

Supplementary Material

Type of the Paper (Article)

Beta-Resorcylic Acid and Eugenol Minimized the Invasion and the Expression of Virulence Genes in Multi-Drug Resistant Avian *Campylobacter jejuni* isolates

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Table S1. Distribution of antimicrobial resistance patterns among multidrug-resistant *C. jejuni* isolates

Antimicrobial resistance pattern	No. of resistant <i>C. jejuni</i> isolates (%), source
AM, E, SXT	1 (0.9), Cg
AM, E, KF, SXT	3 (2.7), 2Ctm, 1Cbm
AM, E, CIP, TE, SXT	1 (0.9), Cg
AM, E, NA, CIP, KF	1 (0.9), Cg
AM, E, NA, KF, TE	2 (1.8), Cg
AM, E, NA, TE, SXT	2 (1.8), 1Cns, 1Cg
AM, E, NA, CIP, TE	2 (1.8), Cns
AM, E, NOR, KF, SXT	4 (3.5), H
AM, E, KF, TE, SXT	12 (10.6), 3H, 2Ccs, 2Ccp, 2Cns, 1Cbm, 2Cl
AM, E, NA, CIP, KF, SXT	2 (1.8), Cl
AM, E, NA, NOR, TE, SXT	1 (0.9), Cbm
AM, E, NA, NOR, KF, TE	1 (0.9), Cbm
AM, E, NOR, KF, TE, SXT	1 (0.9), H
AM, E, NA, KF, TE, SXT	10 (8.8), 4H, 1Ccp, 2Ctm, 1Cbm, 2Cl
AM, E, NA, CIP, TE, SXT	21 (18.6), 7H, 5Ccs, 3Ccp, 2Cns, 2Ctm, 2Cbm
AM, E, NA CIP, KF, TE	14 (12.4), 3H, 3Ccs, 2Ccp, 2Ctm, 1Cbm, 3Cl
AM, E, NA, NOR, KF, TE, SXT	4 (3.5), 3Ccs, 1Ctm
AM, E, NA, CIP, KF, TE, SXT	6 (5.3), 3Ccs, 3Ccp
AM, E, NA, NOR, KF, K, TE, SXT	2 (1.8), Cg
AM, E, NA, KF, CN, K, TE, SXT	3 (2.7), 2H, 1Cl
AM, E, NA, CIP, KF, CN, TE, SXT	9 (8), 4H, 1Ccs, 1Ccp, 2Ctm, 1Cbm
AM, E, NA, NOR, KF, CN, TE, SXT	8 (7.1), 1H, 1Ccs, 1Ccp, 2Cns, 1Ctm, 1Cbm, 1Cl
AM, E, NA, NOR, KF, CN, K, TE, SXT	2 (1.8), 1H, 1Ccp
AM, E, NA, CIP, KF, CN, K, TE, SXT	1 (0.9), Ccs
Total	113 (100)

H: human, Ccs: chicken cloacal swab, Ccp: chicken cecal part, Cns: chicken neck skin, Ctm: chicken thigh meat, Cbm: chicken breast meat, Cl: chicken liver, Cg: chicken gizzard, AM: ampicillin, E: erythromycin, NA: nalidixic acid, CIP: ciprofloxacin, NOR: norfloxacin, KF: cephalothin, CN: gentamicin, K: kanamycin, TE: tetracycline, SXT: trimethoprim/sulfamethoxazole.

Table S2. Distribution of virulence gene profiles among human and avian multi-drug resistant *C. jejuni* isolates

Virulence gene profile	No of <i>C. jejuni</i> isolates from different origins (%) harboring virulence gene profile		
	Human (8)	Chicken (17)	Total (25)
<i>virB11, wlaN, flaA</i>	2 (25%)	6 (35.3%)	8 (32%)
<i>virB11, flaA</i>	2 (25%)	3 (17.6%)	5 (20%)
<i>wlaN, flaA</i>	-	1 (5.9%)	1 (4%)
<i>flaA</i>	4 (50%)	7 (41.2%)	11 (44%)

Table S3. Jaccard Coefficient similarity matrix between poultry and human *C. jejuni* isolates falling in ERIC-PCR clusters II-V

ERIC-PCR clusters (<i>C. jejuni</i> isolate No)	II (33Ccs)	II (51Ccp)	III (74Ctm)	III (86Cbm)	IV (85Cbm)	IV (52Ccp)	V (106Cg)
II (5H)	20%	18.2%	0	0	0	0	0
III (7H)	0	0	28.6%	0	0	0	0
III (86Cbm)	0	0	50%	100%	0	0	0
IV (6H)	0	0	0	0	0	25%	0
IV (8H)	0	0	0	0	0	20%	0
IV (85Cbm)	0	0	0	0	100%	25%	0
V (2H)	0	0	0	0	0	0	22.2%
V (4H)	0	0	0	0	0	0	16.7%

H: human, Ccs: chicken cloacal swabs, Ccp: chicken cecal parts, Ctm: chicken thigh meat, Cbm: chicken breast meat, Cg: chicken gizzard.

