

INTERUNIVERSITY PROGRAMME ON MOLECULAR BIOLOGY (IPMB)  
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# Creating cDNA Libraries

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# DEFINITIONS

## **Complementary DNA (cDNA)**

mRNA cannot itself be ligated into a cloning vector so cDNAs are complementary DNA copies of RNA that are generated by the enzyme Reverse Transcriptase then the cDNA produced can be ligated to a vector to produce a cDNA library.

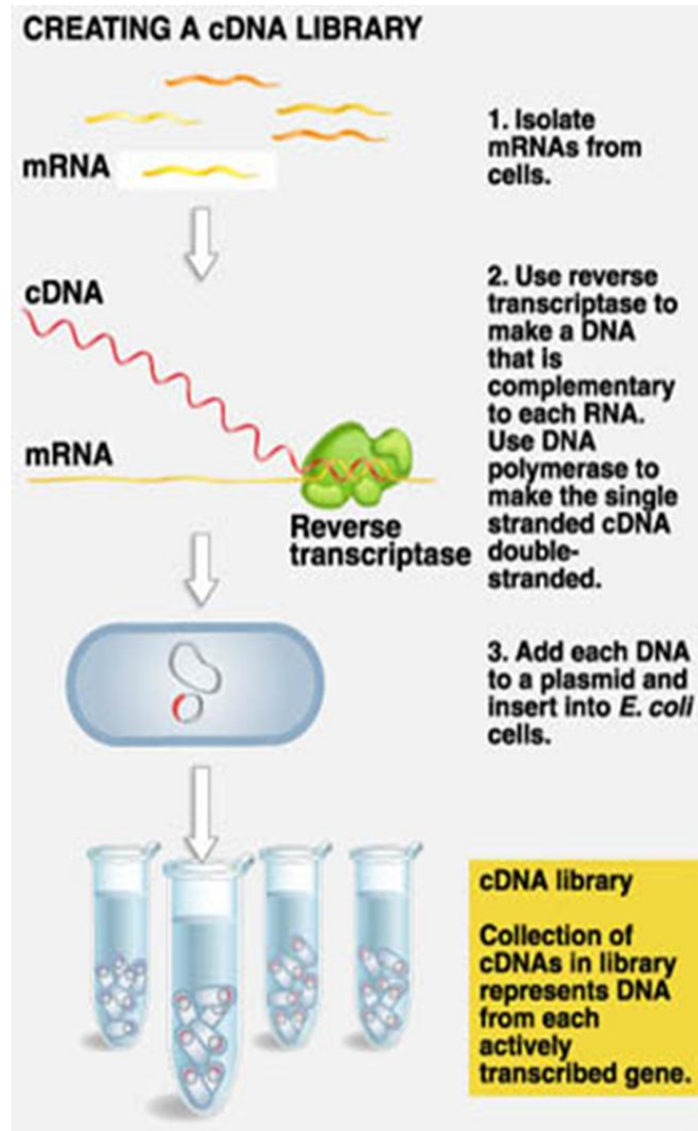
## **Complementary DNAs libraries**

Are processed nucleic acid sequences harvested from the RNA pools of cells or tissues and represent all the cDNA sequence prepared at a certain time for genes expressed in certain cells or tissues.

