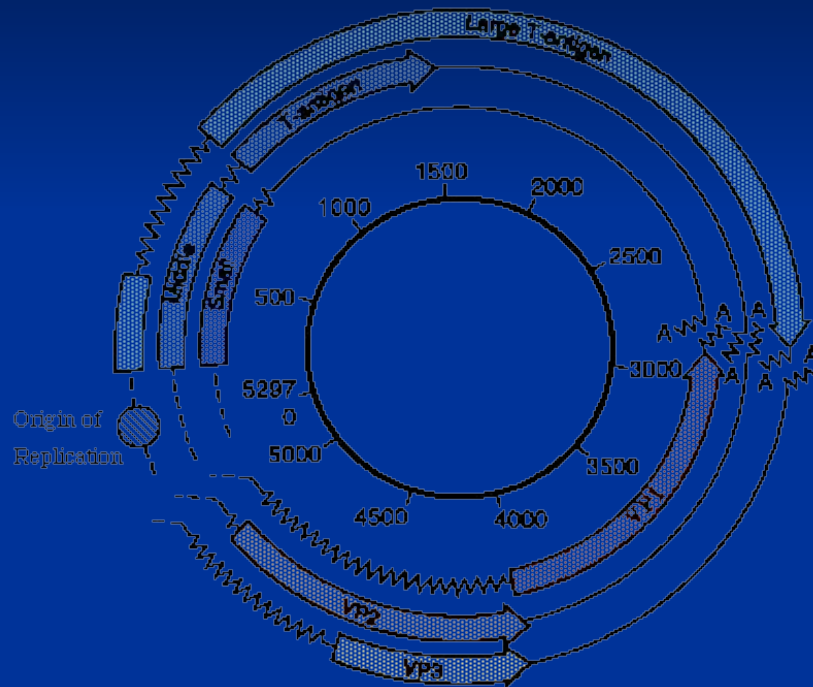
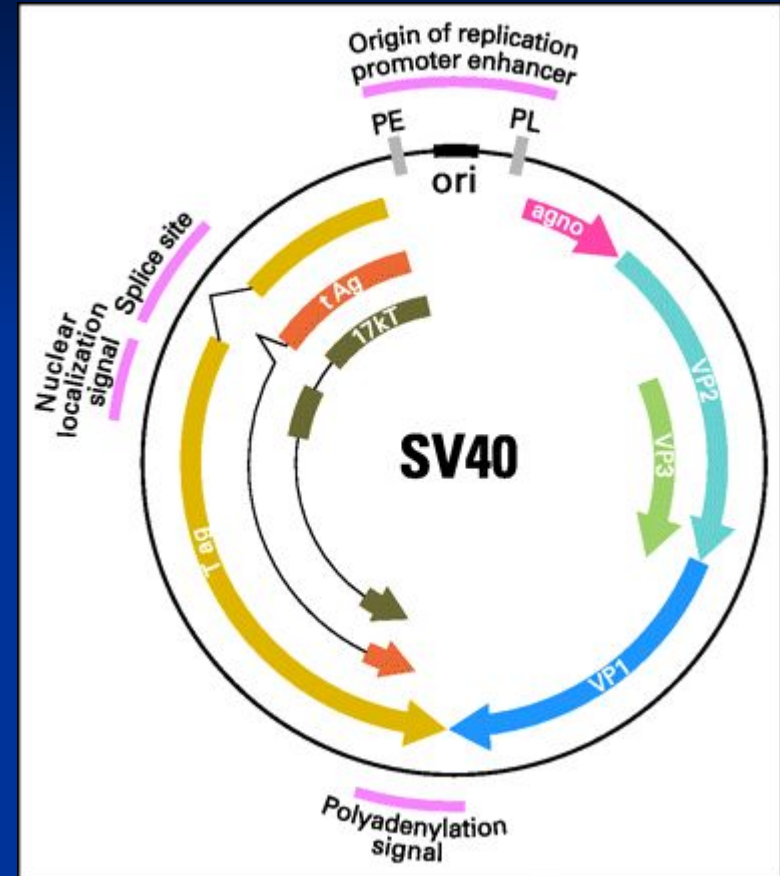


dsDNA

Генетична карта поліомавірусів



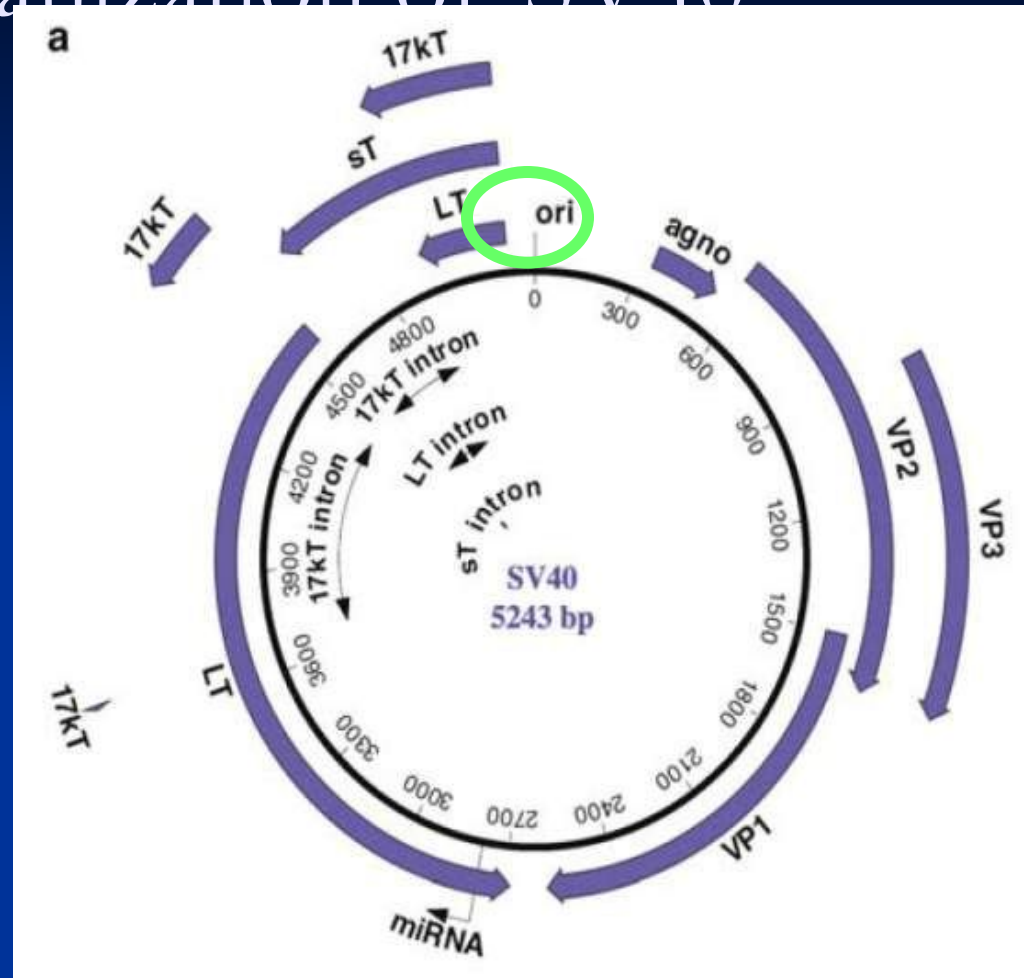
вірусу поліоми



вірусу **SV-40**

Genome Organization of SV40

- **Early unit:** large T antigen (LT), small t antigen (sT), 17K T antigen (17KT).
- **Late unit:** VP1, VP2, VP3, the agnoprotein (agno) and a pre-microRNA (miRNA).



The regulatory region (ori)

- For the early and late promoter and the origin of replication.

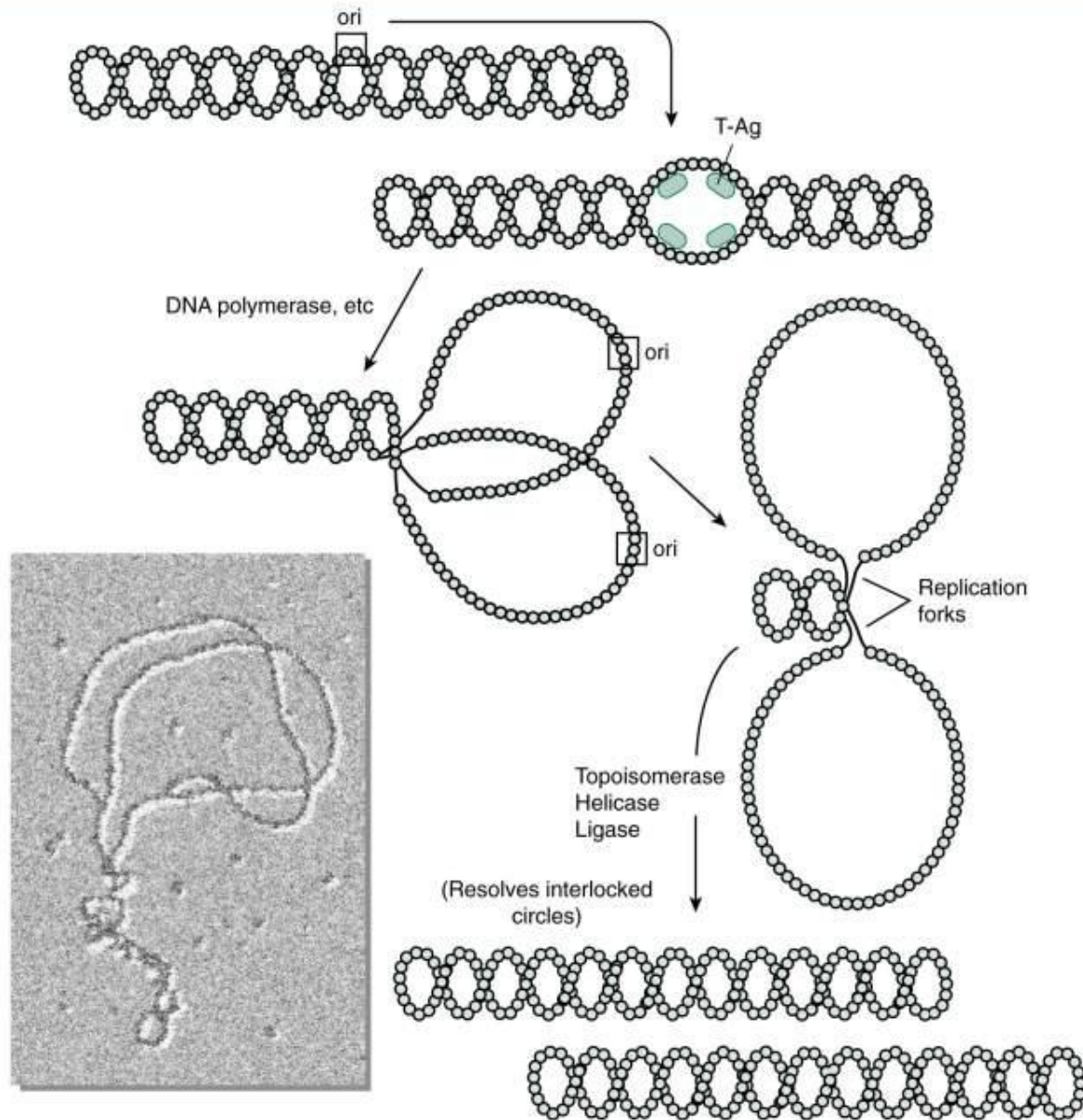
Functional organization of SV40 large T antigen

- 1. Activation of cellular DNA and RNA synthesis
 - binding the cellular Rb and p53
 - causes the infected cell to begin a round of DNA replication.
- 2. Blockage of apoptosis
 - inactivate p53 at inappropriate times in the cell cycle.
- **3. Binding to the SV40 ori to initiate viral DNA replication**
- 4. Shutting off early viral transcription
- 5. Activating late transcription
- 6. Virion assembly

