGGTGGAGTAT	
<i>cdtC</i>	cdtC-F	182	TTGGCATTATAGAAAATACAGTT	[31]
	cdtC-R		CGATGAGTTAAAACAAAAAGATA	
<i>ciaB</i>	ciaB-F	527	TGCGAGATTTTTCGAGAATG	[32]
	ciaB-R		TGCCCGCCTTAGAACTTACA	
<i>pldA</i>	pldA-F	385	AAGAGTGAGGCGAAATTCCA	[32]
	pldA-R		GCAAGATGGCAGGATTATCA	
<i>cadF</i>	cadF-F2B	400	TTGAAGGTAATTTAGATATG	[33]
	cadF-R1B		CTAATACCTAAAGTTGAAAC	
<i>flpA</i>	Cj1279c-F	832	TCAGAAGATGGCAAGGTTATAGAAG	[34]
	Cj1279c-R		GTTATTGCTATTGATTGACTGGAC	

### Bacteriology results

**Isolation and identification** A direct microscope slide from small intestine sample stained with Gram method showed numerous Gram-negative, thin, helical rods with almost no other biota (Supplementary Fig. 6). After incubation on mCCDA plates (direct inoculation), medium-numerous, medium-sized, round, flat, grey colonies with no gloss were obtained in pure culture. After pre-propagation on the supplemented Preston Broth, on Columbia Blood Agar plates we obtained growth of the pure culture of medium-sized, round, flat-convex, greyish and non-haemolytic colonies. Grown bacterial colonies were both catalase and oxidase positive. Microscopic slide from microbial cultures on blood agar plates, stained with Gram method, showed Gram-negative, thin, helical rods. Wet-mount slide from blood agar culture showed thin, motile, helical rods with characteristic corkscrew-like movement.

As a result of the PCR assay with mapAF and mapAR primers, we obtained single amplification product, about 600bp in size during the electrophoresis in 1% agarose gel in 1X TAE buffer, the same as for positive control, which allowed us to identify isolate as *Campylobacter jejuni*, which sequence was uploaded to GenBank and assigned accession number OM927984. We obtained no product with Mu3 and Mu4 primers (for *C. coli* identification).

### Antimicrobial agents susceptibility of *Campylobacter jejuni* isolate

Additionally, as a result of sequencing of the fragment of *gyrA* gene, point mutation (transition) in position 257 (257C>T) was found, resulting in amino acid substitution in codon 86 (Thr-86-Ile), which is the most common and frequent fluoroquinolones resistance mechanism among *Campylobacter* genus [35].

**Virulence factors genes detection** We have detected all of the selected genes responsible for motility (*flaA*, *flaB*), cytolethal distending toxin production (*cdtA*, *cdtB*, *cdtC*) and adhesion and internalization process (*ciaB*, *pldA*, *cadE*, *flpA*) by obtaining single product of expected size (Table 3) in each PCR assay.

### Discussion and conclusions

Necrotic enteritis in poultry is a disease caused mainly by *Clostridium perfringens* [36]. Other bacterial, parasitic, and viral factors have also been reported to cause similar changes in poultry, but this was not *Campylobacter* spp. [37]. Previous studies [9–11] show that, *C. jejuni* is not often isolated from peafowl. So far, no case of a peafowl disease caused by this bacteria has been described. However, in other bird species, *C. jejuni* was isolated from the intestinal tract of clinically affected and asymptomatic birds [2, 4]. Clinical signs of avian campylobacteriosis



have been observed in pet birds (mainly *Passeriformes*) and generally were associated with subacute to chronic hepatitis, include lethargy, anorexia, diarrhea and emaciation [4]. At necropsy, the liver is enlarged, pale or greenish, congested, with or without hemorrhage. Coalescing necrotic hepatitis is a common histological finding [4].

In poultry, *Campylobacter jejuni* has been considered as a commensal microorganism which colonizes its primary host rather than infecting it, in the absence of any obvious clinical signs, however, recent studies show possible pathogenicity of this bacterium for chickens [38]. The clinical signs of campylobacteriosis were experimentally induced in young chickens. Infected birds showed symptoms of diarrhea, weight loss, and even died [39]. Microscopic changes were found, ranging from moderate infiltration of mononuclear cells in ileum and cecum [39], to villus atrophy in the jejunum [40], mucosal damage, notably thickening, shortening and fusion of villi in the ileum [41]. In the presented case, the changes in the small intestine were similar, and their greater advancement may be caused by the concomitant parasitic invasion.

