

**Figure S2.**

Genetic organization of the *cetABCZ* loci in the *Campylobacter* genus based on available genome sequences. Genes are drawn roughly to scale and additional flanking genes are hashed. Pseudogenes are shown by interrupted boxes. The protein sequences encoded by the *cet* genes were searched against a FASTA file containing all open reading frames for each genome using a local BLAST search, using both BLASTP and TBLASTN (BioEdit - <http://www.mbio.ncsu.edu/bioedit/bioedit.html>). Homologs of the Cet proteins were then re-checked against the NCTC 11168 sequences to confirm the match and gene order confirmed using Artemis. In *C. jejuni* subsp. *doylei* strain 269.97, an *aer1* ortholog is present but interrupted by several stop codons and therefore considered to be a pseudogene. The *cetABC* genes are conserved in the *jejuni* species of the *Campylobacter* genus, with the exception of *C. jejuni* subsp. *doylei*, where *cj1191c* is present as a pseudogene, suggesting functional redundancy. Other species from the *Campylobacter* genus show variations of this gene arrangement: *C. coli* and *C. upsaliensis* are most similar to *C. jejuni* with similarly arranged loci. *C. concisus*, *C. curvus*, *C. rectus*, and *C. showae* have genes encoding proteins with a single PAS domain upstream of a gene encoding a CetA homolog, and no gene encoding a

CetZ homolog; while *C. lari* contains two genes encoding CetC homologs upstream of genes for CetA and a CetZ homolog. The *C. fetus* genome encodes a CetB homolog upstream of a *cetA* pseudogene, and a number of genes encoding other proteins that contain PAS domains, including a CetZ homolog (Cff8240\_0322) and two proteins that contain PAS, GGDEF, and EAL domains that may be involved in cyclic di-GMP signalling [1]. A full description of chemotaxis proteins in *C. fetus* is described in [2]. *C. gracilis*, and *C. hominis* appear to lack both the *cetABC* and *cetZ* loci entirely. Interestingly, the *cet* loci are absent in the *Helicobacter* species *H. pylori*, *H. acinonychis*, and *H. hepaticus*. A chemotaxis protein, ChePep, has recently been identified in *H. pylori* lacking any similarity to known chemotaxis proteins except for a CheY-like receiver domain [3,4]. Moreover, *H. pylori* employs three CheV proteins, each with a distinct role in chemotaxis [5], and lacks CheR and CheB. These differences may reflect host adaptation in *H. pylori* [6,7] where both energy and pH taxis systems appear to be important for colonization of their particular niche [8,9].

## References

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