FALL 2014

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RIKEN Center for Life Science Technologies
Researchers at the Division of Structural and Synthetic Biology in Yokohama are advancing technologies for the fundamental structural analysis of macromolecular complexes using electron cryomicroscopy (left), x-ray crystallography and nuclear magnetic resonance spectroscopy.

RIKEN, Japan's flagship research institute, conducts basic and applied experimental research in a wide range of science and technology fields including physics, chemistry, medical science, biology and engineering.

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ISSN 1883-3519

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A greener future

Cover story: Researchers at the RIKEN Center for Sustainable Resource Science are developing a new interdisciplinary science of green solutions for resilient agriculture, biomanufacturing and renewable energy. **Page 21**

Welcome to the second issue of *RIKEN RESEARCH* in its new quarterly format. In this issue, a "Perspectives" article by Kazuo Shinozaki, director of the RIKEN Center for Sustainable Resource Science, presents RIKEN's roadmap for research in the vital area of sustainable resource science (see "Cultivating a renewable future" on page 21). As a publicly funded organization, it is of particular importance for RIKEN to carry out research, either basic or applied, that will eventually be put to use for the betterment of society. In this context, the creation and management of sustainable resources through the integration of biology and chemistry is an important area for us.

Elsewhere in the magazine, we present "Research highlights" that focus on the work being performed by our scientists in a variety of fields, including cognition and memory, bioinspired catalysts and quantum computing. In our regular "Places" feature, we look at RIKEN's productive collaboration with Brookhaven National Laboratory in the United States and highlight a number of the significant achievements that have resulted from this partnership. These include the observation of a plasma similar in character to that of the primitive Universe, which is enabling scientists to better understand its earliest moments.

Our "People" section features interviews with Emiko Hiyama, a principal investigator who carries out her theoretical physics research in a laboratory lined with chalkboards filled with colorful equations, and Jafar Sharif who moved from Bangladesh to Japan to complete work in the field of epigenetics and gene silencing. As a young researcher at RIKEN, Jafar has been able to take advantage of a rigorous mentoring program that offers him enjoyable "mental jousting".

RIKEN recently published its *2013–2014 Annual Report*, which provides a summary of the research carried out during the past fiscal year. This is complemented by a smaller booklet, *At a Glance*, which presents readers with an easy-to-understand overview of the organization. Both are available to download from our website at **www.riken.jp/en/pr/publications/annual_report** and are useful tools for those who wish to take a more general look at RIKEN.

Meanwhile, we hope you enjoy reading this issue of *RIKEN RESEARCH*. We would be happy to hear feedback from our readers on what we are doing right, wrong or might do differently. To let us know what you think, please email **rikenresearch@riken.jp**.

A few-body view of the hypernucleus

Emiko Hiyama

Associate Chief Scientist

Strangeness Nuclear Physics Laboratory
RIKEN Nishina Center for Accelerator-Based Science

Please describe your role at RIKEN.
As an associate chief scientist, one of my main responsibilities is to manage my laboratory and team of researchers. The Strangeness Nuclear Physics Laboratory is a theoretical physics group tasked with expanding a quantum few-body calculation method developed by Kyushu University and applying it to various fields, including hypernuclear physics, hadron physics and the physics of unstable nuclei.

RIKEN is one of the most famous institutes for nuclear physics research.

How did you become interested in your current field of research?
During my master's degree at Kyushu University, I attended a lecture by Professor Osamu Hashimoto, an experimentalist in the field of strangeness nuclear physics. Hashimoto described the appeal of hypernuclear physics and the importance of studying the hypernucleus, which is a nucleus that contains at least one hyperon—a subatomic particle composed of quarks. I also learned that strange quark matter exists in the cores of neutron stars. Therefore, to understand the structure of neutron stars, it is important to study the structure of hypernuclei. This association between nuclear physics and astrophysics really impressed me.

What made you decide to become a scientist?
As a third-year undergraduate student also at Kyushu University, I attended a lecture on nuclear physics by Professor Masayasu Kamimura. In his talk, Kamimura elaborated on fundamental and current aspects of nuclear physics. I found the latest developments in the field fascinating and decided that I wanted to collaborate with Kamimura in conducting research at the cutting edge of nuclear physics.

