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An Editorial Note on Whole Genome Sequencing

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Editorial

Whole Genome Sequencing (WGS), also known as full genome sequencing, complete genome sequencing, or entire genome sequencing, is the method of determining the entirety, or almost the entirety, of an organism's DNA sequence all at once. This entails sequencing all of an organism's chromosomal DNA, as well as mitochondrial DNA and chloroplast DNA in plants. Whole genome sequencing has primarily been utilised in research, but clinics began using it in 2014. Whole genome sequence data may be a significant tool for guiding therapeutic intervention in the future of personalised medicine. The technology of SNP-level gene sequencing is also used to detect functional variants from association studies and improve the knowledge available to evolutionary biologists, perhaps laying the groundwork for predicting disease susceptibility and medication response.

Whole genome sequencing is not to be confused with DNA profiling, which simply indicates the chance that genetic material comes from a specific person or group and provides no extra information on genetic ties, origin, or disease risk. Furthermore, whole genome sequencing should not be confused with technologies that sequence specific portions of the genome, such as whole exome sequencing (1-2% of the genome) or SNP genotyping (0.1%).

In the 1970s and 1980s, manual DNA sequencing methods such as Maxam–Gilbert sequencing and Sanger sequencing were utilised. These approaches were used to sequence entire bacteriophage and animal virus genomes, but the change to faster, automated sequencing methods in the 1990s made it easier to read bigger bacterial and eukaryotic genomes. Bacteriophage MS2 was the first virus to have its entire genome sequenced in 1976. The yeast chromosome III was the first chromosome to be entirely sequenced in 1992. In 1995, *Haemophilus influenzae* became the first organism to have its whole genome sequenced. Following that, the genomes of other bacteria and archaea were sequenced first, owing to their modest genome sizes. The genome of *H. influenzae* is 1,830,140 base pairs long.

Eukaryotes, including unicellular and multicellular organisms like *Amoeba dubia* and humans (Homo sapiens), have substantially larger genomes (see C-value paradox). *Amoeba dubia* has a 700 billion nucleotide pair genome that is spread out over thousands of chromosomes. Although humans have fewer nucleotide pairs (approximately 3.2 billion in per germ cell - note that the exact amount of the human genome is still being reviewed), their genome size dwarfs that of individual bacteria [1-3.]

Shotgun sequencing was used to sequence the first bacterial and archaeal genomes, including that of *H. influenzae*. The first eukaryotic genome (*Saccharomyces cerevisiae*) was sequenced in 1996. *S. cerevisiae*, a model organism in biology, has a genome of only about 12 million nucleotide pairs and was the first unicellular eukaryote whose entire genome had been sequenced. *Caenorhabditis elegans* was the first multicellular eukaryote and animal to have its entire genome sequenced in 1998. Shotgun sequencing of short DNA fragments and sequencing of larger DNA clones from DNA libraries such as Bacterial Artificial Chromosomes (BACs) and yeast artificial chromosomes are two methods used to Sequence Eukaryotic Genomes (YACs).

The complete DNA sequence of human chromosome 22, the shortest human autosome, was published in 1999. By the year 2000, the genome of the fruit fly *Drosophila melanogaster*, a popular model organism in experimental research, had been sequenced, making it the second animal and second invertebrate (yet first insect) genome to be sequenced. By 2000, the *Arabidopsis thaliana* model organism's genome had also been fully sequenced. A draught of the entire human genome sequence was published in 2001. In 2002, the genome of the laboratory mouse *Mus musculus* was completed. The Human Genome Project released an incomplete version of the human genome in 2004. The first female human genome was sequenced in 2008 by a group from Leiden, The Netherlands. [4,5]

Conflict of Interest

None

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