

Course: MSc MICROBIOLOGY SEMESTER II  
Subject: Virology (MIC 204)

**Lecture 2**  
**Classification of Viruses**

Dr Shilpa Kaistha  
Dept of Microbiology  
IBSBT, CSJMU, Kanpur

# Virology; the study of viruses

Viruses have one major characteristic in common: they are obligate intracellular parasites.

Viruses are UNABLE to grow and reproduce outside of a living cell. No virus is able to produce its own energy (ATP) to drive macromolecular synthesis.

However, in many other respects, they are a highly diverse group.

# How are viruses named?

- Based on:
  - the disease they cause  
poliovirus, rabies virus
  - the type of disease  
murine leukemia virus
  - geographic locations  
Sendai virus, Coxsackie virus
  - their discoverers  
Epstein-Barr virus
  - how they were originally thought to be contracted  
dengue virus (“evil spirit”), influenza virus (the “influence” of bad air)
  - combinations of the above  
Rous Sarcoma virus

# Virus classification and nomenclature

- Latin binomials were proposed first by Holmes in 1939
- Various other schemes proposed between 1940 and 1966
- 1966 the International Committee for the Nomenclature of Viruses formed; met in 1970
- Changed to the International Committee for the Taxonomy of Viruses in 1973

- Viruses not classified as members of Kingdoms
- Do not obey biological taxonomy
- Based
  - Classical system: host based
  - Genomics: Baltimore classification
  - Serology: Diagnostic virology Corona virus have antigenic differences but very few host or genetic differences (single/double mutant variants)

# Virus Classification

Taxonomy from Order downward

- Family often the highest classification. Ends in -viridae.
- Many families have subfamilies. Ends in -virinae.
- Bacterial viruses referred to as bacteriophage or phage (with a few exceptions).

## Examples

family *Myoviridae*

genus T4-like phages

type species *Enterobacteria phage T4*

family *Herpesviridae*, subfamily *Betaherpesvirinae*

genus *Muromegalovirus*

type species *Murine herpesvirus 1*

# Holme's Classification

- 1948. Linnaean Taxonomy with binomial nomenclature
- Group I : Phaginae
- Group II: Phytophaginae
- Group III: Zoophaginae
- Rejected as no consideration for morphological characteristics

# LHT System of Classification

- **1962. Lwoff, Horne and Tournier** proposed system adopted by Provisional Committee on Nomenclature of Viruses (PCNV) formed by International Association of Microbiological Society
- LHT based on
  - Nature of NA
  - Symmetry of viral particle
  - Envelop presence or absence
  - Diameter of capsid
  - Number of capsomere
- Phylum Vira
  - Subphylum Deoxyvira and SubPhylum Ribovira
    - Class
      - Order
        - » Family
- Disadv: No evolutionary relationship , not a natural classification (traits to find similarity/dissimilarity)



- **1967. Bellet classification** based on
  - MW
  - % GC
  - Phenotypic, serological and antigenic properties also considered
- **1969. Gibbs system of classification** for Plant Viruses (135 viruses into 6 broad groups)
  - Shape of Capsid
  - Mode of transmission
  - Type of vector
  - Symptoms on host
  - Name of accessory particles

- **1975. Casjens and King's Classification**
  - NA type
    - (4 :ssRNA,dsRNA,ssDNA,dsDNA)
  - Capsid symmetry
    - (Helical, Iscosahedral, Icosahedral complex)
  - Presence /absence of envelop
  - Site of assembly of envelop (nuclear or cytoplasmic)

# The Baltimore classification system

1971- 2008. David Baltimore: Based on genetic contents and replication strategies of viruses. According to the Baltimore classification, viruses are divided into the following seven classes:

1. dsDNA viruses
2. ssDNA viruses
3. dsRNA viruses
4. (+) sense ssRNA viruses (codes directly for protein)
5. (-) sense ssRNA viruses
6. RNA reverse transcribing viruses
7. DNA reverse transcribing viruses (added later- modified Baltimore Classification)

where "ds" represents "double strand" and "ss" denotes "single strand".

