

# John Craig Venter (1946- )

John Craig Venter helped map the genomes of humans, fruit flies, and other organisms in the US in the late 1990s and early 2000s, and he helped develop an organism with a synthetic genome. In February 2001, Venter and his team published a human genome sequence after using a technique known as Expressed Sequence Tags, or ESTs. Venter worked to bridge commercial investment with scientific research. Venter founded a number of private companies, including the for-profit Celera Genomics, headquartered in Alameda, California, as well as research institutes, such as the not-for-profit J. Craig Venter Institute, located in Rockville, Maryland, and La Jolla, California.

Venter was born in Salt Lake City, Utah, on 14 October 1946. In his childhood he moved with his parents, John Eugene Venter and Elizabeth Jeanne Wisdom, to Millbrae, California. As a child and adolescent, Venter struggled in school, graduating from Mills High School with a number of Cs and Ds. After high school, Venter worked small jobs. In 1964 he enrolled in the Orange Coast Junior College in Costa Mesa, California, but shortly after he was drafted to join the US military effort in the Vietnam War. His father, a former Marine Officer, persuaded Venter to talk to a navy recruiter. In 1965 Venter enlisted in the United States Navy, enrolled in a three-year program, and opted for hospital corps school. Venter trained at Balboa Navy Hospital in San Diego, California, then worked in an emergency room at the naval station at Long Beach, California. He was deployed in Vietnam on 25 August 1967. In Vietnam he worked in the intensive care unit of the Da Nang Navy field hospital until the end of 1968. While working in a hospital, Venter decided to study the life sciences. At one point in Vietnam, however, Venter decided to commit suicide by swimming out into the ocean, hoping to be overcome by exhaustion. As he later told the journalist James Shreeve, he changed his mind and decided to swim back to shore.

Back to the United States, Venter received a BSc in biochemistry in 1972, starting at the College of San Mateo in California and later transferring to the University of California (UC), San Diego. In December 1975 he received a PhD in physiology and pharmacology, also from the UC San Diego, studying neurotransmitters and adrenaline under the biochemist Nathan O. Kaplan. While in graduate school, Venter met and married Barbara Rae, who was also a PhD student at UC San Diego.

Venter's first job as a graduate of UC San Diego was as assistant professor at the State University of New York (SUNY) at Buffalo and the Roswell Park Cancer Institute, also in Buffalo, New York. He researched mammalian receptor proteins using techniques based on immunology and tissue culture, which was a novel approach at the time. He published the article, "Autoantibodies to beta 2-adrenergic receptors: a possible cause of adrenergic hyporesponsiveness in allergic rhinitis and asthma" in 1980. While at SUNY Buffalo, Venter divorced his first wife and married his graduate student Claire M. Fraser. In 1984, Venter joined the US National Institutes of Health (NIH) in Bethesda, Maryland, where he developed Expressed Sequence Tags, or ESTs, also known as shotgun sequencing, for rapid gene discovery. A year later his wife Fraser joined Venter at the NIH.

Venter used ESTs to sequence parts of the genomes of a number of microbial organisms, with the ultimate aim to map the human genome. He co-authored a paper titled, "Caenorhabditis elegans expressed sequence tags identify gene families and potential disease gene homologues," in 1992. Venter's colleagues argued that the EST technique, which seemed to be working for the simpler genomes of some bacteria, would not be robust and precise enough to map the more complex human genome. In 1992, two years after the NIH and the Department of Energy launched the Human Genome Project in the US, Venter left the NIH. He recruited private resources to map the human genome himself, with his own methods. Venter has been criticized for using the initial work of the NIH on genome mapping for his personal gain.

After Venter left the NIH he founded The Institute for Genomic Research (TIGR), a not-for-profit research institute in Rockville, Maryland, in 1992. Fraser followed Venter to the newly installed TIGR, where she became vice president of research. In 1995, Venter and his team decoded the genome of the first free-living organism, the bacterium *Haemophilus influenzae*, using Venter's whole genome EST technique. In 1996, Venter published a paper, "A new strategy for genome sequencing," arguing that the advances made in EST and mapping a bacterial genome made it feasible to apply the method to the human genome and complete the project before 2005 at a projected cost of three billion dollars.

Noting that critics opposed the EST method of genome sequencing, in 1998 Venter founded Celera Genomics, a for-profit company. Venter planned to sequence the human genome using tools and techniques that he and his team developed. Celera worked with TIGR, which Venter's wife directed. TIGR focused on decoding and analyzing the genomes of several organisms, including the bacteria responsible for Lyme disease, syphilis, tuberculosis, and meningitis, while Celera focused on the human genome.

Venter's approach to sequencing the human genome differed from that of the NIH. The techniques developed by Venter were faster and focused only on genes, which are the protein producing pieces of the genome, roughly five percent of the human genome. The NIH's team worked to describe all of the nucleotides in human DNA, not just those in genes. With these two approaches running parallel to one another, the United States Congress called Francis Collins, the director of the National Human Genome Research Institute (NHGRI) of the NIH, and Venter, of Celera, to testify before Congress in Washington D.C. in June 1998. With Venter's efforts underway, Congress asked why it should continue to fund the NIH genome efforts.

During the testimonials to Congress, the director of the NIH, Harold Varmus, alongside Collins, argued that the human genome effort had room for both the NIH and Celera's approach. Elsewhere they claimed that Venter's approach was sloppy and not up to the standards of the NIH's project. Furthermore, they were concerned about the public availability of the human genome data, noting the for-profit orientation of Celera. These worries were picked up by Congress, who posed them to Venter during his hearings.

Venter defended his approach and told Congress that his company did not intend to patent most of their data, except for 100 to 300 sequences that he said were sufficiently novel, not obvious, and useful. At the time, congress found no problem with Venter's statements on the intellectual property of the human genome.

After the hearings, the race between Celera and the NIH to map the human genome accelerated. Venter and Collins appeared alongside US President Bill Clinton and UK Prime Minister Tony Blair to announce the completion of the preliminary draft of the human genome in 2001. NIH and Celera both published a first draft of the human genome ahead of schedule on 16 February 2001, in the journals *Nature* and *Science*, respectively. Shortly after that, Venter and Collins discussed their findings at the American Association for the Advancement of Science's annual meeting in San Francisco, California.

Venter's team sequenced the fruit fly, mouse and rat genomes in 2000, 2002, and 2004 respectively. Venter's EST technique became widely used by researchers. Using this technique, Venter's Global Ocean Sampling Expedition, launched in 2003, aimed to assess the genetic diversity of marine microbial communities.

Shortly after these accomplishments, however, Venter left Celera over disputes about company's future and genetic sequence patents. In 2002, Venter announced that most of the DNA in Celera's human genome efforts was his own. In 2005, Venter and his wife divorced, and Venter married Heather Kowalski in 2008. In 2006, Venter founded the J. Craig Venter Research Institute, which incorporated the TIGR and The Center for the Advancement of Genomics, The J. Craig Venter Science Foundation, The Joint Technology Center, and the Institute for Biological Energy Alternatives.

On 20 May 2010, Venter and his team announced the development of a bacterium, *Mycoplasma laboratorium*, with an entirely synthetic genome. All of the organism's genes were designed with an arrangement of base pair series that are not known to occur in nature. Some scientists argued

that the first synthetic genome is a major step forward from genetic engineering of individual genes. Others argued against the method used by Venter's team to design a synthetic bacterial genome, and some argued that the synthetic genome does not equate to synthetic life.

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