Supplemental materials

Table S1. Primer and probe sequences used in this study.

Purpose	Target		Primer sequence	Detection	Reference[a]	Annealing temperature (°C)	Amplicon Size (bp)
Genus detection	16S	forward reverse 1 reverse 2	GGATGACACTTTTCGGAGC CATTGTAGCACGTGTGTC CATTGTAGCACGTGTGTA	Genus	Modified, D Linton[1]	55	800
	23S	forward reverse probe	GATCCAGTGAAATTGTAGTGGAGGT GGCTCATATACAACTGGCGTCATA GACGGARAGACCC	Genus	Pholwat, S.[2]	60	158
Speciation and phylogenetic analysis	atpA	forward reverse 1 reverse 2	ATGGACTTAAGAATATTATGGC ATAAATTCCATCTTCAAATTCC CACGYTCAAGTTGTTTTCTACT(sequence)	C. jejuni/C. coli	Modified, Dingle[3]	50	1300
		forward reverse	GARCCAATTGAYGCTAAAGG TTTAADAVYTCAACCATTCTTTGTCC	C. lari	Miller[4]	53	924
		forward reverse	GGTATGGCHTTAAACCTTGAAGA TGACCACGCTCWARTTGTTTTCT	C. Sp (RM12651)	This study	52	1060
		forward reverse	GGTGATGCTTTAATTGGTCGTG AACGGATACAATGCTGCTTCA	C. volucris	This study	60	1091
	cpn60	forward reverse	GATCAAGCAGGCGATGGAAC GCTTTTCTTCTATCGCCAAAACCTG	C. jejuni	Hill, J. E[5]	60	614
		forward reverse	CTTGAAAATATGGGYGCTTCAC GCTTTTCTTCTATCKCCAAAACCT	C. coli	This study	58	665
		forward reverse	GAAAATATGGGTGCTTCTTTRGT GAAATCACTTCACCACCTGTT	C. lari	This study	56	707
		forward reverse	CAAGCAGGAGATGGAACTACAAC CGTTCCACCTGTTAAGATTGC	C. Sp (RM12651)	This study	60	651
		forward reverse	AAGCWGGTGATGGAACAACAAC GAAATCACTTCGCCACCTGT	C.ornithocola/ C. subantarcticus	This study	60	655
		forward reverse	CTGATCAAGCAGGAGATGGA TGTTCTTCCAAGCTCTTCTGAG	C. volucris	This study	59	680
	hipO	forward reverse probe	CTTGCGGTCATGATGGACATAC AGCACCACCCAAACCCTCTTCA TGCTTGCTGCAAAGTATT	C. jejuni	Liu, J.[6]	60	122
	glyA	forward reverse probe	AAACCAAAGCTTATCGTGTGC AGTGCAGCAATGTGTGCAAT TAAGCTCCAACTTCATCCG	C. coli	Liu, J.[6]	60	125

