

Review Article

Review on Classification and Nomenclature of Viruses

Solomon Bimrew^{1,*}, Merkuz Abera²

¹Department of Plant Science, Woldia University, Woldia, Ethiopia

²Department of Plant Science, Bahirdar University, Bahirdar, Ethiopia

Email address:

solomonbimrew07@gmail.com (Solomon Bimrew), merkuzabera@yahoo.com (Merkuz Abera)

*Corresponding author

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Abstract: Viruses are subcellular, infectious, non-living creatures that can only replicate and metabolize inside the cells of living hosts. Virus taxonomy is the classification of viruses into categories called taxa. The classification and nomenclature recently gained importance due to the exponentially increasing number of new viruses discovered. Hence the current review on classification and nomenclature of virus aimed to provide sufficient and updated information to readers. Current virus classification is increasingly performed using more complex phylogenetic approaches that move researchers closer to a rudimentary understanding of the origin, evolution, relatedness, and diversification of viruses. In the taxonomic hierarchy of virus, the highest taxa are real and the lowest rank is species. To categorize viruses, phenotypic traits like morphology, nucleic acid type, and mechanism of replication, host organisms, and the sort of disease they cause are taken into consideration. Mostly based on 1. Classical- e.g. Animal, plant, or bacterial virus system- e.g. Naked or enveloped virus. 2. Genomic-Baltimore classification by seven categories: I: dsDNA viruses (e.g. Adeno viruses, Herpes viruses, Pox viruses) II: ssDNA viruses (+ strand or "sense") DNA (e.g. Parvo viruses) III: dsRNA viruses (e.g. Reo viruses) IV: (+) ssRNA viruses (+ strand or sense) RNA (e.g. Corona viruses, Picorna viruses, Toga viruses) V: (–) ssRNA viruses (– strand or antisense) RNA (e.g. Orthomyxo viruses, Rhabdo viruses). VI: ssRNA-RT viruses (+ strand or sense) RNA with DNA intermediate in life-cycle (e.g. Retro viruses). VII: dsDNA-RT viruses DNA with RNA intermediate in life-cycle (e.g. Hepadna viruses). 3. Serology (a corona virus). There isn't a standardized format for virus species names yet, in contrast to the binomial nomenclature used for cellular species. The ICTV now requires that a species name comprise as few words as possible while still being distinct, and must not merely contain the term virus and the host. By responding to a series of questions based on contrasting traits, a species can be identified using the dichotomous key method.

Keywords: Classification, Dichotomous Key, Hierarchy, Nomenclature, Taxonomy, Virus

1. Introduction

Viruses are contagious organisms that have a diameter of typically lower than 400 in a nanometer and it only multiply and metabolize inside the cells of living hosts. Viruses are sub cellular, infectious, non-living creatures that only join a system that is alive once they have infected host cells, giving them a sort of temporary existence [69]. International Committee on Taxonomy of Virus (ICTV) Executive Committee approved the formal definition of a "virus" in November 2020, and it was ratified in March 2021. It states

that a "virus" is a MGE (mobile genetic element) that encodes at least one protein that is a significant part of the virion that contains the nucleic acid of the relevant MGE [34].

The gene that actually encodes the major virion protein or MGEs that can be conclusively shown to be ancestors of such types of significant virion protein - coding organisms. Every monophyletic element of MGEs that descends from an ancestor expressing virion proteins ought to be categorized as a member of viruses [40].

The process of classification of viruses is based on gathering and comparing several characteristics that describe the virus and can be used to differentiate one virus from

another [39]. Characters can be any trait or characteristic of the virus, such as the molecular make-up of the genome, the virus's capsid structure and whether or not it is enveloped, the gene expression program that produces the virus's proteins, the host range, pathogenicity, and sequence similarity [14].

Similarity, phylogenetic relationships have emerged as two of the most essential categories of characters for defining and separating viral taxa. A hierarchical relationship is developed based on character evaluation that classifies viruses with related traits. Each lower level taxon shares the characteristics that distinguish higher-level taxa [45].

ICTV is responsible for classifying viruses taxonomically and designating virus taxa [3]. The International Union of Microbiological Societies' Division of Virology has tasked the ICTV with creating, enhancing, and maintaining universal virus taxonomy [62].

In contrast to other groups of biological organisms, the ICTV is charged with establishing standards for taxonomic classification of viruses as well as developing standards for taxonomic naming of taxa. It is also responsible for approving proposed taxonomy and names before they are adopted as official definitions. The ICTV Statute set forth for the standards for the ICTV and its operations [13], while an International standard set to classify and name a given virus specifies the guidelines for naming and creating virus taxa. ICTV is an organization that was first founded in 1966 as international committee on virus nomenclature [1, 3, 29].

Numerous virus species can cause diseases, and numerous new viruses are found every year. In order to assure accurate detection, classification, and identification of the desired viral species, this circumstance has increased interest in viral taxonomy. In order to give adequate and current information regarding the classification and naming of viral species, the current review on virus nomenclature set out to do so. Thus, it lets users to arrange, classify, and locate the information they're looking for.

2. Classification of Virus and Nomenclature

2.1. Overview of Virus Taxonomy

The taxonomic order of viruses explains the relationships between infectious entities. When a virus is classified, its name is given and it is put into a taxonomic system that is comparable to the classification systems used for biological entities. Viruses aren't considered to be part of the kingdoms. Do not follow biological taxonomy. In order to categorize viruses, phenotypic traits like morphology, nucleic acid type, and mechanism of replication, host organisms, and the sort of disease they cause are taken into consideration. Mostly based on 1. Classical- e.g. Animal, plant, or bacterial virus system- e.g. Naked or enveloped virus 2. Genomic-Baltimore classification 3. Serology, a taxonomy based on diagnostic virology, such as the infectious bronchitis virus (IBV) of chickens (a corona virus) [20].

The increasing number of reported viral nucleic acid

sequences allows the construction of phylogenetic trees based on a single gene or a group of genes. Sequence comparisons by themselves have not satisfactorily provided a clear classification of all viruses together but are widely used at the order, family, and genus levels. Recently the National Center for Biotechnology Information (NCBI) in Washington developed a system of pair wise sequence comparisons (the so-called PASC system) between viral sequences which allows a new virus to be assigned to known taxa. It seems probable that, in future, virus classification will make increasing use of sequence data [21].

