

VIROLOGIA 2006/2007

APRESENTAÇÃO 2

**(Variabilidade genética dos vírus de
RNA)**

Maria Filomena Caeiro

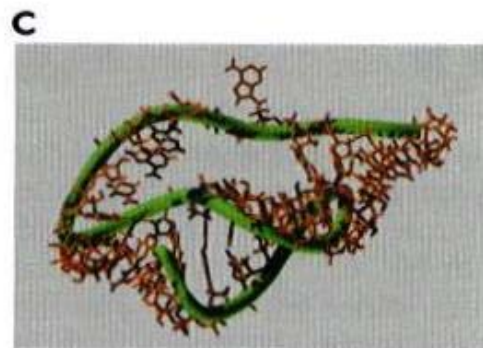
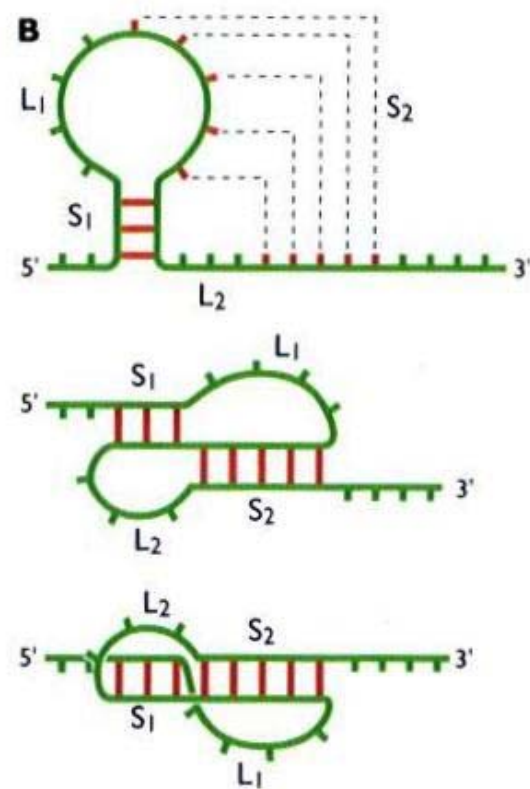
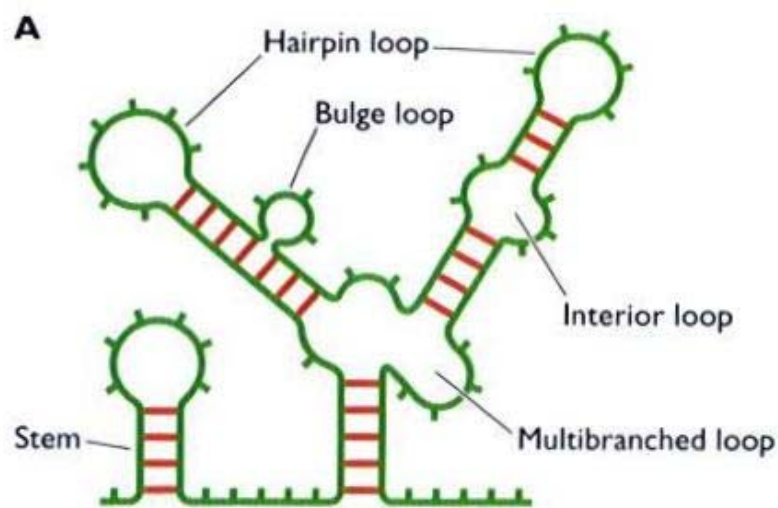
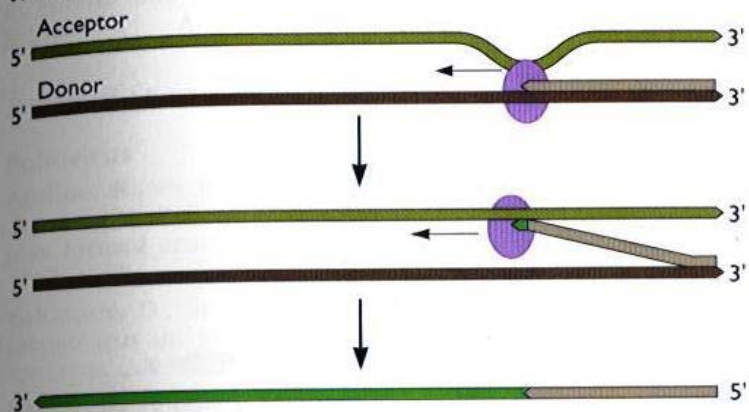


