Genomic Library

Introduction

A **genomic library** is a collection of the total genomic DNA from a single organism. The DNA is stored in a population of identical vectors, each containing a different insert of DNA. In order to construct a genomic library, the organism's DNA is extracted from cells and then digested with a restriction enzyme to cut the DNA into fragments of a specific size. The fragments are then inserted into the vector using DNA ligase. Next, the vector DNA can be taken up by a host organism - commonly a population of Escherichia coli or yeast - with each cell containing only one vector molecule. Using a host cell to carry the vector allows for easy amplification and retrieval of specific clones from the library for analysis.

There are several kinds of vectors available with various insert capacities. Generally, libraries made from organisms with larger genomes require vectors featuring larger inserts, thereby fewer vector molecules are needed to make the library. Researchers can choose a vector also considering the ideal insert size to find a desired number of clones necessary for full genome coverage.

Genomic libraries are commonly used for sequencing applications. They have played an important role in the whole genome sequencing of several organisms, including the human genome and several model organisms.

What is genomic library?

“A genomic library is a collection of bacteria which have been genetically engineered to hold the entire DNA of an organism”. A genomic library is a collection of genes or DNA sequences created using molecular cloning. These libraries are constructed using clones of bacteria or yeast that contain vectors into which fragments of partially digested DNA have been inserted. These bacteria and yeast are subsequently grown in culture and when these microorganisms replicate their genome, they also replicate the vector genome contained within them, that is, they replicate DNA fragments that had been inserted in vectors producing clones of the orignal genome. This collection of clones, in theory, contains all sequences found in the original source, including the sequence of interest. Genomic libraries can be constructed using various hosts like plasmids, bacteriophagelambdas , cosmids, YACs and many more.

Construction of Genomic Library involves following steps

(a) Isolation of target DNA:

Genomic libraries can be constructed by isolation of complete DNA from bacteria, virus, plants and animals. In eukaryotes, high molecular weight DNA is isolated by CTAB or SDS methods. The isolated DNA is then purified by caesium chloride and other methods.

(b)Restriction Fragments

Fragmentation can be done by mechanical shearing or using suitable restriction enzymes. Partial digestion is essential to procure proper size DNA fragments. Therefore, treatment times and concentration of enzyme is very important for desirable result.

(c) Cloning the fragments in vector:

The restricted digested DNA sample is electrophoresed and subjected to. Target DNA fragments are identified by hybridization with probes and then cloned in suitable vectors like lambda or cosmid vectors and maintained as library.

(d) Screening of Genomic library:

Genomic library can be screened for clones by hybridization with probe, western blotting to detect protein product and also screening of protein activity.

Importance of Genomic Library

- Used to explore the genome of an organism and to learn more about the genomic structure and function.
- Used to create a genomic map and to identify the locations of specific genes.
- Used to study the genetic variations such as mutations (Cancer).
- Useful in recombinant DNA technology, like transgenic plants or animals through genetic engineering (B.T cotton).
- It is the first step in any DNA sequencing projects.

What are the uses of Genomic Library?

- Researchers can explore the genome of an organism to learn more about genomic structure and function .
- They can map the genome, identifying the locations of specific genes.
- Helps to develop tests which can be used to locate genetic variationsϖ including mutations
- Useful in Recombinant DNA Technology, helps to genetically modify organisms and produce clones of desired types.
- Genomic library construction is the first step in any DNA sequencingϖ projects.
- Genomic library helps in identification of the novel pharmaceutically important genes.

Problems and Solutions of Genomic Library

1. Problem in Genome Library

The gene may be cut internally with the restriction enzyme used, therefore a singleθ required sequence is not obtained. The gene of interest obtained by the restriction enzyme may be larger than the vector.

2. Solution

Random cloning of DNA fragments of large size ≥ 20 kbθ

REFERENCES

1. www.google.com
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3. www.studymafia.org