Journal of Genetic Syndromes & Gene Therapy

OPEN ACCESS Freely available online

Perspective

General Features and Importance of the Human Chromosome 7

Willard Gray*

Research Institute of Green Science & Technology, Shizuoka University, Ohya, Shizuoka, Japan

DESCRIPTION

Human chromosome 7 is a part of human genetics, because of the cystic fibrosis gene and the numerous cytogenetic alterations linked to different types of cancer more than 153 million base pairs, or 99.4% of all bases, are present in the euchromatic sequence of chromosome 7, is the first metacentric chromosome to be complete segmentally duplicate sequence which make up an unusually high percentage of the sequence 8.2% and the two arms of the sequence differ noticably from one to another. When the sequence was first discovered to there are 941 pseudogenes, and 1,150 protein-coding genes, which have been confirmed by complementary DNA sequences [1,2].

Clone-by-clone shotgun sequencing was used to sequence human chromosome 7, and the obtained sequence broken up into 11 contigs the separations between contigs are often small, and the majority are calculated using fluorescence *in situ* hybridization of DNA fibers or by comparing the distance to the location in the mouse genome sequence the exceptions include the centromere and one gap near the long arm's terminal end in bacteria- or yeast-based methods, such as the screening of numerous large-insert genomic libraries that provided cumulatively 100-fold coverage of the human genome, the DNA in these last gaps is repetitive or has proven challenging to clone the known sequence covers 99.4% of the euchromatic sequence, which is larger than the projected sizes of these gaps.

Protein-coding genes

To produce the frame work for the human chromosome 7 gene catalog as the first step toward a thorough understanding of all the functional elements encoded by the chromosome,[3] while also acknowledging the challenges of gene annotation first, 1,073 human mRNAs from *REFSEQ19* and the Mammalian Gene Collection 20 were manually edited to produce 605 non-overlapping human mRNAs with a splicing alternative of 45%the only known genes associated with chromosome 7 that were not detected in the sequence.

Symptoms

Different individuals may have various degrees and types of partial monosomy 7p (chromosome 7)-related bodily indications and symptoms however, many afflicted individuals have developmental abnormalities during pregnancy and beyond (prenatal and postnatal growth retardation) additionally, various levels of mental and psychomotor impairment may be connected to the disease premature closure of one or more cranial sutures, or fibrous joints, connecting certain skull bones,[4] is a common feature of monosomy 7p an abnormally shaped head and a malformed skull can result from Craniosynostosis.

Causes

A piece of the short arm is removed in people with partial monosomy of chromosome 7. (Monopolized) everybody cell's nucleus contains chromosomes. Each person possesses a few genetic traits. Human chromosomal pairs are numbered from 1 to 22, with a 23rd unbalanced pair made up of an additional pair of X and Y chromosomes for males and two X chromosomes for females each chromosome consists of three parts: a concave region connecting the two arms, [5] which is indicated by the letter "q," a small arm marked by the letter "p," and a long arm (centromere).The chromosome-making bands are further divided into groups and assigned numbers away from the centromere bands on chromosome 7's short arm (7p), Bands on 7p, for example, are 7p21–p22, and 7pter is the name for the end of 7p for example, 7p11–p15.

CONCLUSION

An important advancement in the Human Genome Project is the description of the human chromosome 7 sequence as a component of numerous other human chromosomes as chromosome sequences advance from their initial "draught" phase to a high-accuracy comprehensive stage, the ability to conduct in-depth analysis becomes more dependable and the molecular environment becomes more visible chromosome 7 enabled thorough gene analyses that increased our capacity to discern between genuine genes and false genes. Chromosome 7

Correspondence to: Dr. Willard Gray, Research Institute of Green Science & Technology, Shizuoka University, Ohya, Shizuoka, Japan, E-mail: Willard.Gray@shizuoka.ac.jp

Received: 03-Jun-2022, Manuscript No. JGSGT-22-18677; **Editor assigned:** 07-Jun-2022, Pre QC No. JGSGT-22-18677 (PQ); **Reviewed:** 21-Jun-2022, QC No. JGSGT-22-18677; **Revised:** 27-Jun-2022, Manuscript No. JGSGT-22-18677 (R); **Published:** 04-July-2022,DOI:10.35248/2157-7412.22.13.366.

Citation: Gray W (2022) General Features and Importance of the Human Chromosome 7. J Genet Syndr Gene Ther.13: 366.

combines a high-quality, nearly full sequence with a partial mouse genome that has been sequenced.

Chromosome 7 has a significantly higher incidence of intra chromosomal duplication than the other chromosomes that have been studied so far, and it also produces more segmental duplications than other chromosomes, according to genome-wide analysis of the segmental an index of the chromosome's genes.

REFERENCES

1. Riethman HC, Xiang Z, Paul S, Morse E, Hu XL, Flint J, et.al. Integration of telomere sequences with the draft human genome sequence. Nature. 2001;409(6822):948-951.

2. Lander ES. Initial sequencing and comparative analysis of the mouse genome. Nature. 2002; 420:520-562.

3. Rowen L, Koop BF, Hood L. The complete 685-kilobase DNA sequence of the human β T cell receptor locus. Science. 1996:21;272(5269):1755-1762.

4. Dunham I, Hunt AR, Collins JE, Bruskiewich R, Beare DM, Clamp M, et. al. The DNA sequence of human chromosome 22. Nature. 1999; 402(6761):489-495.

5. Eddy SR. A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. BMC Bioinform.2002;3(1):1-6.