2.1.1. Historical Systems

Virus taxonomy, which is described as the grouping of viruses into similar groups, determining the degree of intra as well as inters closeness in the groups, and naming such groups, is an activity that has just recently been undertaken [53]. Earlier, viruses were frequently categorized according to what disease they are responsible for. According to [35] he emphasized the importance of applying additional criteria for virus identification in addition to infection responses and associated hosts. He proposed naming of virus entities by prefixing popular names of its hosts in which they were discovered with a number, such as tobacco virus 1 for TMV.

Descriptive keys on the bases of five characteristics was created by [36]:

- (i) Transmission methods,
- (ii) Differential or natural hosts,
- (iii) Longevities invitro, (iv) thermodynamic death points,
- (iv) and symptoms that are distinct or precise.

Fifty viruses were recognized and categorized using the aforementioned key. [65] Presented a grouping system for the identified virus particles or viral illnesses and split up with 51 classes. The basic characteristics of many viruses that were not at all linked were grouped together. Grouping mostly on the basis of disease symptoms and methods of transmission was published by [28]. He named items using a trinomial system from Latin.

Viruses can be categorize into three groups under one order, the Virales, according to Holmes classification [63]. They are arranged as follows: Group I: Phaginae (attacks bacteria). Group II: Phytophaginae (attacks plants). Group III: Zoophaginae (attacks animals). Because it ignored morphological similarities, the system was rejected by others [43]. Various plans to a virus infecting plants alone or to any virus particles were set forth between 1940 and 1966. The foundation of the International Committee on the Nomenclature of Viruses was during the period of 1966, indicating the start of an international organization. After that, at a time of 1973, International Committee on the Taxonomy of Viruses (ICTV) was come in to existence [13].

2.1.2. Virus Taxa Descriptions

Virus classification continues to evolve with the technologies available for describing viruses. The first wave of descriptions, those before 1940, took into account mostly the visual symptoms of viral diseases along with modes of viral transmission. A second wave, between 1940 and 1970,

brought together an enormous amount of information from studies of virion morphology (electron microscopy, structural data), biology (serology and virus properties), and physicochemical properties of viruses (nature and size of the genome, number and size of viral proteins) [21].

The impact of descriptions on virus classification has been particularly influenced by electron microscopy and the negative-staining technique for virions in the 1960s and 1970s. With this technique, viruses could be identified from poorly

purified preparations of all tissue types and information about size, shape, structure, and symmetry could be quickly provided. As a result, virology progressed simultaneously for all viruses infecting animals, insects, plants, and bacteria. Since 1970, the virus descriptors list (Tables 1&2) has included genome and replication information (sequence of genes, sequence of proteins), as well as molecular relationships with virus hosts [21].

Table 1. *Virus family descriptors used in virus taxonomy [21].*

I. Virion properties
A. Morphology properties of virions
Size, shape, Presence or absence of an envelope and peplomers, capsomeric symmetry and structure
B. Physical properties of virions
Molecular mass, buoyant density and sedimentation coefficient, pH stability, thermal stability, cation (Mg^{++} , Mn^{++}) stability, solvent stability, detergent stability and radiation stability
C. Properties of genome
Type of nucleic acid – DNA or RNA, strandedness – single stranded or double stranded, linear or circular, sense – positive, negative, or ambisense, number of segments, size of genome or genome segments, presence or absence and type of 5' -terminal cap, presence or absence of 5' -terminal covalently linked polypeptide, presence or absence of 3' -terminal poly (A) tract (or other specific tract) and nucleotide sequence comparisons)
D. Properties of proteins (number of proteins, size of proteins, functional activities of proteins (especially virion transcriptase, virion reverse transcriptase, virionhemagglutinin, virion neuraminidase, virion fusion protein) and amino-acid-sequence comparisons)
E. Lipids (presence or absence of lipids and nature of lipids)
F. Carbohydrates (presence or absence of carbohydrates and nature of carbohydrates)
II. Genome organization and replication
A. Genome organization B. Strategy of replication of nucleic acid C. Characteristics of transcription D. Characteristics of translation and post-translational processing E. Site of accumulation of virion proteins, site of assembly, site of maturation and release F. Cytopathology, inclusion body formation
III. Antigenic properties (A. Serological relationships B. Mapping epitopes)
IV. Biological properties
A. Host range, natural and experimental B. Pathogenicity, association with disease C. Tissue tropisms, pathology, histopathology D. Mode of transmission in nature E. Vector relationships F. Geographic distribution

Table 2. *List of criteria demarcating different virus taxa [21].*

I. Order
Common properties between several families including: Biochemical composition Virus replication strategy Particle structure (to some extent) General genome organization
II. Family
Common properties between several genera including: Biochemical composition Virus replication strategy Nature of the particle structure Genome organization
III. Genus
Common properties within a genus including: Virus replication strategy Genome size, organization, and/or number of segments Sequence homologies (hybridization properties) Vector transmission
IV. Species
Common properties within a species including: Genome arrangement Sequence homologies (hybridization properties) Serological relationships Vector transmission Host range Pathogenicity Tissue tropism Geographical distribution

2.2. Classification of Viruses

2.2.1. Classification of Viruses by International Committee on Taxonomy of Viruses (ICTV)

Although the Baltimore classification method can be used to classify viruses into one of seven groups depending on how they synthesize mRNA, the formal taxonomic categorization of viruses is the responsibility of ICTV. The ICTV has established specific naming conventions and other classification rules. It has been suggested to create a list of all known viruses, and in 2013, some early efforts were under way [66].

Any biological classification system is based on species. Prior to 1982, it was believed that viruses could not be altered to conform to Ernst Mayr's conception of a species as a

reproductive unit and were therefore not amenable to such treatment. The ICTV began defining a species as "a cluster of strains" that have distinctive distinguishing characteristics in 1982. A more explicit theory was developed in 1991, which explains the idea in which a virus species is a polythetic class of viruses that comprises reproducing descendants and resides in certain ecological habitats [18].