How and when did you join RIKEN?
While working as an associate professor at Nara Women's University, I felt that I wanted to pursue a role with a stronger focus on research. The position of associate chief scientist at RIKEN was exactly what I was looking for, so I decided to apply for it, and I succeeded in getting it. As a result, I moved to RIKEN in April 2008.

What is the best thing about working at RIKEN?
RIKEN is one of the most famous institutes for nuclear physics research. Many researchers from abroad have shown an interest in joining or visiting my laboratory. Here at RIKEN, I have the resources to welcome a number of postdoctoral researchers and to travel abroad to discuss new findings with fellow collaborators. This enables me to both expand the scope of my research and network, something that has been very advantageous as it allows me to venture into new fields of physics. I am really enjoying my work here at RIKEN.

Please tell us about your professional and personal goals.
I have developed a calculation method for the quantum-mechanical few-body problem, which I have thus far been able to use in solving up to the five-body problem. One group of researchers has been able to calculate the motions of up to 12 bodies. I would like to develop my method beyond the 12-body problem to become a leading researcher in few-body physics.

How do you balance family life with your work at RIKEN?
Physics is my life. My husband is also a scientist and understands my research. We enjoy discussing our research together. ■

Spinning nature's thread

Jafar Sharif

Research Scientist

Laboratory for Developmental Genetics
RIKEN Center for Integrative Medical Sciences

How did you become interested in your current field of research?
I have always been fascinated by evolution and the fact that all living and extinct species are linked by a common thread—DNA, the basic code of life. During the time when I was an undergraduate student, Dolly the sheep was cloned from an adult somatic cell. This news really excited me because it revealed that a single cell can be reprogrammed to create an entire animal. I chose my current field of research as it allows me to ask questions about the evolution of DNA and the reprogramming of cells.

What made you decide to become a scientist?
I am from Bangladesh, which is a treasure trove of subtropical flora and fauna. The mangrove forest—now a world heritage site—near the rural area where I was born is home to the majestic Bengal tiger and beautiful spotted deer. Hordes of monkeys used to steal mangoes from our orchard and I would have to fight them away with a stick! Growing up around such marvelous animals and plants, I decided to become a scientist to learn more about them.

How and when did you join RIKEN?
During my PhD research, I had the opportunity to collaborate with my current supervisor, Haruhiko Koseki, at RIKEN. After obtaining my doctoral degree in 2008, I decided to join his lab. At first, I was supported by a Japan Society for the Promotion of Science fellowship. Then in April 2014, I became a permanent staff scientist under RIKEN's Foreign Postdoctoral Researcher program.

What is the best thing about working at RIKEN?
Probably, the rigorous mentoring program for young researchers like me. I still attend a weekly, one-on-one session with my supervisor. The meetings offer a bit of mental jousting, which I really enjoy, and an opportunity to learn. The overall international atmosphere at RIKEN is also encouraging for foreign researchers.

> *The best thing about RIKEN is its rigorous mentoring program for young researchers like me.*

What do you wish you had known before you came to RIKEN?
I wish I had known that the science at RIKEN was so tough! It took me two years to get used to the relentless and thorough style of research at my lab and the center as a whole.

Please tell us about your professional and personal goals.
My personal goal is to bring happiness to myself, my family and the people around me through my work. Professional goals include becoming independent and pursuing challenging and exciting fields of research. I am very fond of Japan and expect to spend a large part of my professional and personal life here. Both my wife and daughter are Japanese.

How do you balance family life with your work at RIKEN?
I am grateful for the mental support offered by my wife. This year, my daughter was born and she has brought absolute joy to my life. There is a natural equilibrium between my family and my work and I hope to maintain it. ■

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Polycomb-group proteins bind to DNA and repress expression of developmental genes.

Gene regulation turned upside down

DNA binding by complexes that regulate developmental gene expression occurs in the reverse order to that expected

Molecular modification of DNA and the histone proteins it is bound to is one of the key mechanisms responsible for regulating gene expression. Polycomb-group proteins play an important role in some of these modification processes, but the molecular mechanisms by which they bind to DNA and exert their effects have been poorly understood.

