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GENOME ANNOUNCEMENT

The Complete Genome Sequence of Bacteriophage CP21 Reveals Modular Shuffling in *Campylobacter* Group II Phages

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***Campylobacter* group II phages described so far share a high degree of sequence similarity. We report the 182,833-bp genomic sequence of the closely related group II phage CP21 and show that it has a completely different genomic organization. As in other group II phages, the CP21 genome is composed of large modules separated by long DNA repeat regions which obviously trigger recombination and modular shuffling.**

Campylobacter is one of the most important food-borne pathogens. Infections are caused mainly by the consumption of undercooked poultry (7). Application of bacteriophages is a promising tool to control *Campylobacter* (1, 3, 6, 9), though the genomes of the phages have to be stable and free from critical genes. Up to now, five *Campylobacter* phages have been characterized (2, 4, 5, 8), and three of them (CP220, CPt10, and vB_CcoM-IBB_35) belong to the closely related group II phages (genome size, ca. 175 kb) that show some relationship to T4-type phages.

Here we report the complete nucleotide sequence (182,833 bp) of phage CP21, isolated from an organic farm in Berlin, Germany. Like other group II phages, CP21 is a myovirus infecting *Campylobacter jejuni* and *Campylobacter coli* strains. The phage was propagated and purified as previously described (4). Whole-genome sequencing was performed with the Roche 454 genome sequencer FLX Titanium system. Assembling of reads (Newbler Assembler v2.6) yielded contigs with a >30-fold sequence coverage. Gaps were closed by PCR and Sanger sequencing.

We identified 259 possible open reading frames (ORFs) on the linear, circularly permuted CP21 genome. For 111 ORFs (43%), functional assignments could be made. Most (85%) of the predicted CP21 products are 80 to 100% identical to proteins of CP220, CPt10, and vB_CcoM-IBB_35. Moreover, typical for group II phages, the CP21 genome contains genes for tRNAs (Pro, Thr), homing endonucleases, transposases, and radical *S*-adenosylmethionine proteins. However, the CP21 genomic organization is divergent. The genome consists of four modules (A to D, 28 to 56 kb) separated by long DNA repeat regions (RR1 to RR4, 1.0 to 2.9 kb) that comprise multiple copies of a core repeat unit that shows only a few sequence polymorphisms. Three regions (RR1, RR2, and RR4) contain inverted repeats, and one (RR3) contains direct repeats. Notably, region RR4 encloses five CP21 ORFs (255 to 259), while ORF 187, probably encoding a head completion protein, is embedded in RR3. CP220 and CPt10 possess very similar modules and repeat regions and an identical core repeat unit, but the order (B, D, A, C) and orientation (B and C are reversed in CP220/CPt10) of the modules are different from those in CP21. As a result, CP21 and CP220/CPt10 exhibit coding sequence (CDS) strand bias values of 43% and 89%, respectively. In addition, unlike CP21, CP220 and CPt10 contain two inverted and two direct repeat regions. We propose the repeat regions to be substrates for recombination, causing extensive genomic rearrangements. This speculation is backed by the finding that in CP21 and CP220/CPt10, the repeat region containing the head completion protein gene is flanked by different modules. Thus, the related repeat regions may trigger both intragenomic and intergenomic rearrangements. It is conceivable that transposases encoded by the phages are involved in this modular shuffling. Interestingly, the five vB_CcoM-IBB_35 contigs which could not be joined (2) correspond well with the described modules. We suspect that in vB_CcoM-IBB_35, the contigs are similarly linked by long DNA repetitions impeding DNA sequence determination.

Nucleotide sequence accession number. The genome sequence of CP21 is available in GenBank under accession number HE815464.

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