A species is a monophyletic group of viruses whose characteristics may be recognized from those of other species by a number of criteria, according to a revision in the ICTV definition of species that took effect in July 2013 [2]. These requirements include the capsid's structure, the presence of an envelope, the gene expression program for its proteins, the range of the organism's hosts, its pathogenicity, and, most crucially, the similarity of the genetic sequences and their

evolutionary relationships [33; 34]. Depending on the taxon, the actual standards are different and occasionally inconsistent (using arbitrary similarity thresholds) or unrelated to lineage (based on geography) [56]. For many individuals, the situation is still open [18].

In the early 1970s, an organization the so called International Committee on the Taxonomy of Viruses started developing as well as implementing guidelines in order to name and group viruses. The International Union of Microbiological Societies has exclusively entrusted the ICTV with the responsibility of generating, maintaining, and updating the universal viral classification and nomenclature [46].

Numerous characteristics of the system, like taxon structure, are shared with a classification scheme significant for living entities. An organization of International Code of Zoological Nomenclature as well as an International Code of Nomenclature of Algae's, Fungi and Plants both have their own nomenclature systems, but there are some variations as well, such as the requirement that all taxonomic names be italicized [31]. Following, with the taxonomic suffixes in parenthesis, is how viruses are classified, starting at the realm level [31].

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*) and Species.

2.2.2. Structure-Based Virus Classification

Some viral groups that infect hosts from various domains of life have been found to share comparable virion assembly and structure. Examples include bacterial tecti viruses, eukaryote adenoviruses, and prokaryote Caudovirales as well as eukaryote herpes viruses [7, 8].

Because of this, it has been recommended that the structural relationships between viruses be used as a foundation for establishing higher-level taxa - structure-based viral lineages - that might supplement the ICTV classification scheme of 2010 [42]. By exploiting relationships found in protein folds, the ICTV has gradually added a large number of higher-level taxa.

2.2.3. Baltimore Classification

Depending on a combination of their nucleic acid (DNA or RNA), strandedness (single-stranded or double-stranded), sense, and mechanism of reproduction, viruses are divided into one of seven types (Figure 1). These groups are identified by Roman numbers and are named for the scientist Baltimore D., the recipient of a Nobel Prize. Other categories are based on the illness the virus causes or its morphology, neither of which are appropriate because various viruses might either produce the same illness or have a striking resemblance [11, 28].

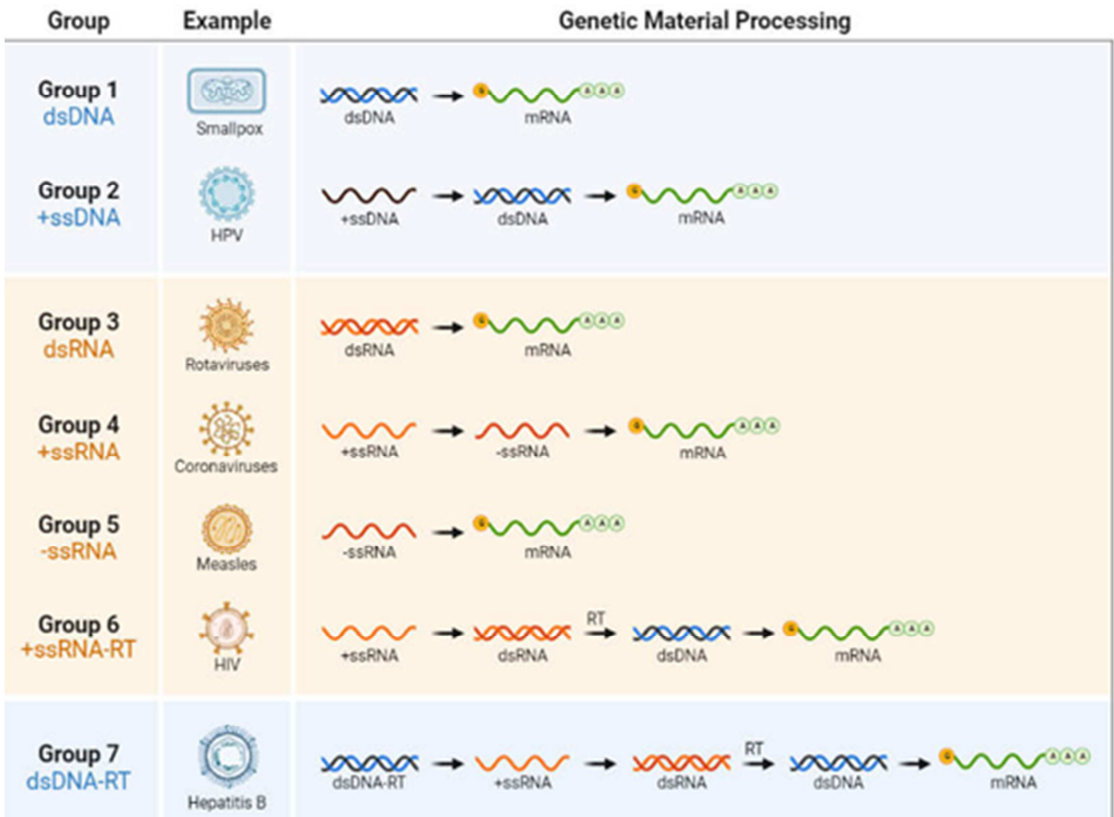


Figure 1. Baltimore classification of viruses based on mRNA synthesis (Biorender template).

Furthermore, determining viral structures under the microscope is frequently challenging. When viruses are grouped together based on their genomes, they will all exhibit

behaviors that are similar, providing some guidance for future research. One of the following seven categories can be used to classify viruses [11].

- (i) *dsDNA viruses* (e.g. Adeno viruses, Herpes viruses, Pox viruses).
- (ii) *ssDNA viruses (+) sense DNA* (e.g. Parvo viruses).
- (iii) *dsRNA viruses* (e.g. Reo viruses).
- (iv) *(+) ssRNA viruses (+) sense RNA* (e.g. Picorna viruses, Toga viruses).
- (v) *(-) ssRNA viruses and (-) sense RNA viruses* (eg, Orthomyxo viruses, Rhabdo viruses).
- (vi) *ssRNA-RT viruses (+) sense RNA with DNA intermediate in life-cycle* (e.g. Retro viruses).
- (vii) *dsDNA-RT viruses* (e.g. Hepadna viruses).