Takashi Kondo and colleagues from the Laboratory of Developmental Genetics at the RIKEN Center for Integrative Medical Sciences, in collaboration with researchers from the University of Oxford in the United Kingdom, have now shown that modifications involving Polycomb proteins occur in a manner that contradicts existing models[1].

Polycomb-group proteins are found in two complexes, known as PRC1 and PRC2, and there are two forms of PRC1—the canonical and variant forms. Molecular modifications involving these complexes play crucial roles in gene regulation, cellular differentiation and development. "Polycomb-group proteins repress gene transcription by binding to DNA," says Kondo. "This is the main system that regulates transcription of developmental genes, and Polycomb systems are also related to some cancers. Understanding their mechanism of action is therefore biologically very significant."

PRC1 and PRC2 complexes always work together, but exactly how has remained unclear. For some time, it has been thought that PRC2 must first bind to the DNA, which then allows binding or 'recruitment' of PRC1. However, as recent evidence suggests

that this might not be the case, Kondo and his colleagues developed a new approach to investigate.

The researchers inserted human DNA into mouse embryonic stem cells to cause the PRC1 complex to bind at specific sites. They found that the variant form of PRC1, but not the canonical form, was able to recruit PRC2 to the DNA—the reverse of the long-accepted mechanism of PRC2 binding prior to recruiting PRC1.

This process is dependent on a component of the PRC1 complex called KDM2B, and deleting part of this protein prevented PRC1 from binding to DNA in cells. In live mice, genetically disrupting the function of KDM2B, thereby preventing PRC1 binding and PRC2 recruitment, had serious consequences: complete loss of KDM2B function was lethal before birth, while partial loss caused abnormalities in the skeleton due to incorrect development.

"Our findings indicate that the Polycomb regulatory mechanisms possibly rely on the activity of variant PRC1 rather than PRC2 or canonical PRC1," explains Kondo. "This means that studies on variant PRC1 may be more fruitful for investigating the mechanisms of developmental regulation and cancer development." ■

Reference

1. Blackledge, N. P., Farcas, A. M., Kondo, T., King, H. W., McGouran, J. F., Hanssen, L. L. P., Ito, S., Cooper, S., Kondo, K., Koseki, Y. *et al.* Variant PRC1 complex-dependent H2A ubiquitylation drives PRC2 recruitment and polycomb domain formation. *Cell* **157,** 1445–1459 (2014).

How brains remember and correct

High-frequency nerve signals let mice remember how to make the right move

Information processing in the brain is complex and involves both the processing of sensory inputs and the conversion of those inputs into behavior. The passing of electrical oscillations between networks of neurons in different parts of the brain is thought to be a critical component of cognition as well as conscious perception and awareness, but so far there has been little direct evidence linking specific neuronal oscillations to discrete thinking and behavior events.

Jun Yamamoto and colleagues from the RIKEN–MIT Center for Neural Circuit Genetics have now detected a brief burst of nerve activity oscillating in two specific parts of the mouse brain just before a correct choice is made, either when planning an action or when correcting a mistake[1].

The researchers searched for evidence of specific neuronal oscillations by studying mice navigating a T-shaped maze with a reward at the end of one arm of the T. Just before trained mice made the correct choice of direction, Yamamoto and his colleagues observed a brief burst of synchronized high-frequency gamma waves oscillating in specific parts of the entorhinal cortex and hippocampus.

In mice navigating a simple maze, a synchronous oscillation of high-frequency gamma waves occurs in two specific parts of the brain just before a correct navigation choice is made.

Yamamoto was fascinated to notice that the burst of gamma waves also occurred just before mice that had originally turned in the wrong direction realized their mistake and turned round. He called this the "oops" moment, and the results indicate that similar neuronal activity occurs when making a correct choice either immediately or on realization of an error. No such gamma-wave activity was detected when mice made the wrong choice without correcting it.

To further test the link between the gamma synchrony and the memory recall process, the researchers genetically engineered mice with light-activated ion channels that could block the gamma waves. When these channels were activated, the gamma waves ceased and the mice could no longer accurately choose the right direction or correct their wrong choices.

