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Annals of Biological Research, 2022, 13 (3):127-128
(http://scholarsresearchlibrary.com/archive.html)

ISSN 0976-1233
CODEN (USA): ABRNBW

A Short Note on Comparative Genomics

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Received: *14-Mar-2022, Manuscript No. Abr-22-60764;* ***Editor assigned:*** *16-Mar-2022, PreQC No. Abr-22-60764 (PQ);* ***Reviewed:*** *28-Mar-2022, QC No Abr-22-60764;* ***Revised:*** *06-Apr-2022, Manuscript No. Abr-22-60764 (R)* ***Published:*** *13-Apr-2022. Doi: 10.4172/ 0976-1233.004*

DESCRIPTION

FComparative genomics is a branch of biology that compares the genomic characteristics of different animals. The DNA sequence, genes, gene order, regulatory sequences, and other genomic structural landmarks are examples of genomic characteristics. Whole or substantial portions of genomes arising from genome projects are compared in this branch of genomics to investigate basic biological similarities and differences, as well as evolutionary relationships between organisms. Comparative genomics' main idea is that similar traits of two organisms are frequently encoded within their evolutionarily conserved DNA. As a result, comparative genomic techniques begin with some kind of genome sequence alignment, followed by a search for orthologous sequences (sequences that share a common ancestor) in the aligned genomes and a determination of how conserved such sequences are. On the basis of them, genome and molecular evolution can be deduced, which can then be applied to phenotypic evolution or population genetics, for example. Comparative genomics has become a common component of the analysis of every new genome sequence since the entire genomes of two organisms became accessible in 1995 [1]. This discipline has gotten increasingly sophisticated as a result of improvements in DNA sequencing technologies, particularly next-generation sequencing methods in the late 2000s, which made it possible to deal with several genomes in a single study. Comparative genomics has found striking similarities between closely related organisms like humans and chimps, as well as surprising similarities between seemingly distantly related organisms like humans and the yeast. It also revealed the tremendous diversity of gene makeup across evolutionary lineages. In the early 1980s, comparative genomics began with the comparison of viral genomes [2]. For example, researchers analysed tiny RNA viruses that infect mammals (picornaviruses) and those that infect plants (cowpea mosaic virus) and discovered that they share significant sequence similarities and, in part, gene order. The first large-scale comparative genomic analysis was published in 1986, comparing the genomes of varicella-zoster virus and Epstein-Barr virus, both of which had over 100 genes apiece. The first whole genome collection of a mobile organism, that became frist discover in 1995. The 2nd genome sequencing paper became of the small parasitic bacterium *Mycoplasma genitalium* posted withinside the identical year. Starting from this paper, reviews on new genomes unavoidably have become comparative-genomic studies. The first high-decision entire genome evaluation device became evolved in 1998 with the aid of using Art Delcher, Simon Kasif and Steven Salzberg and implemented to the evaluation of complete fairly associated microbial organisms with their collaborators on the Institute for Genomic Research (TIGR). The device is known as MUMMER and became defined in a guide in Nucleic Acids Research in 1999. The device facilitates researchers to pick out big rearrangements, unmarried base mutations, reversals, tandem repeat expansions and different polymorphisms. In bacteria, MUMMER allows the identity of polymorphisms which can be chargeable for virulence, pathogenicity, and anti-biotic resistance. The device became additionally implemented to the Minimal Organism Project at TIGR and ultimately to many different comparative genomics projects. Saccharomyces cerevisiae, the baker`s yeast, became the primary eukaryote to have its whole genome collection posted in 1996 [3,4]. After the guide of the roundworm

Caenorhabditis elegans genome in 1998 and collectively with the fruit fly genome in 2000, Gerald M. Rubin and his crew posted a paper titled “Comparative Genomics of the Eukaryotes”, wherein they in comparison the genomes of the eukaryotes *D. melanogaster, C. elegans,* and *S. cerevisiae*, in addition to the prokaryote *H. influenzae*. At the identical time, Bonnie Berger, Eric Lander, and their crew posted a paper on entire-genome evaluation of human and mouse [5]. With the guide of the big genomes of vertebrate’s withinside the 2000s, inclusive of human, the Japanese pufferfish *Takifugu rubripes*, and mouse, precomputed outcomes of big genome comparisons had been launched for downloading or for visualisation in a genome browser. Instead of mission their personal analyses, maximum biologists can get admission to those big cross-species comparisons and keep away from the impracticality resulting from the dimensions of the genomes [6-10].

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