SV 40 DNA replication

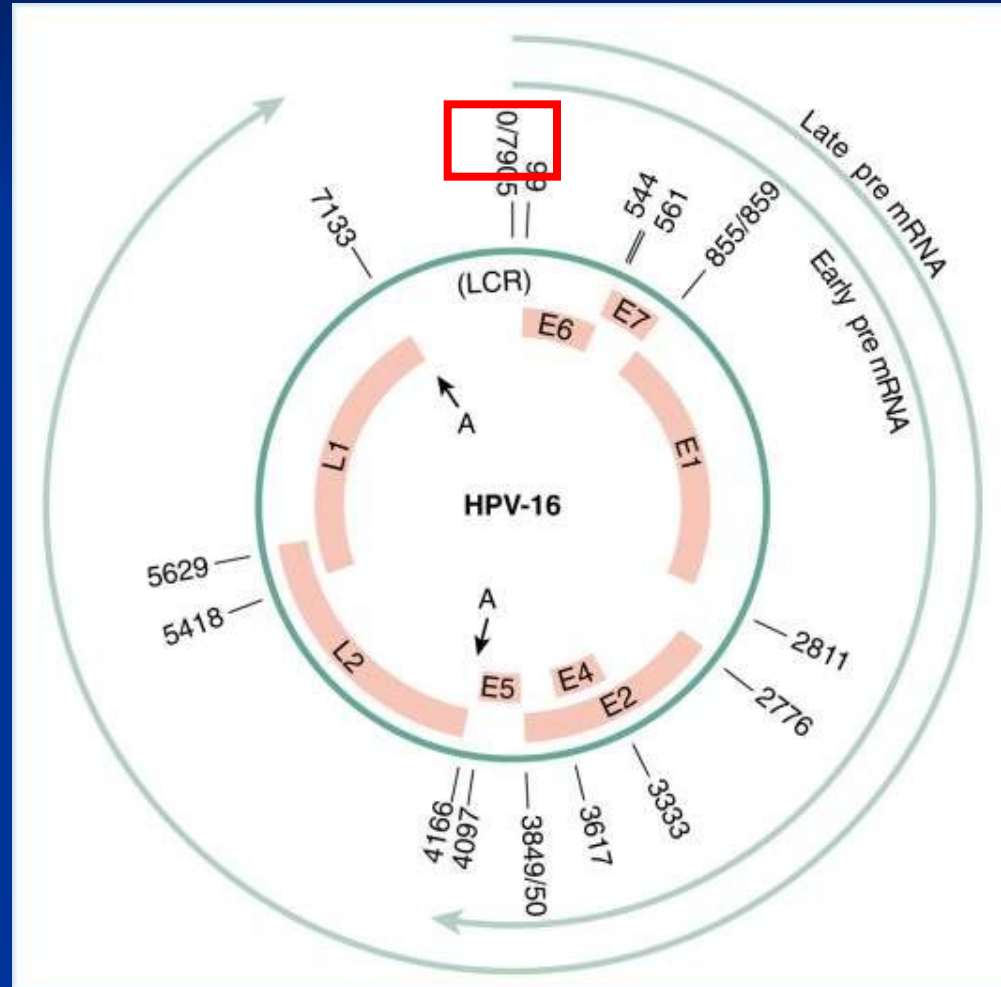
- In the nucleus.
- Large T antigen binds to the SV40 origin
- Using the host cell DNA polymerase,
 - which recognizes the viral origin of replication if the T antigen is present.
- Bi-directional replication
- Host histones complex with the newly made DNA.

The replication of SV40 DNA



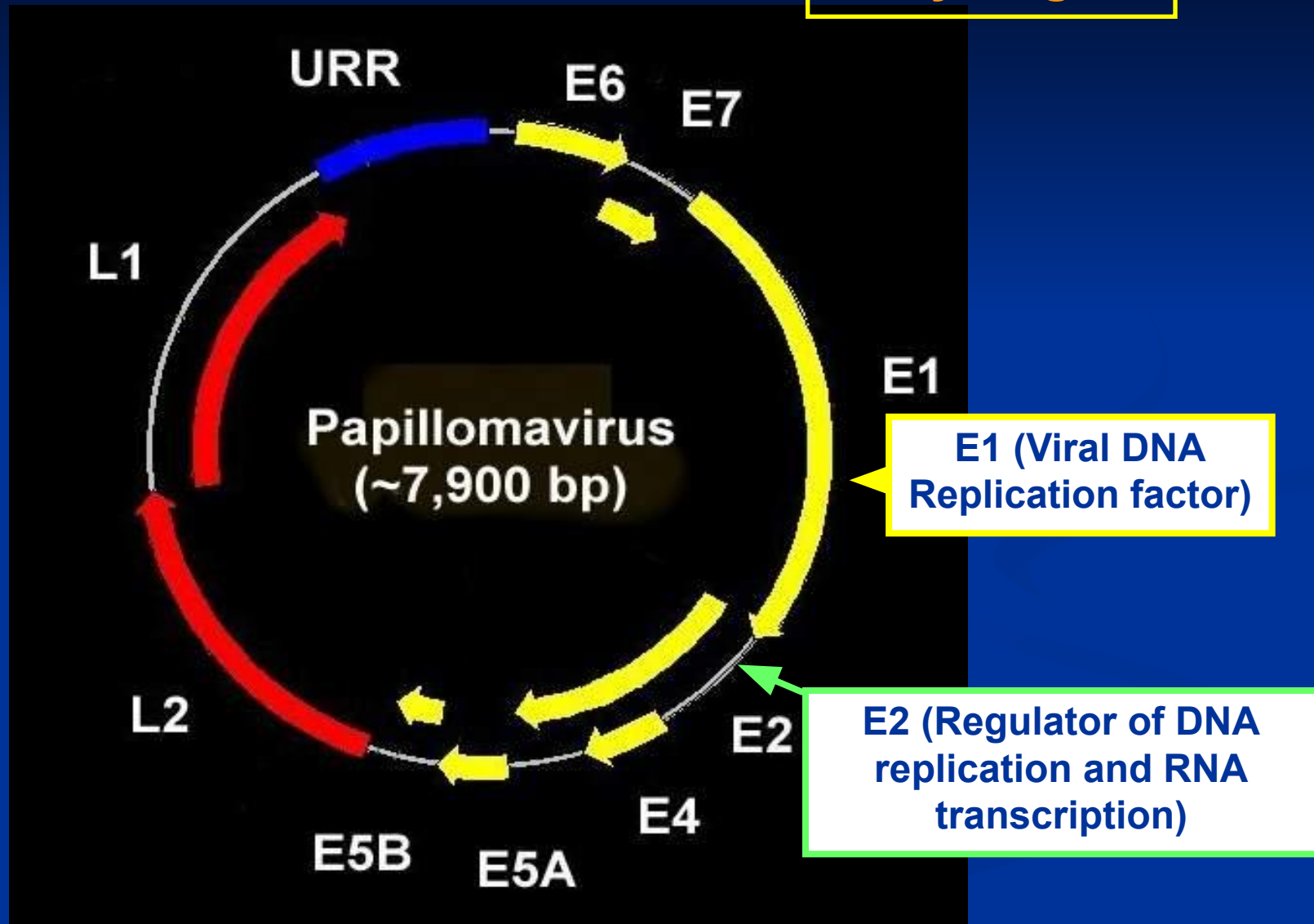
Genomic Organization of Papillomavirus

- Genome
 - 7Kb circular genome
 - Encode all proteins on the same DNA strand
 - RNAs splicing
 - Long control region (LCR) contains transcriptional and replication regulatory elements

