Supporting Information

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SI Materials and Methods

Mutant Construction. Mutants in the genes *cj0481*, *cj0483*, *cj0486*, *cj0487*, and *cj0490* were constructed using a mutagenesis and gene-replacement strategy. The target gene was PCR-amplified using the primers listed in Table S3 and the genomic DNA of NCTC 11168 was used as the template. All primers used for these cloning reactions were designed for use with the In-fusion Dry down PCR cloning kit (Clontech). The PCR products were cloned into BamHI-digested pUC19 plasmids using the manufacturer's protocols. Once recombinant plasmids were obtained, they were used as a template for an inverse PCR, so as to delete regions within the gene, and create a site for the insertion of a chloramphenicol resistance cassette (*cat*). The primers used for the inverse PCR are listed in Table S3. The *cat* gene was amplified from pRY111 using Pfx polymerase (Invitrogen) and the primers indicated in Table S3. The *cat* gene was then cloned into the inverse PCR product using the Clontech kit, as above. Constructs were confirmed by sequencing and the recombinant plasmids were naturally transformed into motile *Campylobacter jejuni* NCTC 11168, as described previously (1, 2) by selecting for chloramphenicol resistance on MH agar. The exception to this protocol was the mutation of *cj0486*. The *C. jejuni cj0486* mutant was created by blunt insertion of the SmaI-cut 1488 bp kanamycin cassette from pWM2 into the SpeI-cut *C. jejuni cj0486* cloned into pBR322 described above. Electroporation of 1 μg of this plasmid into *C. jejuni* NCTC 11168 was performed, as described previously (3), selecting for kanamycin-resistant *C. jejuni* transformants. Constructs were confirmed by PCR and sequence analysis of the recombinant gene.

***C. jejuni* Mutant Complementation.** The plasmid used to construct CjWM227a was kindly provided by Qijing Zhang (Iowa State University, Ames, IA). This construct contained the amplified region *cj0486-cj0490,* cloned into the pRRK vector (4) as described in by Muraoka et al. (5). This construct was transformed into the *Δcj0487* mutant to create the *cj0486–cj0490* complemented *Δcj0487*strain. To construct the *Δcj0486+ (cj0486–cj0490)* strain, the pRRKCj0486-cj0490 plasmid was digested with MfeI-HF to remove the kanamycin-resistance cassette and replace it with a chloramphenicol-resistance cassette. The resultant plasmid pRRC486-490 was transformed into the *Δcj0486* mutant.

Complementation of an *Escherichia coli fucP* Mutant with *Ec-fucP* and *cj0486*. The *fucP* genes from *Escherichia coli* and *C. jejuni* (*cj0486*) were PCR-amplified to contain ribosome binding sites. A 1,354-bp PCR product containing the *E. coli fucP* gene was obtained with oligonucleotides EfucP_F, EfucP_R, and chromosomal DNA of *E. coli* K12; a 1,317 bp *C. jejuni-fucP* containing PCR product was obtained using oligonucleotides CfucP_F, CfucP_R, and chromosomal DNA of *C. jejuni* NCTC11168. Full-length *E. coli fucP* and *C. jejuni cj0486* genes were cloned into BamHI or SalI cut pBR322 within the tetracycline gene. For further complementation analysis of the *E. coli fucP* mutant plasmid, pCE111-28 was linearized with EcoRV and ligated with the *fucP* gene containing PCR products. One positive candidate after restriction analyses with PstI (for the insertion and correct orientation of the *E. coli fucP* gene) or HindIII (for the insertion and correct orientation of the *C. jejuni fucP* gene) was used to complement the *E. coli fucP* mutant strain.

Mucin Isolation and Electrospray Ionization Mass Spectrometry Analysis. Intestinal sections (duodenum, jejunum, ileum, and cecum) recovered from killed piglets, or ceca recovered from broiler chicks, were cut longitudinally to reveal the mucus lining. Luminal contents were removed by washing with PBS buffer and the internal surface was scraped into a microcentrifuge tube using a scalpel. The mucus was emulsified with 15% vol/vol 1× PBS buffer and was centrifuged twice at 28,400 × *g* for 20 min to remove solid material. The crude mucin was washed in 70% ethanol and then dialyzed in MilliQ water and lyophilized overnight. All mucin samples were then treated with $NaBH_4$ and NaOH overnight at 42 °C (β-elimination) to release the *O*-linked glycans (6). Purified mucin *O*-glycans were analyzed using a 4000 Q-Trap (AB/MDS Sciex) equipped with a microspray interface. Precursor ion scans at *m/z* 224, corresponding to the fragment ion of the reducing end, were acquired with a scan time of 2 s at a step size of 0.5 Da. The collision energy was ramped from 40 to 80 V over the scan range of *m/z* 600 to 1,400.

Confirmation of Operonic Structure. The organization of the genes *cj0481* to *cj0490* was confirmed to be in an operonic structure by PCR amplification of regions spanning neighboring genes using cDNA as a template. Total RNA was extracted from cultures grown in medium containing L-fucose, as described earlier. The total RNA was converted to cDNA using SuperScript II reverse transcriptase (Invitrogen), following the manufacturer's protocols. To amplify the regions in between genes, the primers previously used for the inverse PCR step of mutant construction were used (Table S3). PCR products from the cDNA template were compared against products from a control genomic DNA template.

