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Comparative Genomics and Evolutionary Trajectories of Viral ATP Dependent DNA-Packaging Systems

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Abstract

We present an overview of comparative genomics of ATP-dependent DNA packaging systems of viruses. Several distinct ATPase motors and accessory proteins have been identified in DNA-packaging systems of viruses such as terminase-portal systems, the ϕ 29-like packaging apparatus, and packaging systems of lipid inner-membrane-containing viruses. Sequence and structure analysis of these proteins suggest that there were two major independent innovations of ATP-dependent DNA packaging systems in the viral universe. The first of these utilizes a HerA/FtsK superfamily ATPase and is seen in prokaryotic viruses with inner lipid membranes, large eukaryotic nucleo-cytoplasmic DNA viruses (including poxviruses) and a group of eukaryotic mobile DNA transposons. We show that ATPases of the ϕ 29-like packaging system are also divergent versions of the HerA/FtsK superfamily that functions in viruses without an inner membrane. The second system, the terminase-portal system, is dominant in prokaryotic tailed viruses and typically functions with linear chromosomes. The large subunit of this system contains a distinct ATPase domain and a C-terminal nuclease domain of the RNase H fold. We discuss the classification of these ATPases within the P-loop NTPases, genomic demography and positioning of their genes in the viral chromosome. We show that diverse portal proteins utilized by these systems share a common evolutionary origin and might have frequently displaced each other in evolution. Examination of conserved gene neighborhoods indicates repeated acquisition of Helix-turn-Helix domain-containing terminase small subunits and a third accessory component, the MuF protein. Adenoviruses appear to have evolved a third packaging ATPase, unique to their lineage. Relationship between one major type of packaging ATPases and cellular chromosome pumps like FtsK suggests an ancient common origin for viral packaging and cellular chromosome partitioning systems.