

Microbial genome application

Microbial genomes are widely variable and reflect the enormous diversity of bacteria, archaea and lower eukaryotes. Bacterial genomes usually consist of a single circular chromosome, but species with more than one chromosome (eg. *Deinococcus radiodurans*), linear chromosomes (eg. some *Bacillus subtilis* strains) and combinations of linear and circular chromosomes (eg. *Agrobacterium tumefaciens*) also exist.

One major difference between the genomes of microorganisms and higher eukaryotes, is the presence of circular, extra-chromosomal DNA called plasmids. Plasmids can be transferred via horizontal DNA transfer from one cell of the same generation to another, mediating the rapid evolution of many different organisms.

The study of microbial genomes helps us to better understand the broader biology of bacteria, and how their genetic composition contributes to their tangible characteristics. The study of genomics is also important to infer the evolution of bacteria. Bacteria often evolve not just through small, single nucleotide level changes but through quantum evolutionary events. These include through the transfer of plasmids between species and also the transposition of large genetic elements within single cells. Understanding these processes allows us to determine the origins of bacteria and map the transfer of genes such as those conferring antibiotic resistance.

Methods of studying microbial genomes

In the years preceding the development of full genome sequencing techniques we were restricted to studying microbial genomes in the lab using techniques such as PFGE.

Pulsed Field Gel Electrophoresis (PFGE)-

The principle underlying PFGE is very similar to normal gel electrophoresis. PFGE however allows us to resolve far large, 'genome scale' pieces of DNA (greater than 20 kilobases in size). PFGE is still an important technique used to estimate the size of microbial genomes and in epidemiology studies.

DNA Sequencing

DNA sequencing has been an enormous advancement in the field of microbial genomics and indeed genetics as a whole, allowing us to amass vast amounts of genetic data from our organisms of choice. The first method for sequencing DNA was developed by Frederick Sanger and his group in 1977. Their method, termed Sanger Sequencing was a platform for innovation in the field of DNA sequencing, and we now have methods for sequencing entire bacterial genomes with relative ease. Whole genome sequencing produces immense amounts of data from which we can derive a catalogue

of important information. From the need to analyse this data, the field of bioinformatics has flourished and become an integral part of genetics research.

Methods for whole-genome analysis of microbes:

The method that was successfully used to determine the complete genome sequence of *H. influenzae* is a shotgun sequencing strategy. Before 1995, the largest genome sequenced with a random strategy was that of bacteriophage lambda with a genome size of 48,502 base pairs (bp), completed by Sanger et al. in 1982. Despite advances in DNA-sequencing technology, the sequencing of whole genomes had not progressed beyond lambda-sized clones (about 40 kbp) because of the lack of sufficient computational approaches that would enable the efficient assembly of a large number of independent random sequences into a single contig. For the *H. influenzae* and subsequent projects, we have used a computational method that was developed to create assemblies from hundreds of thousands of complementary DNA sequences 300–500-bp long. This approach has proved to be a cost-effective and efficient approach to sequencing megabase-sized segments of genomic DNA. This strategy does not require an ordered set of cosmids or other subclones, thus significantly reducing the overall cost per base pair of producing a finished sequence, while providing high redundancy for accuracy and minimizing the effort required obtaining the whole genome sequence. The availability of improved technologies for longer sequence lengths (more than 700 bp) reduces problems associated with repetitive elements in the final assembly.

Microbial Genome Applications

In the field of Microbial Genome Applications of bioinformatics is covered following areas :

- **Waste Clean-up:** In bioinformatics bacteria and microbes are helpful in cleaning waste. *Deinococcus radiodurans* Bacterium is point out in the Guinness Book of World Records and this bacterium has the ability to repair damaged DNA and small fragments from chromosomes by isolating damage segments concentrated area. This is because it has additional copies of its genome. Genes from other bacteria have been inserted into *D. radiodurans* for environmental clean-up. It was used to break down organic chemicals, solvents and heavy metals in radioactive waste sites.
- **Climate Change:** All concerned areas of science and technology including bioinformatics plays a main role in the control of climate change to some level. Bioinformatics is also assisting in climate change studies. In the last few years, various genome sequencing and metagenomic projects have produced large amounts of genetic data for cyanobacteria. This wealth of data affords researchers with a new basis for the study of molecular adaptation, ecosystem and evolution of cyanobacteria, as well as for developing biotechnological applications. It also helps the use of multiplex techniques, i.e., expression profiling by high-throughput technologies such as microarrays, RNA-sequence, and

proteomics. Microbe *Deinococcus radiodurans* is known for radiation resistance and being used for cleaning up the waste sites that contain toxic chemicals. There are many organisms which use carbon dioxide as their sole carbon source and increasing levels of carbon dioxide emission is one of the major causes of the global climate change. The study of genomes based on microbial organisms, which is possible using bioinformatics, helps in decrease the carbon dioxide content. Climate change is caused by factors that contain oceanic methods variations in solar radiation received by Earth. By studying microorganisms genome scientists can begin to understand these microbes at fundamental level and isolated the genes that give them their unique abilities to survive under extreme conditions.

- Nanotechnology and Biotechnology: The concept of biotechnology includes a wide range of procedures for altering living organisms according to human drives, going to training of animals, farming of plants, and enhancements based on breeding programs that employ artificial selection techniques. Advance usage also contains genetic, cell and tissue culture engineering technologies. In the field of bioinformatics and biotechnology identified organisms and microorganisms which are very beneficial in dairy industry and food manufacturers. *Lactococcus Lactis* is very important microorganisms involved in the dairy industry. Nanotechnology is the impacts on an atomic, molecular, and super molecular scale.

Suggested reading:

<https://www.sciencedirect.com/science/article/pii/S0923250800001157?via%3Dihub>

<https://www.nature.com/articles/35021244>