Total RNA Extraction for Real-Time PCR and Microarray Studies. Cultures of *C. jejuni* NCTC 11168 were inoculated into filter-sterilized MEMα medium containing 20 μM $FeSO_4$ and 25 mM L-fucose, UV-sterilized MEMα medium containing 2 mg/mL porcine gastric mucin (Sigma) or control medium of MEMα containing 20 mM sodium pyruvate and 20 μM $FeSO_4$. Cultures were grown to an OD at 600 nm of 0.2, representing midlog phase, at which point the RNA quality was preserved by one of two methods. A 1/10-volume stop solution of 10% buffer saturated phenol (pH 4.3) and ethanol was added to the fucose-containing culture. However, this stop solution proved insufficient to preserve RNA quality in the mucin-containing culture so a 1/1 volume of RNA-later (Ambion) was used in this case. Total RNA was extracted using a hot-phenol extraction method as described previously (1, 2, 7). The RNA was treated twice with Dnase I (Epicentre) and the absence of genomic DNA was confirmed by PCR. Final RNA quality and quantity was ascertained using BioRad's Experion StdSensRNA system using the manufacturer's protocols.

Microarray Hybridization and Analysis. Microarray slides and labeled cDNA probes were prepared and hybridized as described previously (1, 2, 7). Complementary DNA probes from control cultures grown in MEMα containing pyruvate were labeled with indocarbocyanine [Cy3], and experimental samples, from cultures containing L-fucose or mucin were labeled with indodicarbocyanine [Cy5]. Once prepared, the arrays were scanned with a laser-activated confocal scanner (ScanArray Gx; Perkin-Elmer) at a resolution of 10 μm. The signal intensities of each spot were collected using ScanArray software. Spots exhibiting hybridization anomalies were excluded from the analysis. The raw median fluorescence intensity values were background-subtracted, and spots with background-subtracted values less than three times the SD of the local background in both channels were also excluded from further analysis.

Subsequently, the background-subtracted fluorescent intensity in each wavelength (channel 1 for Cy3 and channel 2 for Cy5) was normalized using the MIDAS software (available from TIGR, http://www.tigr.org/software/) and by applying a locally weighted linear regression (Lowess), as previously described (7). Microarray data were collected from three independent biological replicates and three technical replicates for each biological replicate, for a total of nine microarray slides for each condition. Each slide contained triplicates of each probe, yielding a total of 27 replicate spots for analysis. Finally, the ratio of channel 2 to channel 1 was converted to $\log_2$, and the data were statistically analyzed using the empirical Bayes method, as previously described (7).

Quantitative RT-PCR. Quantitative RT-PCR was conducted using the Applied Biosystems 7300 DNA analyzer and the Qiagen Quantitect SYBR Green RT-PCR kit using the manufacturer's protocols and as described previously (1). Each sample used total RNA that was extracted from cultures of *C. jejuni NCTC11168*, *Δcj0481*, *Δcj0486*, *Δcj0487*, and the complemented strains: *Δcj0486+(cj0486–cj0490)* and *Δcj0487+(cj0486–cj0490)*, grown in MEMα supplemented with 25 mM L-fucose. RNA expression relative to the wild-type control was determined for the genes *cj0480c*, *cj0481*, *cj0486*, and *cj0487*, with *rpsL* acting as an endogenous control.

SI Results

Intestinal Mucin *O*-glycan Compositions Differ in Chickens and Pigs. Because intestinal mucin glycoproteins are heavily glycosylated with *O*-linked glycans, we characterized the neutral and acidic *O*-glycans released from porcine and chicken gastrointestinal mucins to identify differences in glycan composition between these two model systems that may be relevant to *C. jejuni* disease. Although both chicken and pig mucin *O*-glycans showed similar levels of fucosylation, the fucosylated oligosaccharides from chicken mucin were predominantly sulfated (38% versus 11–14% in the pig samples) and contained relatively low amounts of NeuAc (Fig. S5). In contrast, the pig mucin *O*-glycans showed very little modification with sulfate, but contained greater amounts of NeuAc and also NeuGc (Fig. S5). The lack of detectable NeuGc in chick mucins is consistent with what has recently been reported (8).

Genes *cj0481* to *cj0490* Exist as a Single Operon. We used PCR of sections spanning neighboring genes and cDNA derived from extracted total RNA to confirm that the genes *cj0481* to *cj0490* are expressed as a single transcript. PCR products were obtained from regions spanning each pair of genes *cj0481-cj0483*, *cj0483-cj0484*, *cj0484-cj0485*, *cj0485-cj0486*, *cj0486-cj0487*, and *cj0487-cj0490*. Each of these products was of equal size to the product obtained from a genomic DNA template. The exception to this was the region in between *cj0480c* and *cj0481*. As these genes are oriented in opposite directions, they should not be transcriptionally linked. A product was obtained from the genomic DNA template, but none from the cDNA template.

Other Genes Transcriptionally Regulated in the Presence of L-Fucose. Cultures grown in the presence of L-fucose also exhibited an upregulation of metabolic genes, including most of the citric acid cycle, proline metabolism (*putAB*), and genes involved in aspartate/glutamate transport and metabolism (*peb1A*, *cj0919*, *cj0920*, *pebC*, *aspB*). Notable groups of genes exhibiting down-regulation included oxidative stress response genes (*ahpC*, *sodB*, *tpx*), elements of the electron transport chain (*cydAB*, *petABC*), chemotaxis (*cetAB*, *tlp4*), and the outer membrane protein (*omp50*).

