



Molecular Biology of Vibrio cholerae Bacteriophage CP-T1
and its Host Interactions

Angelo Guidolin, B.Sc. (Hons.) (Adelaide)
Department of Microbiology and Immunology
The University of Adelaide

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Abstract

Bacteriophage CP-T1 exhibits several interesting properties in its relationship with its host, Vibrio cholerae. The aim of this project was to study this bacteriophage at the molecular level in order to characterize these features, which would explain the observed properties of CP-T1, and to subsequently utilize such features for manipulations within the host bacterium. A detailed examination of the viral genome has been undertaken in order to facilitate these goals.

Preliminary studies on the phage particle revealed that CP-T1 consists of a polyhedral head connected to a contractile tail possessing a baseplate structure with spikes or tail fibres.

The viral nucleic acid consists of a single, linear, double-stranded DNA molecule which is both terminally redundant, and partially circularly permuted. A physical map of the phage genome has been constructed for the restriction endonucleases HindIII, EcoRI, PstI, BamHI, SstI and XbaI. Restriction patterns of CP-T1 DNA were consistent with the viral chromosome being terminally redundant and circularly permuted.

Approximately 30% of the CP-T1 genome has been cloned into the plasmid vector pBR322, and these clones cover several regions of the genome. The repeated inability to clone particular portions of the CP-T1 chromosome, and also the high level of deletions generated in some cloning experiments suggests that some regions of the viral genome appear to be lethal in Escherichia coli K-12. Phage encoded