"Our work is telling us about how the brain recalls remembered information at critical moments," says Yamamoto. "It suggests that synchronized gamma oscillations actually

contribute to the animal's correct choice rather than being a consequence of their choice." The finding sheds light on the fundamental mechanism underlying the successful retrieval of working memory. Yamamoto now intends to see if these initial findings apply to other brain regions.

The results also provide new insight into the phenomenon of animal consciousness. "Our findings provide evidence that animals employ a behavior monitoring process called metacognition that typically requires conscious awareness," says Yamamoto.

Reference

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An all-or-nothing proposition

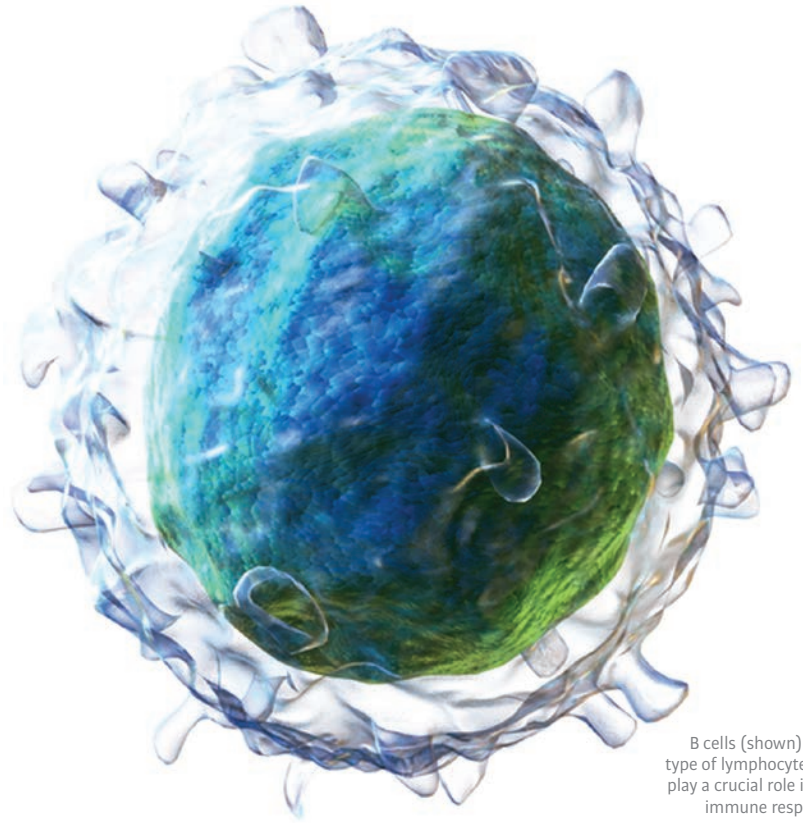
A feedback signaling system forms the foundation for a cellular on–off switch that regulates immune response

The immune system contains a vast array of cell types and signaling pathways that help to regulate immune response. Among these cell types are B cells, which have the unique ability to bind to specific antigens due to a transmembrane receptor protein known as the B cell receptor (BCR) on the cell surface. Through a combination of biochemical and mathematical modeling experiments, a research team led by Mariko Okada-Hatakeyama from the RIKEN Center for Integrative Medical Sciences has now gained a deeper understanding of the interplay between BCRs and another key component of the immune response, the NF-κB protein complex[1].

When a BCR recognizes a potential threat, it sets into motion a series of cellular events that promote a broader immune response. A key step in this process occurs when BCR signaling causes NF-κB to migrate from the cytoplasm to the nucleus, where it directly binds and activates numerous target genes that stimulate B cell maturation and antibody production.

Okada-Hatakeyama and her colleagues uncovered evidence that BCR-stimulated NF-κB activation operates via a binary switch mechanism in which any signal that crosses a set threshold triggers strong, long-lasting activation. Initial cell culture experiments showed that the core machinery of this switch resides in the interaction between two proteins: TAK1 and IKKβ. BCR signaling is initially transmitted from TAK1 to IKKβ, which in turn activates NF-κB. However, the researchers also discovered a 'positive feedback' loop, wherein activated IKKβ gives a further boost to TAK1 activation and thereby increases NF-κB activity. Computational simulations supported this model and confirmed that interference with this feedback loop effectively kills the switch-like response.

