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EDITORIAL

Featured articles dedicated to the 20th anniversary of the human genome

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The year 2021 is the 20th anniversary of the publication of the draft human genome [1,2]. The sequencing of the human genome has brought life sciences into a new era, the era to understand the information systems of life in a quantitative manner. Such understanding lights up the bright future of individualized precision medicine, and enables the rational design of synthetic biological systems that can benefit mankind in broad aspects from industry, agriculture to environment and health. Using the human genome sequence as a basic reference has becoming a routine practice in current biological and medical studies. It is so common that people almost take the existence of the reference genome as granted. But the launching and completion of the Human Genome Project (HGP) was far from a routine practice. It was revolutionary in the history of science in the scientific vision, technological advancement, as well as in the joint efforts of multiple disciplines to accomplish the big scientific goal, in starting the culture and building the infrastructure of data sharing, and in the effective international multi-center collaboration.

Twenty years later, *Quantitative Biology* (QB) is proud to publish a series of featured articles to celebrate the anniversary. They are from leading scientists who have played major roles and made significant contributions in the Human Genome Project or have evidenced its major progresses and influences. We believe such a collection will not only help to uncover the stories behind the revolutionary project, but will bring many insights that will shed light on the future development of quantitative biology. The articles will be published in multiple issues through the year. The first issue starts from two key articles, from Dr. Michael S. Waterman, and Dr. Michael Q. Zhang, respectively.

The first article is “The Human Genome Project: the Beginning of the Beginning” by Michael S. Waterman [3]. Professor Waterman (Fig. 1) is one of the founders in computational biology and bioinformatics. The famous Smith-Waterman algorithm he developed with Temple F. Smith is the fundamental algorithm for comparison and alignment of DNA, RNA and protein sequences. The Lander-Waterman theorem he published with Eric Lander in 1988 established a theoretical cornerstone for DNA sequencing and mapping, which played a fundamental role in the Human Genome Project. Michael Waterman is currently University Professor Emeritus at the University of Southern California, and Distinguished Research Professor at University of Virginia. He is a Member of the National Academy of Sciences USA, the National Academy of Engineering USA, and the American Academy of Arts and Sciences. He is a Foreign Member of the French Academy of Sciences and of the Chinese Academy of Sciences. He was a Cao Xingcheng Chair Professor at Tsinghua University in 2008–2017, and received the Friendship Award of PRC in 2013. His article in this issue brings us the vivid picture of the meeting at University of California Santa Cruz in 1985. That was the first meeting that eventually led to the launching of HGP, before the historical DOE (the Department of Energy) meeting in Santa Fe in 1986.

The article “A personal journey on cracking the genomic codes” by Michael Q. Zhang presents a complete

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This article is dedicated to the feature in 20th anniversary of Human Genome (Eds. Michael Q. Zhang and Xuegong Zhang).

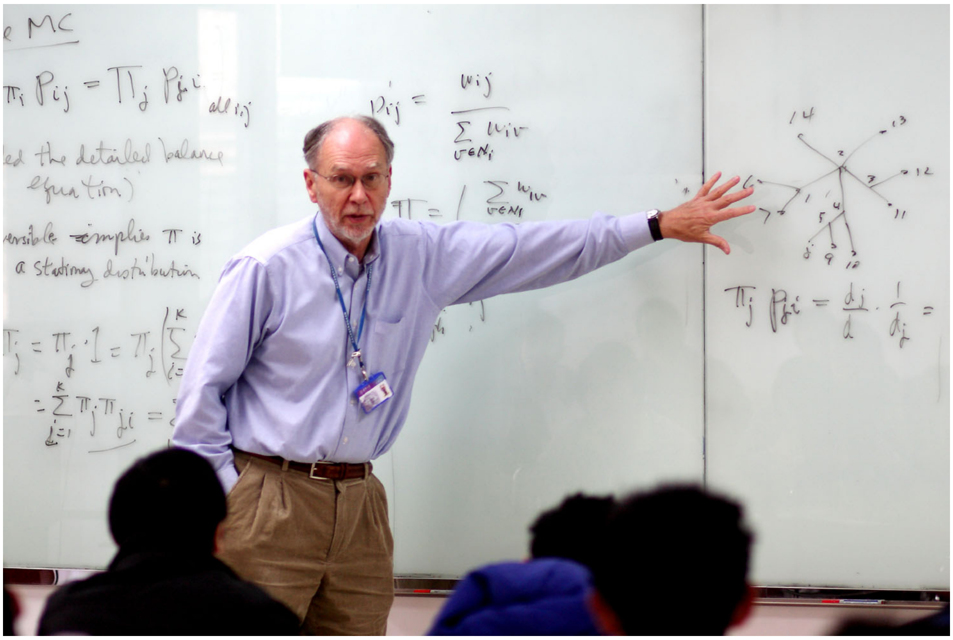

Figure 1. Michael Waterman lecturing in Tsinghua University in 2011. Photo by Xuegong Zhang.

review of the long journey for a trained physicist to become a bioinformatician along the start and progress of the HGP [4]. Professor Michael Zhang is a leading scientist in computational biology and genomics. He was one of the earliest young scientists devoted to decoding the signals in genomes with computational approaches. His early contribution includes the development of the first human gene and promoter prediction algorithms. And his work on analyzing the dynamic yeast gene expression and cell-cycle regulated genes using DNA chips was among the first to open the new era of computational functional genomics. Michael Zhang and Chao Tang are the founding Editors-in-Chief of *Quantitative Biology*. Currently Michael Zhang is the Cecil H. and Ida Green Distinguished Chair Professor of Systems Biology at University of Taxes Dallas, and the Director of the Center for Systems Biology. He was a professor at the Watson School of Biological Sciences at Cold Spring Harbor Laboratory for many years before moving to Dallas. He has also served as an adjunct professor and distinguished guest chair professor at Tsinghua University (Fig. 2). From his article in this issue, we can feel the trajectory of the emerging and evolution of research focuses around the human genome from reading out the sequences to understanding the functions that they encode.

Figure 2. Michael Zhang at a conference in Tsinghua University. Photo courtesy of Tsinghua University News.

In the coming issues of QB throughput this year, we'll have more featured articles dedicated to the anniversary from multiple angles. The impact of the Human Genome Project is far beyond the reference genome sequence itself. The pioneering thinking and determination that led to the start of the seemingly impossible mission, the informatics and mathematical view of the fundamental questions in life sciences, the organization of multi-labs across the globe toward the common goal, and the culture and infrastructure of big data sharing are all important heritages from the human genome science. We hope the publication of the featured articles, together with the rest, in this issue and in this year (and perhaps in subsequent centennial issues) will be inspiring for all readers of QB in many different disciplines and future generations.

REFERENCES

1. Lander, E. S., Linton, L. M., Birren, B., Nusbaum, C., Zody, M. C., Baldwin, J., Devon, K., Dewar, K., Doyle, M., FitzHugh, W., *et al.* (2001) Initial sequencing and analysis of the human genome. Nature, 409, 860–921
2. Venter, J. C., Adams, M. D., Myers, E. W., Li, P. W., Mural, R. J., Sutton, G. G., Smith, H. O., Yandell, M., Evans, C. A., Holt, R. A., *et al.* (2001) The sequence of the human genome. Science, 291, 1304–1351
3. Michael, S. Waterman (2021) The Human Genome Project: the beginning of the beginning. Quant. Biol., 9, 4–7
4. Michael, Q. Zhang (2021) A personal journey on the cracking of the genomic codes. Quant. Biol., 9, 8–22