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Classification:

Classification seeks to describe the diversity of viruses by naming and grouping them on the basis of similarities. In 1962, Andre Lwoff, Robert Horne, and Paul Toumier were the first to develop a means of virus classification, based on the Linnaean hierarchical system.

This system based classification on phylum, class order, family, genus, and species. Viruses were grouped according to their shared properties and the type of nucleic acid forming their genomes.

In 1966, the international committee on Taxonomy of Viruses (ICTV) was formed. The system proposed by Lwoff, Horne and Tournier was never fully accepted by the ICTV because small genome size viruses and their high rate of mutation make it difficult to determine their ancestry beyond order

ICTV classification:

The International Committee on Taxonomy of Viruses (ICTV) developed the current classification system and wrote guidelines that put a greater weight on certain virus properties to maintain family uniformity.

A unified taxonomy (a universal system for classifying viruses) has been established. Only a small part of the total diversity of viruses has been studied. As of 2019, 4 realms, 9 kingdoms, 16 phyla, 2 subphyla, 36 classes, 55 orders, 8 suborders, 168 families, 103 subfamilies, 1,421 genera, 68 subgenera, and 6,589 species of viruses have been defined by the ICTV.

The general taxonomic structure of taxon ranges and the suffixes used in taxonomic names are shown hereafter. As of 2019, the ranks of subrealm, subkingdom, and subclass are unused, whereas all other ranks are in use.

Realm (*-viria*)

Subrealm (*-vira*)

Kingdom (*-virae*)

Subkingdom (*-virites*)

Phylum (*-viricota*)

Subphylum (*-viricotina*)

Class (*-viricetes*)

Subclass (*-viricetidae*)

Order (*-virales*)

Suborder (*-virineae*)

Family (*-viridae*)

Subfamily (*-virinae*)

Genus (*-virus*)

Subgenus (*-virus*)

Species

Baltimore classification:

The Baltimore Classification of viruses is based on the method of viral mRNA synthesis

The Nobel Prize-winning biologist David Baltimore devised the Baltimore classification system. The ICTV classification system is used in conjunction with the Baltimore classification system in modern virus classification.

The Baltimore classification of viruses is based on the mechanism of mRNA production. Viruses must generate mRNAs from their genomes to produce proteins and replicate themselves, but different mechanisms are used to achieve this in each virus family.

Viral genomes may be single-stranded (ss) or double-stranded (ds), RNA or DNA, and may or may not use reverse transcriptase (RT). In addition, ssRNA viruses may be either sense (+) or antisense (-). This classification places viruses into seven groups:

I: ds DNA: Viruses (e.g. Adenoviruses, Herpesviruses, Parvoviruses)

II: ssDNA Viruses (+ strand or "sense") DNA (e.g. Parvoviruses)

III: dsRNA Viruses (e.g. Reoviruses)

IV: (+) ssRNA viruses (+ strand or sense) RNA (e.g. Coronaviruses, Picornaviruses, Togaviruses)

V: ssRNA Viruses (strand or antisense) RNA (e.g. Orthomyxoviruses, Rhabdoviruses)

VI: ssRNA-RT Viruses (+ strand or sense) RNA with DNA intermediate in life-cycle (e.g. Retroviruses)

VII: dsDNA-RT viruses DNA with RNA intermediate in life-cycle (e.g. Hepadnaviruses)

VZV is in Group I of the Baltimore Classification because it is a dsDNA virus that does not use reverse transcriptase.

Epidemiology:

Viral epidemiology is the branch of medical science that deals with the transmission and control of virus infections in humans. Transmission of viruses can be **vertical**, which means from mother to child, or **horizontal**, which means from person to person.

Vertical transmission include hepatitis B virus and HIV, where the baby is born already infected with the virus.

Horizontal transmission is the most common mechanism of spread of viruses in populations. Transmission can occur when: body fluids are exchanged during sexual activity, e.g., HIV.

Blood is exchanged by contaminated transfusion or needle sharing, e.g., hepatitis C.

Exchange of saliva by mouth, e.g., Epstein–Barr virus;

Aerosols containing virions are inhaled, e.g., influenza virus; and insect vectors such as mosquitoes penetrate the skin of a host, e.g., dengue.

The rate or speed of transmission of viral infections depends on factors that include population density, the number of susceptible individuals, (i.e., those not immune), the quality of healthcare and the weather.

Epidemiology is used to break the chain of infection in populations during outbreaks of viral diseases.

Control measures are used that are based on knowledge of how the virus is transmitted. It is important to find the source or sources of the outbreak and to identify the virus.

Once the virus has been identified, the chain of transmission can sometimes be broken by vaccines. When vaccines are not available, sanitation and disinfection can be effective.

Often, infected people are isolated from the rest of the community, and those that have been exposed to the virus are placed in quarantine.

To control the outbreak of foot-and-mouth disease in cattle in Britain in 2001, thousands of cattle were slaughtered. Most viral infections of humans and other animals have incubation periods during which the infection causes no signs or symptoms.

Incubation periods for viral diseases range from a few days to weeks, but are known for most infections.

Somewhat overlapping, but mainly following the incubation period, there is a period of communicability—a time when an infected individual or animal is contagious and can infect another person or animal.

When outbreaks cause an unusually high proportion of cases in a population, community, or region, they are called **epidemics**. If outbreaks spread worldwide, they are called **pandemics**.