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Editorial Notes on Functional Genomics

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Editorial

The study of how genes and intergenic regions of the genome contribute to various biological processes is known as functional genomics. A researcher in this field typically studies genes or regions on a "genome-wide" scale (that is, all or multiple genes/regions at the same time), with the goal of narrowing them down to a list of candidate genes or regions to investigate further. The goal of functional genomics is to figure out how the various components of a biological system interact to produce a specific phenotype. Functional genomics is concerned with the dynamic expression of gene products in a specific context, such as during a developmental stage or during a disease. In functional genomics, we attempt to use our current understanding of gene function to develop a model that connects genotype to phenotype [1-3]. Transcriptomics, proteomics, and metabolomics are all terms used to describe the transcripts, proteins, and metabolites of a biological system, and the integration of these data is expected to provide a complete model of the biological system under study. Functional genomics is a branch of genomics that focuses on understanding gene function and interactions in order to establish a link between an organism's genome and its phenotype. RNA interference is one technique that is widely used to understand gene/protein function (RNAi).

In addition, we discuss a number of potential bioinformatics pipelines, such as structural and functional annotations (e.g., transposable elements and repetitive sequences). This paper also discusses the significance of data management and how to make data and results Findable, Accessible, Interoperable, and Reusable (FAIR) by depositing them in a public repository and making them available to the research community. To learn more about molecular/cellular mechanisms, gene repertoires, genome architecture, and evolution, genome projects employ cutting-edge DNA sequencing [4,5] mapping, and computational technologies (including multidisciplinary experimental designs). The revolution in new sequencing technologies and computational developments has enabled researchers to drive advances in genome assembly and annotation to make the process better, faster, and cheaper using key model organisms.

Mutagenesis, mass spectrometry, genome annotation, and other techniques are used. The majority of functional genomic research is conducted on model species of plants/animals/humans because model organisms provide a cost-effective way to track gene inheritance through many generations in a relatively short time. Based on the data obtained from model organisms, comparative genomics approaches can be used to better understand larger genomes. Functional genomics encompasses a wide range of techniques aimed at assigning functions to genes using high-throughput methods. Homology searching, structural comparisons, expression profiling (messenger RNA and protein levels), large-scale mutagenesis, and protein interaction analysis are examples of platform technologies.

After explaining the principles behind each platform, this article considers case studies in which expression profiling, mutation analysis, RNA interference, and protein interaction analysis were used to identify and character rise novel genes involved in schizophrenia, manic depressive disorder, and bipolar disorders. Pathogenesis is typically defined by a series of events that occur in a sequential order. System biology, on the other hand, predicts nonlinear cellular states of compensatory feedback loops that depict an organism's true complexity. The creation of a knowledge base that accurately represents network-level molecular expression poses significant challenges in terms of data management, integration, and computational modelling. As these fields progress, the development of approaches that combine model systems and interactome analyses may help to unravel the complexities inherent in biological systems. The application of functional genomics to the study of mechanism of action has advanced our understanding of the biology underlying the harmful effects of chemical and pharmaceutical agents on living systems, the regulatory networks that integrate the signalling cascades involved in toxicity, and the pathogenesis of environmental or drug-induced disease.

Indeed, mechanistic toxicology research has been beneficial in risk assessment, drug development, environmental exposure assessment, and understanding of human and animal variability in response to drugs and chemicals. To date, progress has been hampered by a scarcity of comprehensive time- and dose-related studies, as well as a lack of studies employing exposure paradigms that faithfully reproduce the human condition. Functional genomics has been validated and is now widely accepted in toxicology. Although this chapter focuses on transcriptomics, similar approaches are being used in proteomics and metabolomics. Such studies are now improving our understanding of the underlying biology as well as the regulatory networks that integrate the signalling cascades involved in toxicity.

Conflict of Interest

None.

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