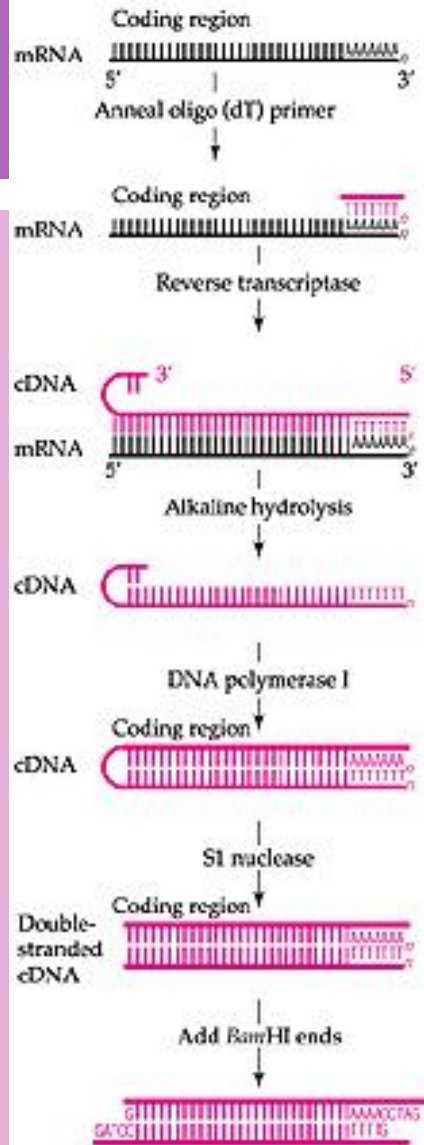
# DIFFERENCES BETWEEN GENOMIC AND COMPLEMENTARY DNA LIBRARIES

- The genomic library contains DNA fragments representing the entire genome of an organism. More commonly used in bacteria.
- The c DNA library contains only complementary DNA molecules synthesized from mRNA molecules in a cell. The size of a c DNA clone needed to contain the complete gene is much smaller than the corresponding length of genomic DNA. Used for animals and other eukaryotes. Lack information about enhancers, introns, and other regulatory elements found in a genomic DNA library.

