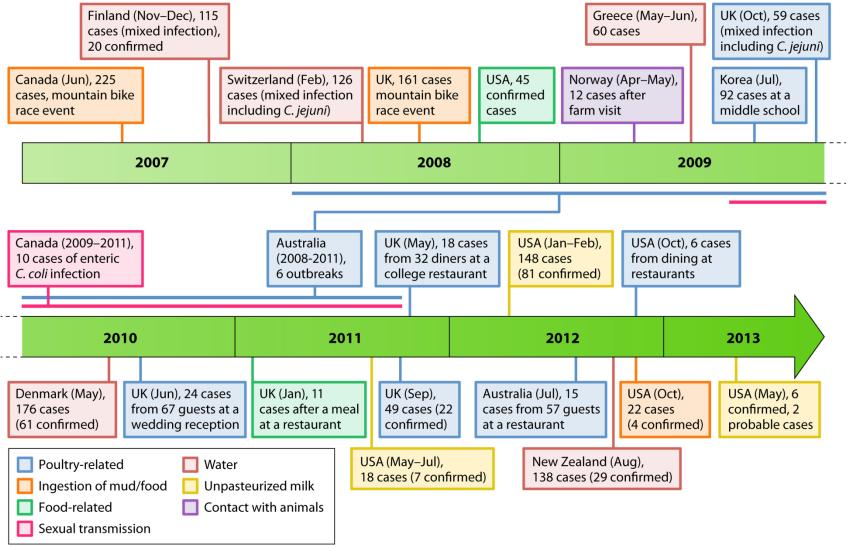




Zoonotic Campylobacter: main microbiological and pathogenic features of a very successful bug

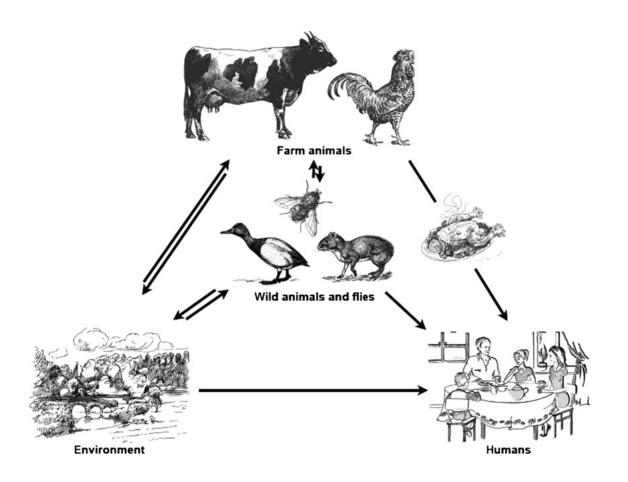
Antonia Ricci Food Safety Department Istituto Zooprofilattico Sperimentale delle Venezie



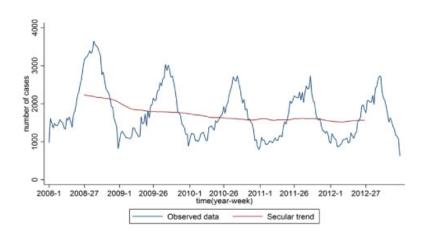




Routes of transmission for Campylobacter jejuni



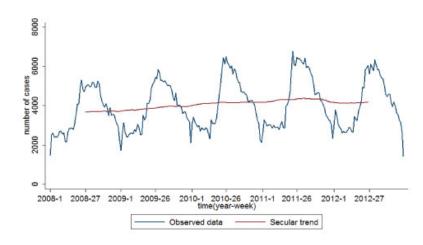
Trend in reported confirmed cases of human salmonellosis in the EU, 2008-2012



Source: 24 MSs: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Latvia, Lithuania, Luxembourg, Matta, Netherlands, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, and United Kingdom. Bulgaria and Poland are excluded as they reported only monthly data. Italy is excluded as its 2012 data were not representative.