Disruption of the L-Fucose Permease Gene *cj0486* Disrupts Expression of Genes both Up and Downstream. Quantitative RT-PCR was conducted on the mutants *cj0481*, *cj0486*, and *cj0487*, as well as mutants complemented with the region *cj0486–cj0490* (Fig. S3). Although the mutant *cj0481* exhibited slightly reduced expression of the downstream genes *cj0486* and *cj0487*, the mutants *cj0486* and *cj0487* saw little to no expression of other genes within the operon (in particular *cj0481* was not expressed in either mutant). Although restoring copies of the genes into an rRNA cluster within the genome partially restored expression of the target genes, this did not restore the expression of other genes within the operon. This finding could indicate that a higher level of transcription of the permease genes is necessary to allow for sufficient uptake of L-fucose to stimulate transcription of the operon.

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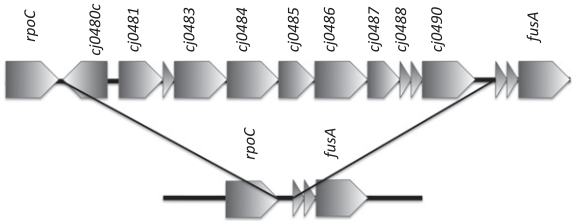

Fig. S1. Genomic region surrounding the putative fucose permease (*fucP, cj0486*). The upper strand is the region as it appears in *C. jejuni* strains NCTC 11168, RM1221, CF93-6, 84–25, *C. jejuni* subsp. *doylei* 269.97, and *C. coli* RM2228. The lower strand is the region as it appears in the strains lacking *fucP: C. jejuni* 81–176, CG8486, HB93-13, 260.94, and 81116.

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EcFucP          MGNTSIQTQSYRAVDKDAGQSRSYIIPFALLCSLFFLWAVANNLNDILLPQFQQAFTLTN 60
Cj0486          ------------------MTDSKNIKIAIVLVTSLFFLWGVSYGLIDVMNKNFQNHLHISQ 43
Cj0484          -------MKHANSIKLELVCKKISWRILPLIVLMFCLSMLDRTNISFVKSHIEIDAGIGE 53

EcFucP          FQAGLIQSAFYFGYFIIPIPAGILMKKLSYKAGIITGLFLYALGAALFWPAAEIMNYTLF 120
Cj0486          HESGFLQFAYFGAYFIIALPAGYIANRFSYKMGIIFGLALYAIGALLIIPATNLASFHLF 103
Cj0484          AAYALGAGIFFIGYAIFEVPSNLFLHKLGAKIWLSRIMITWGLVTMAMIFIQGEISFYVL 113

EcFucP          LVGLFIIAAGLG--CLETAANPFVTVLGPESSGHFRLNLAQTFNSFGAIIAVVFGQSLIL 178
Cj0486          LFAFFILACGIG--SLETSANPYMTKLGDEKNASFRINAAQSFNGLGQFVGPIIGGALFL 161
Cj0484          RFLLGLTEAGFSPGIILYLSYFFPAIYRSKAYGIYQMGVPIAFVFGSLISGFILDYTPNI 173

EcFucP          SNVPHQSQDVLDKMSPEQLSAYKHSLVLSVQTPYMIIVAIVLLVALLIMLTKFPALQSDN 238
Cj0486          SITKQE-----EGASKEQIQAALVANMGNVQLVYIGIAVIVILILIAFVANKLP--EGSA 214
Cj0484          YFKNWQWMFLIEGGITVLVGIFCLFYLDSHPKDAKWLDIKEKDILLKHIEISNTKAKDYS 233

EcFucP          HSDAKQGSFSASLSRLARIRHWRWAVLAQFCYVGAQTACWSYLIRYAVEEIPGMTAGFAA 298
Cj0486          VSDDYKQKDDSKPIYVFKHRHFNLGLLAQFLYIANQVAAGAFFINYVVEHNEGLKDAQGA 274
Cj0484          IKDIFKS-------------ILVWKFVFVYFCIQLSVYGVLFYLPSKIAQILQINVGFEV 280

EvFucP          NYLTGTMVCFFIGRFTGTWLISRFAPHKVLAAYALIAMALCLISAFAGGHVGLIALTLCS 358
Cj0486          YYFSIALVAFMLGRIVSTPLMKIIKGEKILGFYSLINVLICFSLYFASGFFSIVLLIALF 334
Cj0484          GLLN--AIPWIFVFIALPIFTSLADKKHSWNLHAILFLLLASLSMIASTFVTNLAAFLFF 338

EcFucP          AFMSIQYPTIFSLGIKNLG-QDTKYGSSFIVMTIIG------GGIVTPVMGFVSDAAGN- 410
Cj0486          FFMSISFPTIFAVATKNLPLNQVKLGGSLLVMSIVG------GAIMPIIIGFINDHYGTG 388
Cj0484          ISLAAIGFIVIQPIFWNLPTQVLKGKGAAAAIALIGSLGNLGGFVAPTLKTYIENHFGVE 398

EcFucP          IPTAELIPALCFAVIFIFARFRSQTATN-- 438
Cj0486          AGYLAMAPLFLYVAWYGFIGSKVRKNAKDF 418
Cj0484          FGLIVLALIAIL------------------ 410
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Fig. S2. The sequence aligment between the *E. coli* FucP, and the *C. jejuni* Cj0486 and Cj0484 proteins. The alignment was done using the online program ClustalW2 from EMBL-EBI, http://www.ebi.ac.uk/Tools/msa/clustalw2/. Highlighted in green are the amino acid residues Asp46, Glu135, and Asn146.