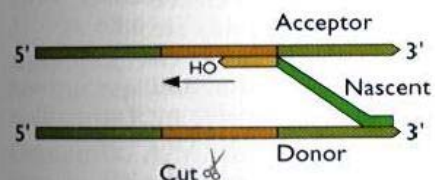
Figure 6.8 RNA secondary structure. (A) Schematic of different structural motifs in RNA. Black bars indicate base pairs, and open bars, unpaired nucleotides. (B) Schematic of a pseudoknot. (Top) Stem 1 (S_1) is formed by base pairing in the stem-loop structure, and stem 2 (S_2) is formed by base pairing of nucleotides in the loop with nucleotides outside the loop. (Middle) A different view of the formation of stems S_1 and S_2 . (Bottom) Coaxial stacking of S_1 and S_2 resulting in a quasi-continuous double helix. (C) Structure of a pseudoknot as determined by nuclear magnetic resonance. The sugar backbone is highlighted with a tube. Stacking of the bases in the areas of S_1 and S_2 can be seen. Adapted from C. W. Pleij, *Trends Biochem. Sci.* **15**:143–147, 1990, with permission.

Flint, S. J., Enquist, L. W., Krug, R. M., Racaniello, V. R. and Skalka, A. M. (2004). "Principles of Virology. Molecular Biology, Pathogenesis, and Control". 2nd edition. ASM Press.

RNA recombination

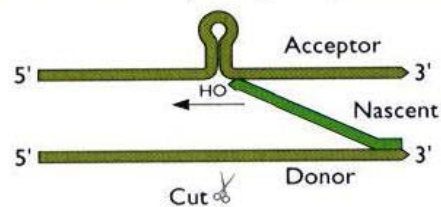


Class 1: Base pairing dependent



RNA-dependent RNA-polymerase
internal pausing/termination
or RNA breakage

Class 2: Base pairing independent



Class 3: Base pairing assisted

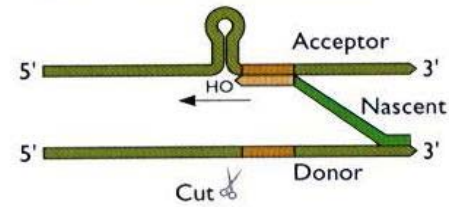
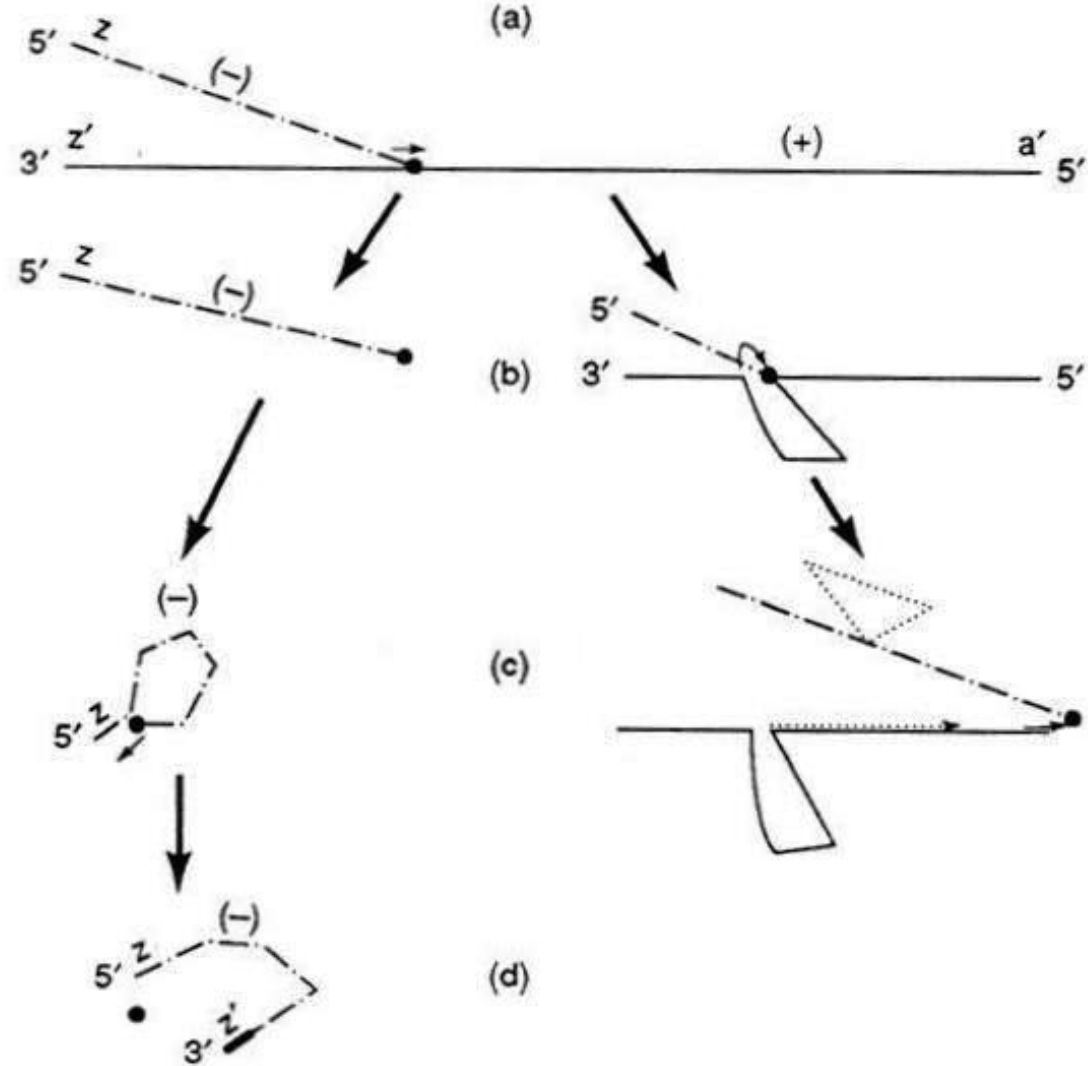


