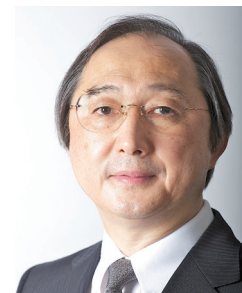


For outstanding contributions to advanced cancer research, such as whole-genome sequencing, through the utilization of supercomputers



Dr. Satoru Miyano

Positions and Organizations :

Specially Appointed Professor and Director, M&D Data Science Center, Tokyo Medical and Dental University
Professor Emeritus, The University of Tokyo

Date of Birth : December 5, 1954

Degree :

Ph.D. (Kyushu University, 1984)

Brief Biography :

1977 BS, Department of Mathematics, Faculty of Science, Kyushu University
1979 MS, Department of Mathematics, Graduate School of Science, Kyushu University
1979 Withdrew from Ph.D. Program in Graduate School of Science, Kyushu University
1979 Assistant, Faculty of Science, Kyushu University
1984 Doctor of Science, Kyushu University
1985 Researcher, Alexander von Humboldt Foundation
1987 Associate Professor, Faculty of Science, Kyushu University
1993 Professor, Faculty of Science, Kyushu University
1996 Professor, Human Genome Center, Institute of Medical Science, The University of Tokyo
2014 Director, Human Genome Center, Institute of Medical Science, The University of Tokyo
2015 President, Kanagawa Cancer Center (concurrent post)
2020 Director, M&D Data Science Center, Tokyo Medical and Dental University
Professor Emeritus, The University of Tokyo

Main Awards and Honors

1994 Japan IBM Science Prize
1994 IPSJ Sakai Special Researcher Award
2013 Fellow, International Society for Computational Biology
2016 Uehara Prize
2020 The Healthy Society Award

Main Achievements:

To understand the pathogenesis of cancer, which arises due to genomic variations in cells, it is vital to identify abnormalities in the genome related to the onset of cancer and to elucidate their functional consequences. Innovations in genome sequencing technology in 2008 made it possible to decode an entire cancer genome and comprehensively identify genomic abnormalities related to cancer. At the same time, analyzing, on a large scale and to a high degree of precision, gene expression data and variations that manipulate cellular systems as consequences of such genomic abnormalities, has become a crucial aspect of research.

Dr. Satoru Miyano designed a system that enables cancer genome research at the world's highest level, even before the advent of the era of large-scale genomic data analysis. This system was realized in the form of the supercomputer "SHIROKANE" at the Human Genome Center under the University of Tokyo's Institute of Medical Science. Currently, much of Japan's whole-genome sequencing research for cancer relies heavily on the supercomputer at this

Center, and it is not an exaggeration to say that this has been underpinned by Dr. Miyano's dedicated efforts.

With the idea of fusing supercomputers and mathematical methods with cancer research, Dr. Miyano brought together leading figures in cancer research in Japan and established the new academic fields of "systems cancer" and "new dimensions in systems cancer" under Japan's Ministry of Education, Culture, Sports, Science and Technology (FY2010–2019). One of the notable achievements is the joint research with Professor Seishi Ogawa (currently Professor at the Graduate School of Medicine, Kyoto University) on elucidating the causative genes for myelodysplastic syndromes (MDS) (*Nature*, 2011). In addition to being a landmark study in elucidating the pathogenesis of MDS, this study was also the first in the world to demonstrate the involvement of RNA splicing somatic mutations in human cancer development, making it a historical discovery in the field of cancer genomics. Starting with this breakthrough in MDS elucidation, Dr. Miyano, as a pioneering figure in innovative cancer research, organized an analytical framework based on supercomputing for the extensive analysis of cancer genome sequencing data and gene expression data. Along with collaborating researchers, he realized many prominent achievements that led the world in the field of cancer pathogenesis. As a result of whole-genome sequencing, he shed light on the fact that structural abnormalities in the untranslated region of the right end of the *PD-L1* gene, which is a component of immune checkpoints, are involved in the mechanism by which cancer cells evade the immune system. This achievement garnered global attention (*Nature*, 2016). In recognition of this series of achievements, he was awarded the Uehara Prize in 2016 jointly with Professor Ogawa. He also contributed to the utilization of the "K" and "Fugaku" supercomputers in generating research outcomes. Thus, Dr. Miyano has been a world-leading figure for many years in the field of computational biology, using supercomputers in cancer research and other areas of study. In 2013, his significant contributions were acknowledged when he became the first Asian to be elected as a Fellow of the International Society for Computational Biology. In 2011, he formed a team at the University of Tokyo's Institute of Medical Science and realized genomic medicine for cancer based on whole-genome sequencing. His achievements have been consistently featured in various media outlets, including those from overseas. In 2020, he was presented with the Healthy Society Award (Pioneer Category).

Dr. Satoru Miyano has made advanced contributions to cancer research, such as whole-genome sequencing, through the utilization of supercomputers. In recognition of these contributions, he is hereby awarded the Okawa Prize.