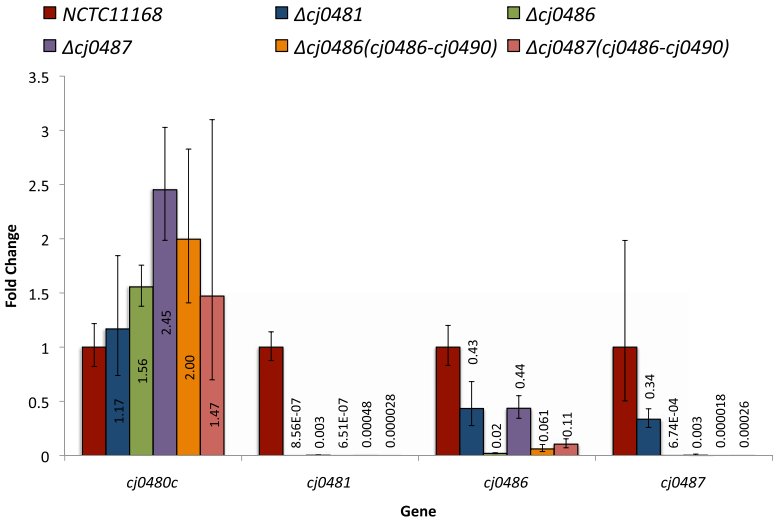

Fig. S3. Expression of the genes *cj0480c*, *cj0481*, *cj0486*, and *cj0487* as determined by real-time PCR from total RNA extracts from *C. jejuni NCTC11168*, *Δcj0481*, *Δcj0486*, *Δcj0487*, and the complemented strains: *Δcj0486+(cj0486–cj0490)* and *Δcj0487+(cj0486–cj0490).* Results are displayed as fold-change relative to the *C. jejuni* NCTC11168 wild-type.

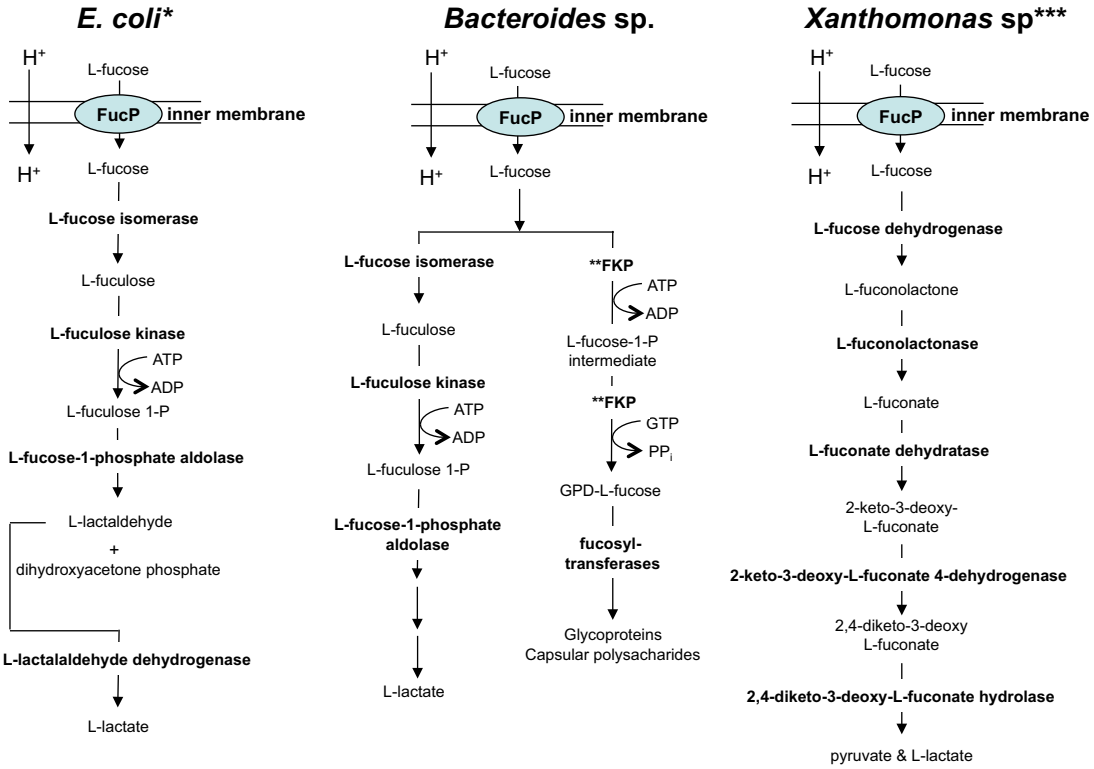

Fig. S4. General pathways for fucose uptake and utilization in *E. coli*, *Bacteroides* sp., and *Xanthomonas* sp. are depicted. FucP, fucose proton symporter of the major facilitator family; FucK, fuculose kinase. Biosynthetic proteins are in bold; *adapted from Baldomà and Aguilar (1), **FKP: bifunctional L-fucokinase/GDP-fucose pyrophosphorylase (2, 3); ***modified from Yew et al. (4)