Figure 6.17 RNA recombination. (Top) Schematic representation of RNA recombination occurring during template switching by RNA polymerase, or copy choice. Two parental genomes are shown. The RNA polymerase (purple oval) has copied the 3' end of the donor genome and is switching to the acceptor genome. The resulting recombinant molecule is shown. (Bottom) Three classes of RNA recombination. All three classes involve RNA polymerase-mediated template exchange. Events that occur after the exchange are shown by an arrow. The hairpin symbolizes various RNA features required for class 2 and 3 recombination. In base-pairing-dependent recombination, substantial sequence similarity between parental RNAs is required and is the major determinant of recombination. In base-pairing-independent recombination, sequence similarity is not required but may be present. Recombination may be determined by other RNA features, such as RNA polymerase-binding sites, secondary structures, and heteroduplex formation between parental RNAs. Base-pairing-assisted recombination combines features of class 1 and class 2 recombination. Sequence similarity influences the frequency or site of recombination, but additional RNA features are required. Adapted from P. D. Nagy and A. E. Simon, *Virology* **235**:1–9, 1997, with permission.

Generation of DI RNAs by a "copy choice" or "jumping polymerase" mechanism. (a) The viral replicase falls off or slides along its genomic RNA template during negative-sense strand synthesis. (b) Still carrying the nascent negative-sense strand, the replicase reinitiates synthesis—either on the original template or near the 5' terminus of the nascent negative-sense strand. (c and d) Completion of the elongation reaction yields a shortened negative-sense strand containing either an internal deletion (right) or complementary termini (left). Slipping backward rather than jumping forward generates sequence repeats rather than deletions, whereas more complex rearrangements require repeated template switches. (From J. J. Holland. (1990) In *Virology*, 2d ed., eds. B. N. Fields and D. M. Knipe. Chapter 8. Raven Press, New York)



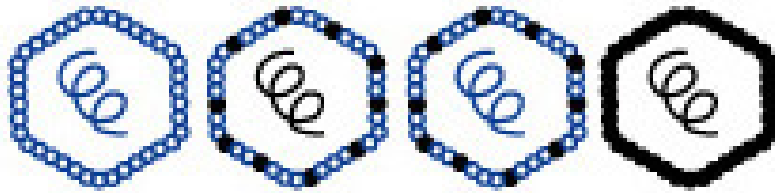
Virus A:
Genome A
Capsid A



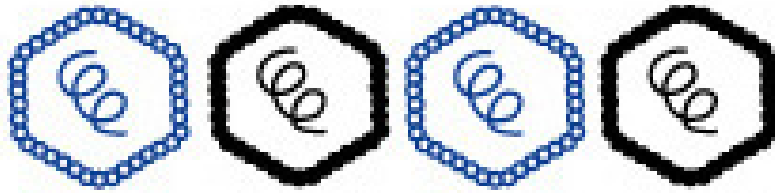
Virus B:
Genome B
Capsid B



Mixed infection



Phenotypically
mixed progeny
virions



Second passage:
Phenotype is
determined by
virus genome

Virus A

Virus B

Virus A

Virus B