Adenoviruses

members of the family Adenoviridae are medium-sized (90–100 nm), no enveloped (without an outer lipid bilayer) viruses with an icosahedral nucleocapsid containing a double stranded DNA genome. Their name derives from their initial isolation from human adenoids in 1953. They have a broad range of vertebrate hosts; in humans, more than 50 distinct adenoviral serotypes have been found to cause a wide range of illnesses, from mild respiratory infections in young children (known as the common cold) to life-threatening multi-organ disease in people with a weakened immune system.

This family contains the following genera:

Genus Atadenovirus; type species: Ovine atadenovirus D Genus Aviadenovirus; type species: Fowl aviadenovirus A Genus Ichtadenovirus; type species: Sturgeon ichtadenovirus A

Genus Mastadenovirus (including all human adenoviruses); type species: Human mastadenovirus C

Structure

Adenoviruses represent the largest nonenveloped viruses. They are able to be transported through the endosome (i.e., envelope fusion is not necessary). The virion also has a unique "spike" or fiber associated with each penton base of the capsid that aids in attachment to the host cell via the receptor on the surface of the host cell.

Genome

The adenovirus genome is linear, non-segmented double-stranded (ds) DNA that is between 26 and 48 Kbp. This allows the virus to theoretically carry 22 to 40 genes. Although this is significantly larger than other viruses in its Baltimore group, it is still a very simple virus and is heavily reliant on the host cell for survival and replication. An interesting feature of this viral genome is that it has a terminal 55 kDa protein associated with each of the 5' ends of the linear dsDNA. These are used as primers in viral replication and ensure that the ends of the virus' linear genome are adequately replicated.

Adenovirus-Associated Human Disease

Pharyngitis

Acute Respiratory Disease

Pneumonia

Pharyngoconjunctival Fever

Epidemic Keratoconjuntivitis

Genitourinary Infections (cervicitis, urethritis, hemorrhagic cystitis)

Gasteroenteritis

Some asymptomatic and persistent infection

Transmission

Ingestion/Fecal-Oral Route

Respiration (through respiratory droplets)

Contact/Hand-to-eye transfer

Venereal

* Papillomaviridae

Papillomaviruses are non-enveloped, meaning that the outer shell or capsid of the virus is not covered by a lipid membrane. A single viral protein, known as L1, is necessary and sufficient for formation of a 55–60 nanometer capsid composed of 72 star-shaped capsomers. Like most non-enveloped viruses, the capsid is geometrically regular and presents icosahedral symmetry. Self-assembled virus-like particles composed of L1 are the basis of a successful group of prophylactic HPV vaccines designed to elicit virus-neutralizing antibodies that protect against initial HPV infection. As such, papillomaviridæ are stable in the environment.

papillomavirus genome: is a double-stranded circular DNA molecule ~8,000 base pairs in length. It is packaged within the L1 shell along with cellular histone proteins, which serve to wrap and condense DNA.

Family is one of the many virus families associated with human disease. The Papovavirus is divided into two subfamilies or genera, Polyomavirus and Papillomavirus. However, the family name is more indicative of the history of the virus, than of its component subsets. Papova is derived not from the combination of the subfamilies, but from the first described viruses used to define the family:

Rabbit PApilloma virus

Mouse POlyoma virus

Simian VAcuolating virus

For centuries, it had been suspected that warts were caused by some infectious agent. The transmissibility of the condition from person to person had long been recognized. But it wasn't until 1933 that the first papillomavirus was scientifically described. The Shope papillomavirus of the rabbit soon became the first specific experimental example of viral association with warts.

Human papillomaviruses types

human papillomavirus types have been completely sequenced. They have been divided into 5 genera: Alphapapillomavirus, Betapapillomavirus, Gammapapillomavirus, Mupapillomavirus and Nupapillomavirus.

✤ Herpesviridae

Herpesviridae is a large family of DNA viruses that cause diseases in animals, including humans. The members of this family are also known as herpesviruses. The family name is derived from the Greek word herpein ("to creep"), referring to the latent, recurring infections (typical of this group of viruses. Herpesviridae can cause latent or lytic infections.