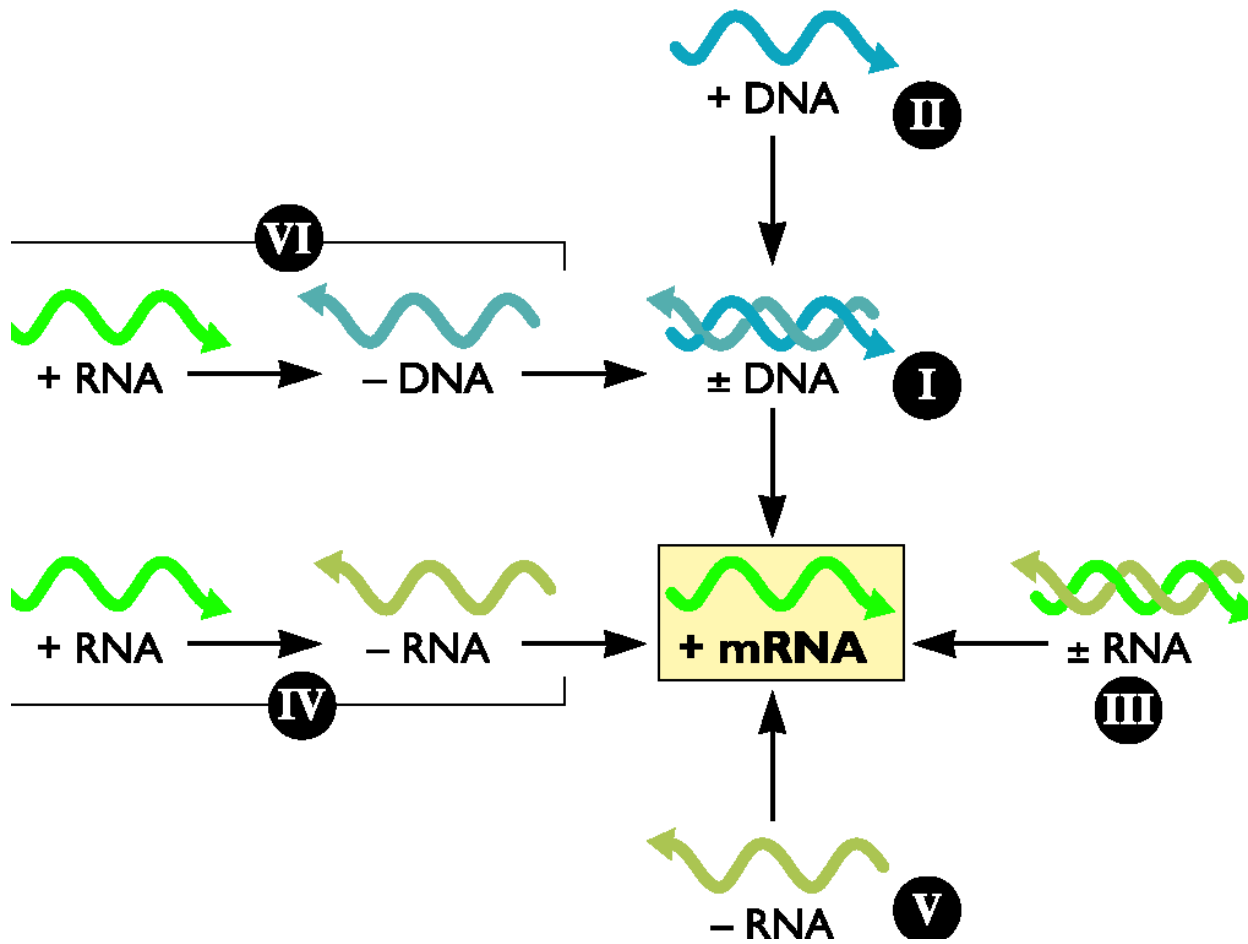
# Dimmock's modified Baltimore Classification

- 2001. Dimmock classified viruses into 6 sections (based on host preference): animal, plant, fungi, bacteria, satellite and viroid.
- Each section divided into 7 Classes (revised Baltimore scheme) and each class into family