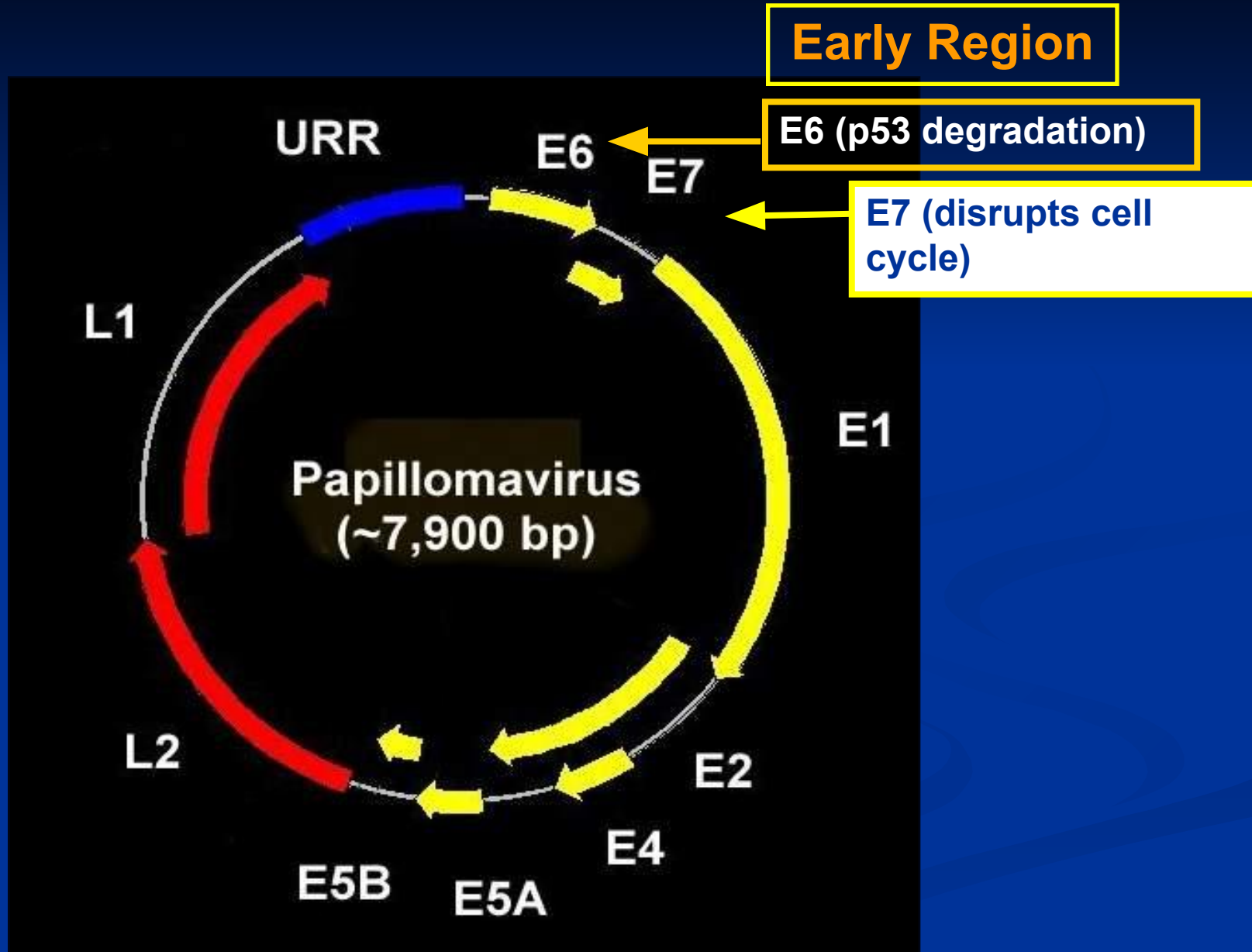


Functional Assignments of Viral Early Proteins

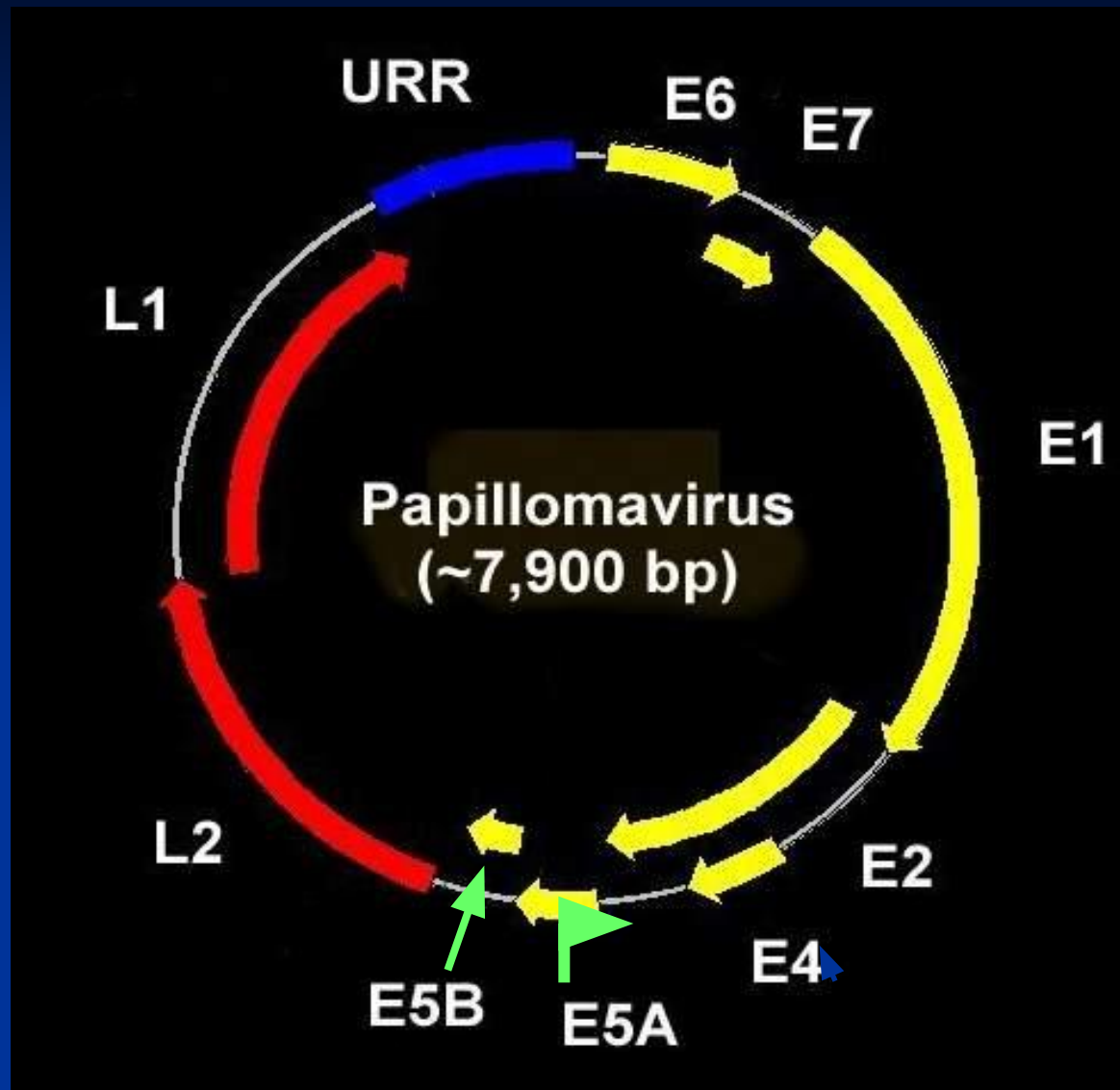
Early Region



Functional Assignments of Viral Early Proteins



Functional Assignments of Viral Early Proteins



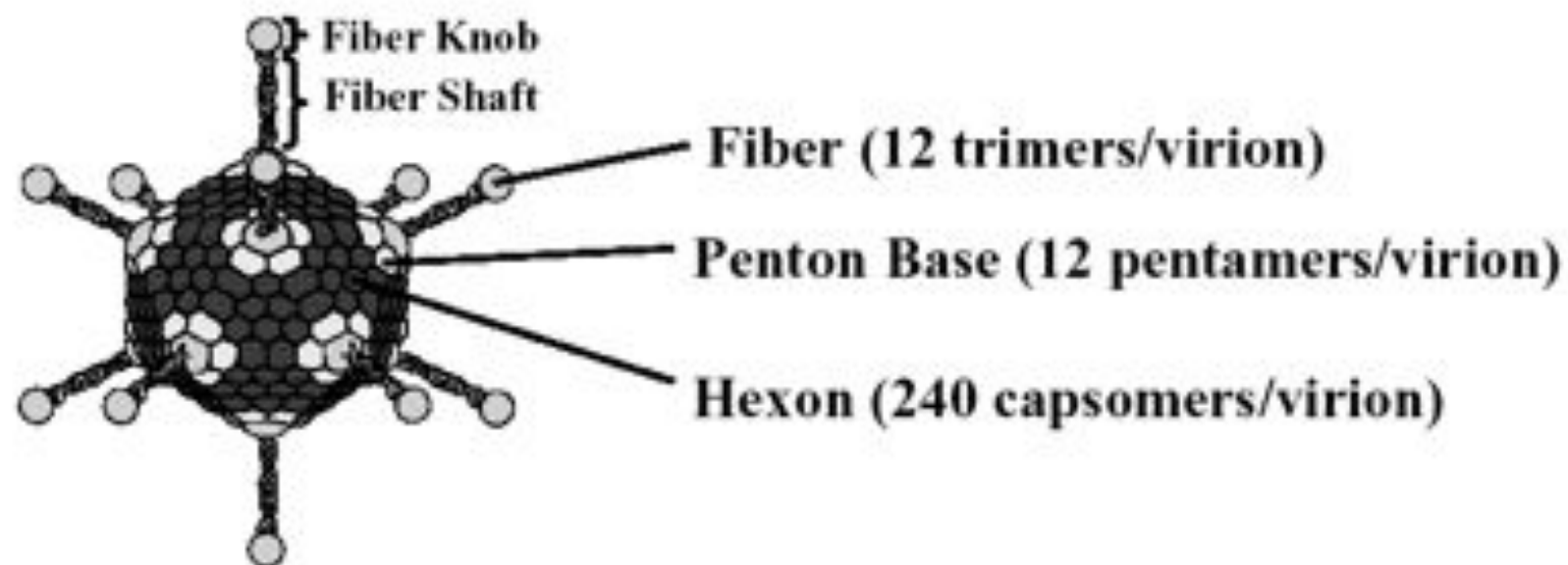
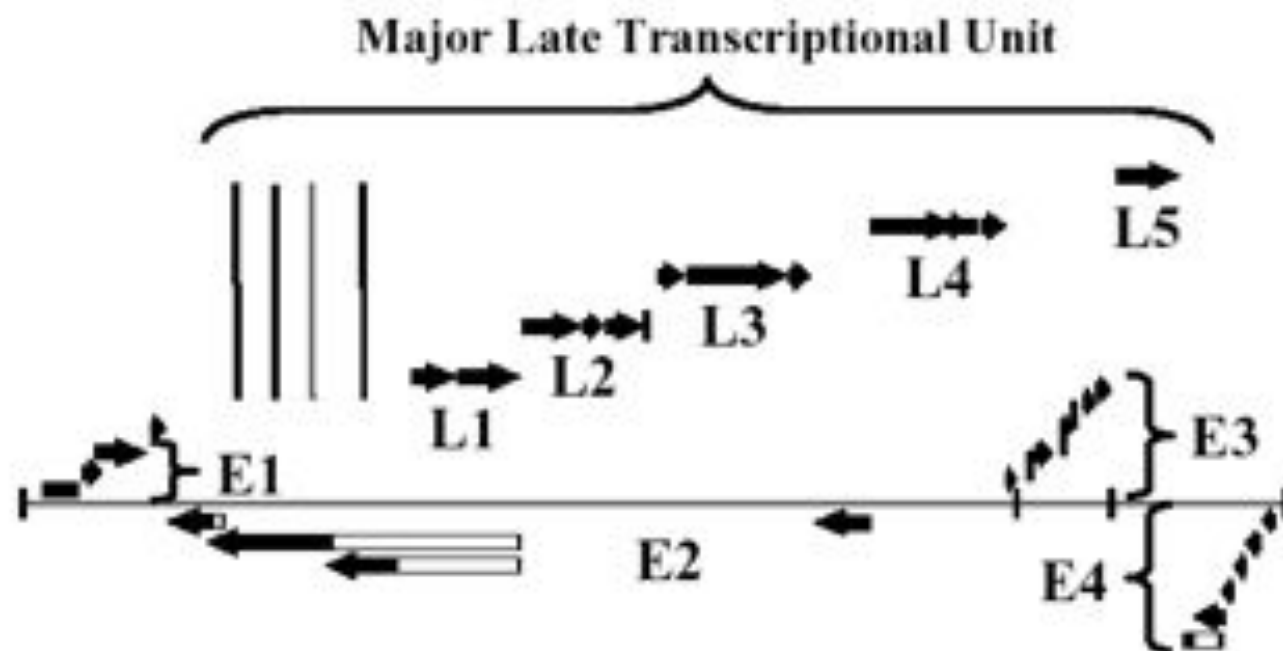
Early Region

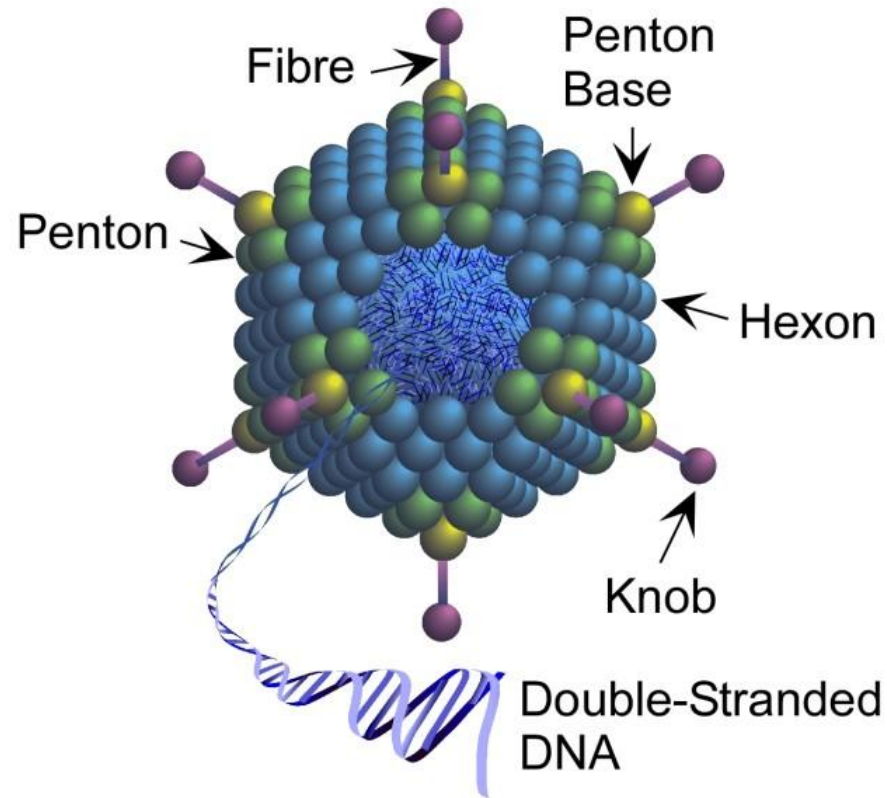
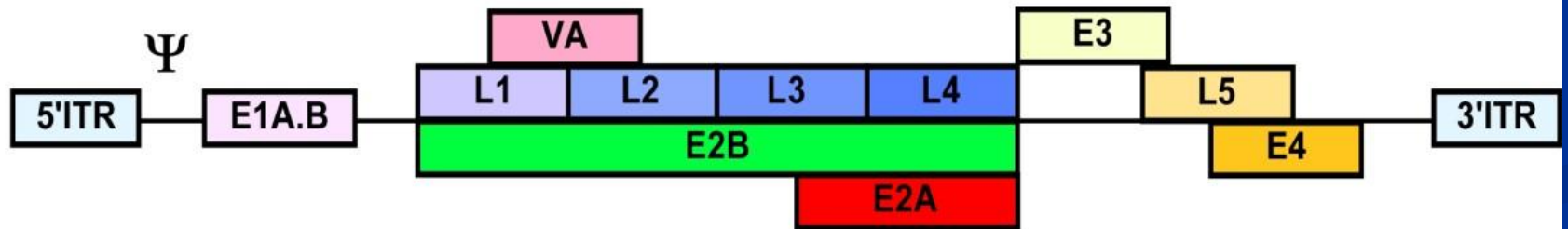
Modulation of growth regulatory mechanisms