New virus proteins are encoded by mRNA molecules that are transcribed from viral genomes prior to viral nucleic acid replication. In some RNA viruses, the virus genome involved in the manufacturing of viral messenger RNA, while in others, the virion itself serves as the mRNA. In some circumstances, the virion itself contains crucial transcriptional enzymes. mRNA is commonly referred to as being in the plus (+) shape. Its complement is described as having a minus (-) structure. This nomenclature is also used to describe the structure of a single-stranded virus's genome, regardless of whether it is made up of DNA or RNA [60].

2.2.4. Classification of Virus on the Basis of Genetic Material

Small and non-living parasites are known as viruses. They cannot able to reproduce by themselves in the absence of host cell. A virus is made up of genetic material, either DNA or

RNA, covered in a protein. They are so categorized as DNA viruses and RNA viruses. The nucleic acid might be circular, linear, segmented, or unsegmented. It can also be single or double stranded [32].

(i). DNA Viruses

Deoxyribonucleic acid (DNA) serves as the basis for DNA viruses' genetic makeup, which is replicated by an enzyme called DNA polymerase (Table 3). Single-stranded DNA (ssDNA) viruses are those that only have one strand of DNA in their genome, while double-stranded DNA (dsDNA) viruses have two strands of DNA in their genomes. Except for viruses that reverse-transcribes DNA, all viruses that have a DNA genome belong to one of three identified viral realms: Duplodnaviria, Monodnaviria, or Varidnaviria [32].

On the other hand, several families and genera of *Incertain sedis* as well as the order Ligamenvirales are also used to categorize DNA virus particles. Viruses with double stranded DNA molecule are found in the domains of Duplodna viria and Varidna viria; other types of viruses having double stranded DNA molecule are named as *Incertain sedis*. Single-stranded DNA viruses in the domain Monodna viria typically encode a HUH endonuclease; other single-stranded DNA viruses are *Incertain sedis* Group I viruses have DNA that is double stranded. These areas contain the herpes and Chicken pox viruses. Group II viruses have DNA that is single-stranded [32].

Table 3. Examples of DNA viruses [32].

Virus family	Examples (common names)	Virionnaked / enveloped	Capsid symmetry	Nucleic acid type	Group
1. Adenoviridae	Canine hepatitis virus, Some types of the common cold	Naked	Icosahedral	Ds	I
2. Papovaviridae	JC virus, HPV	Naked	Icosahedral	ds circular	I
3. Parvoviridae	Human parvo virus B19, canine parvo virus	Naked	Icosahedral	Ss	II
4. Herpesviridae	Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus	Enveloped	Icosahedral	Ds	I
5. Poxviridae	Smallpox virus, cowpox, myxoma virus, monkeypox, vaccinia virus	Complex coats	Complex	Ds	I
6. Anelloviridae	Torque teno virus	Naked	Icosahedral	ss circular	II
7. Pleolipoviridae	HHPV1, HRPV1	Enveloped		ss/ds linear/circular	I/II

(ii). RNA Viruses

The term "RNA virus" refers to a virus that uses RNA as its genetic material. The genome structures of RNA viruses, which make about 70% of all viruses, differ dramatically. These viruses typically exhibit substantially an increased rate of mutations more than that of DNA viruses can do due to mistakes in the rate of involvement of enzymes during the process of RNA replication. Virus variants that are highly adaptable to new hosts are continuously produced as a result of mutation rates of 10⁻⁴. The viral RNA may be single-stranded (ss) or double-stranded (ds), and the genome may be dispersed over two or more independent segments (segmented genomes) or occupy a single RNA segment (ss) [55].

Additionally, the RNA strand of a single-stranded genome can either be a sense strand (plus strand), which can act as messenger RNA (mRNA), or an antisense strand (minus

strand), which is complementary to the sense strand but cannot translate mRNA into proteins. Since it can act as mRNA and start the translation of the virus's encoded proteins, sense viral RNA can reproduce on its own when introduced into cells. On the other hand, antisense RNA has no role in translation and cannot, by itself, create viral components [55].

Within the domain of Riboviria, the kingdom Orthornavirae is composed of all viruses that have an RNA genome and that encode an RNA-dependent RNA polymerase (RdRp) (Figure 2). Group III viruses, like the rota virus, have double-stranded RNA genomes. Group IV viruses have positive-sense single-stranded RNA genomes. This category contains a number of well-known viruses, such as the picorna viruses (a family of viruses that includes well-known viruses such as Hepatitis A virus, entero viruses, rhino viruses, polio virus, and foot-and-mouth virus), SARS virus, hepatitis C virus, yellow fever virus, and rubella virus. Group V viruses have genomes made of single-stranded RNA with a negative sense.

This process prevents cell lysis and aids enveloped viruses in evading the host's immune response. Additionally, viruses with envelopes are typically more vulnerable to extremes in pH, heat, dryness, and simple disinfectants. The following are examples of enveloped viruses: Influenza, Human cytomegalovirus (HCMV), HIV, Respiratory syncytial virus (RSV), Vaccinia virus, Corona viruses, Herpes viruses, Pox viruses, hepatitis viruses, Flavi viruses, Toga viruses, Hepatitis D, Orthomyxo viruses, Paramyxo viruses, Rhabdo viruses, Bunya virus, Filo virus, Retro viruses [71].

(ii). Non-Enveloped Virus

Viruses that are non-wrapped, commonly called "naked viruses," are typically more virulent than viruses that are enveloped. Due to the fact that they frequently result in host cell lysis. Let's examine why this is one of the key distinctions between non-enveloped and enveloped viruses. Cell lysis is the most frequent host cell departure method for non-enveloped viruses since they lack the additional lipid membrane. As a result of the viruses damaging the cell membrane's integrity throughout this process, the host organism suffers substantial tissue damage and cell death.

Extreme pH, heat, dryness, and straight forward disinfectants are more easily overcome by non-enveloped viruses. Hepatitis A and E viruses, Parvo virus, Papova virus, Picorna virus, Enterovirus, Rhino virus, Norovirus, and Adenovirus are a few examples of non-enveloped viruses [24; 71].

