NOMENCLATURE & CLASSIFICATION OF PLANT VIRUSES

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What is the purpose of classification?

- To make structural arrangement for easy comprehension
- To be able to communicate with each other
- To enable prediction of properties of new viruses
- Possible evolutionary relationships
Viruses are the entities
- whose genome is a nucleic acid, either DNA or RNA,
- which reproduce inside living cells and use their synthetic machinery to direct the synthesis of specialized particles, the virions which contain the viral genome and transfer it to other cells.
Latin binomials were proposed first by Holmes in 1939.

Various other schemes proposed between 1940 and 1966.

International Committee on the Nomenclature of Viruses (ICNV) (1966); met in 1970

- Naming and cataloguing of viruses.
The International Committee on Taxonomy of Viruses (ICTV) has framed 20 rules for virus nomenclature. Among others it recognizes common names, their international meaning and use of existing names.

**ICTV database (ICTVdb)** - A centralized repository of virus information

Collect information from databases around the world.

- facilitated the job of accurate identification and diagnosis of new and important virus diseases.
Until recently, many viruses were not associated with specific taxa and most plant viruses were categorized into groups rather than families or genera.

- As more sequence data have accumulated, more viruses have been placed in newly described or existing taxa,
- and the “group” designation has given way to categorization into families or genera of existing families.
- Some viruses are still not associated with named families, but with the current taxonomic framework solidly in place, this number is being reduced with each report of the ICTV.
Rules of orthography changed in 1999 to require italics, but no true binomial – only modified binomial e.g.

- Family *Reoviridae*
  - Genus *Orbivirus*
    - Species *Bluetongue virus* (24 named strains: BTV-1 to BTV-24)

- 7th Report of the ICTV was published in 2000
  - 56 families, 9 subfamilies, 233 genera, and 1550 virus species
  - Includes retrotransposons, satellites, viroids, prions

- 8th Report 2005
- Criteria for species demarcation vary for different families
ICTV published the ratification on taxonomic proposals in 2008.

As per the ICTV statutes, the final stage in the process of making changes to the universal schemes of virus classification is the ratification of taxonomic proposals by ICTV members.

Ratification is done in plenary meeting of ICTV or by circulation by mail and then followed by ballot.

The review process:
- Contained new genera & spp.
- Changed the status of some viruses.
Various virus classification schemes have been used
- Host & symptoms have been important considerations
- Particle morphology was important after EM developed
- Physico-chemical properties became important later
  - Sedimentation coefficient and density of particles
  - Protein compositions and sizes
  - Nucleic acid types, numbers, and sizes
- Sequence analysis confirmed most relationships that were inferred otherwise, and revealed new ones
  - Molecular phylogeny now a primary tool for classifying viruses
  - Complete genomes can be analyzed relatively quickly
Descriptors used in Virus Taxonomy

Virion properties

- Morphological properties of virion
  - Size; Shape; presence or absence of envelop or peplomers; capsomeric symmetry & structure

- Physical properties of the virus
  - Molecular mass
  - Buoyant density
  - Sedimentation coefficient
  - pH stability, Solvent stability, Radiation stability, detergent stability
  - Cation (Mg²⁺, Mn²⁺, Ca²⁺) stability
Descriptors used in virus Taxonomy

- Properties of genome
  - Type of nucleic acid
  - Strandedness of n/acid
  - Linear or circular
  - Sense: +ve or –ve or ambisense
  - Number of segments
  - Size of genome or genome segments
  - Presence or absence and type of 5’ terminal cap
  - Presence o or absence of 5’terminal covalently-linked polypeptide
  - Presence o or absence of 3’terminal poly (A) tract (or other specific tract)
  - Nucleotide sequence comparisons
Properties of protein
- Number; size; functional activities and Amino acid sequence comparisons

Lipids
- Presence or absence; Nature

Carbohydrates
- Presence or absence; Nature

Genome organization and replication
- Genome organization
- Strategy of replication of nucleic acid
- Characteristics of transcription
- Characteristics of translation and post translational processing
- Sites of accumulation of virion proteins, site of assembly site of maturation and release
- Cytopathology inclusion body formation

Descriptors used in virus Taxonomy
Antigenic properties
- Serological relationship
- Mapping epitopes

Biological properties
- Host range, natural & experimental; pathogenicity, etiology
- Tissue tropism, pathology, histopathology
- Mode of transmission in nature; vector relationship
- Geological distribution
Criteria demarcating different virus taxa

- **Order**
  - Common properties between several families including
    - Biochemical composition
    - Virus replication strategy
    - Particle structure
    - General genome organization

- **Family**
  - Common properties between several families including
    - Biochemical composition
    - Virus replication strategy
    - Nature of particle structure
    - Genome organization
Criteria demarcating different virus taxa

- **Genus**
  - Common properties with a genus including:
    - Virus replication strategy
    - Genome size, organization and/or number of segments
    - Sequence homologies
    - Vector transmission

- **Species**
  - Common properties within a including:
    - Genome rearrangement
    - Sequence homologies
    - Serological relationship
    - Vector transmission
    - Host range
    - Pathogenicity
    - Tissue tropism
    - Geographical distribution
Criteria used for classifying plant viruses

1. Structure of the virus particle
2. Physicochemical properties of the virus particle
3. Properties of viral nucleic acid
4. Viral proteins
5. Serological relationships
6. Activities in the plant
7. Methods of transmission
1. Structure of the virus particle

FIGURE:
Relative shapes, sizes, and structures of some representative plant viruses.
(A) Flexuous thread-like virus.

