

How to Sequence a Genome Lesson

Part I

Organize the main headings in the order that you think is logical for the sequencing process by numbering the headings with Roman numerals. Number any subheadings with Arabic numbers (1, 2, 3, etc.).

Sub clones

Building libraries

Mapping

Preparing DNA for Sequencing

DNA sub clones stored in *E. coli*

Products of Sequencing Reaction

Reading the Sequencing Reaction

Separating the Sequencing Reaction

Sequencing Reaction

Working Draft Sequence

Assembling the Results

Different Strategy

Part II

Organize these topics under the headings above using capital letters under the Roman numerals.

Unique Landmarks identified on chromosomes.

Clones are identified using the markers or landmarks that each contains.

Libraries are created for orderly access to information.

Clone libraries contain fragments of human DNA.

Clones are stored in E. coli bacteria.

Bacterial Artificial Chromosome or BACs are 100,000 to 200,000 bases long.

Contain fragments that are only 200 bases long

Fragments of DNA can be stored indefinitely.

Shaker water baths provide air to help bacterial cells grow and divide.

By heating them to 37 degrees Celsius (our body temperature) the frozen bacteria can be revived.

Billions of copies of the DNA fragments are made in a few hours.

DNA is separated from the bacterial debris after a 24-hour growth period.

A sequencing reaction includes four main ingredients

Template DNA Free bases

Guanine pairs with cytosine

Primers

DNA polymerase

Base pairs

Adenine pairs with thymine

Opposite strands of DNA pairs as C-G and A-T.

Fluorescent dye attached to bases limits the length of the DNA strands.

Completed sequencing reactions contain fragments of various sizes.

The products of the sequencing reactions are placed into an automated sequencing machine.

DNA fragments are separated by electrophoresis.

DNA molecules have a negative charge.

Shorter DNA fragments move more quickly through a gel.

The sequencing machine reads the code of the DNA molecules.

A single sequencing reaction can read a few hundred letters of DNA.

DNA fragment overlaps are identified.

On average, any region of the genome may be sequenced nine times.

Many reactions are done in labs in several different countries.

The results of the sequencing are shared with the public via the Internet.

The finished sequence will be 99.9 percent accurate.

The working draft is 90 percent of the genome had been sequenced and assembled in June of 2000.