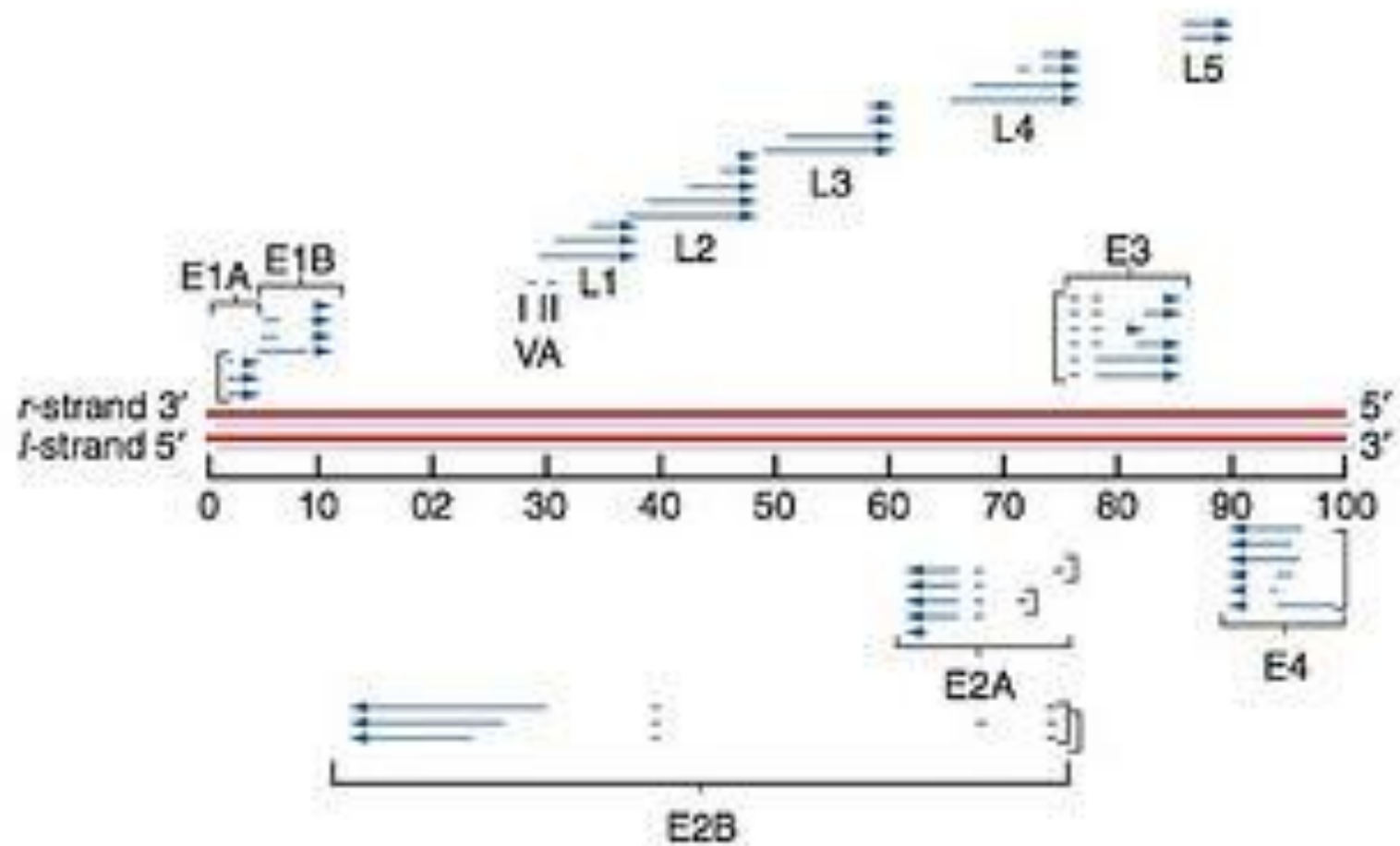
Adenoviruses

Adenoviridae

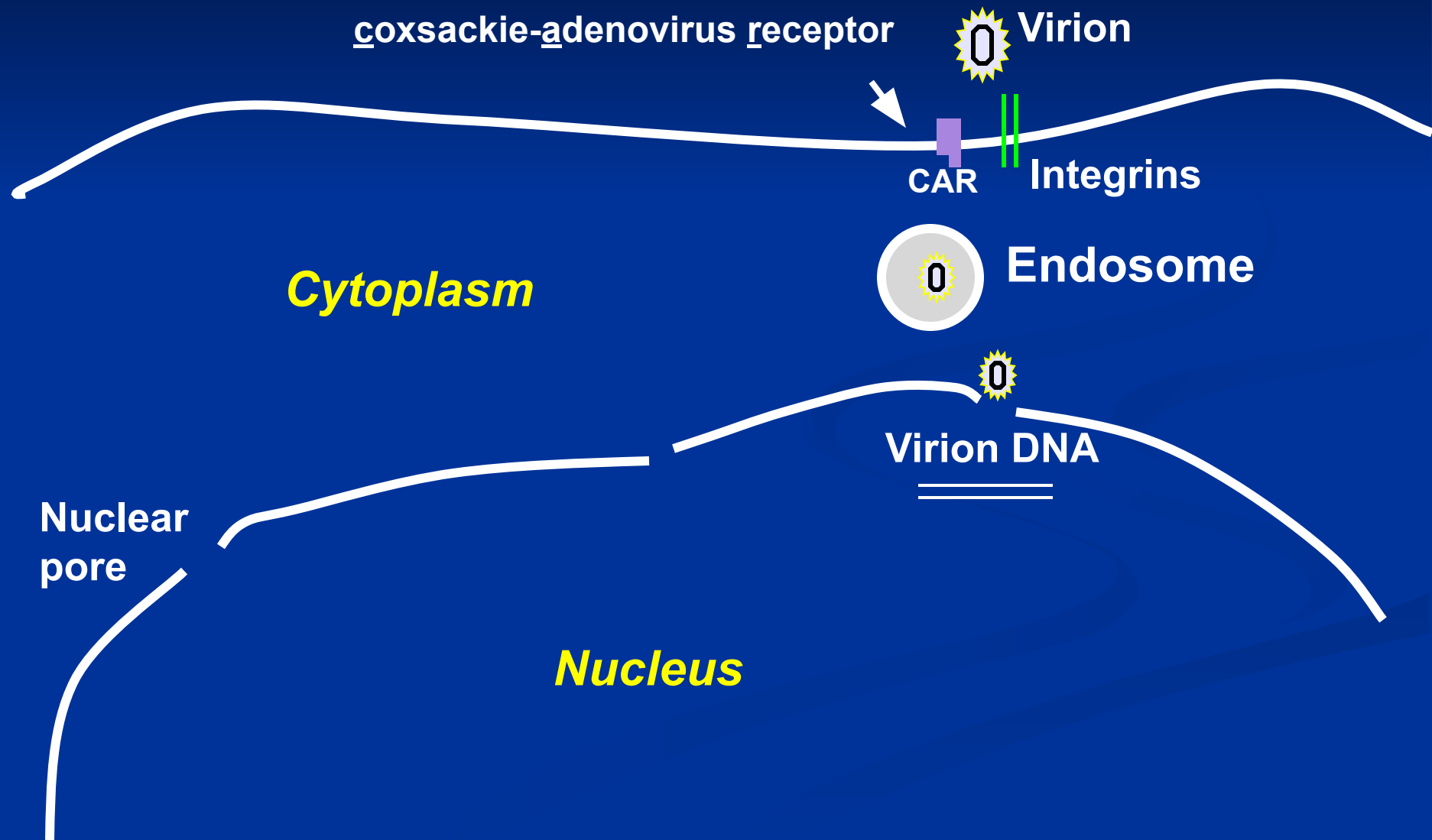
- Characteristics
 - double stranded DNA viruses; linear molecular
 - non-enveloped, icosahedral particles 70 - 90 nm
 - vertices exhibit viral attachment protein(VAP) as fibers or spikes
 - possess hemagglutinin, and type-specific viral antigen
 - capsid proteins are toxic to host cell and may inhibit cellular synthesis
 - viral genome encodes many viral proteins
 - early proteins promote the growth the infected cell
 - E1A/E1B viral proteins bind and inactivate cellular p53 and RB(p1050) genes, thus stimulating cells growth
 - virus also provides its own DNA dependent DNA polymerase
 - some viral proteins suppress the host immune response including inflammation
 - late proteins provide structural proteins and those carried in mature virion
 - viral cycle takes 32 - 36 hours and produces 10, 000 virions
 - virus enters the cell by endocytosis, lyses the endosomal vesicle, and capsid is removed as it delivers the DNA to the nucleus
 - 51 human adenoviruses in groups A - F
 - based upon DNA homology, disease tropism, and fiber antigens

