Comparative genomics of two strains of the human pathogen *Campylobacter jejuni* reveals differences important in *Campylobacter* biology and identification.

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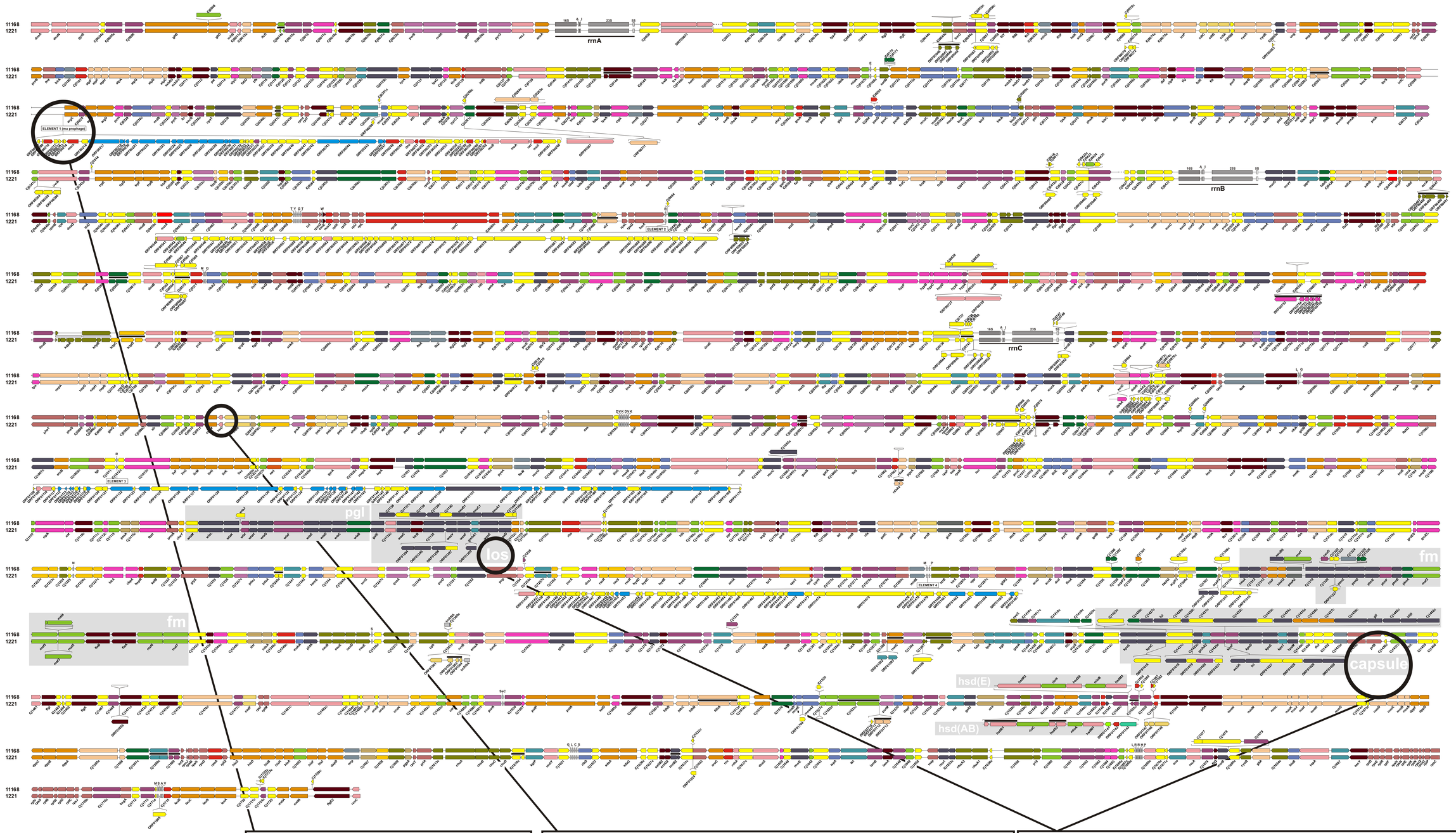
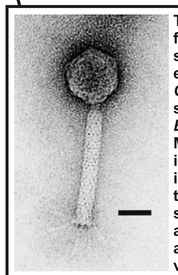
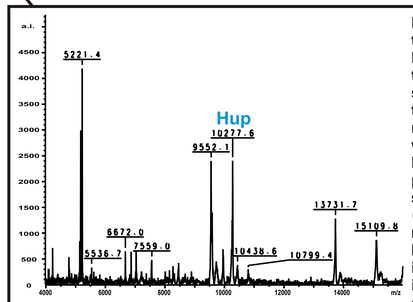


COLOR KEY

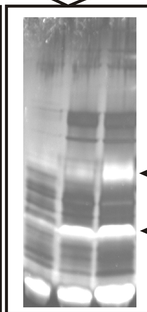
- Information storage and processing; Translation, ribosomal structure and biogenesis
- Information storage and processing; Transcription
- Information storage and processing; DNA replication, recombination and repair
- Cellular Processes; Cell division and chromosome partitioning
- Cellular Processes; Posttranslational modification, protein turnover, chaperones
- Cellular Processes; Cell envelope biogenesis, outer membrane
- Cellular Processes; Cell motility and secretion
- Cellular Processes; Inorganic ion transport and metabolism
- Cellular Processes; Signal transduction mechanisms
- Metabolism; Energy production and conversion
- Metabolism; Carbohydrate transport and metabolism
- Metabolism; Amino acid transport and metabolism
- Metabolism; Nucleotide transport and metabolism
- Metabolism; Coenzyme metabolism
- Metabolism; Lipid metabolism
- Metabolism; Secondary metabolites biosynthesis, transport and catabolism
- Plasmid/Prophage
- Toxin production, antibiotic resistance, and pathogenesis
- Poorly characterized; General function prediction only
- Poorly characterized; Function unknown
- Unassigned

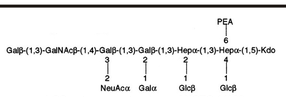


The *C. jejuni* strain RM1221 contains four elements that are not found in strain NCTC 11168. The first of these elements (circled) represents a novel *Campylobacter* mu (mutator) phage similar to the mu phage of *Escherichia coli* (pictured, left). Mutator phage DNA inserts randomly into the bacterial genome and often inactivates bacterial genes. Several toxins involved in virulence (e.g. shiga (O157:H7) and diphtheria toxin) are present on phage. Experiments are underway to determine if virulence genes are present on these unique elements.



Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) is being tested as a rapid and accurate technique for fingerprinting bacteria for species and/or strain differentiation. A typical spectrum (pictured left for RM1221) reveals multiple, soluble, low molecular-weight proteins. One such protein is the DNA-binding protein Hup. While the Hup proteins of RM1221 and NCTC 11168 have the same mass, Hup proteins from different *Campylobacter* species have different masses. Therefore, Hup is a candidate biomarker for species/subspecies identification. Other proteins are being investigated as potential biomarkers for differentiation at the strain level.





LOS outer core structure of NCTC 11168

The LOS, capsule, and flagellar modification (FM) loci are involved in the biosynthesis and modification of *Campylobacter* surface structures. The capsule region is primarily responsible for the *Campylobacter* heat stable (Penner) serotype while the flagellar modification locus is primarily responsible for the heat labile (Lior) serotype. Certain LOS structures have been implicated in Guillain-Barre syndrome, a potentially fatal autoimmune disorder of the human nervous system. 48 Penner serotypes have been described in *C. jejuni*. NCTC 11168 and RM1221 have different serotypes, an obvious reflection of their different genetic makeup at these 3 loci.