In the examined peacock, no changes in the liver were found macroscopically, but microscopic examination showed advanced necrosis and inflammation in the liver and kidneys. It is known that toxins produced by *C. jejuni* may be responsible for necrotic changes in the chicken embryo liver [42].

Antibiotics used in *Campylobacter* infections include macrolides such as erythromycin [43], tetracyclines, streptomycin and furans [8]. The isolate from the studied case additionally showed sensitivity to amoxicillin with clavulanic acid. The resistance of the tested strain to ciprofloxacin determined by single point mutation in the *gyrA* gene, is in line with the recent trends in fluoroquinolone resistance in strains of members of the genus *Campylobacter*, isolated from livestock and clinical samples from several countries [33].

So far, the authors have not observed fatal cases of coccidiosis in adult peafowl and no mortality cause by coccidia in peafowl has been documented in available literature. The only description of *E. pavonina* infestation reported in Europe [20] is a case of marked depression in a young peacock (during winter), while other 33 adult and young peafowl in this place, showed no symptoms of the disease [20]. Interestingly, no parasites were detected in faecal samples from the diseased bird, but in samples of birds from the same and other aviaries [20]. In presented case, although many oocysts were not found in the faeces and intestinal contents, the infestation was confirmed by histopathological examination.

Toltrazuril is a triazinetrione derivative administered orally in the drinking water for the treatment of coccidiosis in chickens and turkeys. The recommended

dose and duration of treatment for chickens and turkeys is 7 mg/kg bw per day for two consecutive days (<https://www.ema.europa.eu/en/medicines/veterinary/referrals/toltrazuril>)- and this is how the described peacock was treated 3 months before his death. In the case described by Hauck et al. [20], treatment with toltrazuril was at the same dose, but twice for 3 days with a break of 5 days. Studies conducted by Gesek et al. [44] with doses of 7 mg / kg bw, 14 mg /kg bw. and 24.5 mg / kg for 2 days in Japanese quails, showed that only a dose of 24.5 mg / kg bw, led to total destruction of the coccidia, but only in two of the six treated birds. However, the use of such high doses causes pathologic toxic changes in the liver and kidneys [44]. Other available drugs that may be used in the treatment of coccidiosis in ornamental *Gallinaceous* birds are sulfonamides. Studies in turkeys have shown that toltrazuril is more effective than sulfonamides [45]. There is therefore a need to test the effectiveness of other triazine compounds, such as aminomizuril and ethanamizuril [46] in peafowl.

In the presented case, *Histomonas meleagridis* was found in the cecum, but no changes typical of this invasion were observed. Much more often cryptosporidiosis was diagnosed as the cause of changes in the intestines in peacocks [47, 48], but in the case described, these parasites were not found in microscopic examination.

Presented case shows that despite the fact that *Campylobacter jejuni* is considered non-pathogenic for most healthy chickens [3], it may induce clinical signs and mortality in peafowl. This case provide guidance to veterinarians who struggle with chronic diarrhea in peafowl, to include campylobacteriosis in diagnostic tests, as well as do not neglect coccidiosis therapy even in adult birds.

#### Abbreviations

mg / kg.: Milligrams per kilogram; mg /l.: Milligrams per liter; spp.: Species; µl: Microliter; bp: Base pair; PCR: Polymerase chain reaction; bw: Body weight; ppm: Parts per million.

#### Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12917-022-03260-1>.

**Additional file 1.**

**Additional file 2.**

**Additional file 3.**

**Additional file 4.**

**Additional file 5.**

**Additional file 6.**

#### Acknowledgments

The authors would like to thank dr Ilona Stefańska from the Department of Preclinical Sciences WULS, for help in the processing of the research results.

### Authors' contributions

AL was responsible for performing and interpretation of clinical examination, necropsy, parasitology and was main contributor in preparing this manuscript. MM was responsible for molecular analysis and interpretation of microbiological data and writing of the manuscript. ID was responsible for histopathology interpretation and writing of the manuscript. DCC was involved in microbiological analysis of sample described in this report. PS supervised the work, was responsible for interpretation of data and design of the work. All authors read and approved the final manuscript.

