Segmented genome

These genes are encoded on either RNA or DNA polymers, and are either single stranded or double stranded. ... While most **genomes** are **non-segmented** (the **genome** is all on one piece of RNA or DNA), some **genomes** are **segmented**, meaning there are several fragments of genetic material that make a complete **virus genome**. eg.

Viruses with Single-Stranded, Segmented, Negative-Sense RNA Genomes

There are three virus families containing a negative-sense RNA genome, which does not exist as a continuous molecule, but is present in several segments. These are the families *Arenaviridae*, *Bunyaviridae* and *Orthomyxoviridae*. Similarly to members of the order *Mononegavirales* , they also require the presence of a special enzyme (RNA-dependent RNA polymerase) to perform the synthesis and replication of messenger RNA (mRNA); it reaches the cell along with other viral components during infection.

A segmented genome enables the virus to generate reassortants. In this process, the RNA molecules of different virus strains are mixed or reshuffled in doubly infected cells during replication and morphogenesis. In this way, progeny viruses can obtain new combinations of RNA segments and thus gain novel properties. This mechanism, which is referred to as antigenic shift, is particularly common and well studied in influenza A viruses, the causative agents of viral influenza or genuine flu.

Viruses with Single-Stranded, Segmented, Negative-Sense RNA Genomes

- Segmented virus genomes are those that are divided into two or more physically separate molecules of nucleic acid, all of which are then packaged into a single virus particle

- Segmentation of the virus genome has a number of advantages and disadvantages. There is an upper limit to the size of a nonsegmented virus genome which results from the physical properties of nucleic acids, particularly the tendency of long molecules to break due to shear forces (and, for each particular virus, the length of nucleic acid that can be packaged into the capsid)
- Segmentation means that the virus avoids “having all its eggs in one basket” and also reduces the probability of breakages due to shearing, thus increasing the total potential coding capacity of the entire genome. The disadvantage of segmentation is that all the individual genome segments must be packaged into each virus particle or the virus will be defective as a result of loss of genetic information. Segmentation means that the virus avoids “having all its eggs in one basket” and also reduces the probability of breakages due to shearing, thus increasing the total potential coding capacity of the entire genome. The disadvantage of segmentation is that all the individual genome segments must be packaged into each virus particle or the virus will be defective as a result of loss of genetic information.

Influenza virus

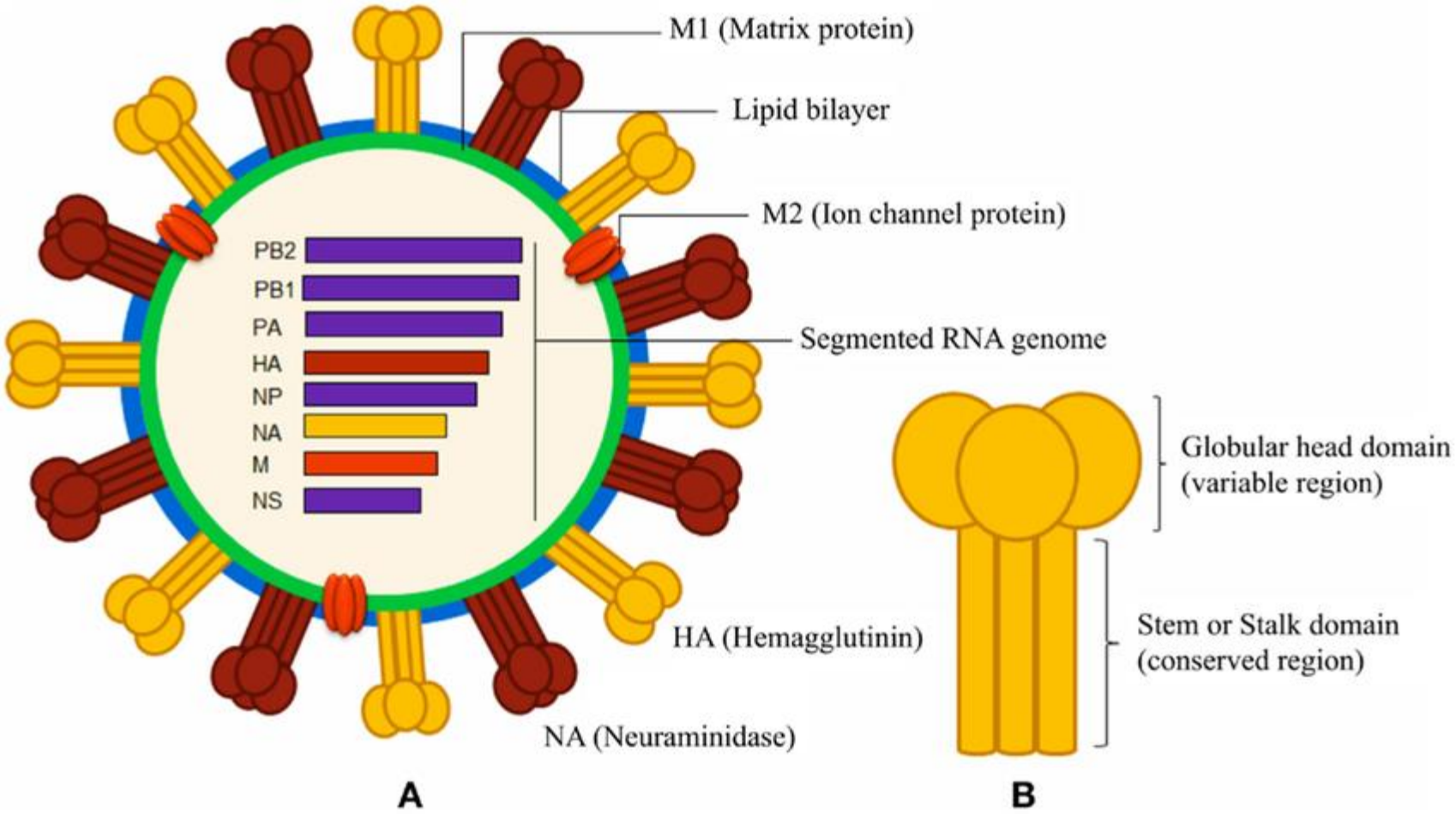
- The influenza A, B, and C viruses, representing three of the five genera of the family *Orthomyxoviridae*, are characterized by segmented, negative-strand RNA genomes.

