Dr. Suman Chauhan

Botany Deptt.

N.A.S. College (P.G.)

B.Sc (Final Year)

Genemic Library

A Genomic library is a **set of recombinant clone** that contain all the **DNA** present in an **individual organism.** A **E.coli** genemic library for e.g. contains all the DNA present in an individual organism i.e. all the **E.coli** genes so any desired gene can be with dram from the **library** and **studied.**

Genemics libraries are prepared by purifying total all **DNA** and then walking a partial restriction digest resulting in fragments that can be cloned into a suitable **vector** usually a **replacement vector** or a **cosmid** for **bacteria yeast** and **fungi** the no. of **clones** needed for a complete **library** will contain so many different clones that identification of the desired one way prove a difficult task with these organism a second type of library. Specific not to the whole organism but to a particular cell type may be more useful. Inspite off all precaution taken in a genomic library. Preparation chances are there of certain fragment being under or over represent of ever mission possibly because certain fragement code for a toxin product or might replicate slowly or night have been altered by recombinational during cloning.

In addition indonuclear cleavage sites are after not recognized equally will certain DNA fragment may therefore never appear in partial digits by a restriction endonuclease used for the construction of genomic library.

To construct a genomic library

For preparation of genomic library the total genomic DNA of an organism is extracted the DNA is broken in to fragments of appropriate size wither by

mechanical sharing or by using suitable restriction endonuclease. For partial digestion is avoided since it generates fragments that are able to heterogenes in size.

For partial digestion restriction enzymes having 4-bse recognition sequence are employed in preference to those having 6-base target sites is expected to occur every 4^4=256 base pairs in a DNA molecule while 6 base target sites would occur molecule while 6 base target sites would occur only after every 4^6=4.096 base pairs therefore fragments produced in partial digests with enzymes having 4 base recognitions sites are more likely to be of appropriate size for cloning than those generated by enzyme having 6 base recognition sites single or mixed digestions with enzyme.

The use of restriction enzyme have the advantage that the same set of fragments are obtained from a DNA each time a specific enzyme is used.

The minimum size (i.e. no. of clones are bacterial colonies) of a genomic library depends on the following factors.

1. The complexity of genome (more complex is the genome large in size)
2. The insert or fragments length used for cloning (smaller the fragment size the larger no. of clones for the same genome).