

Organization Involved in the Genome of Eukaryotic Organisms

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DESCRIPTION

The arrangement of Deoxyribonucleic Acid (DNA) sequences inside the nucleus and the three-dimensional structure of chromosomes are referred to as genome organization. An organism's genetic material, or DNA, is a sequence of four nucleotides arranged in a specific pattern that encodes information. A genomic organization is the linear arrangement of DNA components and their partition into chromosomes. The Watson-Crick double helix structural model controls eukaryotic genomes. In eukaryotic genomes, protein-coding genes are organized in exons and introns, which represent the coding sequence and the intervening sequence, respectively, indicating the functionality of the genome's RNA section. Protein-coding regions, gene regulatory regions, gene-related sequences, and intergenic DNA or extra genic DNA, which includes low copy number and moderate or high copy number repetitive sequences, make up the eukaryotic genome configuration.

Two characteristics of eukaryotic genomes pose a significant information processing challenge. The genome of a typical multicellular eukaryotic cell is significantly larger than that of a prokaryotic cell. Because of cell specialization, many genes can only be expressed in specific types of cells. The reported 35,000 genes in the human genome contain a massive amount of DNA that does not direct the synthesis of RNA or protein. The eukaryotic DNA is highly organized. The DNA-protein complex known as chromatin is not only linked to proteins, but it is also more structurally complex than the DNA-protein complex found in prokaryotes.

Eukaryotic cells contain significantly more DNA in their nuclei than prokaryotic cells. Chromatin is the complex structure of DNA and protein that makes up chromosomes. It is made up of linear unbroken double-stranded DNA. There are two kinds of chromatin-euchromatin and heterochromatin. Multigene families are groups of identical or extremely similar genes, whereas the majority of genes are found in only one copy per haploid pair of chromosomes. These are most likely descended from a single ancestor gene. Members of the multigene family may be grouped or dispersed throughout the genome.

Tandem clusters are formed by multigene families with identical genes. It typically includes genes for histone proteins or RNA products. The transcription unit that encodes the three largest ribosomal Ribonucleic acid (rRNA) molecules is replicated numerous times in tandem. When three rRNA molecules from this transcript are cleaved and combined with proteins and other types of rRNA, ribosomal subunits are formed. Non-identical genes represent the two interrelated families of hemoglobin globin genes, (alpha and beta), which are found on different chromosomes. At different stages of development, each globin subunit expresses its various forms.

Sequences from both families manifest at various stages of development, including embryonic, foetal, and/or adult. The increased oxygen affinity of embryonic and foetal hemoglobin compared to adults ensures oxygen transmission from the mother to the developing foetus. Gene variations are caused by mutations that accumulate in gene copies over several generations. These changes may result in the formation of pseudo genes, DNA segments with sequences similar to true genes but incapable of producing functional proteins.

CONCLUSION

Gene expression in eukaryotes is influenced by a variety of mechanisms, including gene loss, amplification, and rearrangement. The RNA transcripts of differentially transcribed genes are used in a variety of ways. Multiple gene families control the frequency and diversity of gene expression. The current state of knowledge about gene expression in eukaryotes is primarily due to biochemical techniques, rather than conventional genetics. The regulatory regions of eukaryotic genes and the cellular substances that influence gene expression will be discovered using new techniques that allow for the study and manipulation of purified genes with known functions.

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