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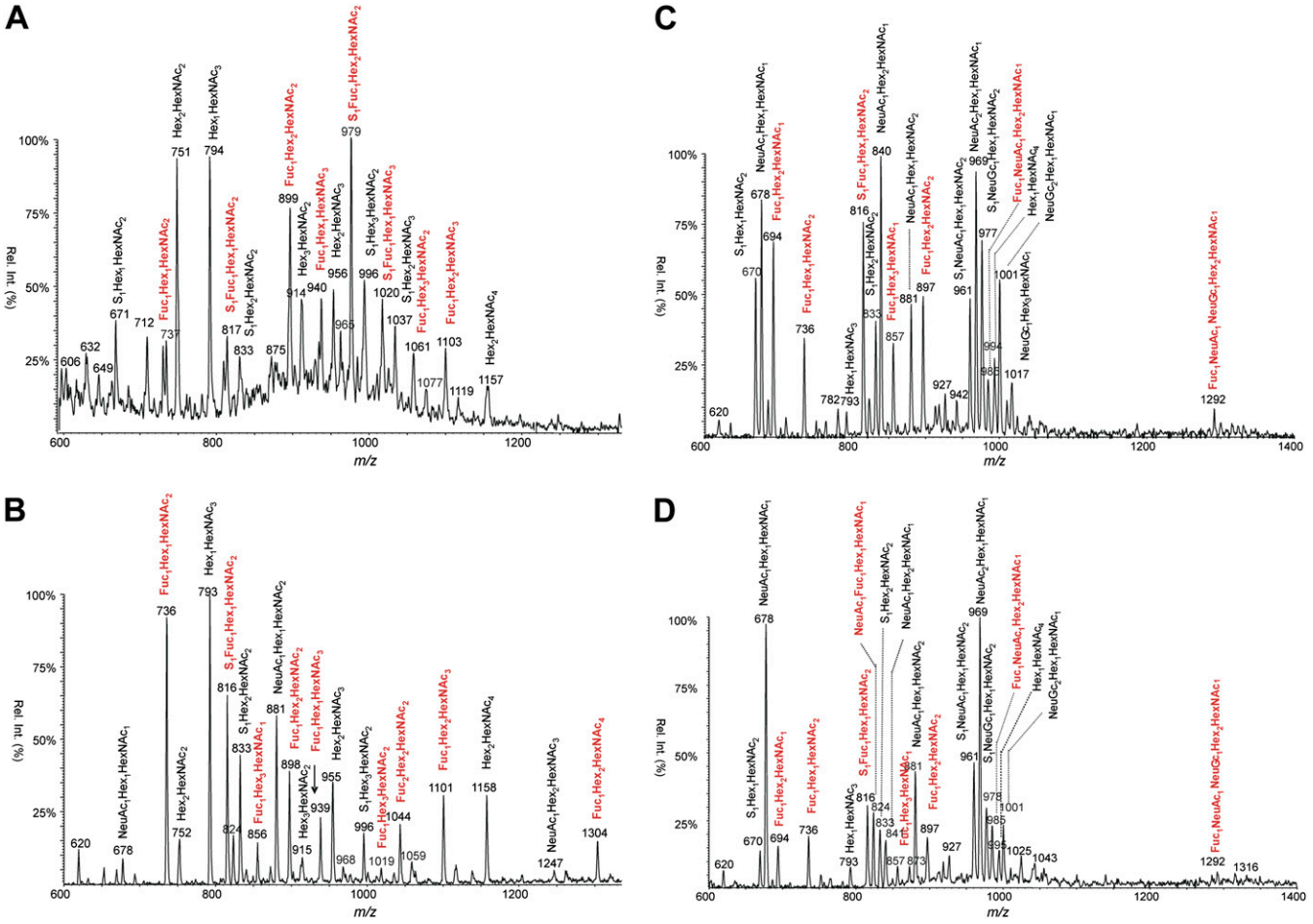

Fig. S5. Precursor ion mass spectra of ion at *m/z* 224 (positive ion detection mode): (*A*) *O*-glycans released from chicken cecal mucin; (*B*) *O*-glycans released from pig gastric mucin (purchased from Sigma); (*C*) *O*-glycans released from piglet ileum; (*D*) *O*-glycans released from piglet cecum.

Table S1. Complete list of genes identified to be differentially expressed in *C. jejuni* NCTC 11168 when grown in minimal media in the presence of 25 μM L-fucose compared with growth in media lacking L-fucose: Fucose microarray