(B) Rigid rod-shaped virus. (B-1) Side arrangement of protein subunits (PS) and nucleic acid (NA) in viruses A and B. (B-2) Cross-section view of the same viruses. HC, hollow core.
(C) Short, bacillus-like virus. (C-1) Cross-section view of such a virus.
(D) Isometric polyhedral virus. (D-1) Icosahedron representing the 20-sided symmetry of the protein subunits of the isometric virus.
(E) Geminivirus consisting of twin particles.
2. Properties of viral nucleic acid

- Most important for placing viruses into families, and genera and
- Establishment of new family or genus.
  - E.g. luteoviruses were earlier recognized as group consisting of BYDV, SbDV and RPV, RMV and SGV strains of BYDV in 2nd ICTV report
  - but over the next few years information obtained about their genome properties they were named as *Luteovirus* genus in 6th report (Murphy et al., 1995) ; the species were divided into two subgroups typified by BYDV-PAV and PLRV.
  - Again their classification was again revised based on the differences in genome sequences and presences of different polymerase enzymes in different species so ultimately divides into three genera in the family *Luteoviridae* (Reganmortel et al., 2000)

- 2nd example is of Caulimoviridae family, in which the four genera (Cassava vein mosaic virus, Soybean chlorotic virus, Petunia vein clearing virus in the genus *Caulimovirs* and two (Badnavirus and RTBV in the genus *Badnavirus*)
  - These are now divided into different genera
3. Viral proteins

Viral protein properties mainly the amino acid sequences have great importance in virus classification at almost all levels including strains.

- Cp gene sequences have been used to differentiate many virus species within a family or genus e.g. in case of Potyviruses the cp-gene clearly differentiate the virus species and to some extent their strains. However, cp gene has more significance in species differentiation than in strains.

- The three dimensional structure of the viral protein is important to compare the amino acid substitution in different viruses in a group to be correlated with biological functions e.g.
  - In TMV and six related viruses, the aa sequence homologies ranged between 28 to 82% out of which 25 residues were conserved in all the seven sequences.
Phylogenetic tree showing relationship of BCMV strains at coat protein (CP only) (a) and 30 terminal region (b) (comprising Nib and complete CP region)
Maximum-likelihood tree of 61 CP sequences of different strains of bean common mosaic virus (BCMV).
4. Serological relationships

5. Activities in the plant

6. Methods of transmission

7. Methods of transmission
Plant viruses are diverse, but not as diverse as animal viruses – probably because of size constraints imposed by requirement to move cell-to-cell through plasmodesmata of host plants.
**Kingdom: Viruses**

Virus genera not yet assigned into families

RNA viruses

**Single-stranded positive RNA [(+) ssRNA]**

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<th>Genus</th>
<th>Type species</th>
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<td>Fungal transmission</td>
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</table>

**Filamentous particles**

<p>| 1 ssRNA              | —      | Allexivirus | Shallot virus X                        | Eriophyid mite transmission   |
| —                    | —      | Carlaviruses | Carnation latent virus                 | No vector                     |
| —                    | —      | Foveavirus  | Apple stem pitting virus               | By contact only               |
| —                    | —      | Potexvirus  | Potato virus X                         | No vector. Some seed transmission |
| —                    | —      | Capillivirus | Apple stem grooving virus              | No vector. Some seed transmission |
| —                    | —      | Trichovirus | Apple chlorotic leafspot virus         |                               |
| —                    | —      | Vitiviruses | Grapevine virus A                      | Mealybugs, scale insects, aphids |</p>
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<td>Rice tungro bacilliform virus-like</td>
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ssRNA (RT) Pseudoviridae: retrotransposons
Cryptograms

- In 1966, Gibbs et al., and in 1968, Gibbs and Harrison, introduced a system of cryptograms in addition to vernacular name with a view to give concise information about the properties of the virus.
- Cryptogram gives quick summary of the virus properties
- In this different keys are used to denote the viral properties.
Keys to Term

1. I Term: Type of n/a / stranded ness
   1. R: RNA₁ = ss
   2. D: DNA₂ = ds.

   - II Term: mol. wt. of n/a in millions/% of n/a in infective particle.
   - III term: Out line of the particle shape/ outline of nucleocapsid:
     - S: Spherical (isometric)
     - E: Elongated (rod)/ E= ends parallel
     - B: Bacilliform
### Keys to Term

**4th term:**

<table>
<thead>
<tr>
<th>Type of host infected/</th>
<th>Type of vector</th>
</tr>
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<tbody>
<tr>
<td>B = BACTERIUM</td>
<td>Ap: Aphid</td>
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<tr>
<td>F = FUNGUS</td>
<td>Au: leafhopper</td>
</tr>
<tr>
<td>i = INVERTEBRATE</td>
<td>Cl: beetle</td>
</tr>
<tr>
<td>S = SEED PLANT</td>
<td>Fu: fungus</td>
</tr>
<tr>
<td></td>
<td>Ne: nematode</td>
</tr>
<tr>
<td></td>
<td>Th: thrips</td>
</tr>
<tr>
<td></td>
<td>W: whitefly</td>
</tr>
<tr>
<td></td>
<td>O: spread without vector</td>
</tr>
<tr>
<td></td>
<td>Se: seed transmitted</td>
</tr>
<tr>
<td></td>
<td>*: information unknown</td>
</tr>
</tbody>
</table>
Cryptogram examples

1st  2nd  3rd  4th

- TMV: R/1:2/5; E/E: S/O, Se
- CMV: R/1: 1.3/18 + 1.1/18 + 0.3/18: S/S: S/Ap, Se
- PVY: R/1: 3.1/6: E/E: S/Ap
- MSV: D/1: 0.7/*/ S/S: S/Au, W