### Funding

This study was funded by Warsaw University of Life Sciences.

### Availability of data and materials

The data generated or analyzed during this study are included in this published article and its supplementary files. The raw data of DNA-sequencing are available from the NCBI database under accession number PRJNA819941. (SRX14610090 and SRX14609836) <https://www.ncbi.nlm.nih.gov/sra/?term=PRJNA819941>.

### Declarations

#### Ethics approval and consent to participate

Not applicable; A case of natural disease in an ornamental bird is described, and the owner agreed to necropsy of the peacock.

#### Consent for publication

Not applicable.

#### Competing interests

The authors declare no competing interests.

#### Author details

<sup>1</sup>Department of Pathology and Veterinary Diagnostics of the Institute of Veterinary Medicine, Warsaw University of Life Sciences, Nowoursynowska 159c, 02-776 Warsaw, Poland. <sup>2</sup>Department of Preclinical Sciences, of the Institute of Veterinary Medicine, Warsaw University of Life Sciences, Nowoursynowska 159c, 02-776 Warsaw, Poland.

Received: 21 November 2021 Accepted: 20 April 2022

Published online: 02 May 2022

### References

- Rosler E, Signorini ML, Romero-Scharpen A, Soto LP, Berisvil A, Zimmermann JA, et al. Meta-analysis of the prevalence of the thermotolerant *Campylobacter* in food-producing animals worldwide. *Zoonoses Public Health*. 2019;66(4):359–69.
- Laconi A, Drigo I, Palmieri N, Carraro L, Tonon E, Franch R, et al. Genomic analysis of extra-intestinal *Campylobacter jejuni* and *Campylobacter coli* isolated from commercial chickens. *Vet Microbiol*. 2021;259:109161.
- Pielsticker C, Glünder G, Rautenschlein S. Colonization properties of *Campylobacter jejuni* in chickens. *Eur J Microbiol Immunol (Bp)*. 2012;2(1):61–5.
- Gerlach H. Bacteria. In: Ritchie B, Harrison G, Harrison L, editors. *Avian Medicine Principles and Application*. Lake Worth: Wingers Publishing, Inc.; 1994. p. 949–65.
- Jackson R. Gastrointestinal disorders. In: Poland G, Raftery A, editors. *BSAVA Manual of Backyard Poultry Medicine and Surgery*. Gloucester: BSAVA; 2019. p. 178–204.
- Colver AF, Pedler SJ, Hawkey PM. Severe *Campylobacter* infection in children. *J Inf Secur*. 1985;11(3):217–20.
- Altekruse SF, Stern NJ, Fields PI, Swerdlow DL. *Campylobacter jejuni*—An emerging foodborne pathogen. *Emerg Infect Dis*. 1999;5(1):28–35.
- Lam KM, DaMassa AJ, Morishita TY, Shivaprasad HL, Bickford AA. Pathogenicity of *Campylobacter jejuni* for turkeys and chickens. *Avian Dis*. 1992;36(2):359–63.
- Hollamby S, Sikarskie JG, Stult J. Survey of peafowl (*Pavo cristatus*) for potential pathogens at three Michigan zoos. *J Zoo Wildl Med*. 2003;34(4):375–9.
- Yogasundram K, Shane SM, Harrington KS. Prevalence of *Campylobacter jejuni* in selected domestic and wild birds in Louisiana. *Avian Dis*. 1989;33(4):664–7.
- Misawa N, Shinohara S, Satoh H, Itoh H, Shinohara K, Shimomura K, et al. Isolation of *Campylobacter* species from zoo animals and polymerase chain reaction-based random amplified polymorphism DNA analysis. *Vet Microbiol*. 2000;71(1–2):59–68.
- Banik DC, Ray HN. On a new coccidium, *Eimeria pavonina* n. sp. from peacock, *Pavo cristatus* Linn. *Bull Calcutta Sch Trop Med*. 1961;9:61.
- Banik DC, Ray HN. On a new coccidium, *Eimeria mandalin* n sp from peacock *Bull Calcutta Sch Trop Med* 1964;12:27.
