

Classification of Pox Viruses

The Poxviridae consists of two subfamilies

- i. Chordopoxirinae (Pox virus of the vertebrates)
- ii. Entomopoxivirinae (Pos virus of insects)

- There are 8 Genera in the Subfamily Chordopoxivirinae.
- Each genus of the Subfamily Chordopoxivirinae contains related virus which generally infect related host
- They are with significant diseases as follows:
- Orthopoxvirus
- Vaccinia
- Variola
- Cowpox
- Feline cowpox
- Horsepox
- Camelpox
- Buffalopox
- Monkeypox
- Parapoxvirus
- Bovine Papular
- Contagious Ecthyma/orf
- Pseudocowpox/milker nodules
- Ectromella/mousepox: An important disease of laboratory and wild mice.
- Capripoxvirus
- Sheeppox
- Goatpox
- Lumpy Skin Disease
- Avipoxvirus
- Fowlpox
- Leporipoxvirus
- Myxomatosis
- Rabbit and Squirrel fibroma: Benign tumors, natural host the cottontail rabbit
- Molluscipoxvirus
- Molluscum contagiosum: A common Disease of children
- Suipoxvirus
- Swinepox
- Yatapoxvirus
- Yaba monkey tumor virus and related viruses

Pox Infections: General

- Poxviruses infect epidermis and produce local lesions that frequently become proliferative and later necrotic
- Rare generalized infections can be fatal
- Poxvirus occur naturally in most Veterinary species except Dog

- Many Poxvirus produce an infection resulting in changes conveniently summarized in order of development as:
 1. Papule
 2. Vesicle
 3. Pustule and
 4. Finally, Scabs or Crusts
- Secondary bacterial infections are not uncommon
- Recovery from poxvirus infection usually is followed by long term immunity
- Many poxvirus can be cultivated on the chorioallantoic membrane of chicken embryo
- Because of their large size Poxviruses can be seen with light microscope in stained smears.
- Virus elementary bodies stained by various procedures including Gutstein's and Giemsa can be readily seen either as aggregates (acidophilic cytoplasmic inclusion) or singly
- Poxvirus may survive for years in dust
- Some mammalian poxvirus are considered oncogenic and have been associated with epidermal and fibromatous hyperplasia
- By far the most studied pox virus is vaccinia virus, the Jennerian small pox virus and some virus which infect cattle and mice.
- Clinical specimen: Vesicular fluid swab, scapping from lesions

Family Asfarviridae

Introduction

This is the family for a category that was referred to previously as African swine fever-like virus it consists of one genus and one species that causes African swine fever.

Viral Characteristics

- The virions of African swine fever are large, complex and in some structural respects resembles poxviruses.
 - This DNA virus consist of a nucleoprotein (70-100nm in diameter) surrounded by an icosahedral capsid and externally by a lipid layer.
 - The genome is linear, double stranded (170-190kb in length), and encodes 150-200 proteins
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- **VIRAL CHARACTERISTIC (CONTD)**
 - The virus replication takes place in the cytoplasm of the host cells (swine macrophages in vivo and in vitro) and soft ticks of the genus Ornithodoros.
 - The dsDNA is used as a template for both mRNA and Progeny genomes
 - The virus particles are stable in the environment being considerably resistant to heat and pH changes. E.g. the virus is stable for 70 days in blood on boards and 140days in salted dried hams

- **Classification**
- The family has only one genus-Asfivirus
- The genus has one species-African Swine fever virus which causes African Swine fever
- African Swine fever infection
- After infection by the oronasal route, the virus replicates in the pharynx, tonsils and dependent lymph nodes
- Viraemia follows by infection of bone marrow, lymph nodes, lungs, kidney and liver where further replication takes place in cells of the lymphoreticular systems
- Clinical specimen: Blood, spleen, tonsil and lymph nodes

FAMILY PARVOVIRIDAE

Introduction

- Are the simplest DNA Animal Virus
- Viral replication is dependent on functions supplied by replicating host cells or by co-infecting helper virus because of the small coding capacity of their genome

VIRAL CHARACTERISTIC

- The genome is single stranded DNA, linear 5, 6kb, MW 1-5—2.0 million
- The virion is icosahedral, 18-26nm diameter and 32 capsomeres
- Has one major and minor protein
- There is no envelope
- Replication is in the nucleus and is dependent on functions of dividing host cells.

