

S-face

SFC makes the future through researches

Exploring the mystery of
life through studying tardigrades,
the “toughest animal”

Kazuharu Arakawa



VOL.

038

2025 Nov. ISSUE

Japanese Color: Sabiseiji-iro

Determining tardigrades' genome sequence and analyzing proteins involved in cryptobiosis

Known as the "toughest animal," tardigrades in cryptobiosis becomes ametabolic and can withstand various extreme environments, such as high and low temperatures, radiation, and vacuum. When rehydrated, tardigrades resume life activities as if brought back to life. We thought this provides a clue to explore the boundaries between life and substantial matter.

However, even if we wanted to rear tardigrades for experiments, their diet was kind of a black box. In addition, their extremely small size (100 - 300 μm) made it difficult to determine their genome. Therefore, we started by exploring ways to rear them, and by establishing a mass rearing system, we laid the foundation for their development as a model organism. Then we developed a technology to analyze ultra-low volumes (which can analyze genomes from 50pg of genomic DNA) and determined the genome sequence of the tardigrade. We also developed a gene transfer technology called TardiVec. These technologies can be applied to analyze genes of various microscopic organisms, as with tardigrades.

One of the findings from our research on tardigrades is the fact that many of the proteins involved in their cryptobiosis are of non-domain type; they do not take specific structures and have no associations between functions and structures/sequences. A number of similar non-domain type proteins are found in many other organisms, including humans, providing emerging evidence that the groups of genes corresponding to these proteins actually have important functions. We also focus on how tardigrades' cell functions and structures are maintained in cryptobiosis without water, with high hopes that studying this will provide important findings about cell damage in all kinds of organisms.

Developing spider silk that does not shrink after washing, by linking genome sequences and physical properties

The other research subject of ours that is as equally important as tardigrades is spider silk. Stronger than iron and as stretchable as nylon, spider silk is the toughest material on earth. Nonetheless, spider silk can be made without relying on petroleum and is even biodegradable. Therefore, it is an ideal next-generation high-functional material.

Spiber, a venture company derived from our research center, the Institute for Advanced Biosciences (IAB), has been successful in putting artificial spider silk fibers to practical use and mass-producing them. However, we are still far from freely manipulating the physical properties of spider silk fibers. Jointly with Spiber, we are attempting to elucidate the principles based on which spider silk is designed from the genome sequence. We collected more than one thousand species of spiders from all over the world, developed a database of their genome information and exhaustively-measured physical properties of their fibers, and performed bioinformatic analysis of the database. Our analysis identified the amino acid sequence involved in the after-wash shrinking of natural spider silk. By replacing the portion corresponding to that sequence, we were successful in designing artificial spider silk that does not shrink after washing.

Unlike enzymes and other proteins that function in aqueous conditions and react in a non-linear manner, spider silk is a protein material whose linear reaction can be observed *ex vivo*, which is an advantage that makes it easy to associate a certain gene sequence with a certain physical property as a phenotype. The design principles elucidated through decoding spider silk will provide a clue to decode other fibrous proteins, such as hair keratin and skin collagen.

Quantitatively defining "life" through biological information on tardigrades and spider silk

What is life? – To answer this eternal question that nobody has been able to answer quantitatively, Professor Kazuharu Arakawa conducts research by using a bioinformatics approach that uses computer-based analysis of enormous biological information.

By studying tardigrades, the "toughest animal" that becomes indestructible by entering cryptobiosis (a reversible suspension of life activities), Professor Arakawa explores the boundaries between life and matter and attempts to quantitatively define "life."

Based in the Tsuruoka Town Campus endowed with rich nature and dietary culture, the professor's laboratory is exploring connections between information and life.

Outreach activities to raise public awareness of tardigrades

While tardigrades are strongest when they are in cryptobiosis and nearly "substantial matter," they are fragile and very difficult to keep when they are active "organisms." We first explored how to rear tardigrades, even though there was little previous knowledge at that time as to what they eat and what environmental conditions are suitable for them. At the same time, we made stuffed tardigrades to let people know about them, provided many free lectures at museums and other places that attract children, and thus raised public awareness of tardigrades as experimental organisms. These outreach activities were necessary also to promote academic research on tardigrades.



Developing a database by measuring spider silk from more than one thousand species of spiders

In our research on spider silk, we created a comprehensive catalog of silk protein gene sequences from 1,098 spider species and characterized their mechanical, thermal, structural, and moisture-retentive properties. By integrating the genome sequences of silk proteins with the corresponding phenotypic properties, we found a number of amino acid sequence patterns that contribute to those properties. This database, called "Spider Silkome Database," has been made publicly available free of charge, with the intention to facilitate the development of next-generation biomaterials.



A world-leading bioinformatics research center



The Institute for Advanced Biosciences (IAB) is a research center for comprehensive analysis of biological data, such as genome, metagenome, transcriptome, proteome, and metabolome, and understanding the massive amounts of data by performing computer-based analysis, modeling, and simulation of the data. The Metabolome Campus has as many as 50 analyzers for metabolomics. In its thriving research environment, the IAB attracts global attention as a pioneer of "integrated systems biology," which is a bioscience based on big data.



Bioinformatics is essential for the development of biology

In the 21st century, it became possible to comprehensively and quantitatively measure all constituents of organisms. We are able to obtain all kinds of information on an organism in the form of data through: genomics, which provides information on DNA which is the blueprint for the organism; transcriptomics, which exhaustively determines the quantities of thousands to tens of thousands of types of messenger RNAs; proteomics, which exhaustively determines the quantities of tens of thousands of types of proteins; and metabolomics, which exhaustively measures thousands of types of low-molecular compounds in cells (a technology developed at the IAB).

Modern biology would not be possible without bioinformatics, which performs computer-based analysis of these enormous amounts of data. Rather than attempting to grasp organisms directly in all their overwhelming complexity, it is through making full use of multiple partial projections that we can reconstruct and understand them as systems. We believe that this environment and information studies-oriented approach is precisely what makes our work at SFC meaningful.

We have developed various open-source software products for that purpose. Our integrated software environment for genomic analysis, the "G-language Genome Analysis Environment," has been cited in hundreds of papers by researchers all over the world. Our tools, such as "E-Cell 3D," which visualizes the whole-cell simulation software E-Cell (also originally developed at SFC), have also been widely used. By utilizing these tools ourselves, we continue to pursue the elucidation of what life is.



Profile

Kazuharu Arakawa

Professor Kazuharu Arakawa is the Director General at the Institute for Advanced Biosciences, Professor at Graduate School of Media and Governance, and Professor at Faculty of Environment and Information Studies, Keio University. He completed the Graduate School of

Media and Governance, Keio University, in 2006. Professor Arakawa holds a PhD in Media and Governance. He has been in the current post since 2022, after serving as Project Research Associate, Project Assistant Professor, and Project Associate Professor at Graduate School of Media and Governance, Keio University, and as Associate Professor at Faculty of Environment and Information Studies, Keio University. Professor Arakawa specializes in systems biology and bioinformatics.

For more details, visit the S-face website!

You'll find more articles and videos featuring Kazuharu Arakawa.

S-face

Search



Keio Research Institute at SFC
Office of Research Development and Sponsored Projects,
Shonan Fujisawa Campus, Keio University
5322 Endo, Fujisawa, Kanagawa, 252-0882, Japan
Tel: +81-(0)466-49-3436
E-mail: info-kri@sfc.keio.ac.jp