Gene number	Gene name	Fold-change $\log_2$	Bayes.p	Genome annotation
Up-regulated				
cj0481	***dapA***	4.36611	3.05E-11	Putative dihydrodipicolinate synthase
cj0483	***uxaA***	4.36413792	4.40E-13	Putative altronate hydrolase
cj0484	***cj0484***	3.74781682	2.32E-11	Putative MFS (Major Facilitator Superfamily) transport protein
cj0486	***cj0486***	3.69370417	1.97E-11	Putative sugar transporter
cj0485	***cj0485***	3.38307458	4.27E-11	Putative oxidoreductase
cj0487	***cj0487***	3.14743458	4.22E-10	Putative amidohydrolase
cj0490	***ald***	2.99369783	6.14E-10	Putative aldehyde dehydrogenase
cj1503c	*putA*	2.65269167	2.78E-11	Putative proline dehydrogenase
cj1502c	*putP*	2.535035	1.03E-10	Putative sodium/proline symporter
cj0917c	*cstA*	2.41062708	2.50E-09	Putative integral membrane protein
cj1537c	*acs*	2.31594208	3.43E-10	Acetyl-CoA synthetase
cj0488	***cj0488***	2.01624375	3.53E-08	Conserved hypothetical protein
cj0482	***uxaA***	1.91812375	1.82E-09	Putative altronate hydrolase
cj0921c	*peb1A*	1.87636	4.81E-08	Aspartate/glutamate-binding ABC transporter protein
cj0919c	*cj0919c*	1.80535083	8.53E-10	Putative ABC-type amino acid transporter permease protein
cj1682c	*gltA*	1.70775458	1.81E-09	Citrate synthase
cj0922c	*pebC*	1.56586042	1.42E-08	ABC-type amino acid transporter ATP-binding protein
cj0920c	*cj0920c*	1.53398875	3.99E-08	Putative ABC-type amino acid transporter permease protein
cj1541	*cj1541*	1.50247792	3.13E-11	Conserved hypothetical protein
cj0021c	*cj0021c*	1.43879667	3.69E-09	Putative fumarylacetoacetate (FAA) hydrolase family protein
cj1158c	*cj1158c*	1.430605	1.42E-05	Small hydrophobic protein
cj0489	***ald***	1.41285565	4.90E-07	Putative aldehyde dehydrogenase
cj0074c	*cj0074c*	1.3800625	2.01E-10	Putative iron-sulfur protein
cj0075c	*cj0075c*	1.3614325	1.57E-09	Putative oxidoreductase iron-sulfur subunit
cj0437	*sdhA*	1.35764458	1.42E-06	Succinate dehydrogenase flavoprotein subunit
cj0438	*sdhB*	1.214365	8.08E-06	Putative succinate dehydrogenase iron-sulfur protein
cj1619	*kgtP*	1.21231	2.21E-05	α-Ketoglutarate permease
cj0073c	*cj0073c*	1.18393542	8.59E-08	Conserved hypothetical protein
cj0835c	*acnB*	1.16229458	1.85E-10	Aconitate hydratase
cj0833c	*cj0833c*	1.11848833	1.83E-09	Putative oxidoreductase
cj0689	*ackA*	1.09401826	5.11E-09	Acetate kinase
cj1681c	*cysQ*	1.04634458	8.37E-11	CysQ protein homolog
cj1192	*dctA*	1.03423458	1.09E-09	Putative C4-dicarboxylate transport protein
cj0533	*cj0553*	1.0199275	5.59E-09	Putative integral membrane protein
cj0832c	*cj0832c*	0.977855	4.56E-13	Putative Na^+/H^+ antiporter family protein
cj0853c	*hemL*	0.96895417	3.07E-09	Glutamate-1-semialdehyde 2,1-aminomutase
cj0688	*pta*	0.96819375	2.66E-08	Putative phosphate acetyltransferase
cj0522	*cj0552*	0.95287417	1.45E-08	Putative membrane protein
cj1625c	*sdaC*	0.92356917	3.00E-10	Amino acid transporter
cj0439	*sdhC*	0.91213167	0.00011757	Putative succinate dehydrogenase subunit C
cj0850c	*cj0850c*	0.90949087	5.03E-12	Putative MFS (Major Facilitator Superfamily) transport protein
cj1388	*cj1388*	0.89035625	1.19E-05	Putative endoribonuclease L-PSP
cj0076c	*lctP*	0.88469348	1.58E-08	L-Lactate permease
cj1542	*cj1542*	0.87182792	9.77E-08	Putative allophanate hydrolase subunit 1
cj0427	*cj0427*	0.84059	4.65E-09	Hypothetical protein
cj0203	*cj0203*	0.82591125	1.92E-12	Putative citrate transporter
cj0903c	*cj0903c*	0.80671125	1.33E-06	Putative amino acid transport protein
cj0982c	*cjaA*	0.79958792	1.36E-11	Putative amino acid transporter periplasmic solute-binding protein
cj0762c	*aspB*	0.78819083	1.35E-06	Aspartate aminotransferase
cj0393c	*mqo*	0.78807833	4.02E-09	Putative malate:quinone oxidoreductase
cj0834c	*cj0834c*	0.78551348	5.66E-08	Ankyrin repeat-containing putative periplasmic protein
cj1543	*cj1543*	0.76831917	3.90E-10	Putative allophanate hydrolase subunit 2
cj1624c	*sdaA*	0.72731542	1.28E-07	L-Serine dehydratase
cj1389	*cj1389*	0.71259182	7.42E-07	Pseudogene (putative C4-dicarboxylate anaerobic carrier)
cj0534	*sucD*	0.70539083	2.65E-11	Succinyl-coA synthetase α chain
cj0554	*cj0554*	0.69407667	2.00E-06	Hypothetical protein
cj0533	*sucC*	0.67438458	1.57E-10	Succinyl-coA synthetase β chain
cj1200	*cj1200*	0.64165539	2.86E-05	Putative NLPA family lipoprotein
cj0531	*icd*	0.63176625	4.58E-09	Isocitrate dehydrogenase
cj1719c	*leuA*	0.62830458	1.63E-09	2-Isopropylmalate synthase
cj0373	*cj0373*	0.61054458	2.23E-10	Putative D-2-hydroxyacid dehydrogenase

Table S1. Cont.

