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Structural Analysis of the Shigella Virus Sf14 Capsid

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Viruses are minimally comprised of a genome that is protected from the environment by a protein coat. Many viruses are spherical, with the coat proteins forming an icosahedral capsid around the genome. The T number, or triangulation number, of a capsid describes the geometry of this icosahedral shell [1]. Of the bacterial viruses—known as bacteriophages or phages—most have icosahedral capsids that display T=7 or T=13 symmetry, which have been analyzed in terms of assembly, structure, and stability [2].

Recently, several members of the Mooglevirus group of phages were isolated from environmental sources in Michigan and Nebraska [3,4]. These were most frequently isolated using the bacterium *Shigella flexneri*. Across two years of sampling, 16 Mooglevirus-like *S. flexneri* phages were found. By contrast, none were isolated on *Salmonella* and only one was found on *E. coli*. Mooglevirus characteristics include an icosahedral head with a long, contractile tail that attaches to the host. These newly isolated Mooglevirus-like phages have an uncommon genome size of 85.0 – 95.0 kilo base pairs, suggesting they may have similarly uncommon capsid geometry. An initial low-resolution structure (15 Å) revealed these phages' capsids exhibit T=9 icosahedral symmetry. From hundreds of available virus structures, only three—including one of these environmental isolates—exhibit T=9 icosahedral symmetry. The other two T=9 capsids are resolved to 14 Å (EMD-1472) and 18 Å (EMD-6043) [5,6].

Using cryo-electron microscopy, we have since obtained a 4.5 Å structure of the Mooglevirus-like Sf14 virion. To our knowledge, this is the first high-resolution structure of a T=9 virus. On the virion, decoration-like proteins bind preferentially to only the hexamers surrounding the pentamers at each icosahedral vertex. These decoration proteins have two immunoglobulin-like domains, which are similar to the single immunoglobulin domain in the T=13 bacteriophage T5 [7]. However, in T5, the decoration protein binds to the center of all hexamers of the capsid. The mechanism conferring hexamer-specific binding in Sf14 has yet to be determined. In addition, the function of this protein is currently unknown but is hypothesized to play a role in capsid stability. Determining the structure and measuring the stability of capsids with or without decoration proteins may indicate how and why these proteins are associated with the virion.

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