Editorial

Dr. J. Craig Venter: A visionary architect of modern genomics

Dr. J. Craig Venter, PhD, founder, Chairman, and CEO of the J. Craig Venter Institute, was a farsighted geneticist, renowned for his pioneering contributions to modern genomics. Dr. Craig Venter died on April 29, 2026, at the age of 79, due to complications from cancer treatment**.**

Craig Venter was born on October 14, 1946, in Salt Lake City, Utah. He earned a BS in Biochemistry in 1972 and a PhD in Physiology and Pharmacology in 1975, both from the University of California, San Diego. In 1976, Craig Venter was appointed Assistant Professor of Pharmacology and Therapeutics at the State University of New York at Buffalo, where he was later promoted to Professor. From 1984 to 1992, he worked at the National Institute of Neurological Disorders and Stroke, a component of the National Institutes of Health (NIH). In 1992, Venter left the NIH to establish The Institute for Genomic Research (TIGR), a non-profit genomics research organization based in Rockville, Maryland, and served as its President until 1998. That same year, he joined Celera Genomics as its President and Chief Scientific Officer. Celera Genomics was established to serve as a definitive hub for genomic, medical, and biological information. In 2002, Venter stepped down from his executive role at Celera Genomics after a disagreement over the commercialization of the genome data, though he briefly continued to serve as the Chairman of its Scientific Advisory Board. He subsequently became the President of the newly established J. Craig Venter Institute (JCVI), where he consolidated his various research activities. It was during the 1990s that the Human Genome Project was launched, a landmark initiative that generated immense enthusiasm among geneticists worldwide. Craig Venter was deeply involved in this ambitious undertaking, initially working within the publicly funded project before establishing Celera Genomics and initiating a parallel effort to sequence the human genome.

The Human Genome Project (HGP) was conceived to determine the sequence of the approximately 3 billion DNA nucleotides that constitute the human genome, identify all human genes, and store and make this information freely available to the public. Another major objective of the project was to examine the ethical, legal, and social implications of emerging genetic technologies and to promote public awareness and understanding of these issues. When the HGP was in its final lap, Celera Genomics, under the leadership of Craig Venter, announced that they were also on a mission to decipher the human genome, expecting to finish it within three years. This created a fierce race between two groups pursuing fundamentally different strategies: the public International Human Genome Sequencing Consortium (IHGSC) utilized a methodical, step-by-step *Hierarchical Shotgun Sequencing* approach, whereas Celera relied on a high-speed, computer-driven *Whole-Genome Shotgun Sequencing* technique.

In the hierarchical shotgun sequencing approach employed by IHGSC, chromosomes were first isolated and digested using restriction enzyme, to generate fragments, roughly 150,000 to 300,000 base pairs long. These fragments were then inserted into Bacterial Artificial Chromosomes (BACs) and replicated inside *Escherichia coli* to establish a genomic library. The cloned DNA fragments were analysed to identify overlapping regions, allowing them to be aligned into a physical map known as BAC contigs. The term "shotgun" was used to imply random fragmentation of the original BAC clone.

Under the leadership of Craig Venter, Celera Genomics utilized the Whole-Genome Shotgun (WGS) sequencing method. Celera bypassed the tedious physical mapping phase entirely, opting

for a faster, computationally heavy approach. The effectiveness of WGS sequencing was convincingly demonstrated in 1995 when Craig Venter and his team at TIGR published the first complete genome sequence of a free-living organism, *Haemophilus influenzae,* comprising approximately 1.83 million base pairs. This achievement came at a time when genome sequencing efforts had largely been limited to much smaller viral genomes.

In the WGS method, the entire human genome was randomly sheared into millions of small fragments of various sizes. These fragments were sequenced simultaneously using automated, high-throughput capillary sequencers. Massive supercomputers running complex assembly algorithms (like the Celera Assembler) searched for overlapping ends among the millions of 'reads' to digitally 'stitch' the entire genome back together from scratch. This approach significantly reduced expenses and saved years of preliminary labour. The process relied heavily on automation and computation rather than manual lab work. However, WGS has its own limitations. Because the entire genome was fragmented at once, the assembly algorithms struggled to accurately place the *highly repetitive DNA sequences*. The computers often misassembled, misplaced, or entirely omitted these regions. Because of the limitations with repetitive regions, Celera could not independently complete a flawless assembly using *only* its shotgun data. Ultimately, they incorporated the publicly available physical mapping data generated by the IHGSC to accurately anchor their sequence fragments correctly.