Gene number	Gene name	Fold-change $\log_2$	Bayes.p	Genome annotation
cj1008c	*aroB*	0.60434	1.59E-09	3-Dehydroquinate synthase
cj0555	*cj0555*	0.60296727	2.30E-09	Putative dicarboxylate carrier protein MatC
cj0069	*cj0069*	0.5911	7.86E-08	Hypothetical protein
cj0981c	*cjaB*	0.58550875	2.96E-07	Putative MFS (Major Facilitator Superfamily) transport protein
cj1717c	*leuC*	0.58027391	1.42E-08	3-Isopropylmalate dehydratase large subunit
cj0374	*cj0374*	0.5777755	6.82E-07	Conserved hypothetical protein
cj0987c	*cj0987c*	0.56922083	1.36E-07	Putative MFS (Major Facilitator Superfamily) transport protein
cj0348	*trpB*	0.56829625	3.04E-06	Tryptophan synthase beta chain
cj0536	*oorA*	0.55900417	1.46E-11	OORA subunit of 2-oxoglutarate:acceptor oxidoreductase
cj0346	*trpD*	0.53065333	6.20E-05	Anthranilate synthase component II
cj0374	*cj0374*	0.52706261	2.98E-08	Conserved hypothetical protein Cj0374
cj0375	*cj0375*	0.513895	6.32E-10	Putative lipoprotein
cj0532	*mdh*	0.50484125	5.74E-09	Malate dehydrogenase
Down-regulated				
cj1185c	*petB*	−0.5030075	2.42E-06	Putative ubiquinol-cytochrome C reductase cytochrome B subunit
cj0912c	*cysM*	−0.5038296	0.00012051	cCsteine synthase
cj1220	*groES*	−0.503845	4.72E-05	10 kDa chaperonin (cpn10)
cj0613	*pstS*	−0.5137573	3.20E-06	Putative periplasmic phosphate binding protein
cj1659	*p19*	−0.5246338	6.47E-08	Periplasmic protein p19
cj1688c	*secY*	−0.5303296	4.35E-06	Preprotein translocase subunit
cj1001	*rpoD*	−0.5452921	9.37E-07	RNA polymerase σ factor (σ-70)
cj0224	*argC*	−0.54543	4.95E-06	*N*-acetyl-γ-glutamyl-phosphate reductase
cj0515	*cj0515*	−0.5500692	2.24E-08	Putative periplasmic protein
cj0118	*cj0118*	−0.5565643	2.52E-05	Conserved hypothetical protein
cj0012c	*rrc*	−0.5577417	3.25E-10	Nonhaem iron protein
cj0281	*tal*	−0.5627229	9.98E-07	Putative transaldolase
cj1511c	*fdhA*	−0.5698267	8.23E-07	Putative formate dehydrogenase large subunit (Selenocysteine containing)
cj1221	*groEL*	−0.5822396	7.97E-08	60 kDa chaperonin (cpn60)
cj0082	*cydB*	−0.5890079	3.96E-05	Cytochrome bd oxidase subunit II
cj0343c	*cj0343c*	−0.6022113	8.88E-05	Putative integral membrane protein
cj0081	*cydA*	−0.6309096	4.68E-05	Cytochrome bd oxidase subunit I
cj1190c	*cetA*	−0.6329646	0.00026076	Bipartate energy taxis response protein
cj0328c	*fabH*	−0.6329863	4.43E-06	3-Oxoacyl-[acyl-carrier-protein] synthase
cj1438c	*cj1438c*	−0.6341713	4.58E-07	Putative CPS glycosyltransferase
cj1181c	*tsf*	−0.6379096	8.15E-08	Elongation factor TS
cj1184c	*petC*	−0.6417317	8.63E-09	Putative ubiquinol-cytochrome C reductase cytochrome C subunit
cj1180c	*cj1180c*	−0.6453832	2.54E-09	Putative ABC transporter ATP-binding protein
cj1514c	*cj1514c*	−0.6476025	4.48E-09	Hypothetical protein
cj0134	*thrB*	−0.6604627	2.90E-07	Putative homoserine kinase
cj1434c	*cj1434c*	−0.6673438	1.24E-07	Putative CPS glycosyltransferase
cj0475	*rplA*	−0.67948	6.65E-10	50S ribosomal protein L1
cj1474c	*ctsD*	−0.6918808	1.11E-07	Putative type II protein secretion system D protein
cj0117	*pfs*	−0.6924929	2.35E-08	5′-methylthioadenosine/S-adenosylhomocysteine nucleosidase
cj1612	*prfA*	−0.7133457	2.08E-07	Peptide chain release factor 1
cj1596	*rplQ*	−0.7141754	1.14E-10	50S ribosomal protein L17
cj0343c	*cj0343c*	−0.7166329	4.91E-05	Putative integral membrane protein
cj1500	*cj1500*	−0.7177971	3.37E-06	Putative integral membrane protein
cj0025c	*cj0025c*	−0.7422229	5.74E-06	Putative sodium:dicarboxylate family transmembrane symporter
cj0190	*cj0190c*	−0.7711905	2.60E-05	Conserved hypothetical protein
cj1189c	*cetB*	−0.7724913	6.90E-06	Bipartate energy taxis response protein
cj0264c	*cj0264c*	−0.7761913	4.05E-08	Molybdopterin containing oxidoreductase
cj0265c	*cj0265c*	−0.8130454	2.87E-09	Putative cytochrome C-type haem-binding periplasmic protein
cj0370	*rpsU*	−0.8188554	2.71E-12	30S ribosomal protein S21
cj1153	*cj1153*	−0.8466967	2.36E-11	Putative periplasmic cytochrome C
cj0779	*tpx*	−0.8684075	1.93E-06	Thiol peroxidase
cj0169	*sodB*	−0.9068563	6.42E-09	Superoxide dismutase (Fe)
cj0379c	*cj0379c*	−0.9803817	1.33E-07	Putative molybdenum containing oxidoreductase
cj0262c	*cj0262c*	−1.0401525	8.48E-11	Putative methyl-accepting chemotaxis signal transduction protein
cj1169c	*cj1169c*	−1.1581492	1.17E-08	Putative periplasmic protein
cj0239c	*cj0239c*	−1.3205179	2.18E-07	NifU protein homolog
cj0334	*ahpC*	−1.3638779	4.18E-13	Alkyl hydroperoxide reductase
cj0415	*cj0415*	−1.3721392	1.12E-06	Putative GMC oxidoreductase subunit