2.2.6. Classification of Virus Based on Capsid Structure and Shape of Virus

Polioviruses and the hepatitis A virus are naked icosahedra viruses. Epstein-Barr virus, Herpes simplex virus, Rubella virus, Yellow fever virus, HIV-1, are examples of enveloped icosahedra viruses. Enveloped helical viruses include Rabies, measles, mumps, and influenza viruses. Naked helical viruses are *Tobacco mosaic viruses*. Other viruses may be complex with several proteins; some others have icosahedra and helical capsid shapes together. For example, T4 bacteriophage, Smallpox virus, Hepatitis B virus, and Herpes viruses are typical for this group [48].

Each virus possesses a protein capsid to protect its nucleic acid genome from the harsh environment. The shape of a virus might be simple or complex. Viral forms might be helical or cylindrical, polyhedral (icosahedral and prolate), spherical, or complicated [50]. The capsid's geometric symmetry helps keep the virus stable and well-structured. The helical virus; this virus has a rod- or filamentous-like structure on its capsid [54].

A central cavity with this kind of structure houses the source of genetic material (nucleic acids) inside. Many viruses in this group are very lengthy, like an 18-wheeler, while others are relatively short, like a two-door vehicle. Helical viruses can be enveloped or naked. The first virus described, *Tobacco mosaic virus*, is a naked helical virus. In fact, most plant viruses are helical, and it is very uncommon that a helical plant virus is enveloped. In contrast, all helical animal viruses are enveloped. These include well-known viruses such as

Influenza virus, Measles virus, Mumps virus, Rabies virus, and Ebola virus [16; 50].

In addition, depending on how the capsomeres are organized, many allow for either a lot of flexibility or a lot of stiffness. Icosahedral viruses are made up of same type of structural subunits that form equilateral or equidistance triangles that are then placed symmetrically. Uniques of icosahedral shape, named as prolate, is a variant of the icosahedral shaped viruses. It is observed in a bacteriophage [16].

With a few notable exceptions, most animal viruses are roughly spherical. These exceptions include the Rabies virus, which has a bullet shape, the Ebola virus, which has a filamentous shape, the Pox virus, which has a brick shape, and the Adenovirus, which has a space craft shape [25]. With a few notable exceptions, most animal viruses are roughly spherical. These exceptions include the Rabies virus, which has a bullet shape, the Ebola virus, which has a filamentous shape, the Pox virus, which has a brick shape, and the Adenovirus, which has a space craft shape [25].

2.2.7. Classification of Virus on the Bases of Structural Symmetry

In order to self-assemble, viral capsids use one of two main symmetry types: icosahedral symmetry, in which the protein subunits form a symmetric shell over the nucleic acid-containing core, and helical symmetry, in which the protein subunits and nucleic acid are arranged in a helix.

- (i) *icosahedral or cubic symmetry viruses* are a polygon with 12 vertices (corners), 20 facet (sides), and 30 edges [25]. Each facet is a triangle with equal sides. Adenovirus, Picorna virus, Papova virus, herpes virus, etc. are a few examples of human pathogenic viruses that have icosahedral capsids, which are the most stable. There are two forms of icosahedral capsids: Pentagon and Pentagonal capsomere at the vertices. Hexagon; vertices have hexagonal caps. Reo and Picorna viruses are examples [25; 37].
- (ii) *A virus with a spiral or helical symmetry*. The capsomere and nucleic acid combine to form a structure that resembles in the form of either of helical structure and spiral tube. All helical viruses are RNA viruses, and the majority of them are enclosed. The *Tobacco mosaic virus* (TMV) is a known RNA virus that has 2130 similar capsomeres organized to form helical structure. It is the archetypal virus with helical symmetry. Paramyxo virus, Orthomyxo virus.
- (iii) *Radial symmetry virus*, such as Bacteriophage, are further instances [37; 59].
- (iv) *Complex symmetry*: Some viruses have a higher degree of complexity since they are made up of numerous distinct capsomeres with their own unique shapes and symmetry [50]. Due to the complexity of their capsid structure, neither icosahedral nor helical symmetry exist in them. Binal symmetry is an example of complex symmetry. Some viruses, like the T-phage (T2, T4, etc.), show intricate symmetry, including a head

and tail. Bacteriophages, which have an icosahedral head and a helical tail, are the most structurally complex viruses. The term "binal symmetry" refers to this structure. Pox virus is another illustration [37].

2.2.8. Classification of Virus on the Bases of Type of Hosts

- (i) *Animal Viruses*: Animal viruses are viruses that infect and survive inside the cells of all animals, including humans. For instance, the Poliovirus, Mumps virus, Rabies virus, Influenza virus, etc. RNA or DNA makes up their genetic makeup.
- (ii) *Plant Viruses*: Plant viruses are known for their ability to infect plants. They still have a protein sheath around their RNA genetic material, which is retained. Viruses that affect plants include the Turnip yellow virus, the Beet yellow virus, the Potato virus, and the Tobacco mosaic virus.
- (iii) *Bacteriophages*: The term "bacteriophage" or "bacteria eaters" refers to viruses that attack bacterial cells. They are genetically composed of DNA. Bacteriophages come in numerous variations. Typically, each type of bacteriophage will only target a single bacterial species or strain [38].

2.2.9. Classification of Virus on the Bases of Mode of Transmission

- (i) Infections spread by the respiratory pathway, such as the Swine flu or the Rhino virus,
- (ii) Viruses spread by the faecal-oral pathway, such as the Rota virus, Polio virus, and Hepatitis A virus,
- (iii) Viral transmission through sex: For instance, the Retro virus (iv). Virus spread by blood transfusions, such as the Hepatitis B and HIV viruses,
- (iv) Virus spread through animal bites (Zoonotic diseases), such as the Rabies, Alpha, and Flavi viruses [12; 17; 47; 61].

2.2.10. Classification of Virus on the Bases of Replication Properties and Site of Replication

- (i) All RNA viruses reproduce and assemble in the host cell cytoplasm, with the exception of the Influenza virus.
- (ii) Host replication in the nucleus and cytoplasmic assembly: Pox and Influenza viruses.
- (iii) Viruses that reproduce and assemble in the nucleus of the host cell include, all DNA viruses, with the exception of the Pox virus.
- (iv) Replication of viruses using ds DNA as an intermediary: All DNA viruses, Retro viruses, and some tumor-causing RNA viruses replicate via ds DNA as intermediates.
- (v) viruses that replicate via ss RNA as an intermediate include; All RNA viruses, with the exception of Reo viruses and tumor-causing RNA viruses [58].