A**B**

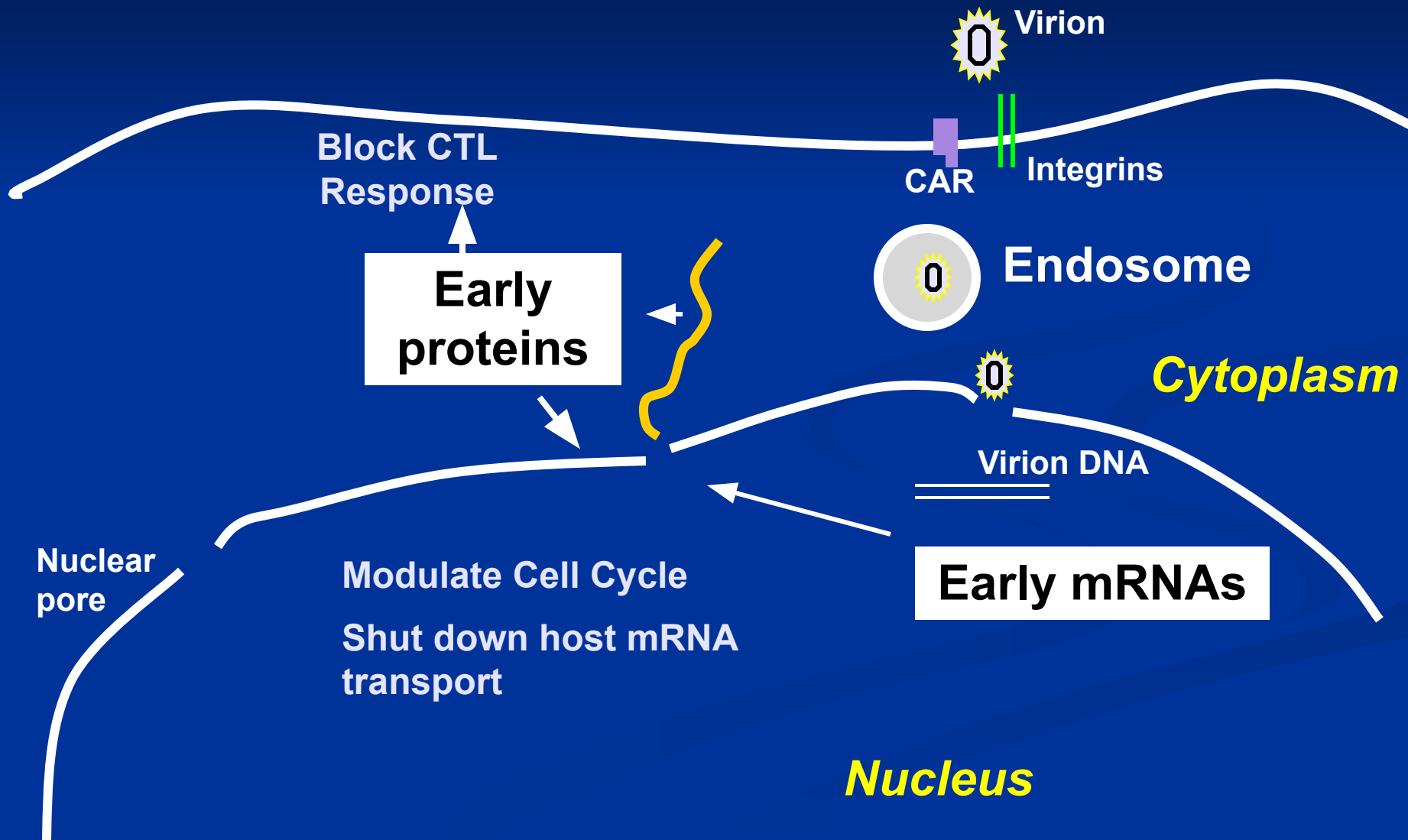
A**B**



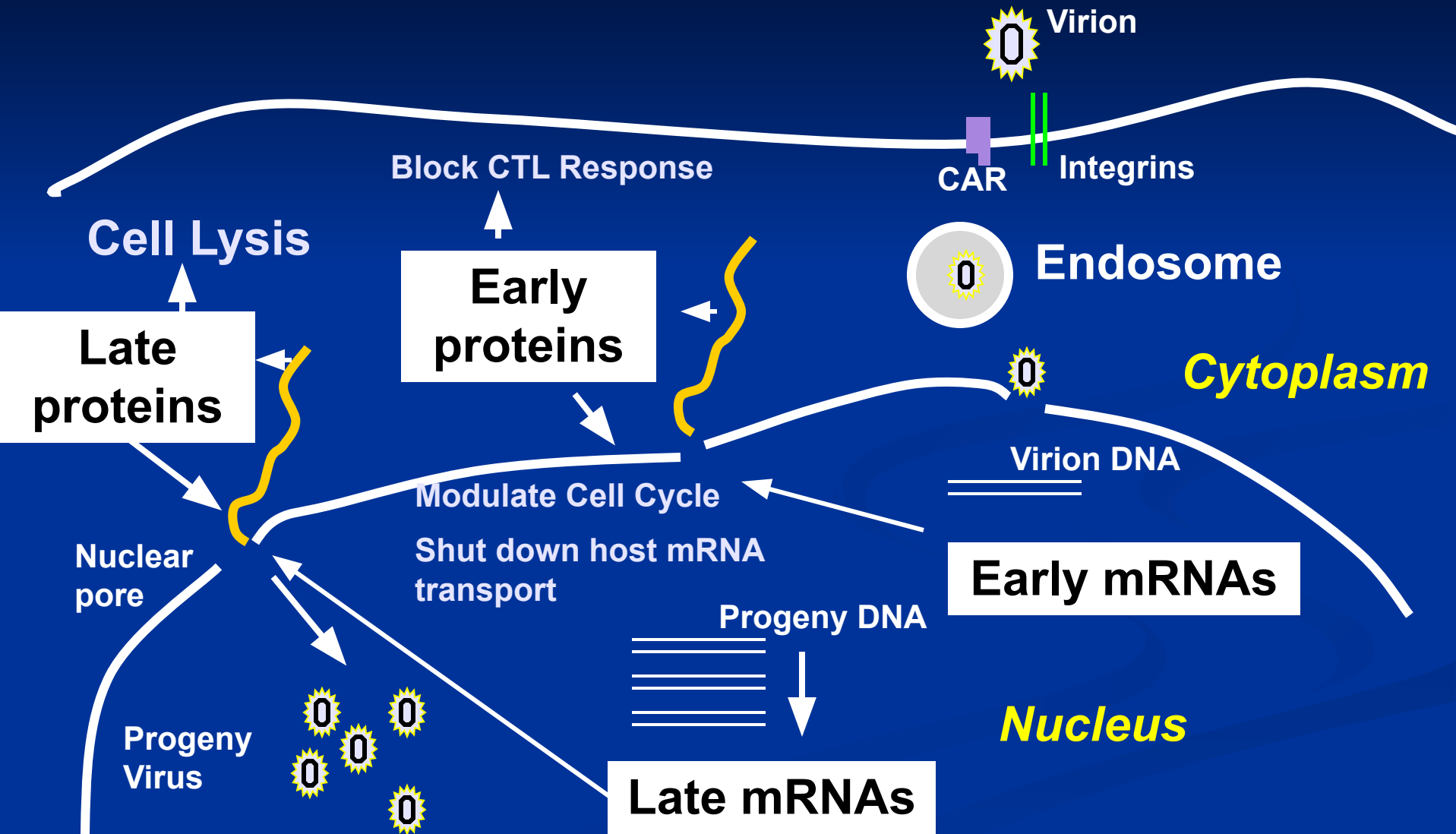
Adenovirus Replication



Adenovirus Replication



Adenovirus Replication



- The early protein include:

- For transcription

- EIA is referred to as an ‘immediate early’ gene)

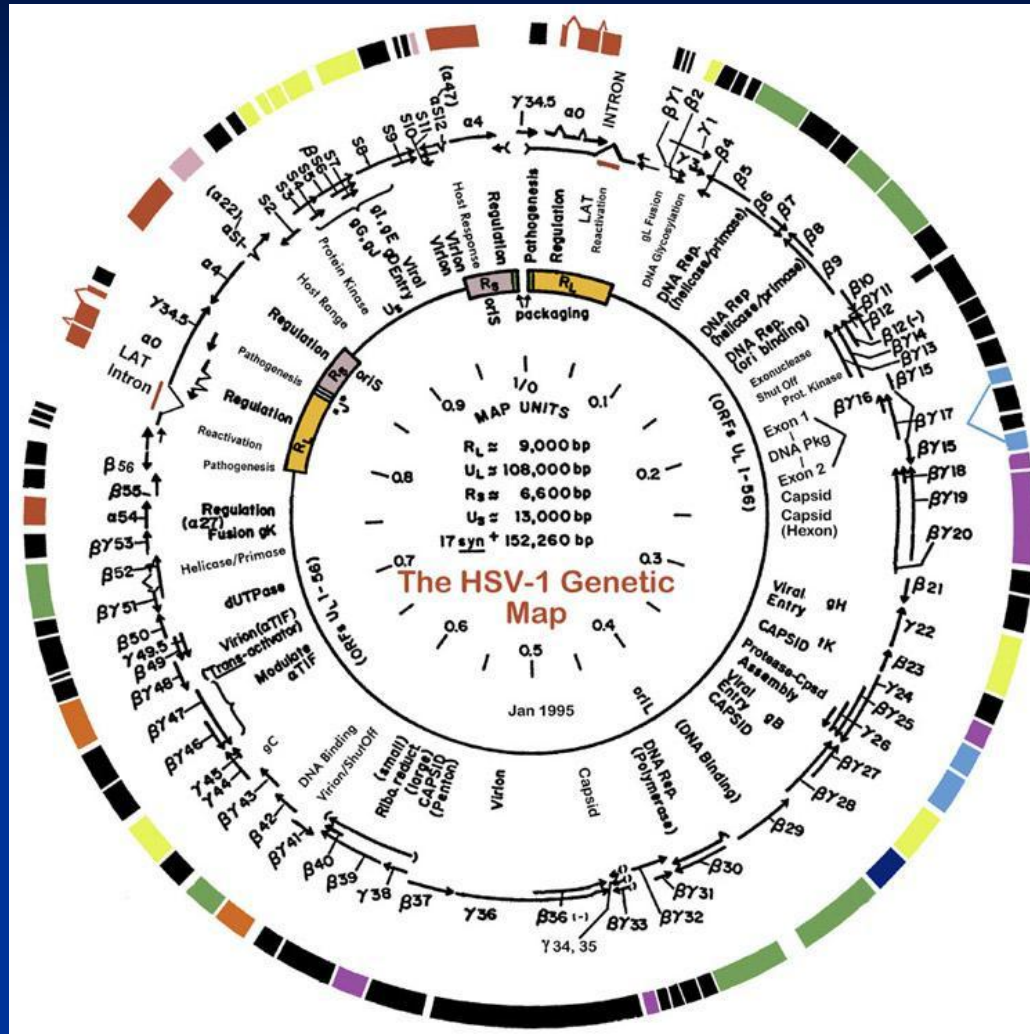
- For adenovirus DNA synthesis

- viral DNA polymerase)

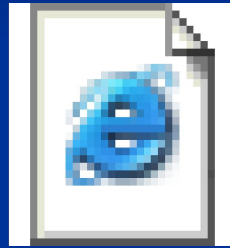
- Alter expression of host cell genes

- Against the host anti-viral response and/or interfere with cell cycle regulation

Генетична карта вірусу простого герпесу

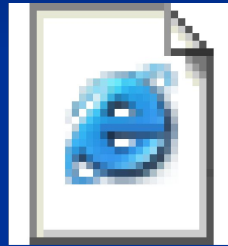


Транскрипція вірусу простого герпесу



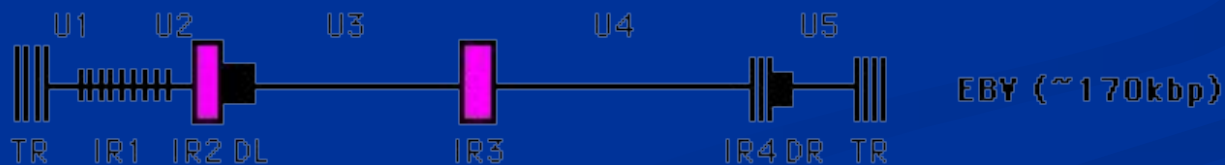
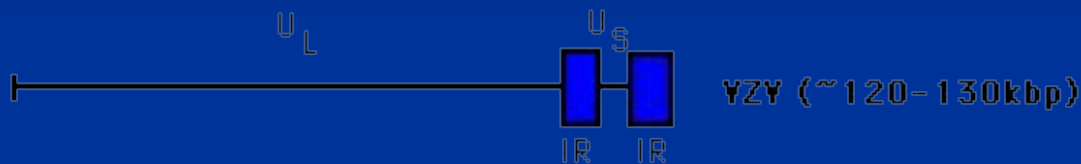
Hsvrna.swf