# Virus Classification I

## - the Baltimore classification

- All viruses must produce mRNA, or (+) sense RNA
- A complementary strand of nucleic acid is (–) sense
- The Baltimore classification has + RNA as its central point
- Its principles are fundamental to an understanding of virus classification and genome replication, but it is rarely used as a classification system in its own right



# Virus classification II - the Classical system

- This is based on three principles -
  - 1) that we are classifying the virus itself, not the host
  - 2) the nucleic acid genome
  - 3) the shared physical properties of the infectious agent (e.g. capsid symmetry, dimensions, lipid envelope)

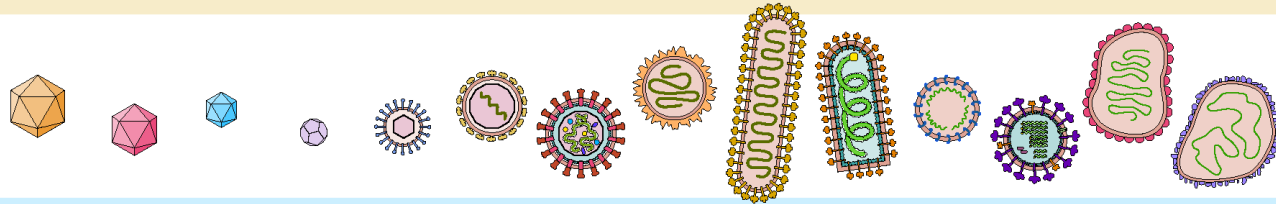
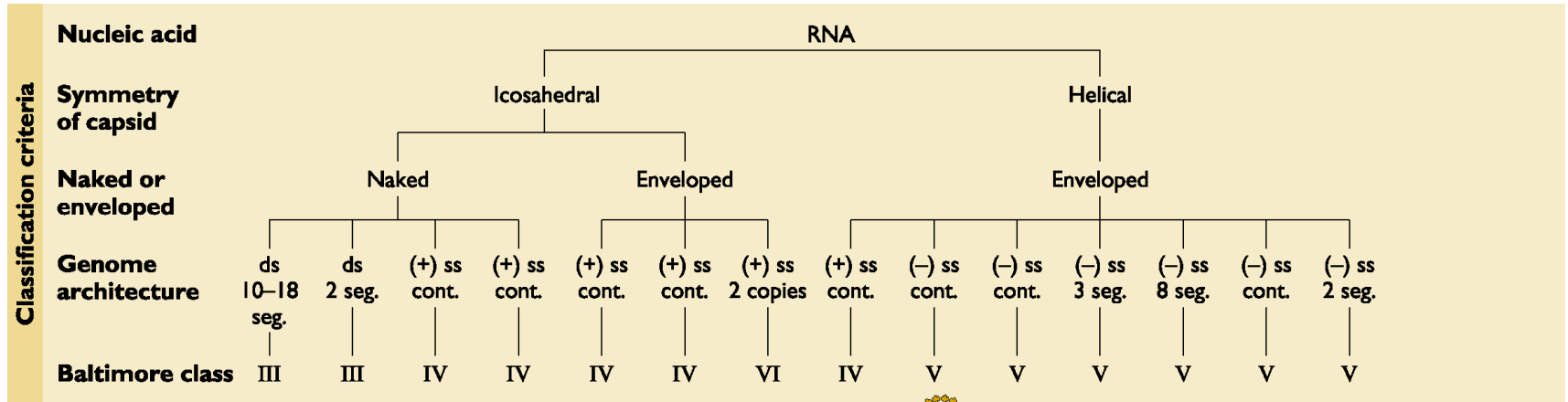
# Virus classification III - the genomic system

- More recently a precise ordering of viruses within and between families is possible based on DNA/RNA **sequence**
- 2019. ICTV agreed to adopt a 15-rank classification system for viruses, ranging from realm to species
- 4 realms, 9 kingdoms, 16 phyla, 2 subphyla, 36 classes, 55 orders, 8 suborders, 168 families, 103 subfamilies, 1421 genera, 68 subgenera, 6590 species ([ictvonline.org/taxonomy](http://ictvonline.org/taxonomy))



