

Characterization of *Campylobacter* sp. bacteriophages

Carla Carvalho¹, Silvio Santos¹, Erika Langohr² Andrew Kropinski²; Desislava Raytcheva³; Cammie Haase-Pettingell³, Jonathan King³; Joana Azeredo¹

¹IBB-Institute for Biotechnology and Bioengineering, Centre for Biological Engineering, Universidade do Minho, Campus de Gualtar 4710-057, Braga, Portugal; E-mail: carlacarvalho@deb.uminho.pt

² Public Health Agency of Canada, Laboratory for Foodborne Zoonoses, 110 Stone Road West, Guelph, ON, N1G 3W4, Canada

³ Department of Biology, MIT, Cambridge, Massachusetts, USA

Campylobacter coli and *Campylobacter jejuni* are commensally inhabitants of chicken's gut and are the major sources of foodborne infections in humans. 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 the present study 47 *Campylobacter* phages were isolated from poultry intestines. The phages were screened against a panel of food and clinical isolates of *Campylobacter coli* and *Campylobacter jejuni*. Three phages (phiCcoIBB_12; phiCcoIBB_35; phiCcoIBB_37) showed the broadest lytic spectra and therefore were further characterized. These 3 phages were investigated by transmission electron microscopy (TEM), pulsed-field gel electrophoresis, restriction endonuclease analysis and by SDS-PAGE. The three phages had icosahedral heads and long contractile tails and were classified as members of the family Myoviridae. Restriction endonuclease analysis demonstrated that DNA from the phages was refractory to digestion by a number of restriction enzymes. The three phages showed similar genome sizes and a similar protein profile which indicates that although they have different lytic profiles and different latent period/burst sizes they must be very similar. The genome of one of the three phages (vB_CcoM-IBB35) was sequenced and the results showed that where homology exists it is primarily to T4-like phages. Several incidences of gene duplications, split genes with intein and introns were present. Unique genes involved in the carbohydrate metabolism, pathogenesis and amino acid metabolism were annotated. Throughout the experiments some difficulties were faced when working with the DNA of *Campylobacter* phages, namely the DNA preparations appeared to contain substances that inhibit Taq and φ29 enzymes. Investigation of the structural proteins and host range differences among phages are continuing.