Outstanding Characteristic

- Very simple virus
- One genus is replicating defective and requires a helper virus

Classification

- The family Parvoviridae is divided into 2 subfamilies
 1. Parvovirinae
 2. Densovirinae – which infects only invertebrates

Parvovirinae has 3 genera

1. **Parvovirus**-contains the autonomous parvoviruses which has widespread and capable of autonomous replication e.g Canine Parvovirus infection, Feline panleukopenia, Porcine Parvovirus infections
2. **Dependovirus** –requires helper virus function for replication
3. **Erythrovirus** e.g. B19 Parvovirus of human bind to erythrocyte antigens for replication

Parvovirus Infection: General

- The Parvovirinae is the subfamily that contains parvovirus that are pathogenic to vertebrates.

Genus	Virus	Host	Disease
Parvovirus	Minute Virus	Mice	Subclinical of Mice (MVM)
	Feline Parvovirus (FPV)	Cat	Enteritis, leucopenia Cerebral ataxia
	Canine Parvovirus (CPV)	Dog	Enteritis, myocarditis
	Porcine Parvovirus (PPV)	Pigs	Reproductive failure
Dependovirus	Adeno-associated Virus (AAV)	Human & Others	Unknown
Erythrovirus B19		Man	Respiratory tract illness Aplastic crisis, Hydrops foetalis, Erythema infectiosum, fifth Disease
	Simian Parvovirus	Monkey	Anaemia

Orthomyxoridae

Introduction

This is a family of negative-sense, single-stranded RNA viruses. They are smaller than the paramyxoviruses and their genome is segmented (7 to 8 segments) rather than consisting of a single piece RNA. Influenza viruses are the only members of Orthomyridae.

Viruses of this family have a predilection for the respiratory tract, but usually do not cause a serious disease on uncomplicated cases. Exceptions are human infections with viruses of avian origin. Principal viruses of veterinary importance are type A influenza viruses, which causes equine, swine, and avian influenza.

Viral characteristics

- i. Viruses have a segmented single-stranded RNA genome, helical nucleocapsids (each RNA segment + proteins nucleocapsid) and an outer lipoprotein envelop.
- ii. The segmented genome facilitates genetic reassortment, which accounts for antigenic shifts. Point mutations in the RNA genome accounts for antigenic drifts that are often associated with epidemics. In wither case, the changes are frequently associated with the HA (hemmagglutinin) and NA (neuraminidase) antigens.

The envelop is covered with two different kinds of spikes, a hamegglutinin (HA antigen) and a neuraminidase (NA antigen). In contrast, the hemagglutinin and neuraminidase activities of prarmuxoviruses are in the same protein spike

In the laboratory, the viruses replicates best in the epithelial cells lining the allantoic cavity of chicken embryos.

The viruses agglutinate red blood cells of a variety of species.

Replication takes place in the nucleus.

The viral RNA=dependent RNA polymerate transcribes the negative-sense genome into mRNA.

Immune Response

The host immune response to influenza viruses includes:

- Non-specific immune response: the release of interferons by the infected cells aids in preventing viral spread to neighboring cells.
- Humoral immune response: IgA in the upper respiratory tract and IgA in the lower respiratory tract.
These antibodies are typically directed against the HA and NA antigens.
- cell-mediated immune respouse: cytotoxic T Lymphocytes are important in recovery

Classification

The family consists of four genera:

Influenza virus A; Viruses cause avian, equine and swine influenza: associated with both epidemics and pandemic; both antigen drift noted. High antigenic variability in the surface glycoproteins HA and NA

Influenza virus B; Members infect only humans; associated with epidemics; antigen drift noted.

Influenza virus C; viruses cause mild, sporadic respiratory infections in humans. May also infect swine.

Thogoto-like viruses: the two species Thogoto and Dhori viruses are tick-borne viruses recovered from cattle, camels, and humans in the regions of Asia, Africa and Europe. They are not considered to be of pathogenic significance for animal.

Antigenic Composition

Knowledge of the antigen nature of influenza viruses is necessary for an understanding of the epidemiology of influenza.