- *Four virus realms are recognized by ICTV based on specific highly conserved traits (based on genomics & proteomics) but no common ancestor (polyphyletic)*
- Duplodnaviria, which contains all double-stranded DNA (dsDNA) viruses that encode the HK97-fold major capsid protein;
- Monodnaviria, which contains all single-stranded DNA (ssDNA) viruses that encode **a circular rep (replication associated protein) encoding ssDNA (CRESS DNA)**, HUH superfamily endonuclease and their descendents;
- Riboviria, which contains all RNA viruses that encode RNA-dependent RNA polymerase and all viruses that encode reverse transcriptase; and ~paraphyletic
- Varidnaviria, which contains all dsDNA viruses that encode a vertical jelly roll major capsid protein.

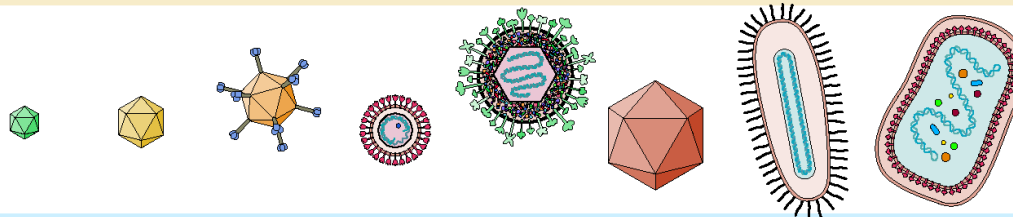
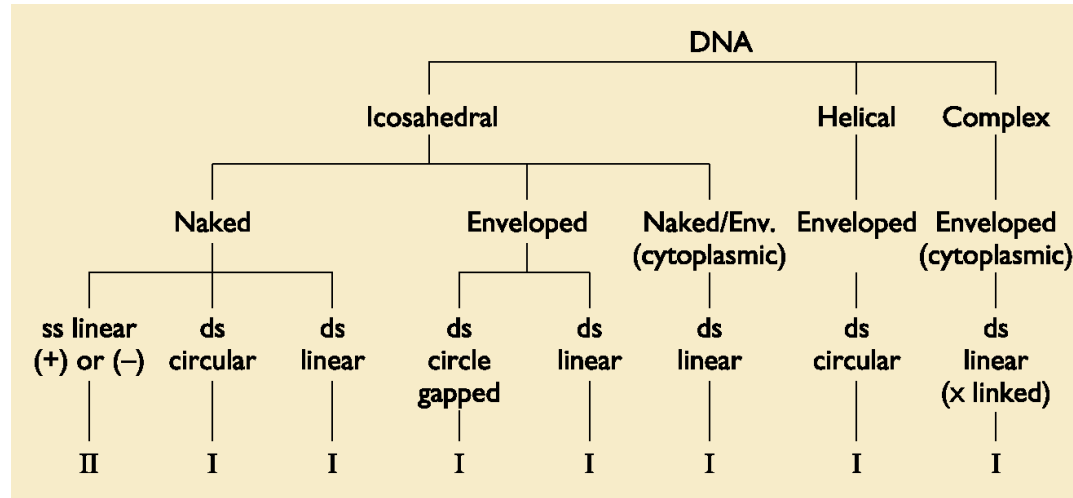
# RNA viruses



Properties	Family name	Reo	Birna	Calici	Picorna	Flavi	Toga	Retro	Corona	Filo	Rhabdo	Bunya	Orthomyxo	Paramyxo	Arena
	Virion polymerase		(+)	(+)	(-)	(-)	(-)	(-)	(+)	(-)	(+)	(+)	(+)	(+)	(+)
Virion diameter (nm)		60-80	60	35-40	28-30	40-50	60-70	80-130	80-160	80 x 790-14,000	70- 85 x 130-380	90-120	90-120	150-300	50-300
Genome size (total in kb)		22-27	7	8	7.2-8.4	10	12	3.5-9	16-21	12.7	13-16	13.5-21	13.6	16-20	10-14