2.3. Phylogenetic Tree in Virus

The relationship between common ancestor, intermediate ancestors, and contemporary species may be likened to the

relationship between root, internal nodes, and terminal nodes (leaves) of a tree respectively [26].

Figure 3 showed an example of phylogenetic relationships within the family *Retroviridae* [13].

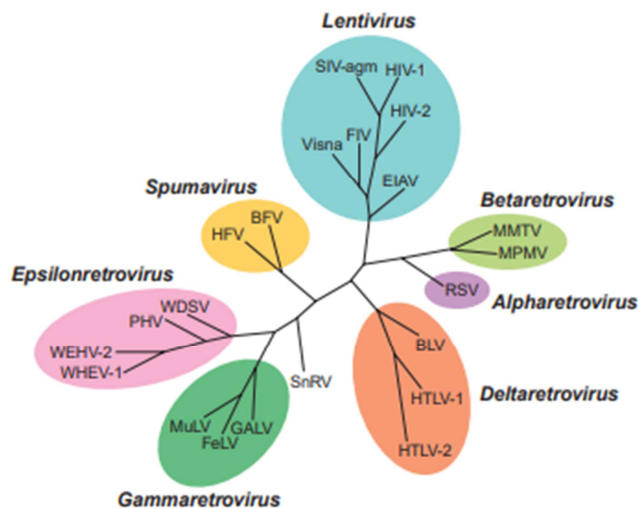


Figure 3. Phylogenetic analyses of conserved regions of the retrovirus polymerase gene [13].

2.4. Latest Classification of Plant Virus

Based on the kind of genome (RNA or DNA), strandedness (single or double stranded), and replication strategy, plant viruses are divided into five main types. Orders, families, genera, and species are present in every group (which is not a recognized taxon). The five groups are single-stranded positive sense RNA (ss (+) RNA), single-stranded negative sense RNA (ss (-) RNA), double stranded RNA (ds RNA), double stranded DNA (ds DNA (RT)), and single stranded DNA (ss DNA) [5].

2.4.1. Single Stranded +ve Sense RNA [(+) RNA] Viruses

Order: Nidovirales:

- (i) *Family Bromoviridae* which includes viruses like Bromo virus (*Brome mosaic virus*, or BMV), Alfamo virus (*Alfalfa mosaic virus*, or AMV), Cucumo virus (*Cucumber mosaic virus*, or CMV), and Ilar virus (*Tobacco streak virus*-TSV),
- (ii) *Family Closteroviridae*; examples include Clostero virus (*Beet Yellows Virus*, or BYV), and Ampelo virus (*Grapevine leaf roll associated virus* GLRaV),
- (iii) *Family Como viridae*, which includes viruses such as Como virus (*Cowpea mosaic virus*), Faba virus (*Broad bean wilt virus*), and Nepo virus (Nematode transmitted polyhedral virus, like *Tobacco ring spot virus*) [51].
- (iv) *Family Flexi viridae*; examples are Potex type of viruses in potato (*Potato virus X*) and Carla viruses (*Carnation latent viruses*),
- (v) *Luteoviridae* family, which includes luteo virus (*Barley yellow dwarf virus*, or BYDV) and polero virus (*Potato leaf roll virus*-PLRV),
- (vi) *Family Potyviridae*, the largest family of plant viruses

has received the most research attention. One of the most effective plant viral diseases is the Poty virus genus. For instance, Poty virus (*Potato virus Y*-PVY), Ipomo virus (*Sweet potato mild mottle virus*-SPMMV), and Bymovirus (*Barley yellow mosaic virus*) are some examples [51].

- (vii) *Family Sequiviridae*, including Waika virus and Sequi virus (*Parsnip yellow fleck virus*-PYFV) (*Rice tungro spherical virus*- RTSV).
- (viii) *Family Tombusviridae*, including Necro virus, Carmo virus, Tombus or TBSV virus (*Tomato bushy stunt virus*) and TNV (*Tobacco necrosis virus*).
- (ix) *Tymoviridae family*, including Tymo virus (*Turnip yellow mosaic virus*- TYMV). A family has not yet been assigned to certain highly significant viruses called 'floating genera', like Tobamovirus (*Tobacco mosaic virus*, or TMV), Tobra virus (*Tobacco rattle virus*, or TRV), Potex virus (*Potato virus X*, or PVX), etc [10].

2.4.2. Negative Sense Single Stranded RNA Viruses [ss (-) RNA] Viruses

Only enveloped plant virus particles can be a part of this group. Order: Mononegavirales,

- (i) *Family: Rhabdoviridae*, which includes Tospo or TSWV virus (*Tomato spotted wilt virus*), GBNV virus (*Groundnut bud necrosis virus*) and Nucleorhabdo or PYDV virus (*Potato yellow dwarf virus*).
- (ii) *Family: Bunya viridae*, which includes Cytorhabdo virus (*Lettuce necrotic yellows virus*-LNYV) and Nucleorhabdo viruses [5].

2.4.3. Double Stranded RNA (ds RNA) Viruses

There is no order assigned

- (i) *Family: Rheoviridae*, including Phytorheo virus and the Fiji virus (*Fiji disease virus*-FDV) (*Wound tomur virus*-WTV).
- (ii) *Family: Partiviridae*, including the White Clover cryptoviruses Alphacryptovirus and Betacryptovirus [5].

2.4.4. Double Stranded DNA Virus [ds DNA (RT) Virus]

The most varied and extensive group of Baltimore classes is double-stranded DNA viruses. These viruses predominate in the bacterial virome and are also widespread in eukaryotes, though not to the same degree as RNA viruses. A phylogenetic tree for this Baltimore class cannot be created even in theory because no single gene is shared by all dsDNA viruses. However, networks of gene exchange and phylogenies of the genes that are conserved in big virus groups offer a practical framework for categorizing dsDNA viruses. No order has been assigned i) *Family: Caulimoviridae*, e.g., Caulimovirus (*Cauliflower mosaic virus*- CaMV) [19].