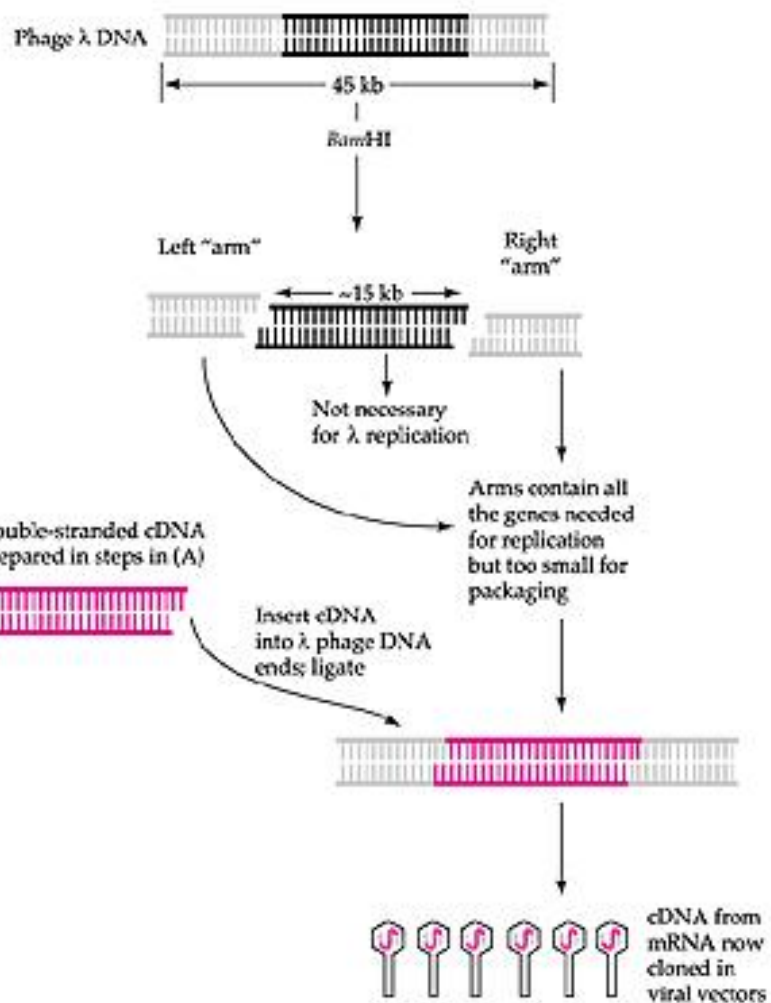
# FIG. 01. FORMATION OF CDNA LIBRARIES



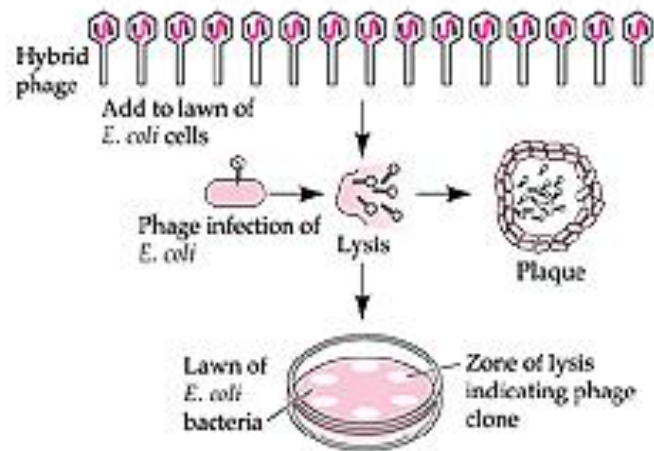
(A) Preparation of clonable cDNA



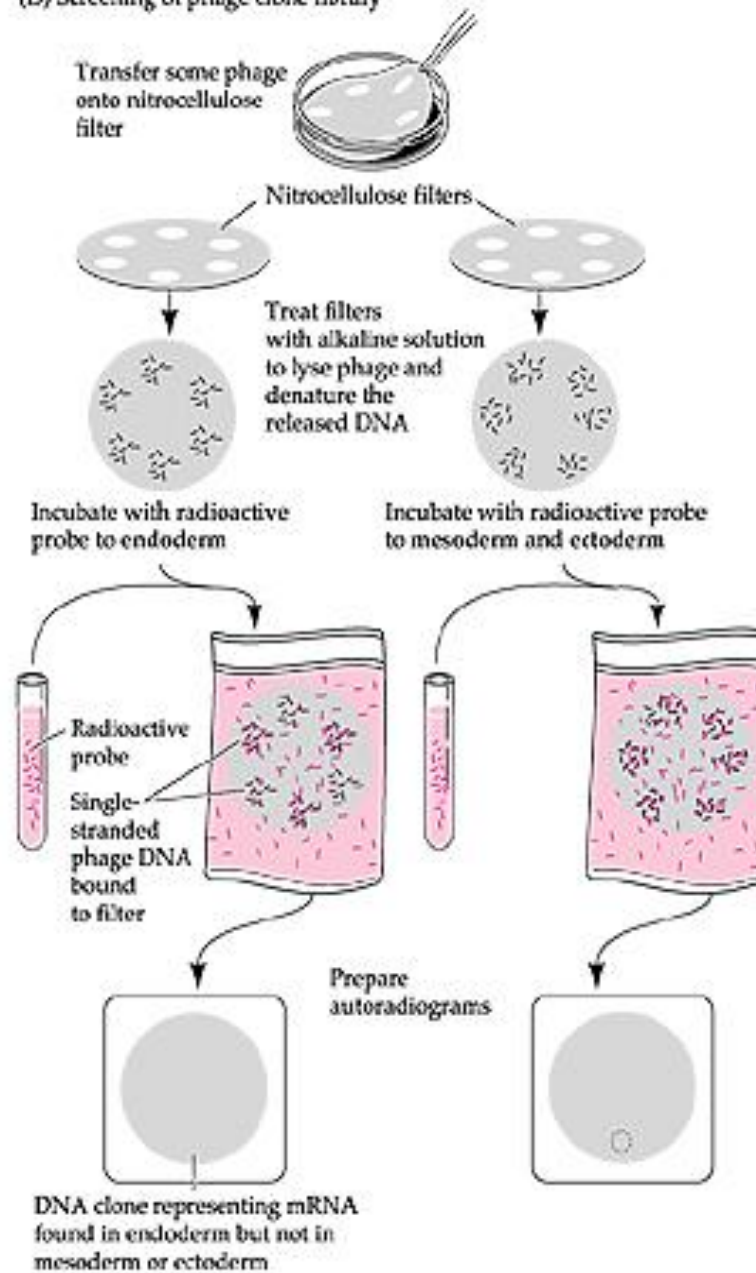
(B) Insertion of double-stranded cDNA into viral vector (bacteriophage  $\lambda$ )