Реплікація ДНК вірусу простого герпесу



Dnarep.swf

Блочний запис генетичної інформації у герпесвірусів



Генетична карта бактеріофагу Т4

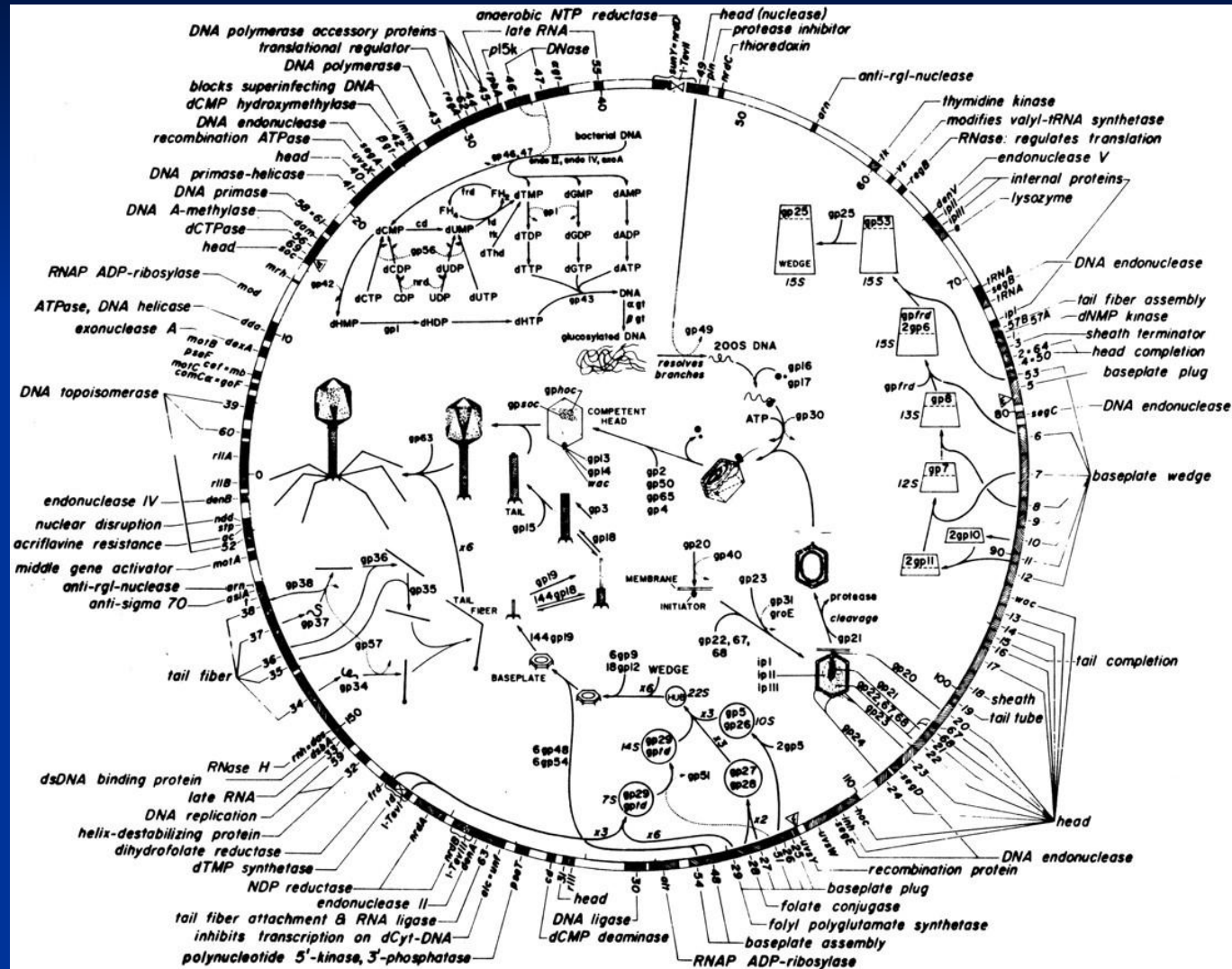
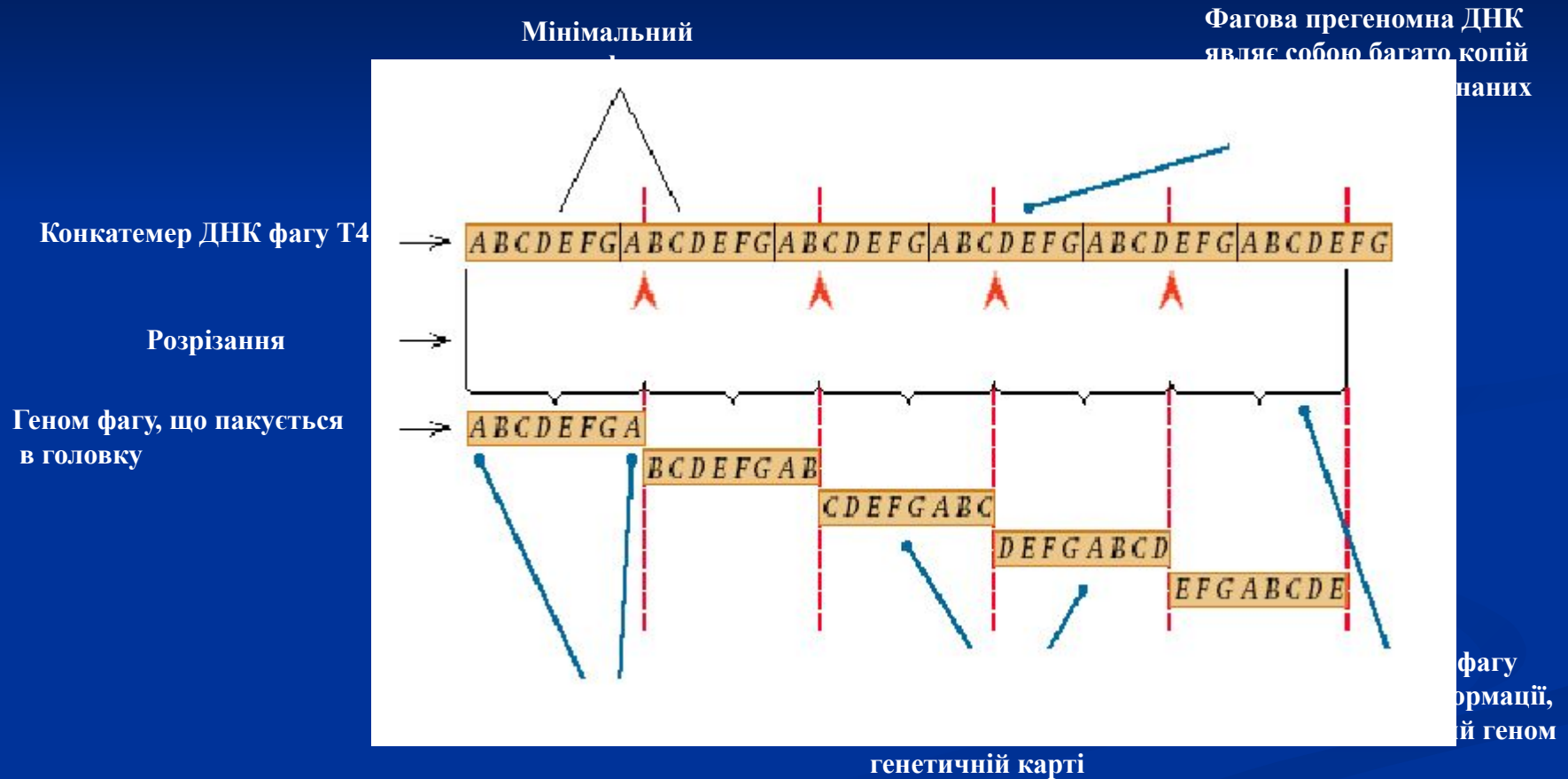
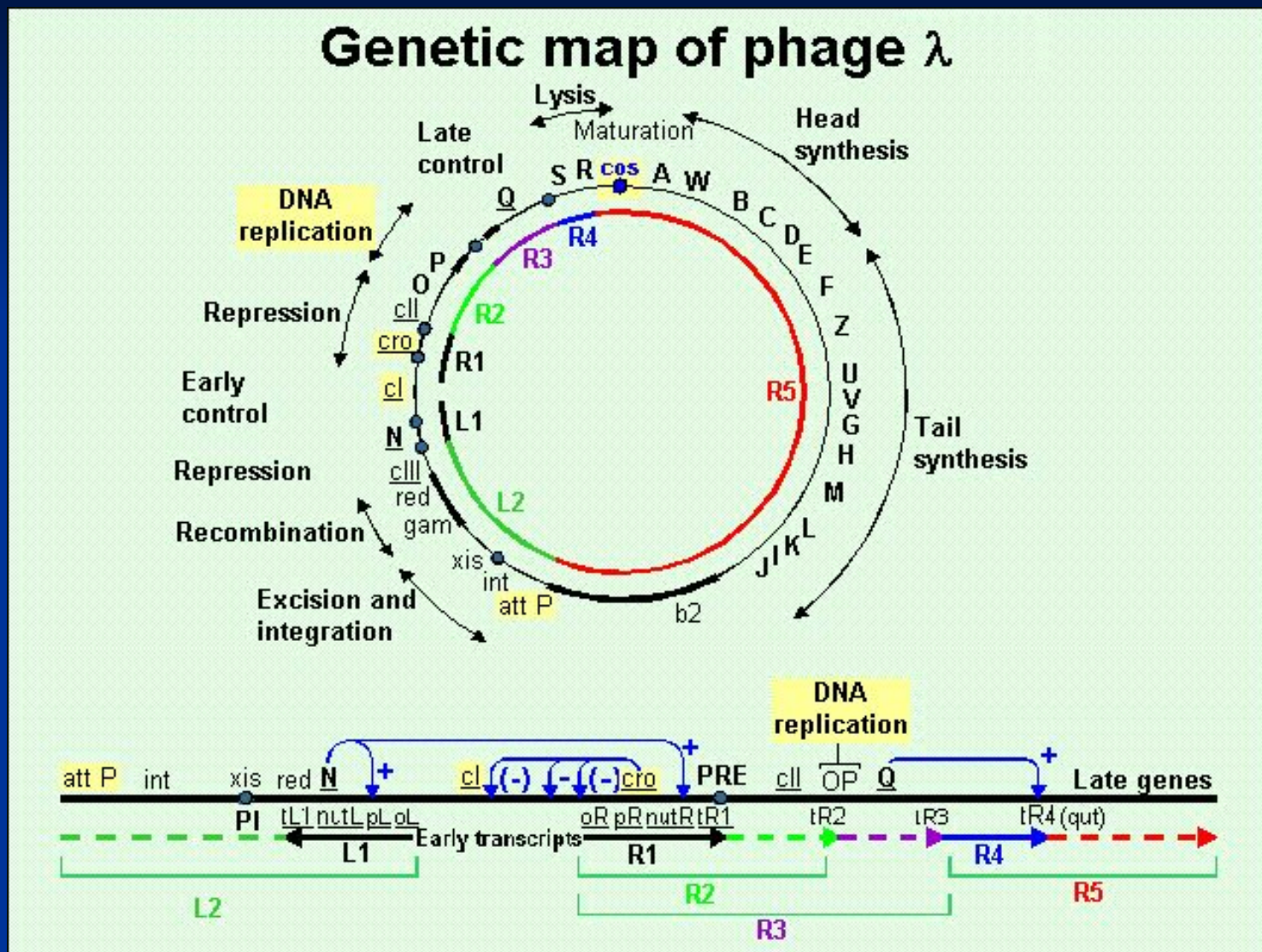


