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Gene Mapping: An Overview

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Editorial

The methods for determining a gene's locus and the distances between genes are referred to as gene mapping. The distances between distinct places inside a gene can also be described via gene mapping. The goal of all genome mapping is to place a collection of molecular markers on the genome in their proper locations. Molecular markers come in a variety of shapes and sizes. Genes can be thought of as a special form of genetic marker that can be mapped in the same way as any other marker in the development of genome maps. In the field of genome mapping, there are two sorts of "Maps": genetic maps and physical maps. While both maps are made up of genetic markers and gene loci, genetic maps employ genetic linkage information to calculate distances, whereas physical maps use real physical distances, which are commonly measured in base pairs. While the physical map may be a more "accurate" representation of the genome, genetic maps can reveal a lot about the nature of different chromosome regions. For example, the genetic distance to physical distance ratio varies a lot at different genomic regions, reflecting different recombination rates, which is often indicative of euchromatic (usually gene-rich) vs heterochromatic (usually gene-poor) regions of the genome.

Researchers start a genetic map by taking blood, saliva, or tissue samples from family members who have a conspicuous disease or trait and those who don't. Saliva is the most commonly utilised sample in gene mapping, particularly in personal genomic studies. Scientists then isolate DNA from the samples and examine it closely, seeking for patterns in the DNA of family members who do carry the disease that aren't present in the DNA of those who don't. Polymorphisms, or markers, are the names given to these distinct molecular patterns in DNA. The development of genetic markers and a mapping population are the first steps in creating a genetic map. The closer two markers are on the chromosome, the more probable they will be passed down in the same generation. As a result, all markers' "co-segregation" patterns can be used to rebuild their order. Keeping this in mind, the genotypes of each genetic marker are recorded for both parents and subsequent generations of individuals. The number of genetic markers on the map and the size of the mapping population are two parameters that influence the quality of genetic maps. The two aspects are connected, as a greater mapping population might boost the map's "resolution" and keep it from being "saturated." Any sequence feature that can be reliably identified from the two parents can be utilised as a genetic marker in gene mapping. In this case, genes are represented as "traits" that can be accurately differentiated between two parents.

The actual gene loci are then bracketed in a region between the two nearest nearby markers, as if they were common markers. The approach is then repeated by looking at other markers that target that region in order to map the gene neighbourhood to a higher precision and eventually identify a single causal locus. This technique is known as "positional cloning," and it is widely utilised in the study of plant species. Maize is one plant species in which positional cloning is used extensively. Genetic mapping has the advantage of being able to determine the relative position of genes merely based on their phenotypic effect [1-5].

References

1. Clazien Bouwmans, Marieke Krol, Hans Severens, Marc Koopmanschap, Werner Brouwe Leona Hakkaart-van Roijen Bouwmans. “The iMTA productivity cost questionnaire: a standardized instrument for measuring and valuing health-related productivity losses.” Human Genet Embryol 13 (2022): 753-758.
2. Sharon O’ Neilla Julie Brault Marie-Jose Stasiabc Ulla and G.Knausa “Genetic disorders coupled to ROS deficiency.” Human Genet Embryol 13 (2022): 36-41
3. Ada Hamosh, Alan F. Scott, Joanna Amberger, Carol Bocchini, David Valle, Victor A. McKusick “Online Mendelian Inheritance in Man (OMIM), a knowledgebase of human genes and genetic disorders.” Human Genet Embryol, 13 (2022),52–55,.
4. Nejat Mahdieh, and Bahareh Rabbani. “An Overview of Mutation Detection Methods in Genetic Disorders” Human Genet Embryol. 13 (2022): 375–388 .
5. V T Ramaekers, G Heimann, J Reul, A Thron, J Jaeken “Genetic disorders and cerebellar structural abnormalities in childhood“ Human Genet Embryol 13 (2022): 1739–1751

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