Genome mapping

Genome mapping is the method by which we get the most accurate idea of gene maps . The basis of mapping is the determination of the **number of chromosomes , the position of genes** on the given chromosomes and in what **order** the genes are located (gene distance). Determining the exact sequence is possible using genome mapping and genome sequencing methods .

One of the main tasks of **medical genetics** is to identify genes, determine their function and reveal the changes that **cause disease** - gene mapping is a prerequisite for this.

Two methods are used to **map the human genome** :

- **genetic mapping**
  - uses the frequency of '*meiotic crossing-overs* to estimate the distance between loci
- **physical mapping**
  - uses **cytogenetic and molecular genetic techniques** for precise localization on the chromosome

Mapping the genome

We are able to determine the number of chromosomes using common methods of cytogenetic examination of the karyotype . **The laws of gene bounds** and the **three-point test** are used to determine the order and distance of genes. Other mapping methods include, for example, the hybridoma method and probe mapping.

Find more detail on: Gene bounds.

Find more details on: Three-point test.

Hybridoma method

It used to be used, nowadays it is rather abandoned. The method is too lengthy and requires experience.

Successful experiments were with hybrids of mice and human cells. Mouse lines were selected with a deficiency of a certain enzyme, the function of which was completely taken over by the corresponding human gene in the offspring. These hybrids tended to **eliminate human chromosomes**. The evaluation took place by monitoring **the presence of the product of the given chromosome**. If only one human chromosome remained in the cell and its product was present, the gene was located on that chromosome.

Using this method, it was possible to localize the gene **complex of the human HLA system** according to its antigenic products and translocation to the distal part of the p-arm of chromosome 6.

Probe mapping method

If we know the protein product of a gene, we can try **a molecular probe**. We will compile a sequence of nucleotides that encode the frequency of the gene under study and we can try **mutual hybridization**.

In DNA - RNA modification , an mRNA strand is used, labeled with a radioactive isotope. The isotope-labeled base hybridizes to the part of DNA where the structural gene is responsible.

Sequencing methods

To determine the exact sequence of nucleotides in DNA, the Sanger and Maxam & Gilbert methods were created. Today, the Sanger method is more widely used.

The Sanger method

It uses the special properties of special nucleotides - 2', 3' dideoxyribonucleotide triphosphates (ddATP, ddCTP, ddGTP and ddTTP), to the end of which another nucleotide cannot be attached.

We amplify single-stranded DNA, add DNA polymerase, the appropriate primers and enough deoxyribonucleotide triphosphates (dATP, dCTP, dGTP and dTTP) (for synthesis) and a certain amount of another type of dideoxyribonucleotide triphosphate (eg ddATP). The primers anneal to the single-stranded DNA and the polymerase completes the sequence of the second strand. When adding dATP to the chain, there is a certain probability that it will add ddATP, the inclusion of which **will terminate the polymerization** . Such a product will end with adenine. If the reaction takes place with ddCTP, ddGTP and ddTTP, we obtain **a mixture of oligonucleotides** terminated with the appropriate base.

Subsequently, we perform **electrophoresis of the given mixture** . We perform the electrophoresis evaluation from below and evaluate the DNA sequence.

Find more details on: Polymerase chain reaction (PCR).

Find more details on: DNA sequencing.

Maxam & Gilbert

It uses a specific **chemical cleavage of DNA** beyond certain nucleotides instead of a polymerization reaction. The evaluation takes place electrophoretically, just as with the Sanger method.

Sanger DNA sequencing method
5'TACAGTTTCAGGA3'

Mapping results

Using knowledge of exact sequences, we are able to **determine the origin of the disease**. The gene that causes the given disability is disabled by a targeted mutation .

For ethical reasons , **such experiments cannot be performed on humans!**

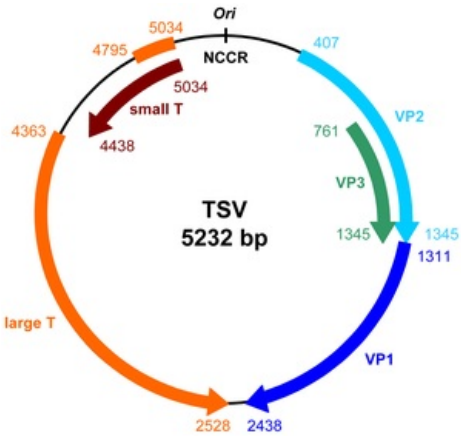
Genetic maps

Based on linkage analysis . **The frequency of meiotic crossing-over** is used to estimate the distance between two loci .

The distance of the respective genes on the chromosome (recombination fraction) is expressed using **Morgan's number**:

$$p = \frac{počet\ recombinationů}{počet\ všech} * 100$$

Morgan's number is expressed in centimorgans [cM].



Genome map

Physical Maps

It helps to determine the exact location of genes in the DNA sequence . Distances between genes are expressed in base pairs. This method uses cytogenetic and molecular genetic techniques.

Links

Related Articles

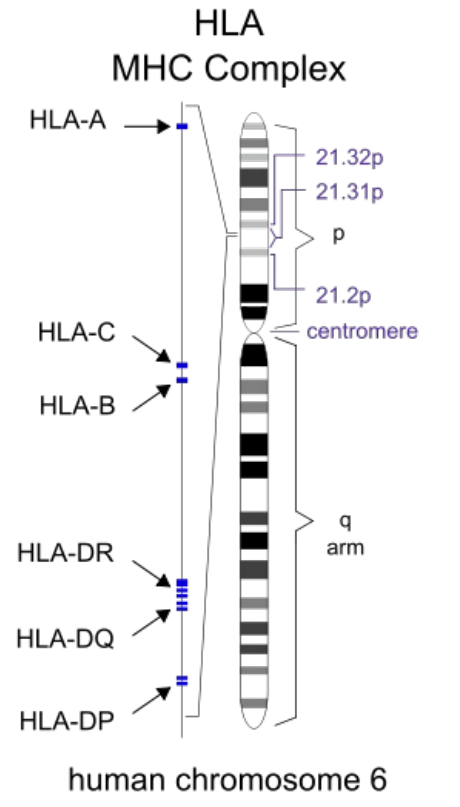
- Genom
- Klinická genetika

External links

- **HUGO** - *Humane Genome Mapping Organization* (http://www.hugo-international.org/)
- Genetika -Biologie; Mapování genomu (http://www.genetika-biologie.cz/mapovani-genomu)

References

- OTOVÁ, Berta, et al. *Lékařská biologie a genetika I. díl.* 1. edition. Karolinum, 2008. 123 pp. ISBN 978-80-246-1594-3.



HLA