(C) Preparing library of phage clones

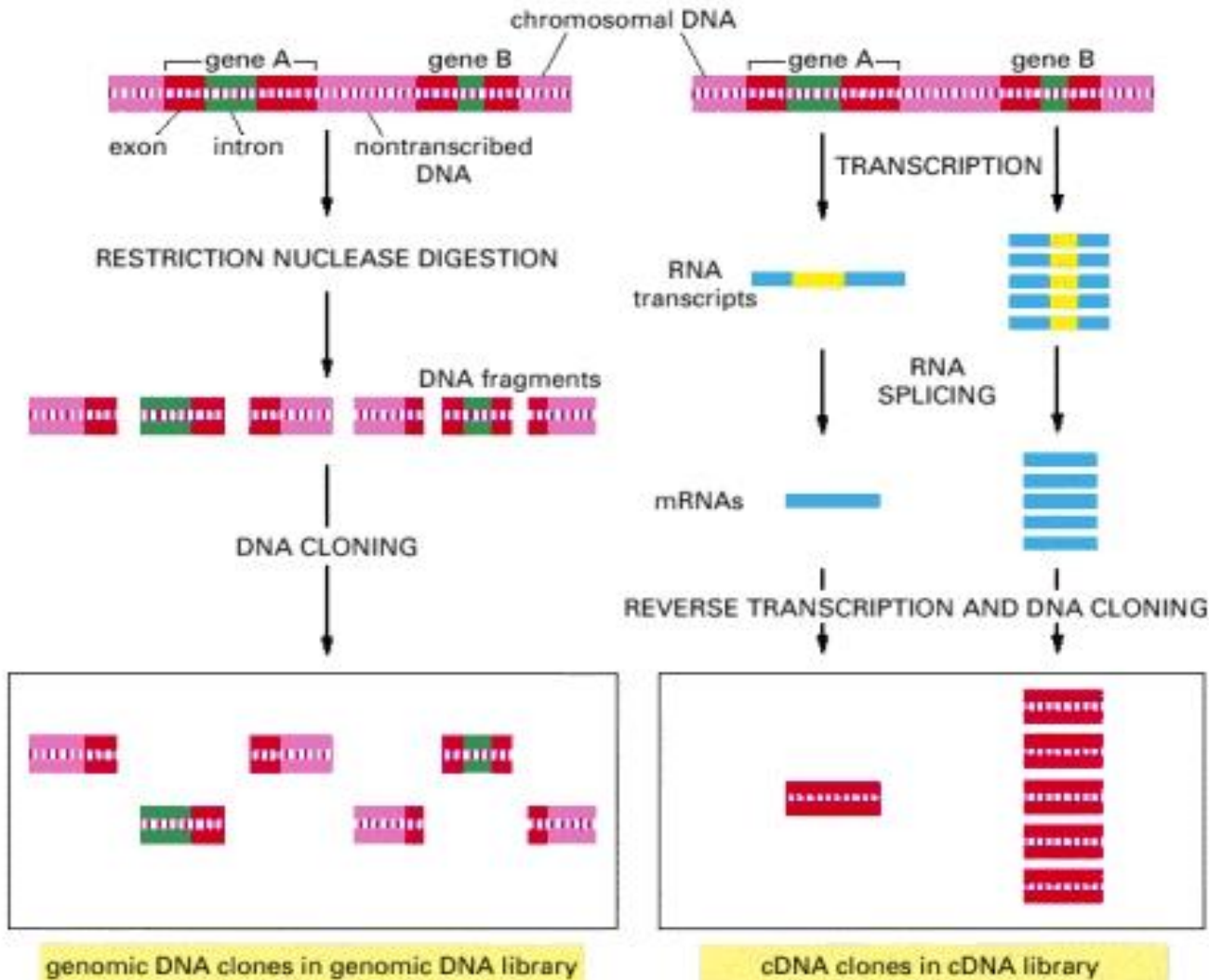


(D) Screening of phage clone library



# TABLE 01. GENOMIC AND CDNA PROCESS OF CLONING LIBRARIES

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# CDNA LIBRARY USES

- ❖ Are commonly used when reproducing eukaryotic genomes, as the amount of information is reduced to remove the large numbers of non-coding regions from the library.
- ❖ To express eukaryotic genes in prokaryotes. Prokaryotes do not have introns in their DNA and therefore do not possess any enzymes that can cut it out during transcription process. cDNA do not have introns and therefore can be expressed in prokaryotic cells.
- ❖ cDNA libraries are most useful in reverse genetics where the additional genomic information is of less use. Also, it is useful for subsequently isolating the gene that codes for that mRNA.
- ❖ To monitor a large number of genes to provide a powerful tool for assessing differential mRNA expression levels for the identification of disease-associated genes.



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**MUCHAS GRACIAS POR SU ATENCION!**