Virulence	*cdtA*	forward	ATCGTACCTCTCCTTGGCG	*C. jejuni*	Poudel, S.[7]	60	440
		reverse	CGGAGCAGCTTTAACGGTTTG				
		forward	GCCAAGGCTAAAATCTCCAAA	*C. coli*	This study	60	192
		reverse	TGCCAAGCTCTTGCATCTC				
		forward 1	CGGTTTGGGCTTTAAATCCA	*C. lari*	This study	58	388
		reverse 1	GCACTAATGCTCCATTGTCTAT				
		forward 2	CAGTTTGGGCCTTAAATCCA				
		reverse 2	GCGCTAACACTCCATTGTCTAT				
		forward	TGGGCGATATGTATGATGATG	*C. volucris*	This study	60	480
		reverse	TCCAAAATTGAGCTTGATTGC				
	cdtB	forward	TGGAGGAACAGATGTAGGAGC	*C. jejuni*	Poudel, S.[7]	60	180
		reverse	GCTTGAGTTGCGCTAGTTGG				
		forward	CTAGYAAGTGGGGGAAATGA	*C. coli*	This study	60	183
		reverse	CGTAGAAGAAGGCGGAACAAC				
		forward	AGAGTDGATGTTGGRGCAAAT	*C. lari*	This study	60	304
		reverse	TACGCGMTCTTAAATCHGSATCA				
		forward	AAAATCACCTGCAACCATCC	*C. volucris*	This study	60	464
		reverse	CTGCAACCACAGAAAGCAAA				
	cdtC	forward	GCTCCAAAGGTTCCATCTTCTAAG	*C. jejuni*	This study	60	269
		reverse	GCCTTTGCAACTCCTACTGG				
		forward	GCCTAGCTTGGATGAATTAG	*C. coli*	This study	60	411
		reverse	TCTATGGCGATACTAGAGTCAG				
		forward	GCAGTTTATAAAYCCTAGAGGTGCTG	*C. lari*	This study	60	315
		reverse	GGAGTTGCTTCAACRATAGCAG				
		forward	TCTAAACCGAAACGCTGCTC	*C. volucris*	This study	60	430
		reverse	GCGTTTGCTGAGATGGAATC				
	cadF	forward	CTGCTAAACCATAGAAATAAAATTTCTCAC	*C. jejuni*/*C. coli*	Liu, J. [6]	60	221
		reverse	CTTTGAAGGTAATTTAGATATGGATAATCG				
		forward	GCTCAATATGGTGCRGGTTT	*C. lari*	This study	60	259
		reverse	CACAACCTATATGATCAAGCAAAGC				
		forward	TGGTTATGAGCACCAAAAAGG	*C.* Sp (RM12651)	This study	60	674
		reverse	TGTCTTCGCTAACACCAGCTT				
		forward	GTGGTATGTTTGCCCAATATGGT	*C. volucris*	This study	60	249
		reverse	AGGCACCTTTTCTTGGTTCTG				
	flaA	forward	ATGCTTCAGGGATGGCGATA	*C. jejuni*/*C. coli*	This study	60	178
		reverse	CCATCTTGAGCCGCTTGAGT				
		Forward 2	GATGATGCTTCKGGKATGGCTA	*C. lari*	This study	59	192
		reverse 2	AGTRCTTTGWCCATCTTGWGC				
		forward	TAACTCTGCTGCTGATGATGCT	*C.* Sp (RM12651)	This study	60	229
		reverse	AGCTTGAAGTGAGCGTCTTGTT				
		forward	AGATGATGCTTCAGGTATGGCTA	*C. volucris*	This study	60	193

	reverse	AGTGCTTTGCCCATCTTGAG				
	forward 1	ATGCTTCAGGTATGGCTATTG	*C. volucris*	This study	56	418
	reverse 1	CTACTTTTAGCTTGAGATCCTGTT				
cheY	forward	TGATGACAGTTCTACTATGAGAAGG	*C. jejuni*	This study	56	362
	reverse	CTTCTCCACTTCCTGTTCCT				
	forward	TGATGACAGTTCTACTATGAGAAGG	*C. coli*	This study	56	283
	reverse	CAGTAATCACCTCAGCCTTG				
	forward	GTAGTTGATGATAGTTCTACCATGAG	*C. lari*	This study	56	248
	reverse	CCACCTTCTGTWGTTACCATGA				
	forward	CAAAGATTAGGTCATGAGGATG	*C.* Sp (RM12651)	This study	56	210
	reverse	TTCTGCTTTACCACCTTCAG				
	forward	GATGTTTTAGAGGCTGAGCA	*C. volucris*	This study	56	198
	reverse	TTCAGCTTTACCACCTTCTG				
CiaB	forward	AGCTGAATTTGCTTGGATGA	*C. jejuni*	This study	58	279
	reverse	CCATAAAATATCATCGGAGTGC				
	forward	GGCTGAATTTGCATGGATGA	*C. coli*	This study	60	306
	reverse	GCAGAAAACAAACCCTTAAGCTC				
	forward	GTTCAAGGTGTGCATAATATAGGTGT	*C. lari*	This study	58	704
	reverse	CCCTTAAGCTCTGCYCCATAA				
	forward	AGACTTCATTCAAGTTGGGCATT	*C.* Sp (RM12651)	This study	60	493
	reverse	TTCGTGTCCAATGGTGCTAA				
	forward	AGCTGAACTTGCATGGATGG	*C. volucris*	This study	60	298
	reverse	AAGTCCTTTAAGCTCTGCTCCA				
gluP	forward	AGCTCCACCCCAATAATAAGC	*C.* Sp (RM12651)	This study	60	604
	reverse	TCAAAATGGTGTTGTAGGTGGA				
hlyB	forward	TAGTTTGCTCTTGCGGTGTAT	*C.* Sp (RM12651)	This study	58	695
	reverse	CGCAAAATTAGGCAGTGAGT				
pgiB	forward	TGGATGATGTAAATGCAGTGCT	*C.* Sp (RM12651)	This study	60	662
	reverse	TGCGATTATATGTGARCCACCA				
gyrA T86I	forward	GCCCGTATAGTGGGTGCTGT	*C. jejuni* fluoroquinolone resistance	Pholwat, S.[2]	60	86
	reverse	TCTTGAGCCATTCTAACCAAAGC				
	probe[W]	ATAAACTGCTGTATCTC				
	probe[M]	AACTGCTATATCTCC				
23S A2075G	forward	GATCCAGTGAAATTGTAGTGGAGGT	*Campylobacter* macrolide resistance	Pholwat, S.[2]	60	158
	reverse	GGCTCATATACAACTGGCGTCATA				
	probe[M]	GACGGAAAGACC				
	Probe[W]	GACGGAGAGACCC				