- The influenza A and B virus genomes each comprise eight negative-sense, single-stranded viral RNA (vRNA) segments, while influenza C virus has a seven-segment genome.

- The eight segments of influenza A and B viruses (and the seven segments of influenza C virus) are numbered in order of decreasing length. In influenza A and B viruses, segments 1, 3, 4, and 5 encode just one protein per segment: the PB2, PA, HA and NP proteins. All influenza viruses encode the polymerase subunit PB1 on segment 2; in some strains of influenza A virus, this segment also codes for the accessory protein PB1-F2, a small, 87-amino acid protein with pro-apoptotic activity

- The genomic organization of influenza C viruses is generally similar to that of influenza A and B viruses; however, the HEF protein of influenza C replaces the HA and NA proteins, and thus the influenza C virus genome has one fewer segment than that of influenza A or B viruses.

THE BIOLOGY OF INFLUENZA VIRUSES
Nicole M. Bouvier and Peter Palese*



Schematic diagrams of influenza A virus and surface hemagglutinin protein. (A) The segmented negative-sense RNA genome of influenza A virus encodes three envelope proteins (hemagglutinin, neuraminidase, and ion channel M2 protein), and internal nucleoprotein (NP), polymerases (PA, PB1, and PB2), matrix protein 1 (M1), and non-structural proteins (NS). The lipid bilayer is derived from host cell membrane. (B) The cylindrical HA is a homo-trimeric protein consisting of a variable globular head and a conserved stem domain.

Multipartite viruses

- Multipartite viruses have genomes segmented in pieces enclosed in different capsids that are independently transmitted.

- This is found for both DNA and RNA plant viruses.

- Although multipartite genomes are also segmented, each genome segment is packaged into a separate virus particle. These discrete particles are structurally similar and may contain the same component proteins, but they often differ in size depending on the length of the genome segment package

Non-segmented genome

A viral genome that consists of one continuous nucleic acid molecule.

Picornaviridae

- The *Picornaviridae* represent a large family of small plus-strand RNA viruses that cause a bewildering array of human and animal diseases ranging from severe (poliomyelitis, encephalitis, meningitis, and hepatitis) to mild (common cold).

- The genome is a single sense-strand RNA (molecular weight, approximately 2×10^6 to 3×10^6) (Fig. 53-3). The RNA strand consists of approximately 7,500 nucleotides and is covalently bonded to a noncapsid viral protein (VPg) at its 5′ end and to a polyadenylated tail at its 3′ end. This genome RNA serves as an mRNA and initiates the synthesis of virus macromolecules.

Medical Microbiology. 4th edition.
Chapter 53Picornaviruses
Marguerite Yin-Murphy and Jeffrey W. Almond.