2.4.5. Single Stranded DNA [ss DNA] Virus

Archaea, bacteria, and eukarya are three separate domains that can each be infected by various ssDNA viruses, which are substantially divergent and reflect the polyphyletically generated groupings. Only the Gemini viridae and Nano

viridae families of eukaryotic ssDNA viruses are acknowledged as important plant diseases out of the six diverse families [15].

There is currently no assigned order: *Family: Gemini viridae*, including Mastrevirus (*Maize streak virus*, MSV), Curtovirus (*Beet curly top virus*, BCTV), Begomovirus (*Bean golden mosaic virus*, BGMV), *Bhendi yellow vein mosaic virus*, BYMV, and *Cassava latent virus*, CLV. I *Family: Circoviridae*; examples include *Nano virus* (*Subterranean clover stunt virus*; *Banana bunchy top virus*-BBTV) [30].

2.5. Typical Virus-Like Agents

Defective Viruses: these virus like agents consist of both viral nucleic acid and proteins but are unable to replicate in the absence of 'helper' virus and need the involvement of helper virus to accomplish its multiplication. During growth many defective viruses are produced in addition to other infectious viruses [49]. **Pseudovirions:** these virus like agents composed of host cell DNA instead of viral DNA within the capsid. It can infect cells but does not replicate. **Viroids:** it comprises solely of a single molecule of circular RNA without a protein coat or envelope. Its RNA is small and does not code for any protein. It can cause several plant diseases but are not implicated in human diseases. **Prions:** Are infectious particles that are contained solely of protein but there is no detectable nucleic acid. It can cause certain slow diseases like Creutzfeldt-Jacob Disease (CJD) in human and scrapie in sheep [57].

2.6. Nomenclature of Virus

There isn't a standardized format for virus species names yet, in contrast to the binomial nomenclature used for cellular species. The ICTV now requires that a species name comprise as few words as possible while still being distinct, and must not merely contain the term virus and the host name [32]. Especially for higher plants and animals, species names frequently have the form of [Disease] virus. The ICTV released a proposal in 2019 for a vote in 2020 to adopt a more defined system of binomial nomenclature for viral species names. Some virologists argued that the debate took place while many in the field were preoccupied owing to the COVID-19 pandemic, which is why they later opposed the prospective modification to the naming system [66].

Many plant viruses are named after the most conspicuous symptom they cause on the first host in which they have been studied. Thus, a virus causing a mosaic on tobacco is called tobacco mosaic virus, whereas the disease itself is called tobacco mosaic; another virus causing spotted wilt symptoms on tomato is called tomato spotted wilt virus and the disease is called tomato spotted wilt, and so forth. Considering, however, the variability of symptoms caused by the same virus on the same host plant under different environmental conditions, by different strains of a virus on the same host, or by the same virus on different hosts, it becomes apparent that this system of nomenclature leaves much to be desired [4].

In formal taxonomic usage, the virus order, family, genus and species names are printed in italics or underlined with first

letter being capitalized. Other words in species names are not capitalized unless they are proper nouns or parts of proper noun. Also in formal usage, names of taxons should precede the name being used e.g. Family Caulimoviridae, the Genus Clostero virus, the species Potato virus Y. However, in less formal instances which are widely used, the taxonomic unit is omitted [32].

Because of the difficulty in creating new official international names for virus species, it has been decided in 1998 by the ICTV to use the existing English vernacular virus names [70]. However, to differentiate virus species names from virus names it has also been decided that their typography would be different, that is, the species names would be italicized, and the first letter of the name capitalized while the virus names would not. In addition ICTV had created an additional category called 'Tentative Species Names' to accommodate viruses that seemed to belong to a new species, but did not have enough data to support this decision; it was also a way to 'reserve' a name already used in literature. In 2005, ICTV decided to replace this category by 'Unassigned Viruses' in the genus [21].

For several years, plant virologists adopted a different nomenclature, using the vernacular name of a virus but replacing the word 'virus' by the genus name: for example, Cucumermosaic, Cucumovirus and Tobaccomosaic, Tobamovirus. This system is called 'the non Latinized binomial system', although the binomial order is the opposite of the typical Latinized binomial system where the genus name ends with the virus name [67]. Though this usage is favored by many scientists, in formal usage, the name of the taxon precedes the name of the taxonomic unit: for example, "the family Picornaviridae" or "the genus Rhinovirus" [21].

In informal vernacular usage, virus order, family, subfamily, genus, and species names are written in lower case roman script; they are not capitalized or italicized (or underlined) – for example 'animal reo viruses'. To avoid ambiguous identifications, it has been recommended to journal editors that published virological papers follow ICTV guidelines for proper virus identification and nomenclature and those viruses should be cited with their full taxonomic terminologies when they are firstly mentioned in an article. The order Mononegavirales, the family Paramyxoviridae, the subfamily Pneumovirinae, the genus Pnemo virus, the species Human respiratory syncytial virus can be an example to this [32].

Since 1966 the classification and nomenclature of viruses at the higher taxonomic levels (families and genera) has been systematically organized by the ICTV. But, hierarchical levels under the species level such as strains, serotypes, variants, and pathotypes are established by international specialty groups and/or by culture collections, but not by the ICTV (Fauquet, 2008). Families are named with a suffix-*viridae*. Subfamilies have the suffix-*virinae*; for an order is '*virales*'; genera the suffix-*virus* [23].

The last word of the species is 'virus. The prefix may be another Latin word or a *sigla*, i.e., an abbreviation derived

from some initial letters. Latinized family, subfamily, and generic names are written in italics; vernacular terms derived from them are written in roman letters. For example, the term poxvirus is used to designate members of the family *Poxviridae*. It is still customary to use vernacular terms rather than Latinized binomials for viral species, e.g., foot-and-mouth disease virus [23].

The names for plant virus groups that were first proposed in 1970, and have been widely used by plant virologists since then. Currently, the rules are as set out below [22]. Various approaches, (do not obey the binomial nomenclature) derived from: 1. Named after the diseases eg. Measles virus, small pox virus: 2. Name after the places where the disease first reported eg. Newcastle disease virus, Ebola virus, Nor walk virus, Bunya viridae: 3. Host and signs of disease eg. Tobacco mosaic virus, Cauliflower mosaic virus brome mosaic virus: 4. Latin and Greek words eg. Corona viridae – "Crown" Parvoviridae "small": 5. Virus discoverers eg. Epstein-Barr virus: 6. How they were originally thought to be contracted eg. Dengue virus ("evil spirit"), influenza virus (the "influence" of bad air): 7. Combinations of the above eg. *Rous Sarcoma virus* [22; 44].

