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Commentary

A Short Commentary on Genomics

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COMMENTARY

Genomics is a branch of biology that focuses on the structure, function, evolution, mapping, and editing of genomes. A genome is a full collection of DNA that includes all of an organism's genes as well as its hierarchical, three-dimensional structural arrangement. In contrast to genetics, which studies individual genes and their functions in inheritance, genomics seeks to characterize and quantify all of an organism's genes, their interrelationships, and their effect on the organism.

Genes can control protein creation with the help of enzymes and messenger molecules. Proteins, in turn, form bodily structures such as organs and tissues, govern chemical processes and transport messages between cells. Genomics also includes genome sequencing and analysis using high throughput DNA sequencing and bioinformatics to assemble and study the function and structure of complete genomes. Advances in genomes have sparked a revolution in discovery-based research and systems biology, making it possible to comprehend even the most complicated biological systems, such as the brain.

Intragenomic (inside the genome) phenomena like epistasis (impact of one gene on another), pleiotropy (one gene affecting more than one attribute), heterosis (hybrid vigor), and other interactions between loci and alleles are being studied.

Genome Analysis

Following the selection of an organism, genome projects consist of three components: DNA sequencing, assembly of that sequence to generate a representation of the original chromosome and annotation and analysis of that representation.

Sequencing

Historically, sequencing was done in sequencing centers, which are centralized facilities (ranging from large independent institutions like the Joint Genome Institute, which sequences dozens of terabases per year, to local molecular biology core facilities) that contain research laboratories with the necessary expensive instrumentation and technical support. However, as sequencing technology advances, a new generation of effective rapid turnaround benchtop sequencers has become affordable to the ordinary university laboratory. Shotgun and high-throughput (or next-generation) sequencing are the two primary types of genome sequencing techniques.

Shotgun Sequencing

Shotgun sequencing is a method of analyzing DNA sequences that are longer than 1000 base pairs, up to and including whole chromosomes. It gets its name from the rapidly expanding, quasi-random discharge pattern of a shotgun. Because gel electrophoresis sequencing can only be utilized for relatively short sequences (100 to 1000 base pairs), larger DNA sequences must be broken down into random tiny parts and then sequenced to acquire reads. Several rounds of this fragmentation and sequencing provide several overlapping readings for the target DNA. The overlapping ends of individual readings are then used by computer systems to combine them into a continuous sequence. Shotgun sequencing is a random sampling procedure that necessitates over-sampling to ensure that a particular nucleotide is represented in the reconstructed sequence; coverage is the average number of reads by which a genome is over-sampled.

For much of its history, shotgun sequencing was based on the classical chain-termination approach, often known as the 'Sanger method,' which is based on the selective incorporation of chain-terminating dideoxynucleotides by DNA polymerase during in vitro DNA replication. Shotgun sequencing has recently been overtaken by high-throughput sequencing technologies, particularly for large-scale, automated genome analysis. However, the Sanger technique is still widely used, specifically for smaller-scale projects and for getting very long contiguous DNA sequence reads (>500 nucleotides). Chain-termination techniques necessitate a single-stranded DNA template, a DNA primer, a DNA polymerase, regular deoxynucleoside triphosphates (dNTPs), and modified nucleotides (dideoxyNTPs) that end DNA strand elongation. These chain-terminating nucleotides lack the 3'-OH group needed to establish a phosphodiester link between two nucleotides, causing DNA polymerase to stop extending DNA when a ddNTP is inserted. For detection in DNA sequencers, ddNTPs can be radioactively or fluorescently labeled. These machines can typically sequence up to 96 DNA samples in a single batch (run) and up to 48 runs per day.

Research Areas

Functional genomics: Functional genomics is a branch of

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molecular biology that aims to understand gene (and protein) activities and interactions by utilizing the large abundance of data generated by genomic initiatives (such as genome sequencing programs). Functional genomics focuses on dynamic features of genomic information such as gene transcription, translation, and protein-protein interactions rather than static parts of genomic information such as DNA sequence or structures. Functional genomics seeks to address issues concerning DNA function at the gene, RNA transcript, and protein product levels. Functional genomics studies are distinguished by their genome-wide approach to these concerns, which often use high-throughput methodologies rather than the more traditional "gene-by-gene" approach.