

# Genomics

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**Genomics** is a discipline in genetics concerning the study of the genomes of organisms. The field includes intensive efforts to determine the entire DNA sequence of organisms and fine-scale genetic mapping efforts. The field also includes studies of intragenomic phenomena such as heterosis, epistasis, pleiotropy and other interactions between loci and alleles within the genome. In contrast, the investigation of the roles and functions of single genes is a primary focus of molecular biology or genetics and is a common topic of modern medical and biological research. Research of single genes does not fall into the definition of genomics unless the aim of this genetic, pathway, and functional information analysis is to elucidate its effect on, place in, and response to the entire genome's networks.

For the United States Environmental Protection Agency, "the term "genomics" encompasses a broader scope of scientific inquiry associated technologies than when genomics was initially considered. A genome is the sum total of all an individual organism's genes. Thus, genomics is the study of all the genes of a cell, or tissue, at the DNA (genotype), mRNA (transcriptome), or protein (proteome) levels."<sup>[1]</sup>

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## History

The first genomes to be sequenced were those of a virus and a mitochondrion, and were done by Fred Sanger. His group established techniques of sequencing, genome mapping, data storage, and bioinformatic analyses in the 1970-1980s. A major branch of genomics is still concerned with sequencing the genomes of various organisms, but the knowledge of full genomes has created the possibility for the field of functional genomics, mainly concerned with patterns of gene expression during various conditions. The most important tools here are microarrays and bioinformatics. Study of the full set of proteins in a cell type or tissue, and the changes during various conditions, is called proteomics. A related concept is materiomics, which is defined as the study of the material properties of biological materials (e.g. hierarchical protein structures and materials, mineralized biological tissues, etc.) and their effect on the macroscopic function and failure in their biological context, linking processes, structure and properties at multiple scales through a materials science approach. The actual term 'genomics' is thought to have been coined by Dr. Tom Roderick, a geneticist at the Jackson Laboratory (Bar Harbor, ME) over beer at a meeting held in Maryland on the mapping of the human genome in 1986.

In 1972, Walter Fiers and his team at the Laboratory of Molecular Biology of the University of Ghent (Ghent, Belgium) were the first to determine the sequence of a gene: the gene for Bacteriophage MS2 coat

protein.<sup>[2]</sup> In 1976, the team determined the complete nucleotide-sequence of bacteriophage MS2-RNA.<sup>[3]</sup> The first DNA-based genome to be sequenced in its entirety was that of bacteriophage  $\Phi$ -X174; (5,368 bp), sequenced by Frederick Sanger in 1977.<sup>[4]</sup>

The first free-living organism to be sequenced was that of *Haemophilus influenzae* (1.8 Mb) in 1995, and since then genomes are being sequenced at a rapid pace.

As of September 2007, the complete sequence was known of about 1879 viruses,<sup>[5]</sup> 577 bacterial species and roughly 23 eukaryote organisms, of which about half are fungi.<sup>[6]</sup> Most of the bacteria whose genomes have been completely sequenced are problematic disease-causing agents, such as *Haemophilus influenzae*. Of the other sequenced species, most were chosen because they were well-studied model organisms or promised to become good models. Yeast (*Saccharomyces cerevisiae*) has long been an important model organism for the eukaryotic cell, while the fruit fly *Drosophila melanogaster* has been a very important tool (notably in early pre-molecular genetics). The worm *Caenorhabditis elegans* is an often used simple model for multicellular organisms. The zebrafish *Brachydanio rerio* is used for many developmental studies on the molecular level and the flower *Arabidopsis thaliana* is a model organism for flowering plants. The Japanese pufferfish (*Takifugu rubripes*) and the spotted green pufferfish (*Tetraodon nigroviridis*) are interesting because of their small and compact genomes, containing very little non-coding DNA compared to most species.<sup>[7]</sup> <sup>[8]</sup> The mammals dog (*Canis familiaris*),<sup>[9]</sup> brown rat (*Rattus norvegicus*), mouse (*Mus musculus*), and chimpanzee (*Pan troglodytes*) are all important model animals in medical research.