The Celera Genomics succeeded in sequencing human genome faster and cheaper than the publicly funded international Human Genome Project (HGP). Although diplomatic efforts to bring Francis Collins (HGP) and Craig Venter (Celera) together began in late 1999, the two initiatives remained highly competitive and continued their work in parallel, instead of engaging in a unified collaboration. This monumental sequencing race between HGP and Celera reached a historic milestone on June 26, 2000, when Francis Collins and Craig Venter jointly announced—alongside President Clinton—that both teams had successfully completed a working draft of the human genome. The competing draft sequences were published concurrently in February 2001, with Celera Genomics' draft appearing in *Science* and the Human Genome Project's draft in *Nature*. The publication of these drafts has had a far-reaching impact across various fields of the life sciences, particularly in precision medicine, providing keys to the diagnosis and treatment of numerous diseases, from diabetes to heart disease to Alzheimer disease.

Arguably, Craig Venter has accomplished at least three Nobel Prize-worthy scientific milestones, though the honour has eluded him for various reasons. The first and most prominent of these is, of course, his revolutionary contribution to DNA sequencing. This began in the early 1990s during his time as an NIH researcher, where he pioneered the use of Expressed Sequence Tags (ESTs)—short sub-sequences of cDNA, that allowed identification of protein-coding genes much faster than traditional mapping methods. Building on this momentum, he achieved another milestone in 1995 by sequencing the first complete genome of a living organism, *Haemophilus influenzae*, and later culminated this phase of groundbreaking work by co-assembling the first draft of the human genome in 2000. In addition to the human genome, Craig Venter and his colleagues at Celera also contributed to the sequencing of the genomes of *Drosophila melanogaster* in 2000 and the rat (*Rattus norvegicus*) in 2004. Subsequently, in 2007, his team published the first complete, high-quality diploid human genome—sequenced from Craig Venter's own DNA—profoundly reshaping our understanding of individual genetic variation.

After leaving Celera, Craig Venter launched a series of global ocean expeditions aboard his yacht, *Sorcerer II*, to collect and sequence marine microbial DNA. This landmark metagenomic initiative provided unprecedented insights into the immense and previously unexplored microbial diversity of the world's oceans.

In 2010, Craig Venter's team at the JCVI achieved a monumental milestone in science by creating the first functional, entirely synthetic genome comprising approximately 1.08 million base pairs. Known as *JCVI-syn1.0*, this chemically synthesized genome was modelled after the bacterium *Mycoplasma mycoides*. When transplanted into a closely related bacterium, *Mycoplasma capricolum*, from which the native DNA had previously been removed, the synthetic genome successfully "booted up" and assumed control of the recipient cell, marking the birth of the world's first synthetic organism. This breakthrough marked the emergence of synthetic biology as a distinct scientific discipline. The news was so profound and controversial that President Barack Obama immediately ordered the Presidential Commission for the Study of Bioethical Issues to evaluate the ethics, safety, and security implications of this emerging technology. Finally, in 2016 Craig Venter's lab engineered a "minimal cell" containing only 473 genes—the bare minimum required for a free-living organism to survive—deepening our basic understanding of what defines life.

Craig Venter was a creative entrepreneur and the co-founder of several important biotechnology companies that include Celera Genomics, JCVI, Synthetic Genomics (later renamed Viridos), and Human Longevity, Inc. Much of his later scientific and entrepreneurial career was devoted precisely to confronting the genetic and molecular constraints on human longevity using deep genomic sequencing and AI. Craig Venter also advocated the use of deep genomic sequencing for monitoring long-term health, which may enable the early presymptomatic detection of chronic diseases. He wished to utilize the same concepts to better women's health, and was involved in the establishment of a transformative, data-driven women's health initiative.

Craig Venter has published more than 250 scientific papers and authored three widely acclaimed books: *A Life Decoded* (2007), *Life at the Speed of Light* (2013), and *The Voyage of Sorcerer II* (2023). He has received numerous prestigious awards and honours and has been elected a fellow of several scientific societies. With the passing of Dr. J. Craig Venter, the scientific community has lost a visionary who dared to pursue bold scientific ideas, a pragmatic researcher who valued both time and resources, and an entrepreneur who transformed innovative concepts into real-world applications. The Editorial Team of *EBIOZ* expresses its heartfelt condolences on his death and pays tribute to his remarkable contributions to science and humanity.

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