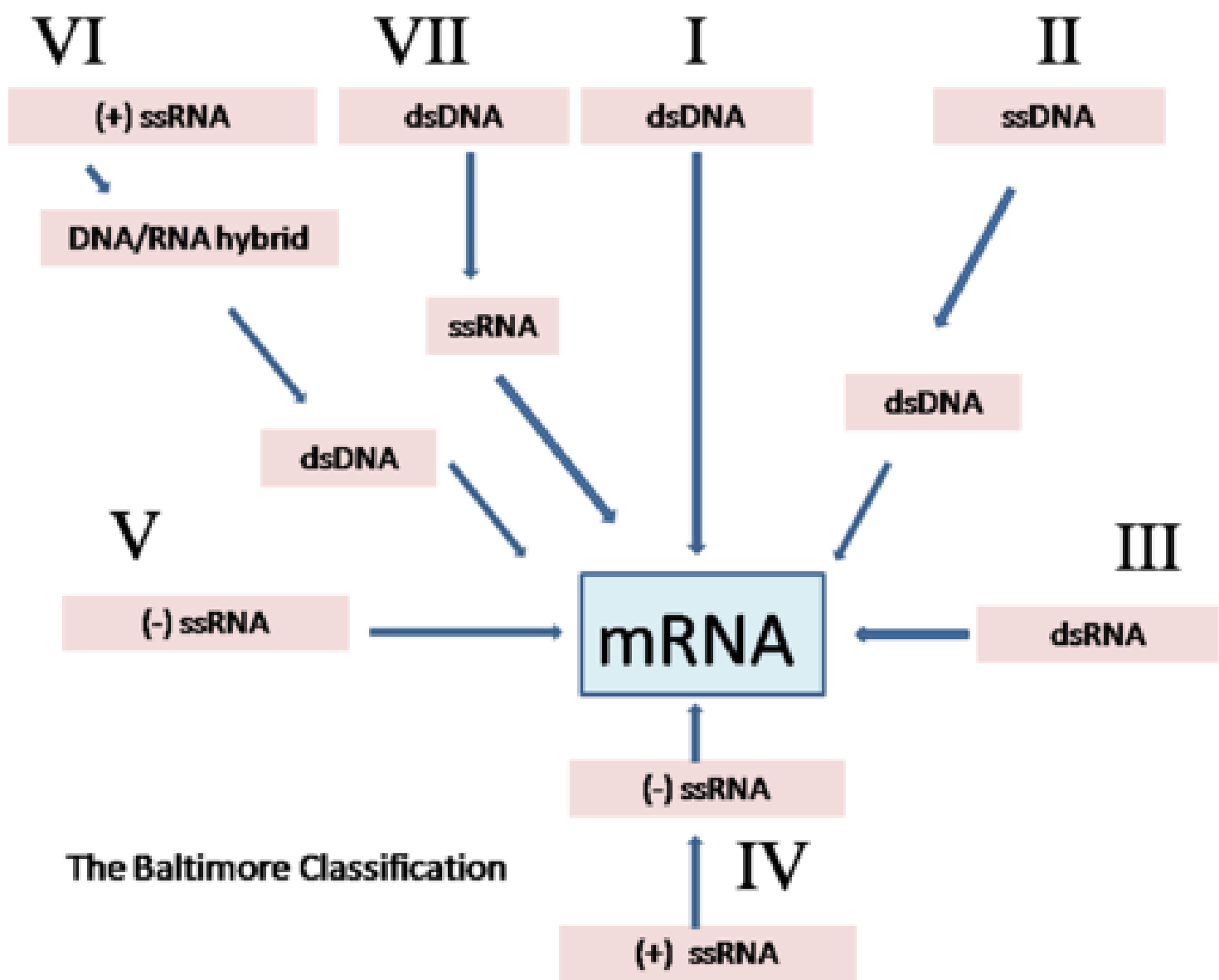
From Principles of Virology Flint et al ASM Press

# DNA viruses



Parvo	Papova	Adeno	Hepadna	Herpes	Irido	Baculo	Pox
(-)	(-)	(-)	(+)	(-)	(-)	(-)	(+)
18-26	45-55	70-90	42	150-200	125-300	60 X 300	170-200 x 300-450
5	5-8	36-38	3.2	120-200	150-350	100	130-280