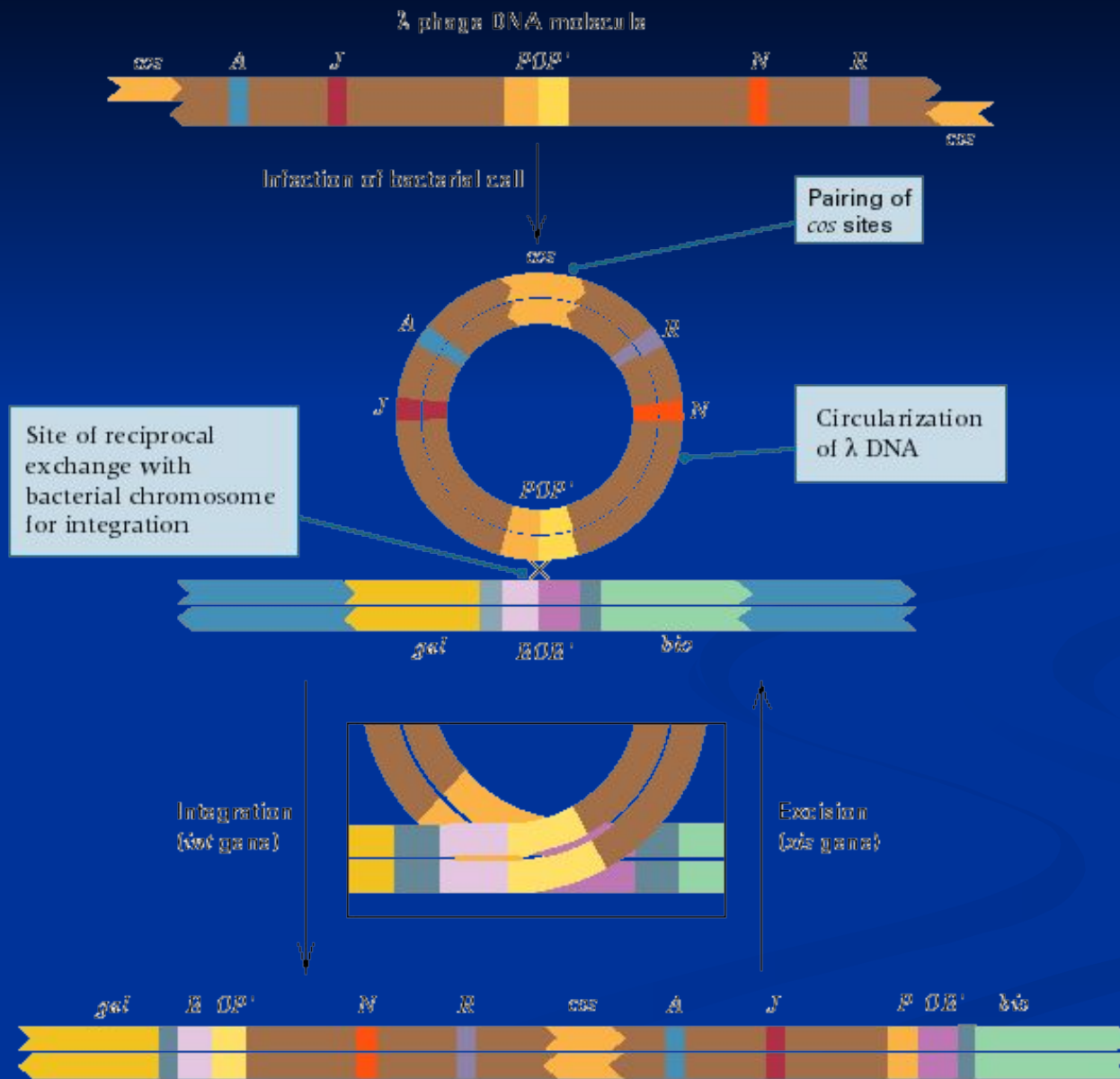
Схема розрізання конкатемеру фага Т4



Генетична карта бактеріофагу лямбда



Інтеграція геному фагу лямбда



POXVIRIDAE

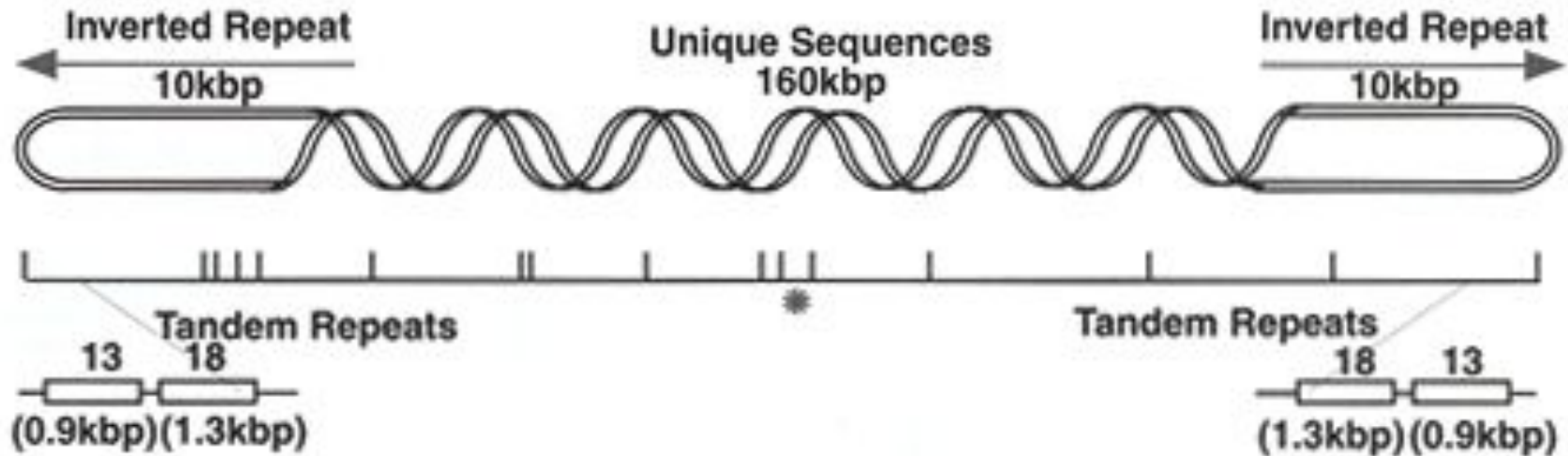


Figure 2 Schematic representation of the DNA of *Vaccinia virus* (VACV) (WR strain): (Top) Linear double-stranded molecule with terminal hairpins and inverted repeats (not to scale). The denatured DNA forms a single-stranded circular molecule. (Bottom) *Hind* III cleavage sites of the *Vaccinia virus* (WR strain) genome, the asterisk indicates the fragment that contains the thymidine kinase gene used in construction of phylogenetic trees. Each 10-kbp terminal portion includes two groups of tandem repeats of short sequences rich in AT. (Redrawn from Fenner, Wittek, and Dumbell, 1989, with permission.)

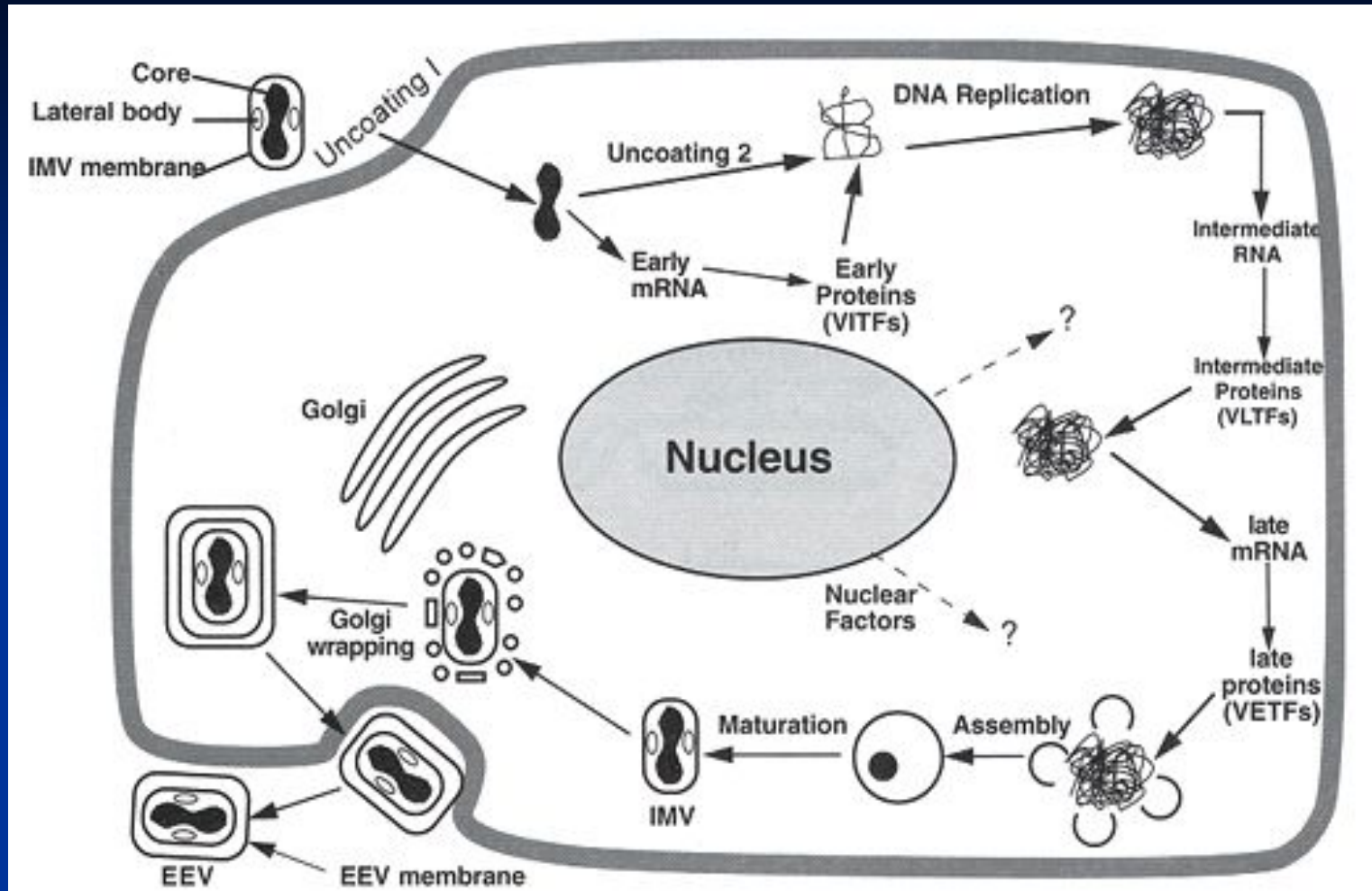
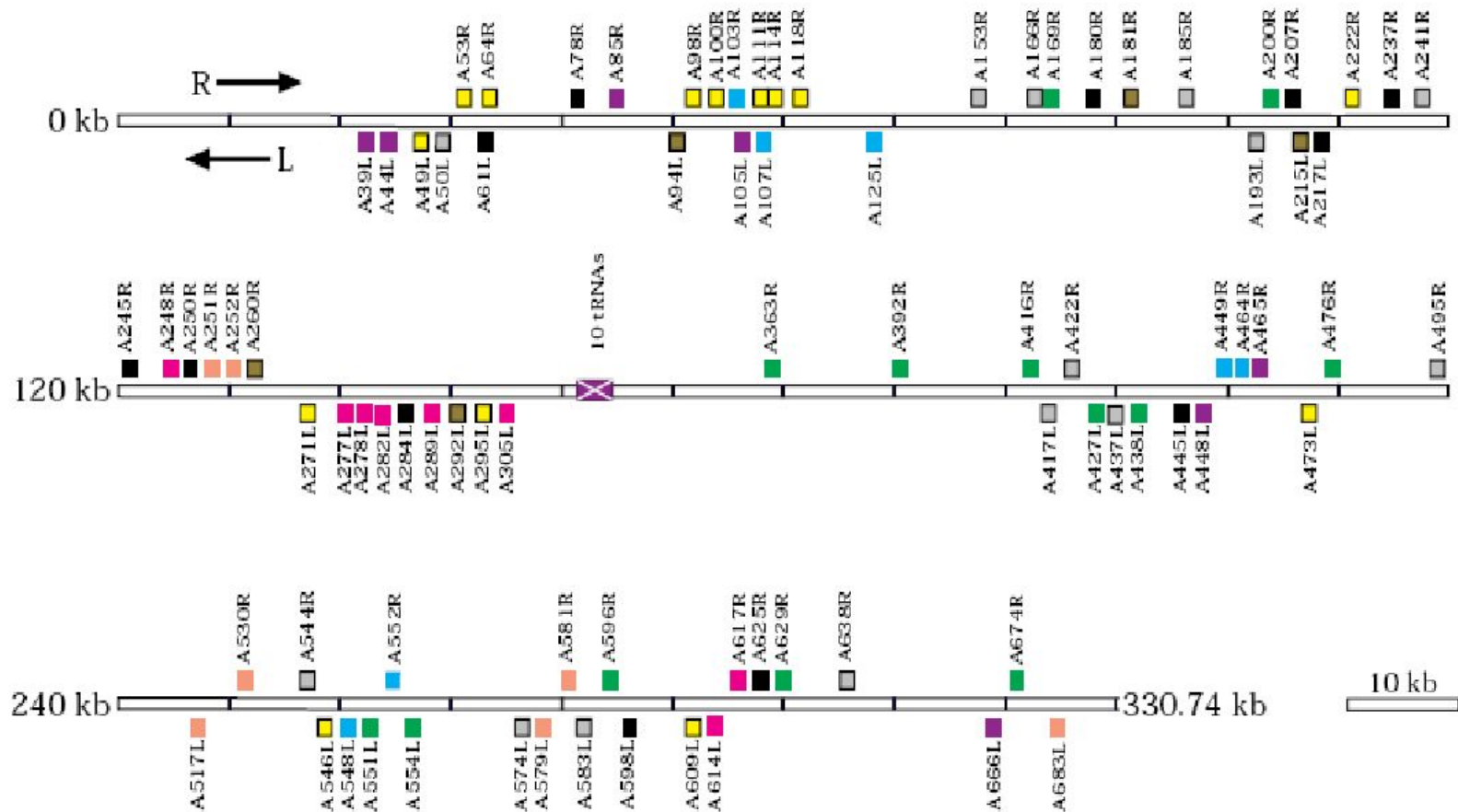


Figure 3 The infectious cycle of *Vaccinia virus* (VACV): IMV, intracellular mature virus; EEV, extracellular enveloped virus; VITF, vaccinia intermediate transcription factor; VLTF, vaccinia late transcription factor; VETF, vaccinia early transcription factor.