This on–off signaling mechanism has important functional consequences. "All-or-none responses are very important because after an 'on' response it is very difficult to return to the basal state," says Okada-Hatakeyama. "This means that if a disease state develops, total recovery is very difficult." These findings could therefore prove helpful



B cells (shown) are a type of lymphocyte that play a crucial role in the immune response.

in understanding the role of NF-κB in certain cancers or inflammatory disorders. On the other hand, such signaling switches can also confer considerable stability to systems, eliminating the signaling 'noise' that can occur in more dynamic signaling networks.

The researchers now hope to explore the final impact of this switch mechanism at the level of NF-κB target gene activity. "We are also planning to rewire and modify this signaling network and see how NF-κB activation and B cell differentiation processes are changed in living systems," says Okada-Hatakeyama. ■

Reference

1. Shinohara, H., Behar, M., Inoue, K., Hiroshima, M., Yasuda, T., Nagashima, T., Kimura, S., Sanjo, H., Maeda, S., Yumoto, N. *et al.* Positive feedback within a kinase signaling complex functions as a switch mechanism for NF-κB activation. *Science* **344,** 760–764 (2014).

A new target for allergy therapies

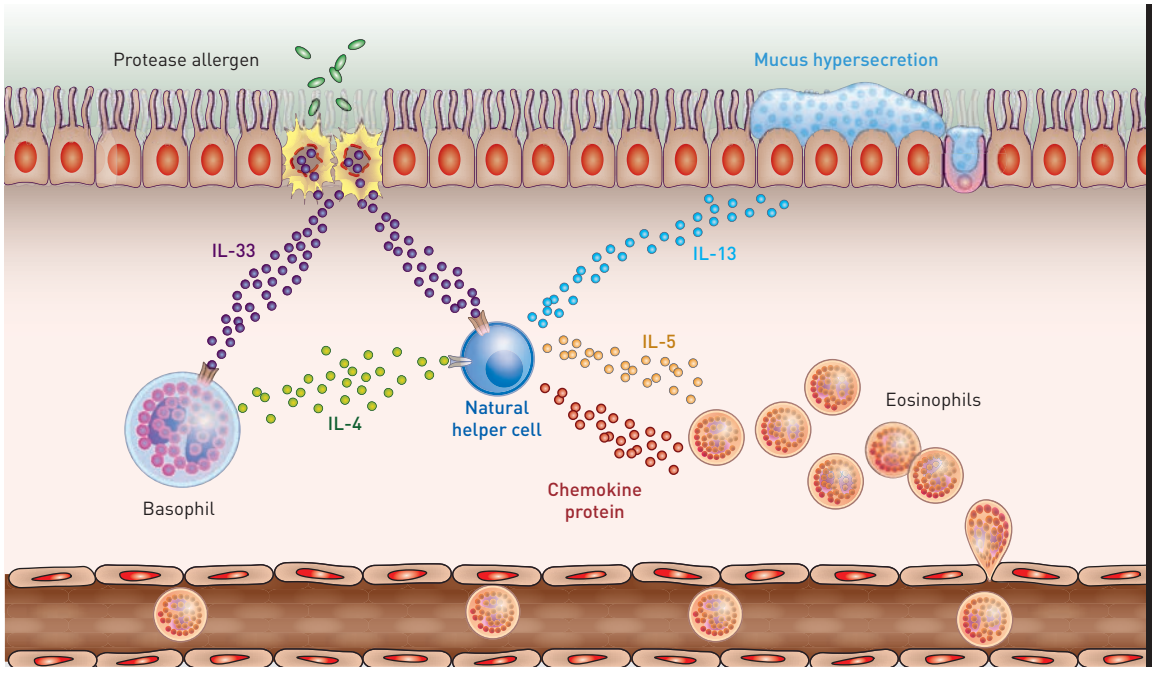
Immune cells called basophils are found to be key drivers of allergy-induced lung inflammation

Many particles and molecules in the environment can trigger allergic asthma in susceptible individuals. The allergic response to some of these allergens results in lung inflammation that can lead to a narrowing of the airways and even severe respiratory difficulty. A research team led by Masato Kubo from the RIKEN Center for Integrative Medical Sciences has now identified that a type of immune cell called a basophil is responsible for initiating a cascade of events that leads to inflammation of the lung in mice after exposure to plant- and dust-mite-derived allergens[1].