The internal proteins consist mainly of nucleocapsid proteins (NC), some matrix proteins (M1) and three polymerase (PA, PB1 and PB2). The proteins NC and M1 determine type specificity. Even being internal, these proteins (or peptides derived from them) may elicit cytotoxic T cells that are important in recovery from infection.

The nucleoprotein antigen (A,B,C) determine the virus type. The HA and NA antigens determine subtypes.

The hemagglutinin (HA) is an envelope antigen (spike) that can attach to erythrocytes and cause agglutination. It is responsible for the attachment of the virion to cell surface receptors (neuraminic acid, sialic acid) if blocked by antibody, attachment of the virus to a susceptible cell is prevented; thus it is very important in protective immunity mediated by neutralizing antibody. A hemagglutinin-inhibition titer of 1/40 is considered to be protective.

Neuraminidase is an envelope protein whose enzymatic activity results in the liquefaction of mucus thus contributing to viral spread. Specific antibody slows down the spread of virus. Neuraminidase also cleaves neuraminic acid to release progeny virus from the infected cell.

Influenza viruses are designated as follows: type/place/time of isolation/H/and N content. In birds, there are approximately 15 H antigens (H1 – H 15) and 9N antigen (N1 – N9), which can be found in all possible combinations. An example would be H7 N3. therefore, the type A type A virus:A/Bangkok/3/79 (H3N2)3, first isolated in 1979, and envelope antigen H3N2.

Antigenic Variation

In brief there are two kinds of antigenic change:

Antigenic shift: These are major changes based on reassortment of segments of the genome. In reassortment, entire segments of RNA are exchanged between two viruses infecting the same host, each of which codes for a single protein, e.g. hemagglutinin. As a result of co-infection by two viruses, a third one may arise.

Antigenic drift: These are minor changes caused by point mutations in the genes encoding the HA and NA glycoproteins.

Genetic Basis for Antigenic Variation

The genes of the type A viral hemagglutinin and neuraminidase are polymorphic, subject to extensive variation. This not the case for types B or C.

The HA and NA genes of types A and B viruses undergo point mutations. When developing a vaccine, the effect of change can be determined by the reciprocal inhibition test. As a result of the change, the immune response generated against vaccine HA or NA is now less effective against mutated (variant progeny) HA or NA.

Influenza A

Equine Influenza

Cause

Equine influenza virus A. The immunologically distinct subtypes involved are usually A/equine/Prague/1/56(H7N7) or A/equine/Miami/2/63 (H3N8). These are also referred to as influenza A/equine 1 and influenza A/equine2. they are also referred to as Type 1 or Equi-1 (Prague) and Type 2 or Equi-2 (Miami). New variants resulting from antigenic drift appear to be infrequent. All recent and current outbreaks have been attributed to A Equi-2.

Clinical specimen: Nasal and ocular swab during a acute phase, Acute and convalescent sera.

Avian Influenza

(Fowl plaque)

Cause

Influenza A virus (avian). There are 15 antigenic groups based on hemagglutinin inhibition and nine based on neuraminidase. The many strains of virus infecting waterfowl provide sources for new mammalian strains, e.g. strain H5N1 a highly pathogenic avian caused influenza with high mortality in humans in Hong Kong. Subtypes H5 and H7 have caused serious outbreaks of avian influenza in commercial flocks of chickens and turkeys. When these pathogenic stains are identified, premises are quarantined and infected flock slaughtered.

Clinical specimen: whole bird or lung, trachea, airsac, spleen, faeces and serum.

Swine Influenza
(Swine flu, Hog flu)
Cause

Influenza virus A. Subtypes H1NA and H3N2 have been frequent causes of swine influenza. More virulent variants H1N1 have appeared in recent years. The H1N2 subtype has also been implicated as a cause of acute swine influenza. It has been suggested that all porcine influenza viruses were derived originally from birds. Secondly infection with *Haemophilus parvis* and other bacteria may contribute to a more severe disease.

Clinical specimen: Nasal swabs and lungs, acute phase, Acute and convalescent sera.

Canine Influenza
(Dog flu)
Cause

Influenza A virus, closely related to subtype H3N8 and presumed to have been acquired from horse(s). Subtype H3N8 virus is a frequent cause of equine influenza.

