SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Proteome analysis comparing protein profiles of wild-type 81-176 and mutant 81-176*cj0415*. Although the downstream *cj0415* gene was insertionally inactivated, both the Cj0415 and Cj0414 proteins are missing in the *cj0415* mutant.

Figure S2. GADH activity of *C. jejuni* 81-176 cell fractions. *C. jejuni* 81-176 cells grown at 42°C were fractionated as described (Myers & Kelly, 2005), and the presence of GADH activity was determined by a coupled enzyme assay. The samples were total membranes (M), cytoplasm (C), periplasm (P), whole cells (WC), or no cell lysate (N) as a negative control.

Figure S3. Growth at 42°C of *C. jejuni* 81-176 supplemented with electron donors. Growth of *C. jejuni* in defined α MEM media containing the electron donors gluconate and formate was monitored by optical density at 600 nm. Electron donors added were: 5 mM formate (open circles), 20 mM D-gluconate (open squares), or no added electron donor (open diamonds). Cultures were inoculated at initial OD₆₀₀ of approximately 0.02 (left panel), 0.06 (center panel), or 0.1 (right panel). Addition of electron donors did not stimulate *C. jejuni* growth.

Figure S4. *In vitro* growth profiles of 81-176 and 81-176*cj0415*. Wild-type and *cj0415* mutant strains were grown individually or mixed in equal concentration prior to inoculation; growth of the three cultures was monitored by OD_{600} (Panel A) and by viable count of the *in vitro* competition (Panel B). Results showed no differences in the growth of the strains either individually or during *in vitro* competition.

Figure S1



Figure S2

GADH activity (pmol DCIP reduced / min / mg)



Figure S3





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TABLE S1. Primers used in this study

Primer	Sequence $(5' \rightarrow 3')^{\dagger}$	Coordinates*
<i>cj0414</i> -F1	AAA <u>CTGCAG</u> ATGCAAGACAATATTATTGATC	380937-380958
<i>cj0415</i> -F1	TGG <u>CTGCAG</u> AGCTTACTAAAGCAGGTT	381740-381757
<i>cj0415</i> -R1	CCC <u>GTCGAC</u> TTTTCCACTTTTATGATATTT	383376-383356
<i>cj0413</i> -F1	AAAAAGATGGACAAATGGCC	380482-380501
<i>cj0417</i> -R1	ACGATGACTTGAATTTGCAT	383712-383693
<i>cj0414</i> -inv1	AA <u>ACCGGT</u> AGCAGATATGGAGAGTTAAA	381647-381666
<i>cj0414</i> -inv2	AAAAAACCGGTGCTAGCAGCCTTGTTCGGCTTTGCCC	381263-381282
<i>cat-</i> Nhe	CTCT <u>GCTAGC</u> GGAGGATAAATGATGCAATT	N/A
<i>cat-</i> Age	AGAG <u>ACCGGT</u> TTATTTATTCAGCAAGTCTT	N/A
<i>cj0414</i> -F2	AAACTGCAGATGCAAGACAATATTATTGATC	380937-380959
<i>cj0415</i> -R2	CCCGTCGACTTTTCCACTTTTATGATATTTT	383376-383354
16S-RT-FOR	GGGTGCTAGTCATCTCAGTAATGC	40161-40187
16S-RT-REV	GGTAAGGTTCTTCGCGTATCTTCG	40210-40176
<i>cj0414</i> -RT-FOR	GGAGAAGGAGCTATAGGTTTAGGC	381177-381201
<i>cj0414</i> -RT-REV	GCGTTGCATAGGAGTTTGATAGCC	381322-381298
<i>cj0415</i> -RT-FOR	GTGGCTGCAGAGCTTACTAAAGCA	381730-381753
<i>cj0415</i> -RT-REV	GCTAAACCACTAGGATCATGGCGA	381908-381885

⁺Underlined nucleotides indicate restriction sites introduced for cloning purposes

*According to NCTC11168 genomic sequence (accession AL111168)

N/A - Not applicable