- The poxvirus genome comprises a linear molecule of dsDNA with covalently closed termini; terminal hairpins constitute two isomeric, imperfectly paired, “flip-flop” DNA forms consisting of inverted complementary sequences. Variably sized, tandem repeat sequence arrays may or may not be present near the ends (Fig. 2). The poxvirus genome comprises a linear molecule of dsDNA with covalently closed termini; terminal hairpins constitute two isomeric, imperfectly paired, “flip-flop” DNA forms consisting of inverted complementary sequences. Variably sized, tandem repeat sequence arrays may or may not be present near the ends (Fig. 2). Replication takes place predominately if not exclusively within the cytoplasm (Fig. 3). Entry into cells of intracellular virus (IMV) and extracellular enveloped virus (EEV) is suggested to be *via* different pathways. After virion adsorption, IMV entry into the host cell is by fusion between the plasma membrane after which cores are released into the cytoplasm and uncoated further. EEV entry, unlike IMV, may necessitate fusion with endosomal membranes to release the core.
- Polyadenylated, capped primary mRNA transcripts, representing about 50% of the genome, are initially synthesized from both DNA strands by enzymes within the core, including a virus-encoded multisubunit RNA polymerase; transcripts are extruded from the core for translation by host ribosomes. During synthesis of early proteins, host macromolecular synthesis is inhibited. Virus reproduction ensues in the host cell cytoplasm, producing basophilic (B-type) inclusions termed “viroplasms” or “virus factories”. The genome contains closely spaced ORFs, lacking introns, some of which may partially overlap preceded by virus-specific promoters that temporally regulate transcription of three classes of genes. One class, the early genes, are expressed from partially uncoated virions prior to DNA replication (these encode many non-structural proteins, including enzymes involved in replicating the genome and modifying DNA, RNA, and proteins designed to neutralize the host response). Early genes also encode intermediate transcription factors. Intermediate genes (which encode late transcription factors), are expressed during the period of DNA replication and are required for subsequent late gene transcription. Finally, late genes are expressed during the post-replicative phase (these mainly encode virion structural proteins but also early transcription factors). Despite a cytoplasmic site of replication, there is mounting evidence for the requirement of host nuclear proteins in post-replicative transcription. The mRNAs are capped, polyadenylated at the 3' termini, but not spliced. Many intermediate, late and some early mRNAs have 5'-poly(A) tracts, which precede the encoded mRNA. Early protein synthesis is generally decreased during the transition to late gene expression, but some genes are expressed from promoters with both early and late activity. Certain proteins are modified post-translationally (e.g., by proteolytic cleavage, phosphorylation, glycosylation, ribosylation, sulfation, acylation, palmitoylation and myristylation). Proteolytic cleavage of late proteins is required for virion morphogenesis.
- The replication of the DNA genome appears to be mainly through the action of viral enzymes. DNA replication appears to involve a self-priming, unidirectional, strand displacement mechanism in which concatemeric replicative intermediates are generated and subsequently resolved via specific cleavages into unit length DNAs that are ultimately covalently closed. Genetic recombination within genera has been shown, and may occur between daughter molecules during replication. Non-genetic genome reactivation generating infectious virus has been shown within and between genera of the *Chordopoxvirinae*.
- Virus morphogenesis begins following DNA replication and expression of early, intermediate and late genes. Particle assembly is initiated with the formation of crescent-shaped membrane structures. Replicated, concatameric DNA is resolved into unit genomes and packaged into immature virion particles, which further mature to form intracellular mature virions (IMVs) which are fully infectious if liberated from cells. A portion of the IMVs are further enveloped by modified Golgi membranes, transported to the periphery of the cell where fusion of the wrapped virions with the plasma membrane ultimately results in release of extracellular enveloped virions (EEVs) by an as yet incompletely understood process. Enveloped virions thereby acquire host cell lipids and additional virus-specific proteins, including the virus hemagglutinin protein. The envelope is closely positioned to the surface membrane. While both IMVs and EEVs are infectious, the external antigens on the two virus forms are different and upon infection, the two forms of virus bind to different cellular receptors and are likely uncoated by different mechanisms. Virus DNA and several proteins are organized as a nucleoprotein complex within the core of all infectious virions. The IMVs contain an encompassing surface membrane, lateral bodies, and the nucleoprotein core complex (see Fig. 1). For *Vaccinia virus*, the core has a 9 nm thick membrane with a regular subunit structure. Within the vaccinia virion, negative stain indicates that the core assumes a biconcave shape (Fig. 1) apparently due to the large lateral bodies, although some evidence suggests the shape may represent an artifact of sample preparation. The lipoprotein surface membrane surrounding the *Vaccinia virus* core and lateral bodies is about 12 nm thick and contains irregularly shaped surface tubules composed of small globular subunits. During natural infections, the virus is likely spread by that population of virus released from the cells (EEV). Although the internal structure of *Vaccinia virus* is revealed in thin sections, the detailed internal structure of parapoxvirus particles is less evident (Fig. 1). In negatively stained preparations of parapoxviruses, superimposition of dorsal and ventral views of the surface filament sometimes produces a distinctive “criss-cross” surface appearance.

Генетична карта вірусу PBCV-1

Partial Gene Map of *Chlorovirus* PBCV-1 (updated December 15, 2000)



Metabolism DNA Replication, Recombination, and Repair

(E)	A185R	δ DNA polymerase
(E)	A544R*	ATP-dependent DNA ligase
(E)	A583L*	DNA topoisomerase II
	A193L	PCNA
	A574L	PCNA
	A399R	RNaseH
	A456L	Superfamily III helicase
(E,L)	A50L*	Pyrimidine dimer-specific glycosylase
	A437L	DNA binding protein
	A417L	Replication factor C
(E)	A166R*	Exonuclease

Nucleotide Metabolism

(E)	A169R*	Aspartate transcarbamylase
	A476R	Ribo. reductase (small subunit)
	A629R	Ribo. reductase (large subunit)
	A427L	Thioredoxin
	A438L*	Glutaredoxin
(E)	A551L*	dUTP pyrophosphatase
	A596R*	dCMP deaminase
	A416R	dG/dA kinase
	A326L	NTP pyrophosphohydrolase
	A200R	Cytidine deaminase
	A674R*	Thymidylate synthase X
	A554L	ATPase
	A392R	ATPase

Transcription

(E)	A107L	Transcription factor TFIIIB
	A125L	Transcription factor TFIIIS
(E)	A552R	Transcription factor TFIIID
	A482R	VLTF2-type transcription factor
(E)	A103R*	RNA guanylyltransferase
	A449R*	RNA triphosphatase
	A153R	Superfamily II helicase
	A363R	Superfamily II helicase
(E)	A464R*	RNase II
	A548L	SWI/SNF helicase
	A241R	Skil helicase
(L)	A612L*	Histone H3, Lys27 methylase

Protein Synthesis, Modification, and Degradation

	A39L	SKP-1 protein
(E,L)	A666L	Translation elongation factor-3
(L)	A85R*	Prolyl 4-hydroxylase
	A105L	Ubiquitin C-terminal hydrolase
	A448L	Protein disulphide isomerase
	A465R	Thiol oxidoreductase
	A604L	Zn metalloprotease
		11 rRNAs

Cell Wall Degrading Enzymes

(E)	A94L*	β -1,3-glucanase
(E)	A181/182R*	Chitinase
(L)	A260R*	Chitinase
(L)	A292L*	Chitosanase
(E,L)	A215L*	Alginate lyase

Sugar and Lipid Manipulation

(E)	A98R*	Hyaluronan synthase
(E)	A100R*	Glucosamine synthase
(E)	A609L*	UDP-glucose dehydrogenase
(E)	A118R*	GDP-D-mannose dehydratase
(E)	A295L*	Fucose synthase
(E,L)	A64R	Mannosyltransferase
	A111R	Glycosyltransferase
	A114R	Fucosyltransferase
	A222/226R	Glycosyltransferase
(E)	A473L	Glycosyltransferase
	A546L	Glycosyltransferase
	A49L	Glycerophosphoryl diesterase
	A53R	2-hydroxyacid dehydrogenase
	A173L	Patatin phospholipase
	A271L	Lysophospholipase
	A297L	Fructose-2,6-bisphosphatase
	A402R	Lipoprotein lipase
	A654L	N-acetyltransferase

Signaling

(E,L)	A250R*	K ⁺ channel protein
	A162L	Ligand-gated channel protein
	A163R	Ligand-gated channel protein
	A34R*	Ser/Thr protein kinase
(L)	A248R*	Ser/Thr protein kinase
	A277L	Ser/Thr protein kinase
	A278L*	Ser/Thr protein kinase
	A282L*	Ser/Thr protein kinase
	A289L*	Ser/Thr protein kinase
	A305L	Tyr phosphatase
	A614L*	Protein Kinase
	A617R	Tyr-protein kinase

DNA Restriction/Modification

	A251R*	Adenine DNA methylase [M. CviAII]
	A252R*	DNA restriction endonuclease [R. CviAII]
(E)	A517L*	Cytosine DNA methylase [M. CviAIII]
(L)	A530R*	Cytosine DNA methylase [M. CviAIV]
(E)	A581R*	Adenine DNA methylase [M. CviAI]
(E)	A579L*	DNA restriction endonuclease [R. CviAI]
	A683L	Cytosine DNA methyltransferase [M. CviAV](E,L)

Integration and Transposition

A625R	Transposase
A134L	Homing endonuclease GIY-YIG
A287R	Homing endonuclease GIY-YIG
A315L	Homing endonuclease GIY-YIG
A351L	Homing endonuclease GIY-YIG
A495R	Homing endonuclease GIY-YIG
A539R	Homing endonuclease GIY-YIG
A651L	Homing endonuclease GIY-YIG
A422R	Homing endonuclease HNH
A87R	Homing endonuclease HNH
A267L	Homing endonuclease HNH
A478L	Homing endonuclease HNH
A490L	Homing endonuclease HNH(L)

Miscellaneous

(E,L)	A207R*	Ornithine decarboxylase
(L)	A237R*	Homoserine synthase
(E)	A78R*	N-carbamoylput amidohydrolase
(E)	A638R*	Agmatine iminohydrolase
	A217L	Monoamine oxidase
	A44L	BCS1 protein
	A61L	O-methyltransferase
	A180R	Fibronectin binding protein
	A245R*	Cu/Zn-superoxide dismutase
	A284L*	Amidase
	A445L	ABC transporter protein
	A598L	Histidine decarboxylase

Structural Proteins

(L)	A430L	Vp54, major coat protein
(L)	A622L	Coat protein-like
	A122R	Glycoprotein Vp260

* Functional enzyme
(E) Early gene
(L) Late gene

Fig. 2 Partial gene map of the PBCV-1 genome. Genes listed above the genome are transcribed from left to right (R, $\rightarrow$), and genes listed below the genome are transcribed from right to left (L, $\leftarrow$). The genes that have similar or related function are assigned into the same group and are labelled by a code in the same colour. *Genes characterized and known to encode functional enzymes. (E) Genes transcribed early; (L) genes transcribed late. For many genes both the transcription patterns and the functions of gene products are unknown.