EFSA, ECDC: EU Summary Report 2012, EFSA Journal 2014,12(2):3547

Figure CA2. Trend in reported confirmed cases of human campylobacteriosis in the EU, 2008-2012



Source: Data for EU trend 24 MSs: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Romania, Slovakia, Slovenia, Spain, Sweden, and United Kingdom. Bulgaria is excluded because only monthly data were reported and Greece and Portugal do not have surveillance systems for this disease.

EFSA, ECDC: EU Summary Report 2012, EFSA Journal 2014,12(2):3547



Despite its importance, the effective control of *Campylobacter* in the food chain and the design of disease prevention strategies are hindered by a **poor understanding** of the genetics, physiology and virulence of this organism.



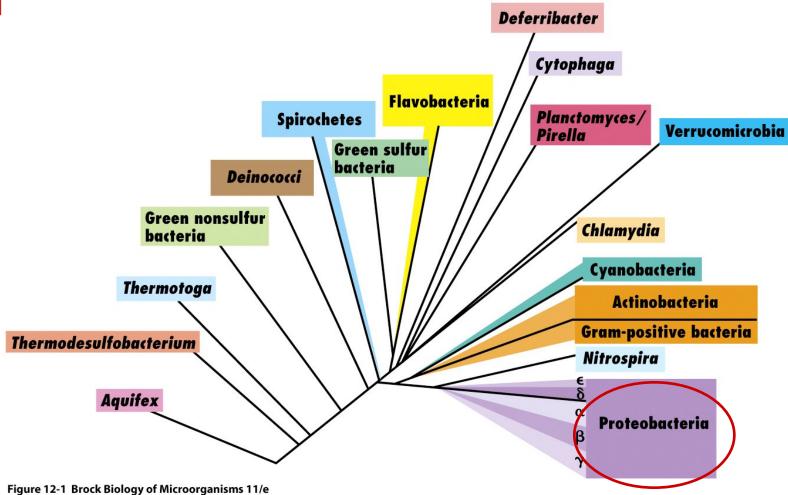


Figure 12-1 Brock Biology of Microorganisms 11/e © 2006 Pearson Prentice Hall, Inc.

The same *phylum*, different classes.....





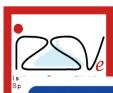


Table 12.1 Major genera of Proteobacteria^a

Subdivision	Genera	
Alpha	Acetobacter	Nitrobacter
	Agrobacterium	Paracoccus
	Alcaligenes	Rhodospirillum
	Azospirillum	Rhodopseudomonas
	Beijerinckia	Rhodobacter
	Bradyrhizobium	Rhodomicrobium
	Brucella	Rhodovulum
	Caulobacter	Rhodopila
	Ehrlichia	Rhizobium
	Gluconobacter	Rickettsia
	Hyphomicrobium	Sphingomonas
	Methylocystis	Zymomonas
Beta	Aquaspirillum	Oxalobacter
	Bordetella	Polaromonas
	Burkholderia	Ralstonia
	Chromobacterium	Rhodocyclus
	Dechloromonas	Rhodoferax
	Gallionella	Sphaerotilus
	Leptothrix	Spirillum
	Methylophilus	Thiobacillus
	Neisseria	Zoogloea
	Nitrosomonas	<u> </u>

^a This table is not meant to be inclusive but only lists some well-described genera of Proteobacteria. For a complete list of genera of Proteobacteria and genera of other lineages of *Bacteria*, see Appendix 2.

Table 12-1 part 1 Brock Biology of Microorganisms 11/e © 2006 Pearson Prentice Hall, Inc.

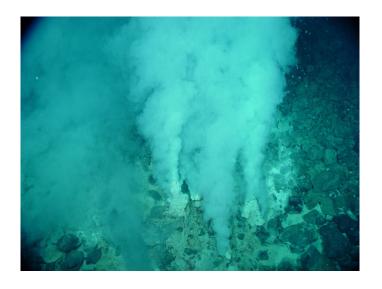
Table 12.1 Major genera of Proteobacteria^a