Protein-chewing enzymes known as proteases that are derived from dust mites and plants can begin to break down cells in the outer layer of the lung, causing damage that can initiate a local inflammatory reaction. While investigating the triggers of this inflammation, the researchers found that these protease allergens induced lung inflammation in normal mice with a complete immune system, but not in mice genetically engineered to lack basophils.

Immune cells, including basophils, secrete the cytokine interleukin-4 (IL-4), which is known to play a role in the induction of asthma. The extent to which basophil-derived IL-4 is involved in the induction of lung inflammation, however, was unknown. Kubo and his colleagues showed that proteases could increase the expression of IL-4 in basophils but not in other types of immune cells. In mice whose basophils were unable to produce IL-4, protease treatment did not cause lung inflammation, suggesting that basophil-derived IL-4 could be the main driver of protease-allergen-induced asthma in mice—a finding that could also extend to humans.

Natural helper (NH) cells are another type of immune cell that is known to play a role in the body's response to allergens. The researchers showed that NH cells express



Lung inflammation that causes asthma is linked to the secretion of interleukin-4 (IL-4) from immune cells called basophils.

the receptor for IL-4, and that NH cells treated with IL-4 increase their expression of cytokines such as IL-5 and IL-3, which are also known to be involved in asthma induction. IL-4-treated NH cells also demonstrate a rise in expression of various chemokine proteins known to attract large numbers of eosinophil immune cells to the lung (see image). This influx of eosinophils triggers inflammation and narrowing of the airway, which leads to asthmatic symptoms such as wheezing.

"The findings suggest that treatments that reduce the numbers of basophils, or that prevent the production of IL-4 by basophils, could be promising for the management of lung inflammation and asthma caused by protease allergens," says Kubo. ■

Reference

1. Motomura, Y., Morita, H., Moro, K., Nakae, S., Artis, D., Endo, T. A., Kuroki, Y., Ohara, O., Koyasu, S. & Kubo, M. Basophil-derived interleukin-4 controls the function of natural helper cells, a member of ILC2s, in lung inflammation. *Immunity* **40,** 758–771 (2014).

Genetic 'junk' may have its uses

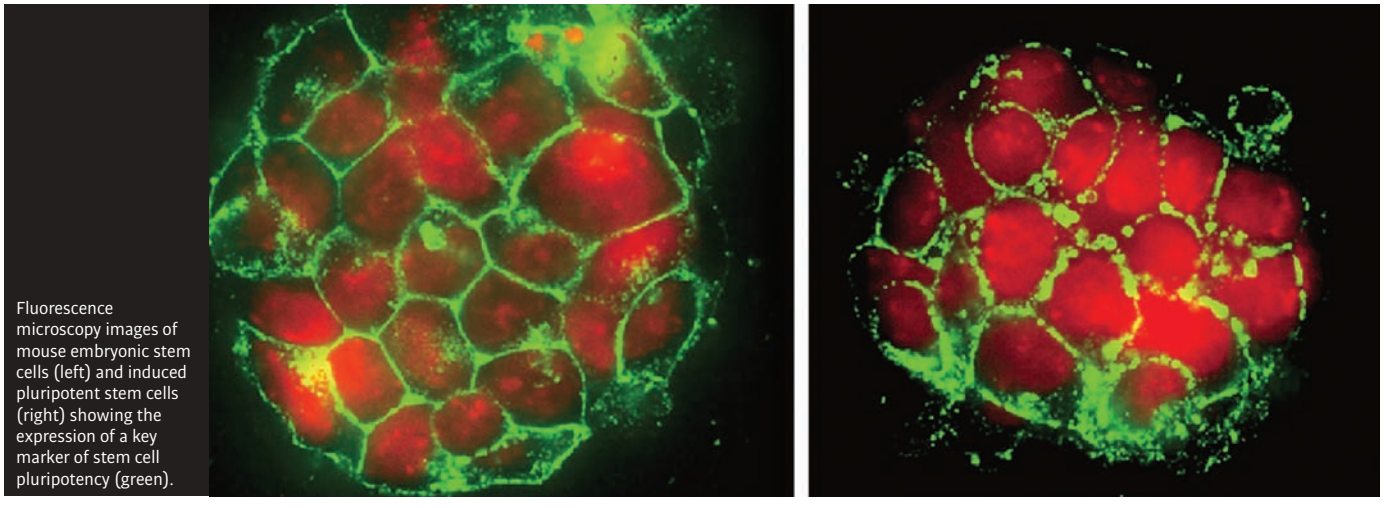
Genome filler could have an important role in maintaining stem cell potency