ᵃ The original primers and probes were used as previously published if it was not indicated as "Modified" or "This study".

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Table S2. Distribution of *Campylobacter* detected in different migratory bird species at 4 habitats.

Migratory birds Order	Family	Genus	Hebei	Heilongjiang	Qinghai	Xizang	Total
Anseriformes	Anatidae	*Anas platyrhynchos*		2			2
		Anser albifrons/fabalis	1	31	1		33
		Anser anser/Anser erythropus			4	1	5
		Anser indicus	13		11	47	71
		Aythya nyroca			1		1
Charadriiformes	Laridae	*Chlidonias leucopterus*	1				1
		Chroicocephalus ridibundus	16			1	17
		Ichthyaetus relictus	1				1
		Larus argentatus	1				1
	Scolopacidae	*Numenius arquata*	2				2
		Tringa erythropus				1	1
	Recurvirostridae	*Recurvirostra avosetta*	2				2
	Charadriidae	*Charadrius placidus*	1				1
		Pluvialis squatarola	1				1
Suliformes	Phalacrocoracidae	*Phalacrocorax carbo*	4			1	5
Strigiformes	Strigidae	*Athene noctua*	1				1
Falconiformes	Falconidae	*Falco peregrinus*		1			1
	Total		44	34	17	51	146

Table S3. Detection of virulence genes in 5 *Campylobacter* species.

Virulence gene	Function	Detection Rate (%)*				
		C. jejuni	*C. coli*	*C. lari*	*C. volucris*	**RM12651-like**
cdtA	Exotoxin	76.5 (13/17)	66.7 (2/3)	81.8 (9/11)	75.0（3/4）	-
cdtB	Exotoxin	76.5 (13/17)	66.7 (2/3)	81.8 (9/11)	50.0（2/4）	-
cdtC	Exotoxin	23.5 (4/17)	33.3 (1/3)	81.8 (9/11)	50.0（2/4）	-
cadF	Adherence	70.6 (12/17)	33.3 (1/3)	91.7 (11/12)	100.0（4/4）	84.3 (59/70)
cheY	Motility	86.7 (13/15)	66.7 (2/3)	91.7 (11/12)	100.0（4/4）	86.3 (63/73)
flaA	Motility	93.3 (14/15)	66.7 (2/3)	100.0 (12/12)	75.0（3/4）	91.8 (67/73)
ciaB	Invasion	80.0 (12/15)	100.0 (3/3)	83.3 (10/12)	100.0（4/4）	84.3 (59/70)
gluP	Immune modulation	-	-	-	-	75.7 (53/70)
pgiB	Immune modulation	-	-	-	-	78.1 (57/73)
hlyB	Exotoxin	-	-	-	-	72.6 (53/73)

*Due to the availability of the samples, no test was done on a few samples. Only samples with complete tests were included for Figure 2 and Figure 3B.

Supplemental Figure Legends
Figure S1. Phylogenetic analysis based on 16S rRNA gene in different habitats and migratory birds. Fasttree was used to construct the tree. *Helicobacter* was used as an outgroup. The figure was prepared with iTOL (Interactive Tree of Life). Different colors in the two columns represent different regions and birds, respectively. The Bootstrap value is displayed only when <0.7.