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ISSN: 2161-1041
Hereditary Genetics: Current Research

Commentary

Short Note on Human Genome

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DESCRIPTION

The human genome is that the complete set of human super molecule sequences encoded as DNA within 23 pairs of chromosomes within the nucleus and within small molecules of DNA found in individual mitochondria. These are usually treated separately because the nuclear and mitochondrial genomes. The human genome contains both protein-encoding DNA genes and non-encoding DNA. The haploid human genome contained in reproductive cells egg and sperm cells that develop during sexual meiosis before fertilization to provide mating cells consists of three billion base pairs of DNA.

The diploid genome found in somatic cells is double. Similar DNA content there are significant differences between the human genomes on the order of 0.1% for single nucleotide polymorphisms, 0.6% for indels, but these are the differences between humans and their closest living relatives, bonobos and chimpanzees. Much smaller than (~1.1% fix single nucleotide polymorphisms, 4% including indel). Although the sequence of the human genome has been almost completely determined by DNA sequencing, it's not yet fully understood. Most though probably not all genes are identified by a mix of high throughput experimental and bioinformatics approaches, yet much work still has to be done to further elucidate the biological functions of their protein and RNA products.

Recent results suggest that the majority of the vast quantities of noncoding DNA within the genome have associated biochemical activities, including regulation of organic phenomenon, organization of chromosome architecture, and signals controlling epigenetic inheritance. Before the acquisition of the total genome sequence, estimates of the quantity of human genes ranged from 50,000 to 140,000 with occasional vagueness about whether these estimates included no protein coding genes. As genome sequence quality and also the methods for identifying protein-coding genes improved, the count of recognized protein-coding genes dropped 19,000 to 20,000. A more complete understanding of the role played by sequences that don't encode proteins and instead express regulatory RNA has pushed the whole number of genes to a minimum of 46,831 plus a further 2300 microRNA genes.

By 2012, functional DNA elements that failed to encode RNA or proteins were identified. The 2018 census revealed an extra 300 million bases within the human genome that aren't included within the reference sequence. The primary human genome sequence was published in February 2001 by the Human Genome Project and Corporation in near-complete draft format. Completion of the sequencing work of the Human Genome Project was announced in 2004, releasing a draft genome sequence that left only a 341 gap within the sequence. It represents other highly repetitive DNA that might not be sequenced with the technologies available at the time.

The human genome is that the first of virtually fully sequenced vertebrates, and as of 2018, quite 1 million individual human diploid genomes are determined using next-generation sequencing. Increase In 2021 it had been reported that the T2T consortium had filled altogether of the gaps within the sex chromosome. These data are used worldwide in bioscience, anthropology, forensics, and other branches of science. Such genomic studies have led to advances within the diagnosis and treatment of diseases, and to new insights in many fields of biology, including human evolution. Some noncoding DNA contains genes for RNA molecules with important biological functions (noncoding RNA, as an example, ribosomal RNA and transfer RNA). The exploration of the function and evolutionary origin of noncoding DNA is a crucial goal of latest genome research, including the ENCODE (Encyclopaedia of DNA Elements) project, which aims to survey the complete human genome, employing a form of experimental tools whose results are indicative of molecular activity. Because noncoding DNA greatly outnumbers deoxyribonucleic acid, the concept of the sequenced genome has become a more focused analytical concept than the classical concept of the DNA coding gene.

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Received: 30-Dec-2022, Manuscript No. HGCR-22-202; **Editor assigned:** 03-Jan-2022, PreQC No. HGCR -22-202 (PQ); **Reviewed:** 17-Jan-2022, QC No. HGCR -22-202; **Revised:** 24-Jan-2022, Manuscript No. HGCR -22-202 (R); **Published:** 31-Jan-2022, DOI:10.35248/2161-1041.22.11.202

Citation: Pritam A (2022) Short Note on Human Genome. Hereditary Genet. 11:202.