Specimen: Nasopharyngeal swab taken within 72 hours of the appearance of signs, paired serum samples with a 3 weeks interval.

Family – Bunyaviridae

This is one of the arboviruses. Arboviruses are defined (WHO Scientific Wasp) as viruses that are maintained in nature principally or to an important extent, through biological transmission between susceptible vertebrate hosts by haematophagous arthropods or through transovarian and possible venereal transmission in arthropods, the viruses multiply and produce viraemia in the vertebrates, multiply in the tissue of the arthropods, and are passed on to new vertebrates by the bites of arthropods after a period of extrinsic incubation.

There are six families containing the arboviruses. Certain viruses within the 6 families are not transmitted by arthropods but maintained in nature within rodents as reservoirs that may transmit the infection directly to human of Hantavirus genus e.g the family Bunyaviridae.

Characteristics of the family Bunyaviridae

Are single stranded negative sense RNA virus they are enveloped. The capsid is helical virus size is 100 – 120nm. The RNA genome has 11 – 12,000 nucleotides the site of capsid assembly

is the cytoplasm by budding through Golgi vesicles. Bunyaviruses have tripartite genome where the genetic material of the virus is divided between 3 pieces of the single stranded RNA termed large (L), medium (M) small (S) segments.

The L RNA segment encodes the RNA – dependent RNA polymerase also termed L protein. The MRNA segment encodes two glycoproteins termed G1 and G2 that are found on the surfaces of the various and the Bunyaviruses, Tospovirus and Phlebovirus genera have a non-structural protein NSM whose function is unknown. The SRNA segment encodes a nucleocapsid (N) protein. The Bunyavirus a genus also contains a non-structural protein termed NSS in an overlapping reading frame while Phlebovirus and Tospovirus genera also contain NSS gene.

The tripartite genome structure enables the bunyaviruses to undergo genetic reassortment whereby a cell infected by two or more bunyaviruses can result in a progeny viruses containing segments from different viruses. Reassortment has been shown to take place in nature between closely related bunyaviruses and is considered to be a process that contributes to genetic variation and evolution.

A virus that has a negative sense RNA genome must contain virus RNA dependent RNA. Polymerase so that its genome can be transcribed in cells to generate m-RNA of different viral genes. In addition the NSm gene of the Tospovirus genus and the NSs gene of this Phlebovirus and Tospovirus genera are encoded as in genes in the positive sense orientation. Thus, the S and M RNA segments of Tospoviruses and the S RNS segment of the Phleboviruses are termed ambience RNAs to denote that the open reading frames of the genes are in opposite orientation

Classification of Bunyaviridae family

The family has 138 members in 5 genera.

1. Genus Bunyaviruse (172) e.g La Gross
2. Nairovirus (34) e.g Crimea Congo haemorrhagic fever Nairobi sheep disease
3. Phlebovirus (51) e.g. Rift valley fever (Zoonotic disease of ruminants)
4. Hantavirus (15) Sin-Nombre (Not arthropod borne)
5. Tospovirus plant viruses

Pathogenesis of the Bunyaviruses

The individual viruses of the family Bunyaviridae are named after the disease or the geographical area where the virus is first isolated. Diseases produced by arbovirus generally may be divided into 3 clinical syndromes.

1. Fever with or without maculopapular rash and is usually benign.
2. Encephalitis – is often with high fatality rate.
3. Haemorrhagic fevers – also frequently severe and fatal .

Specimen for diagnosis: Acute and convalescent sera

Family – Arteriviridae

Characteristics

Single stranded, positive sense RNA virus

Capsid symmetry – Icosahedral

Virion size (nm) - 40 – 60

Genus – Arterivirus

Representative species – Equine arteritis virus.

There is genomic and antigenic variation among the geographically disparate isolates.

The virus strains also vary in their ability to produce disease.

The disease produced by the virus is equine viral arteritis (EVA) which is an acute contagious viral disease of equid.

It is characterised by fever, depression, dependent oedema, conjunctivitis, nasal discharge and sometimes death in young foals.

Specimen for diagnosis. Blood, swab from nasal and conjunctival discharges.