At least five species of Herpesviridae – HSV-1 and HSV-2 (both of which can cause orolabial herpes and genital herpes), varicella zoster virus (the cause of chickenpox and shingles), Epstein–Barr virus (implicated in several diseases, including mononucleosis and some cancers), and cytomegalovirus – are extremely widespread among humans. More than 90% of adults have been infected with at least one of these, and a latent form of the virus remains in most people. There are 9 herpesvirus types known to infect humans: herpes simplex viruses 1 and 2, HSV-1 and HSV-2, (also known as HHV1 and HHV2), varicella-zoster virus (VZV, which may also be called by its ICTV name, HHV-3), Epstein–Barr virus (EBV or HHV-4), human cytomegalovirus (HCMV or HHV-5), human herpesvirus 6A and 6B (HHV-6A and HHV-6B), human herpesvirus 7 (HHV-7), and Kaposi's sarcoma-associated herpesvirus (KSHV, also known as HHV-8). In total, there are more than 130 herpesviruses, some of them from mammals, birds, fish, reptiles, amphibians, and mollusks.

Classification

Alphahernesviringe	Varicella zoster virus (VZV), Human herpes virus 8 (HHV-8, KSHV), B	variable host range, relative short reproductive cycle, rapid spread in culture, destruction of infected cells and capacity to establish latent infection primarily but not exclusively in ganglia
Betaherpesvirinae	herpes virus 6 (HSV-6), Human	restricted host range, long reproductive cycle, infection progresses slowly in culture, and latent in secretory cells, lymphoreticular cells, kidneys and other tissues

	host range characteristic of the family or order of the natural host, infects specifically B or T cells,
Gammaherpesvirinae Epstein-Barr virus (El	latent virus in lymphoid tissue, may cause lytic
Caninalerpesvirillae Epstein-Dari virus (E	fibroblastic cells in lymphocyte, infection may be
	arrested at prelytic or lytic stage but without the production of infectious progeny

Poxviridae

Classification and Taxonomy

Pox viruses are the largest and most complex of all viruses. In fact, they are large enough, with a virion size of 220-350 x 115-260 nm, to be seen under a light microscope. They infect a wide range of hosts, and are divided into two subfamilies: Chordopoxvirinae and Entomopoxviridae. All human pox viruses are in the Chordopoxovirinae subfamily, and most of them belong to either the Orthopoxvirus (variola, vaccinia, cow pox) or the Parapoxvirus (Orf virus) genus. The chicken pox virus does not belong this family! - It is a herpesvirus.

genome: double-stranded DNA, monopartite, linear, noninfectious; encodes over 100 genes, including DNA dependent RNA transcripase

morphology: "complex", ovoid or brick-shaped nucleocapsid

envelope: orthopox are enveloped, parapox are not

replication: takes place in cytoplasm

host range: host range varies by specific virus; zoonoses is common, but small pox only infects humans oncogenicity: may cause benign tumors

Transmission

Pox viruses are most commonly spread by direct contact. In the case of small pox, the virus is found in lesions in the upper respiratory tract, which can be transmitted to others in droplet secretions, and in skin lesions. Although the virus is considered to be highly contagious, this route of transmission makes its spread relatively slow.

✤ Hepadnaviridae

Introduction to the Family

The name is based on "hepato" (liver) "tropic" (replicates and causes infection in the liver) and DNA virus (its nucleic acid). The Hepadna virus family has the smallest genome of all replication competent animal DNA viruses. The single most important member of the family is Hepatitis B virus (HBV). HBV exhibits an extremely limited host range, infecting only chimps and humans. Our presentation will focus very heavily on Hepatitis B as representative of the Hepadna Family and emphasize human pathogenesis.

Genome

Hepadnaviruses have very small genomes of partially double-stranded, partially single stranded circular DNA. The genome consists of two strands, a longer negative-sense strand and a shorter and positive-sense strand of variable length. In the virion these strands are arranged such that the two ends of the long strand meet but are not covalently bonded together. The shorter strand overlaps this divide and is connected to the longer strand on either side of the split through a direct repeat (DR) segment that pairs the two strands together. In replication, this pds genome is converted in the host cell nucleus to covalently-closed-circular DNA (cccDNA) by the viral polymerase.

These five viruses are classified together for the following reasons:

1. They are all enveloped

- 2. They all contain polymerases that can repair the viral DNA genome during replication
- 3. They produce lipoproteins containing envelope proteins
- 4. They infect species that are closely related to that of their natural hosts (narrow host range)
- 5. As the family "hepadna' (for hepatotropic DNA viruses) implies, they can produce chronic infections in liver cells. As stated above, we will focus on the only human virus in the family hepatitis B.