Table S1. Cont.

Gene number	Gene name	Fold-change $\log_2$	Bayes.p	Genome annotation
cj0240c	*iscS*	−1.3789683	4.98E-07	Cysteine desulfurase (NifS protein homolog)
cj0414	*cj0414*	−1.5476567	1.57E-07	Putative oxidoreductase subunit
cj0453	*thiC*	−1.6295863	0	Thiamin biosynthesis protein
cj0017c	*dsbI*	−1.7155813	6.61E-10	Disulphide bond formation protein
cj1170c	*omp50*	−1.8208058	1.07E-08	50 kDa outer membrane protein precursor

Displayed are the gene numbers, name, fold-change in $\log_2$, *P* value, and annotated function. Boldface indicates genes belonging to the fucose operon.

Table S2. Expression of the genes within the operon *cj0481–cj0490* in *C. jejuni* NCTC 11168 when grown in minimal media containing 2 mg/mL porcine gastric mucin compared with the control: Mucin microarray

Gene Number	Gene name	Fold-change $\log_2$	Genome annotation
cj0481	*dapA*	1.862548148	Putative dihydrodipicolinate synthase
cj0483	*uxaA*	1.39661625	Putative altronate hydrolase
cj0484	*cj0484*	1.094871923	Putative MFS (Major Facilitator Superfamily) transport protein
cj0485	*cj0485*	0.98345	Putative oxidoreductase
cj0486	*cj0486*	1.219888462	Putative sugar transporter
cj0487	*cj0487*	0.777173333	Putative amidohydrolase
cj0490	*ald*	0.51669037	Putative aldehyde dehydrogenase

Displayed are the gene numbers, name, fold change in $\log_2$, *P* value, and annotated function.

Table S3. List of primers used in this study

Primer name	Sequence
Gene Cloning	
cj0481L	CGGTACCCGGGGATCCAAAAGGAACTTTACCGGCTTTA
cj0481R	CGACTCTAGAGGATCCTTGCTTCATCAAAGCGAGTG
cj0483L	CGGTACCCGGGGATCCGGAGCAATGCCAATGTTTTT
cj0483R	CGACTCTAGAGGATCCGCTCATCACGCACTTCTTCTT
cj0487L	CGGTACCCGGGGATCCCACCTTTGGGATTTGGAAAA
cj0487R	CGACTCTAGAGGATCCCACTGGATAATTGCTCCCAAA
cj0490L	ATGGCAAGAGATGAAAGCACAC
cj0490R	CCATCAGCTCCGCCTATGC
Inverse PCR	
cj04811	GAACTAAAGGGCGCAGCATAGGTGGAGTTTTTCCAG
cj04812	GAACACCGCCGAGCAACTTGCTCTTCCACGCTCAA
cj04831	GAACTAAAGGGCGCATTTATGAATACACCAGGCAATGA
cj04832	GAACACCGCCGAGCATGCAGCACTTTCAAGCATTT
cj04871	GAACTAAAGGGCGCAGGTTTTAAATCATCTAGGAAGTCCA
cj04872	GAACACCGCCGAGCACGCTAAACAAAACAAAAGATTATGAA
cj04901	AGTGTGCAAAGATGCGGATA
cj04902	TAAAGCAGGTGCCATCTTCC
Chloramphenicol cassette	
catSE	TGCTCGGCGGTGTTCCTTTCCAAG
catAS	TGCGCCCTTTAGTTCCTAAAGGGT
Allelic replacement	
CfucP_F	CGGGATCCTGGGATGAAAACTAAGGAGTA
CfucP_R	ACGCGTCGACAAAGGTGTAGATGAGCATCAA
EfucP_F	CGGGATCCTGAACCTAAGAGGATGCTATG
EfucP_R	ACGCGTCGACTTCAGTTAGTTGCCGTTTG