Rule-1. The code of bacterial nomenclature shall not be applied to viruses.

Rule-2. Nomenclature shall be international.

Rule-3. Nomenclature shall be universally applied to all viruses.

Rule-4. In effort will be made towards a Latinized nomenclature.

Rule -5. Existing Latinized names shall be retained whenever feasible.

Rule-6. The law of priority shall not be observed.

Rule-7. Sigla may be accepted as names of viruses or virus groups, provided that they are meaningful to workers in the fields and are recommended by international virus study groups.

Rule -8. No person's name shall be used.

Rule-9. Names should have international meaning.

Rule-10. The rules of orthography of names and epithets are listed in Chapter 3, Section 6 of the proposed international code of nomenclature of viruses.

Rule-11. For pragmatic purposes the species is considered to be a collection of viruses with like characters.

Rule-12. Numbers, letters, or combinations thereof may be accepted in constructing the names of species.

Rule-13. These symbols may be preceded by an agreed abbreviation of the latinized name of a selected host genus or, if necessary, by the full name.

Rule-14. The genus is a group of species sharing certain common characters.

Rule-15. The ending of the name of a viral genus is '... virus'

Rule-16. A family is a group of genera with common characters, and the ending of the name of a viral family is '... viridae'

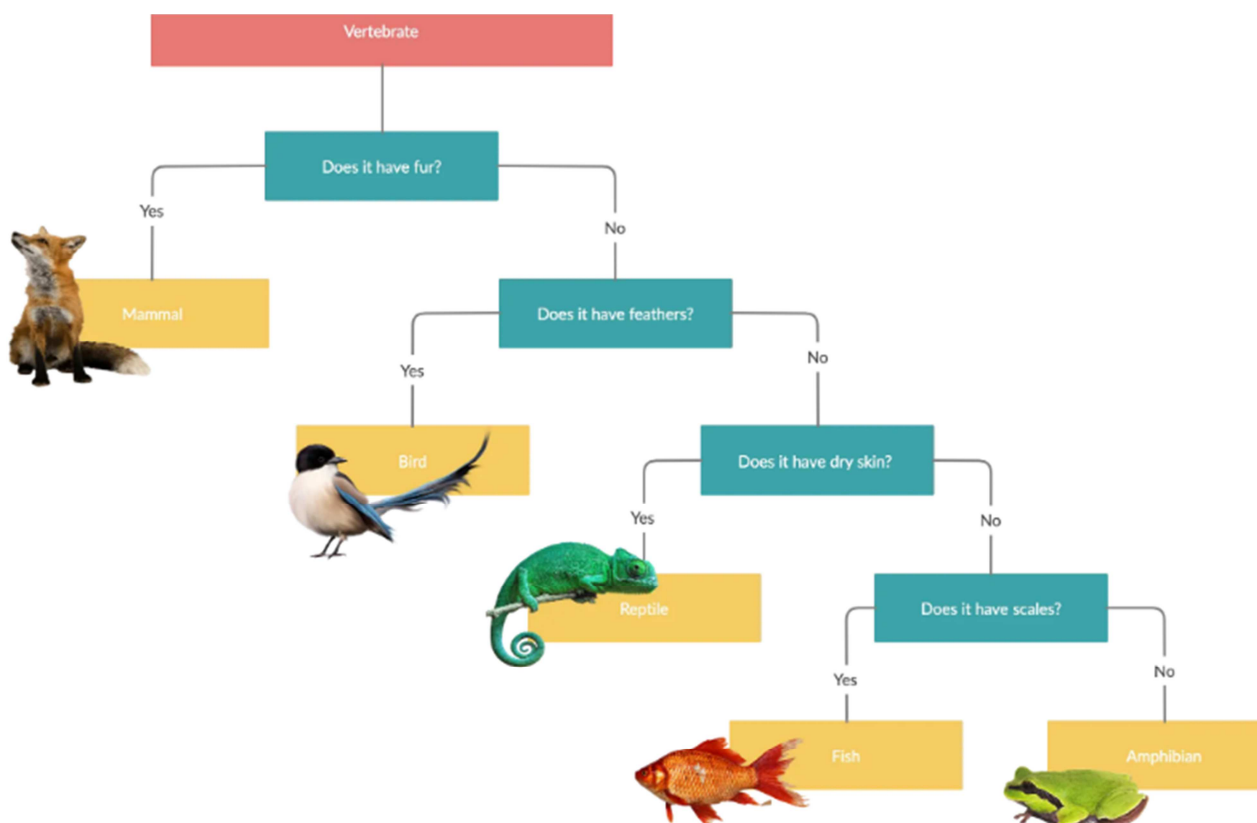


Figure 4. Examples of dichotomous keys [6].

2.7. Taxonomic Keys

Dichotomous” means divided into two parts [6]. The dichotomous key is a chart or classification table that shows the category-wise classification of different objects (Figure 4). Such techniques help to diagnose unknown organisms by providing possible solutions to a series of questions relied on the basis of opposing characteristics (eg: physical features) that yields two possible answers or outcomes [68]. Scientists and specialists can classify animals, plants, viruses, and other species using these dichotomous key charts. It helps the scientists give a clear view of those species and is very helpful for the learners as it makes conceptualization easy. Both qualitative and quantitative factors are considered [6].

3. Conclusion

The need for virus classification is supported by the common human need for organization and acts as scientific tool to compare viruses and extrapolate useful information from one virus to another and from one family to another. Taxonomy of viruses is varied at upper and lower taxonomic ranks where the former organized by ICTV but the latter by international specialty groups and/or by culture collections. For all taxa except species, new names are created following ICTV guidelines.

Naming of viruses is unable to be separated from grouping. Using correct orthography and typography of virus taxa is not simply an exercise meant to complicate the task of virologists

but is based on rules that help scientists to extract useful information from what is written down.

For all these reasons, virus classification and nomenclature have always been very controversial and have led to passionate discussions. The number of classified viruses, as well as the number of each type of taxa, has increased exponentially through time and continues to grow as DNA sequencing has become a routine technique to do so.

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