Subdivision	Genera	
Gamma	Acetobacter	Photobacterium
	Acinetobacter	Pseudomonas
	Azotobacter	Methylococcus
	Chromatium	Methylobacter
	Escherichia	Nitrosococcus
	Ectothiorhodospira	Nitrococcus
	Erwinia	Thermochromatium
	Francisella	Thiomicrospira
	Halomonas	Thiospirillum and
	Halorhodospira	other purple
	Halothiobacillus	sulfur bacteria
	Legionella	Salmonella and other
	Leucothrix	enteric bacteria
	Methylomonas	Vibrio
	Oceanospirillum	Xanthomonas
Delta	Acinetobacter	Geobacter
	Aeromonas	Halomonas
	Bdellovibrio	Moraxella
	Desulfuromonas	Myxococcus and other
	Desulfovibrio and most	myxobacteria
	other sulfate-	Pelobacter
	roducing bacteria	Syntrophobacter
	Francisella	,
Epsilon	Campylobacter	Thiovulum
	Helicobacter	Wolinella
^a This table is not r	neant to be inclusive but only l	lists some well-described

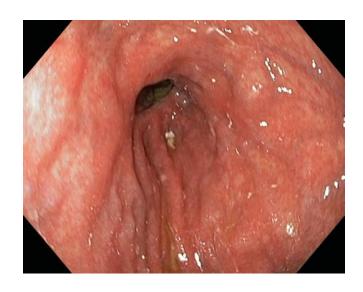
^a This table is not meant to be inclusive but only lists some well-described genera of Proteobacteria. For a complete list of genera of Proteobacteria and genera of other lineages of *Bacteria*, see Appendix 2.

Table 12-1 part 2 Brock Biology of Microorganisms 11/e © 2006 Pearson Prentice Hall, Inc.

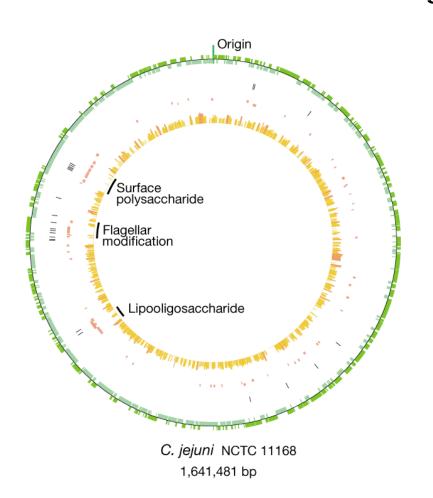
Share the capacity of surviving in hostile environments.....











Some unique features:

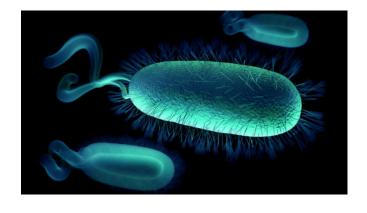
- □Almost complete lack of repetitive DNA sequences (only four);
- ■No functional inserted sequences or phage-related sequences;
- □Little organization of genes into operons or clusters (apart from the two ribosomal protein operons and gene clusters involved in LOS biosynthesis, EP biosynthesis and flagellar modification);
- □Broad set of regulatory systems to adapt to varying environmental conditions;
- □ Presence of high rate of hypervariable sequences commonly found in genes encoding the biosynthesis or modification of surface structures

Parkhill J. et al. Nature (2000) 403:665-668



Motility

Campylobacter demonstrates roughly twice the velocity of rod-shaped bacteria (Salmonella) in substances of low viscosity, and can retain this velocity as viscosity increases 40 to 80 fold.

