tical. Hershey and Chase concluded their paper by saying "the sulfur-containing protein has no function in phage multiplication, and the DNA has some function"[2]. Talk about an understatement. More bons mots from and about Hershey can be found in "*We can sleep later: Alfred D. Hershey and the origins of molecular biology*" which is reviewed on page 18 of this issue. *Boyana Konforti*

1. Luria, S.E. & Delbrück, M. *Genetics* **28**, 491–511 (1943).
2. Hershey, A.D. & Chase, M. *J. Gen. Physiol*. **36**, 39–56 (1952).
3. Avery, O.T., MacLeod, C.M. & McCarty, M. *J. Exp. Med*. **79**, 137–156 (1944).

A DNA wormhole

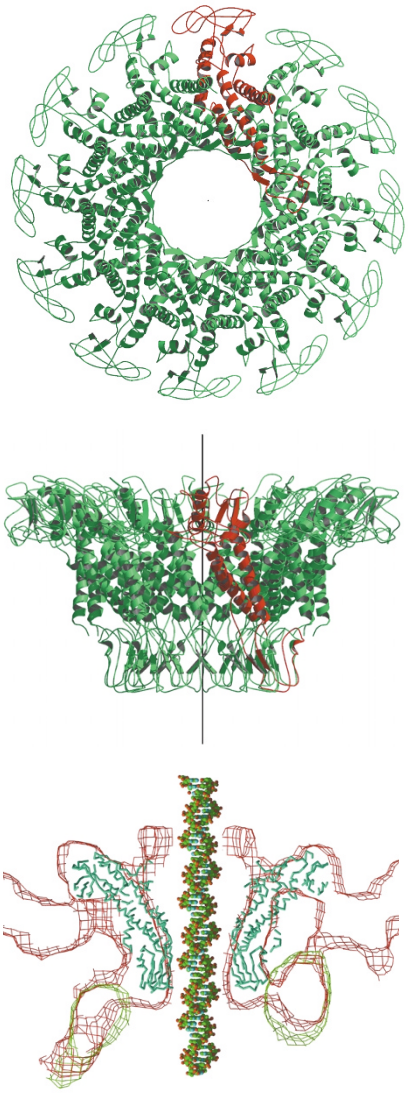
The bacteriophage ϕ29 is a virus that infects the bacterium *Bacillus subtilis*. The mature ϕ29 contains a head region that encloses its genome and a tail region that contacts the cell surface to initiate the infectious cycle. In the late stage of the maturation process from which functional phage particles emerge, the phage genome — a linear double-stranded DNA of ~19,000 base pairs — is packaged into a preassembled empty head (called the prohead). This process requires condensing the viral genome, which would span ~6,400 Å if it were completely extended, into the phage head, which is only ~500 Å in length. How the phage performs this remarkable task is not yet fully understood.

At one end of the phage head is a small opening through which the viral genome enters and exits. A protein complex called the 'connector' — so named because the tail of the phage is connected to the head through this complex — sits at the opening and participates in the DNA packaging process. To understand the structural basis of how the connector regulates DNA packaging, Simpson *et al.* (*Nature*, **408**, 745–750; 2000) have determined its high resolution structure.

The connector complex consists of 12 identical subunits (top and middle panels, one monomer is colored red to illustrate how the subunits are assembled in the complex). The overall shape of the complex is like a bottle stopper (side view; middle panel) with a central channel (top view; top panel). The narrowest part of the channel is ~36 Å in diameter; a double stranded DNA could easily pass through the channel without any steric problems.

To characterize how the connector fits into the phage head, Simpson *et al.* generated a three-dimensional reconstruction of the prohead from cryo-electron microscopy data and then fit the crystal structure into the electron density. The result shows that the narrow part of the connector protrudes outside of the viral shell (bottom panel, a thin section across the center of the prohead along the axis of the connector central channel is shown; the red mesh wire represents the electron density from the prohead and the DNA is modeled in the superposition for illustration purposes). This region of the connector interacts with a phage-encoded RNA (marked by green mesh wire) and possibly a viral ATPase (not present in this reconstruction), both of which had been shown to be important for DNA packaging.

With the translocating DNA as the movable central shaft, the connector, the viral RNA and ATPase appear to constitute a 'motor', with the viral ATPase powering conformational changes in the connector complex. The energy of ATP hydrolysis is converted into a translational motion of DNA. This study thus provides a glimpse of the initial event in the DNA packaging process of bacteriophage ϕ29. *Hwa-ping Feng*



Adapted from Simpson *et al.*