LITERARY REVIEW

Bacteriophages

Bacteriophages are ubiquitous in nature and are known to proliferate wherever their bacterial hosts exist (Hendrix et al. 1999). Virion particles can exist independently outside the host, however all phages are obligate intracellular parasites and need their host to propagate (Jensen et al. 1998). Several phages are highly specific to host cell surface receptors and any slight changes in structure results in little or no interaction between the phage and its host. Therefore, many phage typing schemes for the identification of bacterial species or subspecies are based on this specificity (Welkos et al. 1974).

Bacteriophages are found in almost all environments on Earth, from the depths of the ocean to hot springs, and can be isolated from almost any material that will support bacteria (Dabrowska et al. 2005). There is evidence that the diversity of bacteriophage is about an order of magnitude higher than that of bacteria (Weinbauer and Rassoulzadegan 2004) which has implications in the classification of bacteriophage.

Bacteriophages discovered early by Frederick W. Twort and Felix d’Herelle each one independent. However there has been considerable controversy with regards to who actually discovered the bacterial viruses first. In 1896, British bacteriologist Ernest Hankin described his observations with regards to the presence of antibacterial activity against Vibrio cholerae in the Jumna and Ganges rivers of India. He proposed that an unidentified chemical substance was responsible for the decline in the spread of cholera. A few years later, other researchers made similar observations although they did not investigate their findings further (Sulakvelidze et al. 2001). Nearly 20 years after Hankin’s report, Frederick W. Twort reported on a phenomenon referred to as the ‘glassy transformation’ while working with Vaccinia virus which had been contaminated micrococi. He speculated on the possibility that he had come across an microscopic virus and concluded that the glassy transformation was caused by an infectious agent that killed bacteria and multiplied itself in the process (tuckworth 1976). In 1917, Felix d’Herelle independently discovered ‘ultra
viruses’ that resulted in the death of bacteria (Summers 2001). He proposed the name ‘bacteriophage’ from ‘bacteria’ and ‘phagein’ (Greek word for to eat or devour) therefore implying that bacteriophages ‘eat’ bacteria. D’Herelle believed that a phage was an obligate parasite which is particulate, invisible, filterable, and self-reproducing in nature (Stent 1963).

Structure of *Salmonella*’s Bacteriophage

**Capsid**

The capsid is icosahedral in shape, with rare elongated variations. It appears smooth under electron microscopy and ranges in diameter from 34 to 160nm with a majority at 60nm. Capsomers (the morphological subunits) are also present (Ackermann 2003; Bradley, 1967). The family Myoviridae are generally larger than Podoviridae and Siphoviridae families (Ackermann 1998).

**Tail**

The tail is structured of a hollow tube of fixed length and width, built of packed rows of subunits and generally has a six-fold symmetry (Ackermann 1998). Members of the family Siphoviridae have long non-contractile, flexible tails, the family Podoviridae have short variants on this, while the family Myoviridae have long, rigid, contractile tails (Ackermann *et al.* 1992). The family Myoviridae tails consist of a tail tube surrounded by a sheath, separated from the head by a neck. They are of sixfold symmetry, with subunits arranged in helix format. On contraction, these subunits slide over each other, forming a short cylinder (Ackermann 1998). Tail lengths can vary widely, but are typically conserved within a species. A ruler protein has been identified in some bacteriophage and this acts as a tape-measure around which tail tube monomers polymerize. Alterations to the ruler protein will alter the length of the tail tube (Katsura and Hendrix 1984).
Other Structures

There is a small disk located inside the head at the site of tail attachment which is known as the connector. The connector holds the head and tail together and has functions in head assembly and DNA encapsidation. Tailed bacteriophage can also have base plates, tail spikes and tail fibres, though the number and shape of these can vary (Ackermann 1998).

Genomic Structure

Genomes of Caudovirales consist of linear double stranded (ds) DNA. They range from 17kb to in excess of 700kb in length. Some genomes contain cohesive (cos) sites near end allowing circularisation of the genome after infection. Packaging of DNA can be either of a single genome, or by a headful mechanism, where the genome is continually copied into the capsid until it is full (Streisinger et al., 1967). DNA may be concatemeric (head-to-tail repeats of a sequence) or unit length prior to packaging with concatemeric DNA formed from recombination between linear DNAs or rolling circle replication. Cleavage of concatemeric DNA for packaging can occur at; a) unique sites resulting in blunt mini or cos ends with packaging starting and finishing at a cos site, b) pac sites (sequences recognised by terminase complex) to produce DNA molecules with limited circular permutation and terminal redundancy (excess coding DNA at the terminal end) and where packaging starts at the pac site and continues until the head is full or c) random sites to produce circularly permuted, terminally redundant DNA (Ackermann, 1998; Ackermann 2003; Maniloff and Ackermann 1998).

From comparisons of bacteriophage genomes, it is apparent that bacteriophage genomes have a mosaic nature, with gene order not conserved between species (Chopin et al. 2001; Hertveldt et al. 2005). The following observations of gene order can be made. Genes with related function generally cluster together, though non-structural gene order does not follow any general pattern. Structural genes are generally separate from other genes and, of these head genes precede tail genes (Casjens 2003).