## Human genomics

A rough draft of the human genome was completed by the Human Genome Project in early 2001, creating much fanfare. By 2007 the human sequence was declared "finished" (less than one error in 20,000 bases and all chromosomes assembled). Display of the results of the project required significant bioinformatics resources. The sequence of the human reference assembly can be explored using the UCSC Genome Browser.

## Bacteriophage genomics

Bacteriophages have played and continue to play a key role in bacterial genetics and molecular biology. Historically, they were used to define gene structure and gene regulation. Also the first genome to be sequenced was a bacteriophage. However, bacteriophage research did not lead the genomics revolution, which is clearly dominated by bacterial genomics. Only very recently has the study of bacteriophage genomes become prominent, thereby enabling researchers to understand the mechanisms underlying phage evolution. Bacteriophage genome sequences can be obtained through direct sequencing of isolated bacteriophages, but can also be derived as part of microbial genomes. Analysis of bacterial genomes has shown that a substantial amount of microbial DNA consists of prophage sequences and prophage-like elements. A detailed database mining of these sequences offers insights into the role of prophages in shaping the bacterial genome.<sup>[10]</sup>

## Cyanobacteria genomics

At present there are 24 cyanobacteria for which a total genome sequence is available. 15 of these cyanobacteria come from the marine environment. These are six *Prochlorococcus* strains, seven marine

*Synechococcus* strains, *Trichodesmium erythraeum* IMS101 and *Crocospaera watsonii* WH8501. Several studies have demonstrated how these sequences could be used very successfully to infer important ecological and physiological characteristics of marine cyanobacteria. However, there are many more genome projects currently in progress, amongst those there are further *Prochlorococcus* and marine *Synechococcus* isolates, *Acaryochloris* and *Prochloron*, the N<sub>2</sub>-fixing filamentous cyanobacteria *Nodularia spumigena*, *Lyngbya aestuarii* and *Lyngbya majuscula*, as well as bacteriophages infecting marine cyanobacteria. Thus, the growing body of genome information can also be tapped in a more general way to address global problems by applying a comparative approach. Some new and exciting examples of progress in this field are the identification of genes for regulatory RNAs, insights into the evolutionary origin of photosynthesis, or estimation of the contribution of horizontal gene transfer to the genomes that have been analyzed.<sup>[11]</sup>

## See also

- Full Genome Sequencing
- Computational genomics
- Nitrogenomics
- Metagenomics
- Predictive Medicine
- Personal genomics
- Psychogenomics

## References

1. ^ EPA Interim Genomics Policy (<http://epa.gov/osa/spc/pdfs/genomics.pdf>)
2. ^ Min Jou W, Haegeman G, Ysebaert M, Fiers W (1972). "Nucleotide sequence of the gene coding for the bacteriophage MS2 coat protein". *Nature* **237** (5350): 82–88. doi:10.1038/237082a0 (<http://dx.doi.org/10.1038%2F237082a0>) . PMID 4555447 (<http://www.ncbi.nlm.nih.gov/pubmed/4555447>) .
3. ^ Fiers W, Contreras R, Duerinck F, Haegeman G, Iserentant D, Merregaert J, Min Jou W, Molemans F, Raeymaekers A, Van den Berghe A, Volckaert G, Ysebaert M (1976). "Complete nucleotide sequence of bacteriophage MS2 RNA: primary and secondary structure of the replicase gene". *Nature* **260** (5551): 500–507. doi:10.1038/260500a0 (<http://dx.doi.org/10.1038%2F260500a0>) . PMID 1264203 (<http://www.ncbi.nlm.nih.gov/pubmed/1264203>) .
4. ^ Sanger F, Air GM, Barrell BG, Brown NL, Coulson AR, Fiddes CA, Hutchison CA, Slocombe PM, Smith M (1977). "Nucleotide sequence of bacteriophage phi X174 DNA". *Nature* **265** (5596): 687–695. doi:10.1038/265687a0 (<http://dx.doi.org/10.1038%2F265687a0>) . PMID 870828 (<http://www.ncbi.nlm.nih.gov/pubmed/870828>) .
5. ^ *The Viral Genomes Resource*, NCBI Friday, 14 September 2007 (<http://www.ncbi.nlm.nih.gov/genomes/VIRUSES/virostat.html>)
6. ^ *Genome Project Statistic*, NCBI Friday, 14 September 2007 (<http://www.ncbi.nlm.nih.gov/genomes/static/gpstat.html>)
7. ^ BBC article *Human gene number slashed* from Wednesday, 20 October 2004 (<http://news.bbc.co.uk/1/hi/sci/tech/3760766.stm>)
8. ^ CBSE News, Thursday, 16 October 2003 ([http://www.cbse.ucsc.edu/news/2003/10/16/pufferfish\\_fruitfly/index.shtml](http://www.cbse.ucsc.edu/news/2003/10/16/pufferfish_fruitfly/index.shtml))
9. ^ NHGRI, pressrelease of the publishing of the dog genome (<http://www.genome.gov/12511476>)
10. ^ McGrath S and van Sinderen D, ed (2007). *Bacteriophage: Genetics and Molecular Biology* (<http://www.horizonpress.com/phage>) (1st ed.). Caister Academic Press. ISBN 978-1-904455-14-1. <http://www.horizonpress.com/phage>.
11. ^ Herrero A and Flores E, ed (2008). *The Cyanobacteria: Molecular Biology, Genomics and Evolution*