Table S4. Discriminatory power and profile numbers for different typing methods of 25 *C. jejuni* isolates

Typing technique	Source of isolates (No)	Number of profiles	Discriminatory index (D)
Antibiotyping	Chickens (17)	6	0.7647
	Human (8)	4	0.75
	Total (25)	6*	0.77
Virulotyping	Chickens (17)	4	0.7132
	Human (8)	3	0.7143
	Total (25)	4*	0.69
ERIC-PCR	Chickens (17)	12	0.9559
	Human (8)	6	0.9286
	Total (25)	14*	0.94

*Some profiles of human origin are included within those of the chicken origin

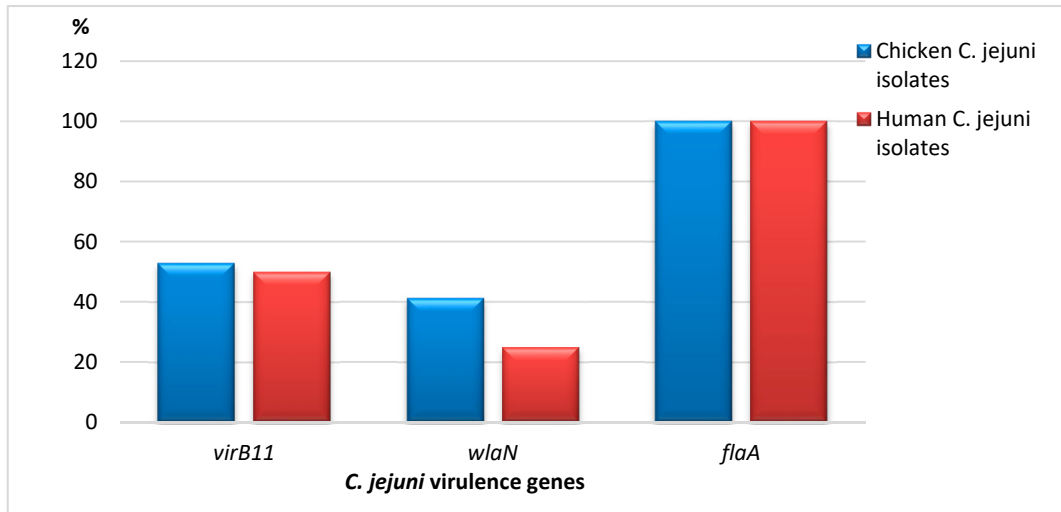


Figure S1. Distribution of *VirB11*, *wlaN* and *flaA* genes among avian and human *C. jejuni* isolates

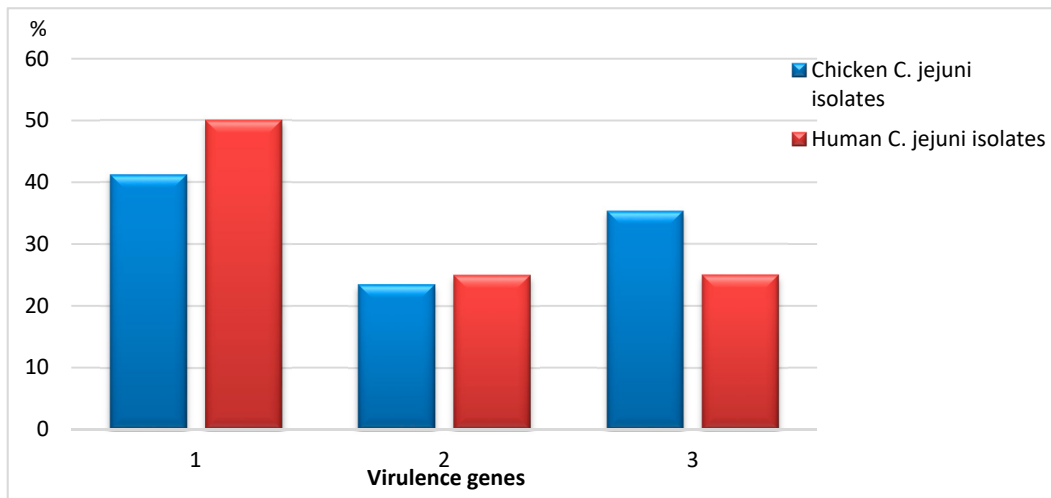


Figure S2. Distribution of one, 2 and 3 virulence genes among avian and human *C. jejuni* isolates