

VIRUSMICROBES2010/173

Genome of *Campylobacter coli* bacteriophage phiCcoIBB_35

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Campylobacter is recognized worldwide as the major etiologic agent in human diarrhoeal disease, being *Campylobacter jejuni* and *Campylobacter coli* the most prevalent species. Bacteriophages are natural predators of bacteria, ubiquitous in the environment, self-limiting, self-replicating and with a high host-specificity. These make them potentially an important biocontrol agent of foodborne diseases. There are only few reports on *Campylobacter* bacteriophages, probably due to the fastidious nature of the host *Campylobacter* which makes the isolation of these phages challenging. Moreover the refractory nature to restriction enzymes digestion of their DNA causes difficulties in characterizing *Campylobacter* phage genomes by common methods such as restriction fragment length polymorphism. In a previous study *Campylobacter* phages were isolated from poultry intestinal contents (Carvalho et al., 2010) and one of these phages (phage phiCcoIBB_35) was selected to be genetically sequenced as it showed broad lytic spectra against food and clinical *Campylobacter coli* and *Campylobacter jejuni* strains. The PFGE analysis indicates that the genome of phage phiCcoIBB_35 is approximately 204kb. However due to the fact that DNA preparations appeared to contain substances that inhibit Taq and KpnI enzymes, the DNA sequence data consists of five DNA contigs in a total of 172 kb that were not possible to be aligned. Annotation indicates that most of the ORFs are unique and that homology exists with members of the *Teequatovirinae* namely for all T4 tail proteins, one head protein (gp23), neck protein (gp20); and baseplate proteins (gp6, gp25, gp48). Moreover homologs were found to T4 proteins involved in morphogenesis, nucleotide metabolism, transcription, DNA replication and recombination. Unique genes involved in the carbohydrate metabolism, pathogenesis and amino acid metabolism were also annotated. Several incidences of gene duplications, split genes with intein and introns and "insertion-like sequences" were present. To our knowledge this study represents the first report of the genomic sequence of a lytic *Campylobacter* phage and therefore is of extreme importance for further comparisons with other phage sequences.

Number of words in abstract: 318

Keywords: Genome - *Campylobacter*

Technical area: Session A: Genomics and Molecular Biology

Special session: Not specified

Presentation: Poster presentation preferred

Special equipment: No special equipment