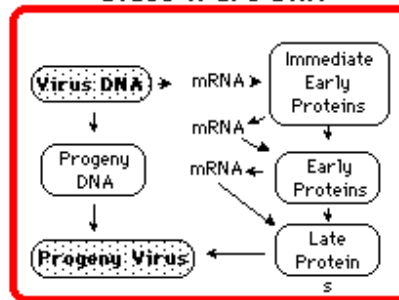
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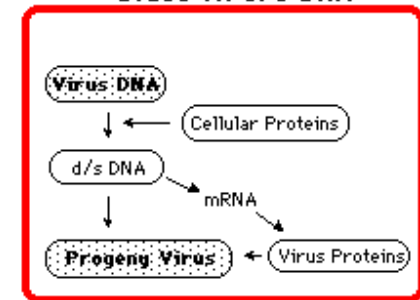
The Baltimore Classification

# The seven “Baltimore” replication classes

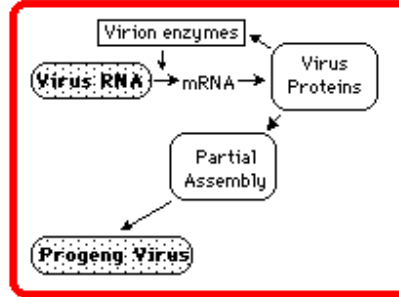
**Class I: d/s DNA**



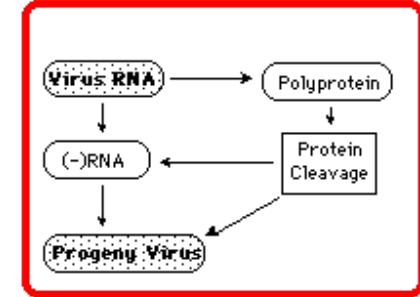
**Class II: s/s DNA**



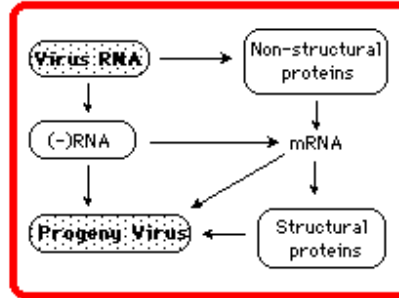
**Class III: d/s RNA**



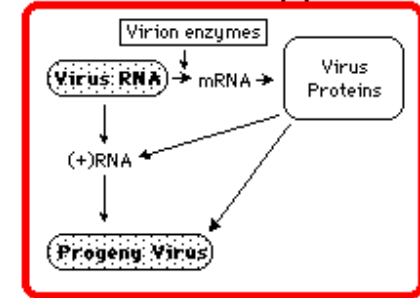
**Class IVa: s/s (+)RNA**



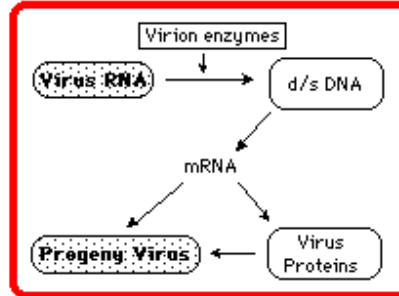
**Class IVb: s/s (+)RNA**



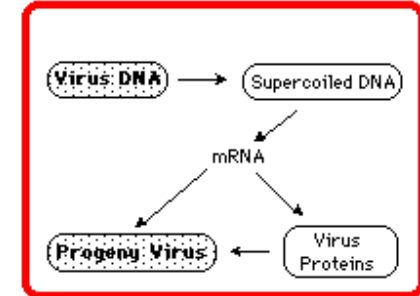
**Class V: s/s (-)RNA**



**Class VI: s/s RNA + DNA**

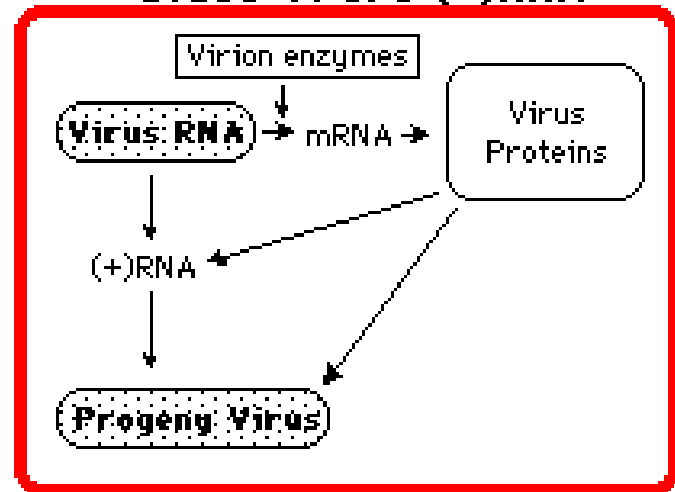


**Class VII: d/s DNA + RNA**

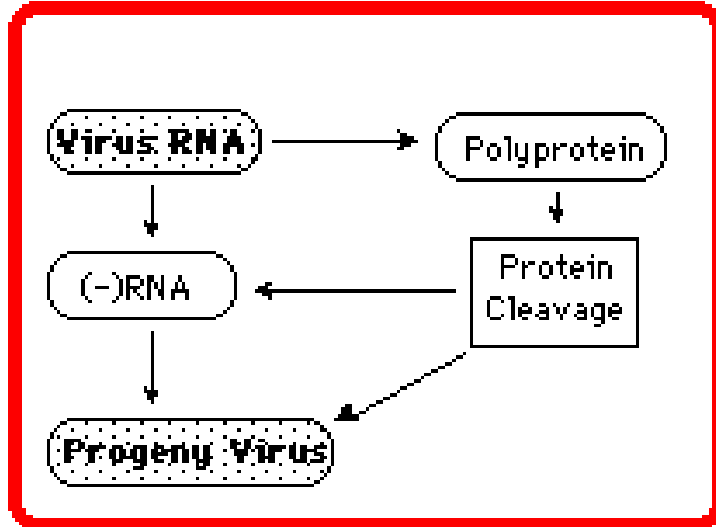