- Mandal AK. Studies on some aspects of avian coccidia (Protozoa: Sporozoa), vol. 3. Five new species of the genus *Eimeria* (Schneider), and a new subspecies of *Eimeria roscoviensis* (Labbe). *Proc Zool Soc (Calcutta)*. 1965;18:47–57.
- Bhatia BB, Pande BP. A new coccidium, *Eimeria mayurai* (Sporozoa. Eimeriidae) from the common peafowl *Pavo cristatus*. *Proc Natl Acad Sci India Section B*. 1966;36:39–42.
- Amoudi MA. Two new species of *Eimeria* from peacocks (*Pavo cristatus*) in Saudi Arabia. *J Protozool*. 1988;3:546–8.
- El-Shahawy IS. *Eimeria pavoegyptica* sp. nov. (Apicomplexa: Eimeriidae) in faeces of Indian peacocks, *Pavo cristatus* Linnaeus, 1758 Galliformes: Phasianidae) from Egypt. *Mem Inst Oswaldo Cruz* 2010;105:965–969.
- Qamar MF, Shahid H, Aftab AMA, Farooq U. Prevalence of Coccidiosis in Peacock at Lahore- Pakistan Available from: <https://www.semanticscholar.org/author/M.-F.-Qamar/50233624>
- Williams RB. Notes on some coccidia of peafowl, pheasants and chickens. *Vet Parasitol*. 1978;4:193–7.
- Hauck R, Hafez HM. Description of *Eimeria pavonina* (coccidia) of peafowl in Germany. *Avian Dis*. 2012;56(1):238–42.
- Macdonald SE, van Diemen PM, Martineau H, Stevens MP, Tomley FM, Stabler RA, et al. Impact of *Eimeria tenella* coinfection on *Campylobacter jejuni* colonization of the chicken. *Infect Immun*. 2019;87(2):e00772–18.
- Loss Chaves S, Dias I, Pomilla C. Extraction of genomic DNA from carnivore fecal samples using QIAamp DNA Stool Mini Kit. (Modified from QIAamp® DNA Stool Handbook) Stool Extraction Protocol; 2010.
- Miska KB, Schwarz RS, Jenkins MC, Rathinam T, Chapman HD. Molecular characterization and phylogenetic analysis of *Eimeria* from turkeys and gamebirds: implications for evolutionary relationships in Galliform birds. *J Parasitol*. 2010;96:982–6.
- On SLW, Jordan PJ. Evaluation of 11 PCR Assays for Species-Level Identification of *Campylobacter jejuni* and *Campylobacter coli*. *J. Clin Micro*. 2003;41(1):330–6.
- The European Committee on Antimicrobial Susceptibility Testing. Breakpoints tables for interpretation of MICs and zone diameters. Version 11.0, 2021. <http://eucast.org>
- CLSI, editor. *Methods for antimicrobial susceptibility testing of infrequently isolated or fastidious Bacteria isolated from animals*. 1st ed. CLSI supplement VET06. Clinical and Laboratory Standards Institute: Wayne; 2017.
- Chatur YA, Brahmabhatt MN, Modi S, Nayak JB. Fluoroquinolone resistance and detection of topoisomerase gene mutation in *Campylobacter jejuni* isolated from animal and human sources. *Int J Curr Microbiol Appl Sci*. 2014;3(6):773–8.
- Nachamkin I, Bohachick K, Patton CM. Flagellin gene typing of *Campylobacter jejuni* by restriction fragment length polymorphism analysis. *J Clin Microbiol*. 1993;31:1531–6.
- Konkel ME, Gray SA, Kim BJ, Gravis SG. Yoon J: identification of enteropathogenes *Campylobacter jejuni* and *Campylobacter coli* based on the cadF virulence gene and its product. *J Clin Microbiol*. 1999;37:510–7.
- Hickey TE, McVeigh AL, Scott DA, Michielutti RA, Bixby A, Carroll SA, et al. *Campylobacter jejuni* cytolethal distending toxin mediates release of interleukin-8 from intestinal epithelial cells. *Infect Immun*. 2000;68:6535–41.
- Datta S, Niwa H, Itoh K. Prevalence of 11 pathogenic genes of *Campylobacter jejuni* by PCR in strains isolated from humans, poultry meat and broiler and bovine faeces. *J Med Microbiol*. 2003;52(4):345–8.