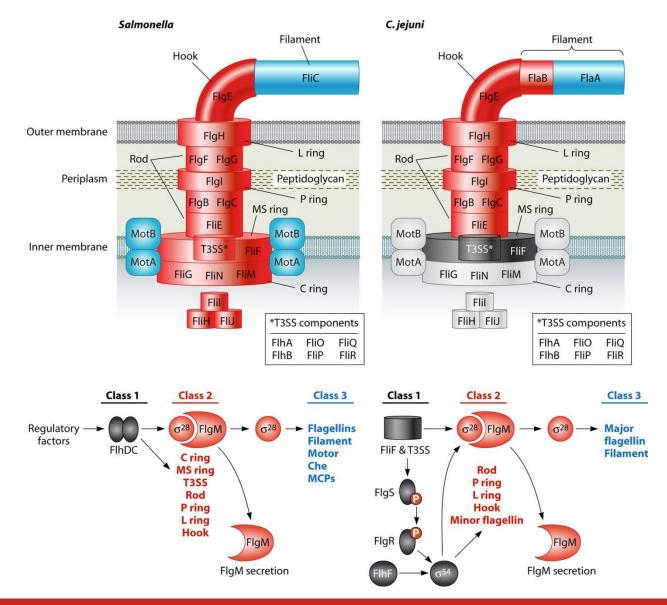


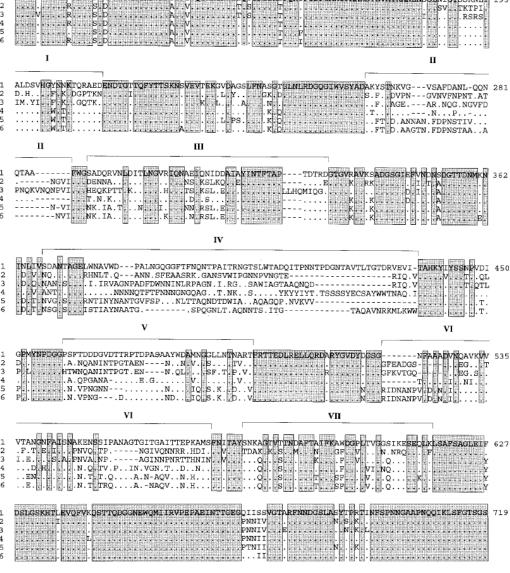
50 m/s

1,74 m/s









NDGLVSSNSASTLTGOA

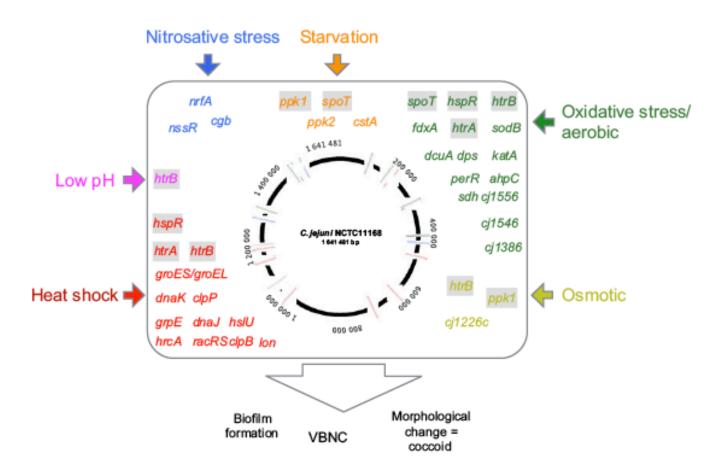
The hook protein

- ☐ Is larger than that of any other bacterial hook known so far (molecular mass in the range of 90 to 94 kDa);
- ☐The large central region of the hook protein exhibits hypervariability among strains of one species and even of one 535 serotype;
 - It confers selective advantages for antigenic diversity and immune escape

Luneberg E. Journal of Bacteriology (1998) 7:3711-3714



Campylobacter jejuni responses to stresses



Bronowski C. et al., FEMS Microbiol Lett (2014) 356:8-19



DNA uptake system of *H. pylori and C. jejuni.*

One unique aspect of natural transformation in some strains of *C. jejuni* is the presence of a plasmid-based (pVir) DNA uptake system

dsDNA B2 **B9** B7 Outer membrane Periplasm/ peptidoglycan **B8** B3 Inner membrane B6 ComEC B10 **B4** ssDNA



Host susceptibility

Key factors are the local microbiota in the intestine, the status of protective processes like the physical barriers at the gastrointestinal mucosal surfaces, and the nonspecific host defense. When such inherent protective processes are overcome, specific acquired host immunity becomes critically important for the outcome of infection.

Havelaar et al., Critical Reviews in Microbiology, 2009; 35(1): 1–22