# RNA virus replication

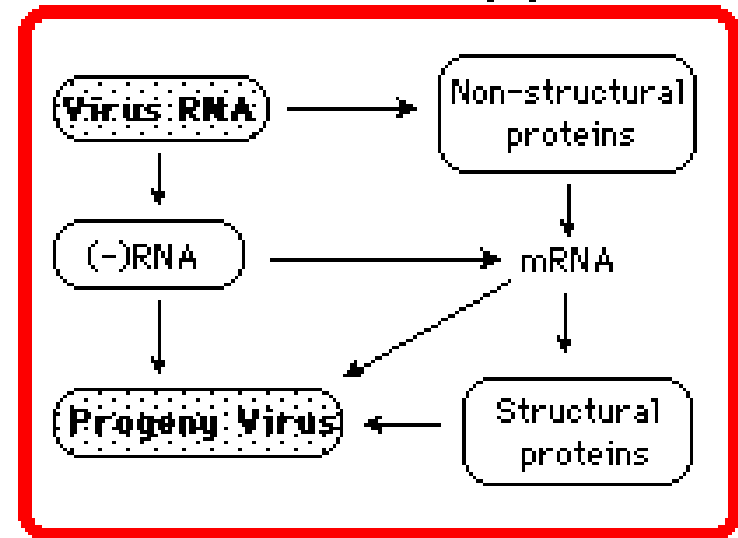
## Class V: s/s (-)RNA



## Class IVa: s/s (+)RNA



## Class IVb: s/s (+)RNA



# Replication Strategy of ss(-)RNA Viruses

## Steps in Replication

1. Primary transcription of virion (-)sense RNA by RNA-Dependent RNA Pol in virion core in cytoplasm, production (mainly) mRNA and (+)sense RNA, formation replicative complex (RC)
2. Translation mRNAs, accumulation of products
3. Virion proteins interact with RC, bias it towards production of full-length (+)sense RNA and therefore of genomic (-)sense RNA
4. Secondary transcription from progeny (-)sense RNA, translation, accumulation structural proteins
5. Nucleocapsid assembly and maturation, budding of nucleocapsid through host membrane containing viral envelope proteins