32. Goon S, Kelly JF, Logan SM, Ewing CP, Guerry P. Pseudaminic acid, the major modification on *Campylobacter* flagellin, is synthesized via the CJ1293 gene. *Mol Microbiol.* 2003;50:659–71.
33. Zheng J, Meng J, Zhao S, Singh R, Song W. Adherence to and invasion of human intestinal epithelial cells by *Campylobacter jejuni* and *Campylobacter coli* isolates from retail meat products. *J Food Prot.* 2006;69:768–74.
34. Flanagan RC, Neal-McKinney JM, Dhillon AS, Miller WG, Konkel ME. Examination of *Campylobacter jejuni* putative adhesins leads to the identification of a new protein, designated FlpA, required for chicken colonization. *Infect Immun.* 2009;77(6):2399–407. <https://doi.org/10.1128/IAI.01266-08>.
35. Sproston EL, Wimalarathna H, Sheppard SK. Trends in fluoroquinolone resistance in *Campylobacter*. *Microb genom.* 2018;4(8):e000198.
36. Cooper KK, Songer JG, Uzal FA. Diagnosing clostridial enteric disease in poultry. *J Vet Diagn Investig.* 2013;25:314–27.
37. Uzal FA, Senties-Cué CG, Rimoldi G, Shivaprasad HL. Non-*Clostridium perfringens* infectious agents producing necrotic enteritis-like lesions in poultry. *Avian Pathol.* 2016;45(3):326–33. <https://doi.org/10.1080/03079457.2016.1159282>.
38. Awad WA, Hess C, Hess M. Re-thinking the chicken-*Campylobacter jejuni* interaction: a review. *Avian Pathol.* 2018;47(4):352–63. <https://doi.org/10.1080/03079457.2018.1475724>.
39. Ruiz-Palacios GM, Escamilla E, Torres M. Experimental *Campylobacter* diarrhea in chickens. *Infect Immun.* 1981;34:250–5. <https://doi.org/10.1128/iai.34.1.250-255>.
40. Lamb-Rosteski J, Kalischuk L, Douglas Inglis G, Buret G. Epidermal growth factor inhibits *Campylobacter jejuni*-induced claudin-4 disruption, loss of epithelial barrier function, and *Escherichia coli* translocation. *Infect Immun.* 2008;76:3390–8. <https://doi.org/10.1128/IAI.01698-07>.
41. Humphrey S, Chaloner G, Kemmett K, Davidson N, Williams N, Kipar A, et al. *Campylobacter jejuni* is not merely a commensal in commercial broiler chickens and affects bird welfare. *mBio.* 2014;5:e01364. <https://doi.org/10.1128/mBio.01364-14>.
42. Clark AG, Bueschkens DH. Response of the chick embryo to live and heat-killed *Campylobacter jejuni* injected into the yolk sac. *Epidemiol Infect.* 1989;103:577–85.
43. Flammer K. Antymicrobial Therapy. In: Ritchie B, Harrison G, Harrison L, editors. *Avian Medicine Principles and Application*. Lake Worth: Wingers Publishing, Inc.; 1994. p. 434–50.
44. Gesek M, Sokół R, Welenc J, Tylicka Z, Korzeniowska P, Kozłowska A, et al. Histopathological observations of the internal organs during toltrazuril (Baycox®) treatment against naturally occurring coccidiosis in Japanese quail. *Pak Vet J.* 2015;35(4):479–83.
45. Greuel E, Mundt HC, Cortez S. Sulfonamide and toltrazuril therapy of experimental turkey coccidiosis. *Dtsch Tierarztl Wochenschr.* 1991;98(4):129–32.
46. Zhang M, Li X, Zhao Q, She R, Xia S, Zhang K, et al. Anticoccidial activity of novel triazine compounds in broiler chickens. *Vet Parasitol.* 2019;267:4–8. <https://doi.org/10.1016/j.vetpar.2019.01.006>.
47. Liu X, Zhu H, Meng W, Dong H, Han Q, An Z, et al. Occurrence of a *Cryptosporidium xiaoi*-like genotype in peafowl (*Pavo cristatus*) in China. *Parasitol Res.* 2019;118(12):3555–9.
48. Rodrigues B, Salgado PAB, Gonzalez IHL, Quadrini A, Holcman MM, Ramos PL, et al. Comparative analyses of coproscopical techniques to diagnose enteroparasites in a group of captive Indian peafowl (*Pavo cristatus*). *Ann Parasitol.* 2020;66(3):397–406.

## Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more [biomedcentral.com/submissions](https://biomedcentral.com/submissions)