(<http://www.horizonpress.com/cyan>) (1st ed.). Caister Academic Press. ISBN 978-1-904455-15-8.  
<http://www.horizonpress.com/cyan>.

## External links

- Genomics Directory (<http://www.genomicsdirectory.com>) : A one-stop biotechnology resource center for bioentrepreneurs, scientists, and students
- Annual Review of Genomics and Human Genetics (<http://arjournals.annualreviews.org/loi/genom/>)
- BMC Genomics (<http://www.biomedcentral.com/bmcgenomics/>) : A BMC journal on Genomics
- Genomics (<http://www.genomics.co.uk/companylist.php>) : UK companies and laboratories\*  
Genomics journal  
([http://www.elsevier.com/wps/find/journaldescription.cws\\_home/622838/description#description](http://www.elsevier.com/wps/find/journaldescription.cws_home/622838/description#description))
- Genomics and Quantitative Genetics (<http://www.knoblauchpublishing.com>) : An international electronic, open access journal publishing, inter alia, genomics research.
- Genomics.org (<http://genomics.org>) : An openfree wiki based Genomics portal
- NHGRI (<http://www.genome.gov/>) : US government's genome institute
- Pharmacogenomics in Drug Discovery and Development  
(<http://www.springer.com/humana+press/pharmacology+and+toxicology/book/978-1-58829-887-4>) , a book on pharmacogenomics, diseases, personalized medicine, and therapeutics
- Tishchenko P. D. Genomics: New Science in the New Cultural Situation (<http://www.zpu-journal.ru/en/articles/detail.php?ID=342>)
- Undergraduate program on Genomic Sciences (spanish) (<http://www.lcg.unam.mx/>) : One of the first undergraduate programs in the world
- JCVI Comprehensive Microbial Resource (<http://cmr.jcvi.org/>)
- Pathema: A Clade Specific Bioinformatics Resource Center (<http://pathema.jcvi.org/>)
- KoreaGenome.org (<http://koreagenome.org>) : The first Korean Genome published and the sequence is available freely.
- GenomicsNetwork (<http://genomicsnetwork.ac.uk>) : Looks at the development and use of the science and technologies of genomics.
- Institute for Genome Sciences ([http://www.igs.umaryland.edu/research\\_topics.php](http://www.igs.umaryland.edu/research_topics.php)) : Genomics research.
- MIT OpenCourseWare HST.512 Genomic Medicine (<http://ocw.mit.edu/courses/health-sciences-and-technology/hst-512-genomic-medicine-spring-2004/>) A free, self-study course in genomic medicine. Resources include audio lectures and selected lecture notes.

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