Electron Cryomicroscopy of Epsilon 15 Phage

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We have used a JEM3000SFF liquid helium electron microscope to record images of Epsilon 15 phage which infects Salmonella anatum. Applying the icosahedral reconstruction, the fold of the capsid protein is derived from the subnanometer resolution density map and found to be homologous to the capsid proteins of HK97 and P22 phage. Using a novel reconstruction algorithm without imposing any symmetry, we are able to determine the complete structure of this phage, including the non-icosahedral components such as the viral genome, the portal complex and the phage tail. The density map is validated by the visualization of the icosahedrally arranged capsid proteins simultaneously with the non-icosahedral components. The viral genome is packed concentrically with a spacing ~25 Å as predicted by the x-ray solution scattering of P22 phage. The portal complex which is the entry point of the viral DNA into the procapsid has 12-fold symmetry spanning across one of the icosahedral 5-fold vertices. The phage fiber has a 6-fold symmetry extending from the portal complex outside the capsid particle. This structure shows for the first time the native structure of an entire virion without any bias in the reconstruction procedure.

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