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Letter

ON THE SEVENTY YEARS OF THE STRUCTURE OF DNA, THE TWENTY YEARS SINCE THE SEQUENCING OF THE HUMAN GENOME AND THE FIFTH INDUSTRIAL REVOLUTION

MANUEL E. CORTÉS

Dirección de Investigación, Innovación y Transferencia Tecnológica, Vicerrectoría Académica, Universidad Bernardo O´Higgins, Chile

E-mail: cortesmanuel@docente.ubo.cl

In an interesting Editorial of *Medicina (Buenos Aires)* twenty years ago[1], Dr. Kotsias highlighted the jubilee of the double helix proposal of deoxyribonucleic acid (DNA). Now, seventy years after this discovery[2] that revolutionized all biomedical sciences from 1953 onwards, it is necessary to remember this outstanding advance for humankind. In addition, this year also celebrates the twenty years of the sequencing of the human genome[3, 4], with which the Postgenomic Era began, whose advances are outlined as protagonists in the Fifth Industrial Revolution that humankind is experiencing[5]. Therefore, this Letter aims to reflect on the seventy years of the structure of DNA, the twenty years since the sequencing of the human genome and the health impacts of the current Fifth Industrial Revolution.

In an intense and competitive race between various research groups[6], the American biologist James D. Watson and the British biophysicist Francis H. C. Crick proposed the molecular structure for DNA, the famous double helix model[2]. With this, the key was obtained to understand the "secret of life", an authentic "Rosetta stone" to decipher the genetic code of all living beings. With this advance, molecular biology was propelled towards its zenith, and new disciplines, such as molecular genetics and structural biology, emerged. Watson and Crick, and Maurice Wilkins received the Nobel Prize in 1962 for this discovery. However, Rosalind Franklin, a skilled British chemist and crystallographer, did not receive this distinction as she died years before. In addition, Franklin's relevant contribution to the Watson and Crick Model would have been intentionally pushed into the background by a team of scientists who, while brilliant, have been considered dysfunctional and prone to rivalries in a culturally discriminatory context and sexist towards the work of a woman scientist[6, 7].

The proposal of the structure of DNA came to answer several relevant questions in genetics. At the same time, it raised other relevant questions and challenges for biological and medical sciences. Solving the DNA structure puzzle was critical for Crick to propose the famous central dogma of molecular biology[8], which establishes that transfer of genetic information from nucleic acid to a nucleic acid or from nucleic acid to protein may be possible[8]; however, transfer from protein to protein, or from protein to nucleic acid is impossible[8].

Among the various scientific challenges that molecular biologists and geneticists faced, thanks to this new knowledge about the biochemistry of nucleic acids, one particularly relevant arose: Knowing the complete sequence of the genomes of several species, especially the human genome[9]. The Genomic Era had arisen. Due to knowledge and technical limitations and the high costs of obtaining DNA sequences, the first genomes sequenced were relatively small, *i.e.*, less than 20 000 nucleotides in length[9]. In the 1980s, the genomes of organelles such as mitochondria, chloroplasts, and some viruses were sequenced[9]. In the 1990s, it was possible to sequence the complete genome of some prokary-

otes and brewer's yeast (*Saccharomyces cerevisiae*), a relatively simple eukaryote[9]. The Human Genome Project was initiated in 1990 and completed in 2003. It aimed to sequence the whole human genome[10]. Here again, a fierce race was observed between scientists from public and private institutions to reveal the secrets of human genetic material, a competition characterized by great scientific rivalries that made spilt much ink[6]. Although this project represented a great advance in understanding the human genome and its complexity, several questions remained unanswered[10]. The fact that only about 20 000 genes are protein and RNA-coding is one of the most striking Human Genome Project results. The human genome is as complex and unique as other organisms. These findings demystified the expectations created around human DNA[10]. However, the information obtained was crucial for the new understanding of health and disease from the molecular diagnosis point of view and for developing a predictive medicine.

The development of the Human Genome Project and various other DNA sequencing initiatives in the last decades has led to the refinement and development of new techniques in molecular biotechnology. The knowledge obtained led to generically called "omics" techniques, including proteomics, metabolomics, and transcriptomics. "Omics" techniques are based on analyzing a large data volume and therefore use bioinformatics and fast, high-throughput automated techniques to integrate the information coherently. Thus, with the completion of the human genome sequencing project, the current Postgenomic Era began.

In concluding remarks, we are living in the Postgenomic Era. But also, we are going through a Fifth Industrial Revolution[5], characterized by mass customization, more environmentally friendly processes, productive approaches focused on users (clients or patients; *i.e.*, personalized medicine), digitization, intelligent manufacturing, cobotics (*i.e.*, robots designed, manufactured and used to interact and cooperate with human beings), the Internet of Things (*i.e.*, physical objects with sensors, processing ability, and software that connect and exchange information with other devices over the internet), smart devices, artificial intelligence, and cyber-physical systems, as well as molecular biotechnology and advanced genetic engineering[5]. In this context, professionals and researchers in biomedical sciences should be prepared to understand the revolutionary technologies of gene editing, synthetic DNA, and the future advent of cyber-biological entities. All the above requires a profoundly academic, bioethical, and legal reflection on the experts and decision-makers regarding regulations in these advanced scientific-technological areas that have emerged to stay.

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