Biotechnologies

Genome sequencing

- **Genomics** is the branch of biology that studies genomes. It is called **functional**, if the purpose is to assign functional roles to the genes, and **comparative** if the sequences of various organisms are compared.
- **Genomic sequences** provide information about the open reading frames (**ORF**) of genes, protein sequences, and regulatory sequences.
- Techniques developed in the nineties have made it possible to sequence the human genome as part of the **Human Genome Project**.
- About 95% of human DNA is not translated into polypeptides (**junk DNA**), but it may have other functions: telomeres and centromeres, introns, regulatory sequences, pseudogenes, transposons, and repeated sequences.

New biotechnologies

- **Biotechnologies** are based on the use of living organisms or their derivatives to produce substances or processes.
- Large quantities of a gene product can be produced in host cells by using **expression vectors**.
- Genetically modified animals can be used to produce drugs by **pharming**.
- In agriculture, biotechnologies are used to obtain **resistant plant** varieties that resist parasites and infections, and especially foods with improved **nutritional characteristics**.
- **Bioinformatics** has made it possible to transition from the study of individual genes and proteins to the study of the entire **transcriptome** and **proteome.**
- The so-called **microRNAs** used in biotechnological manipulation can pair with complementary sequences of some mRNAs and prevent their translation.

Recombinant DNA technology

- This technique consists of identifying a gene, cutting it out and isolating it from the rest of the DNA, joining it to a vector and transferring it into the recipient cell where it is inserted into the genome.
- **Restriction enzymes** cut the DNA into **restriction fragments** corresponding to the sequences of specific bases.
- **Methylation** corresponding to the **restriction sites** permits an organism to protect the DNA from its own restriction enzymes.
- **Gel electrophoresis** can be used to separate the restriction fragments based on their length.
- Many restriction enzymes make staggered cuts in the DNA, leaving **sticky ends** in the fragments.
- The ends of the cut fragments of the same enzyme are **complementary** and can be joined by **DNA ligase**.
- The **DNA fingerprinting** obtained by fragmenting human DNA with restriction enzymes has different characteristics from one person to the next.
- **Single nucleotide polymorphisms** (SNP) and the number of **short tandem repeats** are the most important types of polymorphisms used to establish kinships or to identify a person.

Cloning

- With cloning, many copies of a gene can be obtained as a result of **transfection** of recombinant DNA in host cells.
- A **transgenic** cell has acquired recombinant DNA and can be recognized by the presence of **reporter genes**.
- Host cells may be prokaryotes (bacteria) or eukaryotes (yeasts, or plant or animal cells) depending on the gene they express.
- Once the DNA has entered the host cell, it has to insert itself into a **replicon** to be copied.
- The **vectors** that transport fragments into the host cells may be plasmids, viruses, or artificial yeast chromosomes. They must contain a restriction site and a reporter gene in order to be copied independently of the host cell.
- A **gene bank** is created by fragmenting the genome of a cell and transfecting the host cells with vectors containing the various DNA fragments.
- A **complementary DNA library** (cDNA) is obtained by transfecting the host cells with the cDNA obtained from the mRNAs present in the cell at a given time (transcriptome).
- **Synthetic DNA** can be used to project a gene from a protein. Mutations can be induced in genes to study cause-effect relationships by using techniques of **mutagenesis**.

AUDIO
Summing-up

ebook.scuola.zanichelli.it/sadavabiologiablu