Picornaviridae

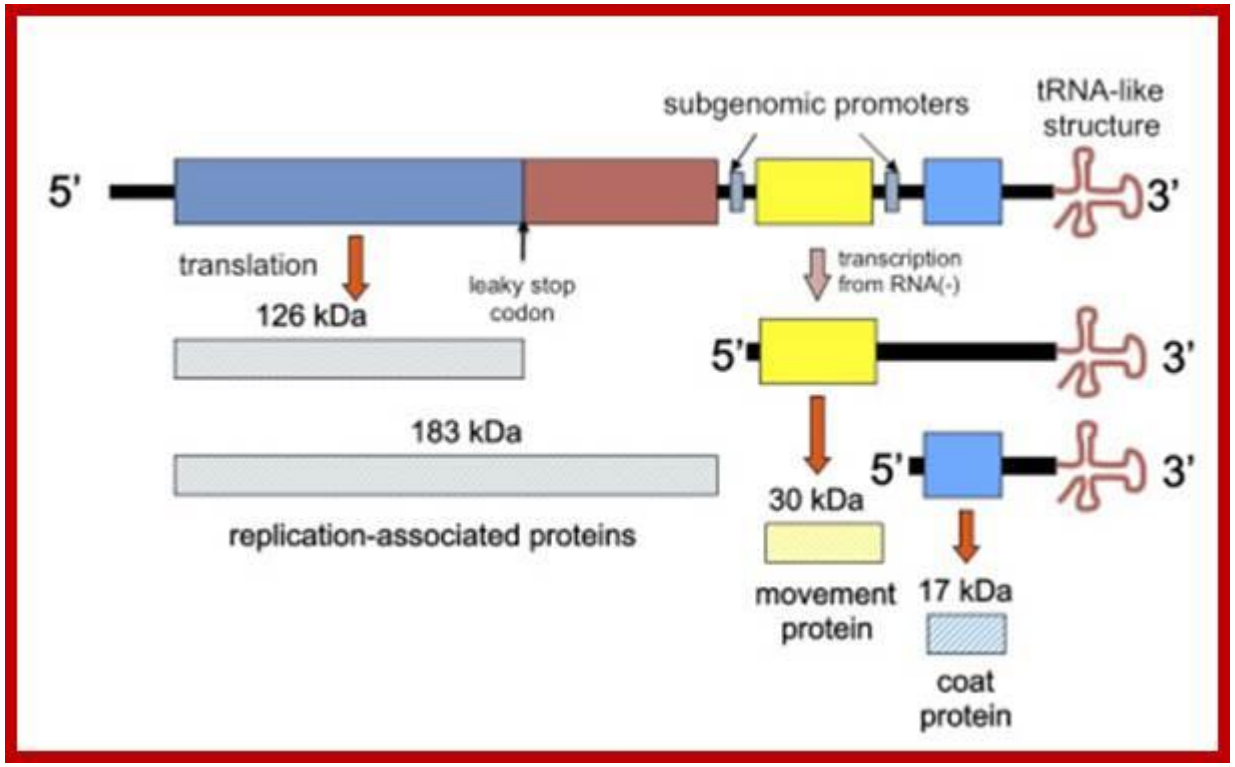
- Positive –strand ,single stranded, nonsegmented RNA genome
- Nonenveloped, icosahedral
- Virion do not contain any enzymes
- **Coxsackievirus**
- **Hepatitis A virus (HAV)** is a member of the genus hepatovirus
- **Poliovirus** (member of the genus enterovirus)
- Infection with poliovirus by ingestion of contaminated food or water
- Polioviruses cause poliomyelitis

Capping and tailing (TMV)

- Most eukaryotic mRNAs have 5 and 3 untranslated regions (UTRs), a methylguanosine [m7G(5)pppG] cap at the 5 end, and a poly(A) tail at the 3 end.
- The cap and the poly(A) tail are required for efficient translation and mRNA stabilization.
- The 5’ end of tobacco mosaic virus (TMV) genomic RNA is capped with 7- methylguanosine.
- TMV belongs to a large group of alphaviruses, which has a 5 cap but lacks the poly(A) tail characteristic of host mRNAs .
- In TMV, the 3 end of the vRNA ends in a series of pseudoknots and a terminal tRNA-like structure that substitutes for the poly(A) tail of mRNAs .
- For mRNAs, and for many vRNAs, the cap structure plays central roles in RNA-associated functions, including transport, translation and turnover and is also a major determinant of RNA decay, protecting the mRNA from degradation by 5 –3 exonucleases. The cap also plays a central role in the recruitment of translation initiation factors .
- All genomic and subgenomic TMV mRNAs contain the same 205-nucleotide 3 UTR region shown to promote efficient translation and increase stability in a cap-dependent manner.

Capping and tailing (TMV)

The genomic TMV RNA is a plus RNA (coding) and 6395 ntds long consists of cap at 5’ end with 67 nucleotide leader sequence with AU rich sequences without any secondary structure, hence it is called ‘W’ sequence. The 5’End cap and structured leader sequence is a distinguishing feature of eukaryotic mRNAs, and TMV RNA has a tRNA like secondary structure at the 3’ end which accepts histidine in the presence of synthase. TMV RNA can be used as plant expression vector, Nobuhiko Takamatsu et al, https://www.ncbi.nlm.nih.gov.



TMV genome, 6395 ntds with Transcription and translation modes; It has three major ORFs. Their was also found to be a **unique hairpin loop-encoding sequence region for assembly initiation** – nicely rounding out pioneering work by **PJ Butler** and colleagues and **Genevieve Lebeurier** and others – both published in **January 1977**,

Capping and tailing (TMV)

Schematic structure of TMV and its mutants with different lengths of internal poly(A) tract (24A, 42A and 62A) introduced before the upstream pseudo-knotted domain (UPD).