A fundamental process in biology is the transcription of genes into various types of RNA. Many RNAs code proteins that are essential for cell function. However, the body of transcripts, or transcriptome, of mammalian cells also contains a diversity of non-coding RNAs, many of which are derived from self-replicating DNA sequences known as retrotransposons that 'jump' around the genome. Generally considered to be genetic filler, the biological functions of retrotransposons and their transcripts, particularly in mammalian stem cells, remains largely unknown.

Piero Carninci, Alexandre Fort, Kosuke Hashimoto and colleagues from the RIKEN Center for Life Science Technologies and RIKEN Center for Integrative Medical Sciences have now led research that has revealed that a number of retrotransposon-derived transcripts are implicated in maintenance of the undifferentiated or pluripotent state of stem cells[1].

Retrotransposons can quickly make copies of themselves in the genome and are responsible for evolutionary increases in the size of the genome, as well as the introduction of genetic variations. Among the many types of retrotransposons, long terminal repeat (LTR) retrotransposons share common features with retroviruses, leading many scientists to regard them as inactive remnants of ancient viral invasions that have been incorporated into host genomes during evolution.

To better understand the non-coding part of the stem cell transcriptome, Carninci's team performed deep profiling of nuclear and cytoplasmic transcriptomes from a representative set of human and mouse stem cell lines, including embryonic and induced pluripotent stem cells, using four complementary high-throughput sequencing technologies (see image). The research team identified thousands of non-annotated transcripts—genomic sequences not annotated as transcribed (or RNA-producing) regions. By characterizing these transcripts and



Fluorescence microscopy images of mouse embryonic stem cells (left) and induced pluripotent stem cells (right) showing the expression of a key marker of stem cell pluripotency (green).

highlighting those found only in stem cells, the researchers revealed that an important fraction of these non-annotated stem transcripts (NASTs) originated in LTR retrotransposons.

Manipulation of four LTR-associated NAST candidates induced the differentiation of pluripotent iPS cells. The findings suggest that LTR retrotransposons and their transcripts are likely to be involved in the maintenance of pluripotency.

"Our work has just begun to unravel the scale of unexpected functions carried out by retrotransposons and their derived transcripts in stem cell biology," says Carninci. "We were extremely surprised to learn from our data that what were once considered genetic 'junk' are in reality symbiotic elements that work closely with other genes to maintain embryonic and induced pluripotent stem cells in their undifferentiated state. This is quite different from the image given by textbooks." ■

Reference

1. Fort, A., Hashimoto, K., Yamada, D., Salimullah, M., Keya, C. A., Saxena, A., Bonetti, A., Voineagu, I., Bertin, N., Kratz, A. *et al.* Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. *Nature Genetics* **46,** 558–566.

Steering the filaments of the developing brain

The direction of nerve fiber growth during brain development is controlled by signaling molecules that regulate the loss or addition of cell membrane at the tips of growing fibers

During brain development, nerve fibers grow and extend to form brain circuits. This growth is guided by molecular cues (see image), but exactly how these cues guide axon extension has been unclear. Takuro Tojima and colleagues from the RIKEN Brain Science Institute have now uncovered the signaling pathways responsible for turning growing nerve fibers, or axons, toward or away from guidance cues[1].

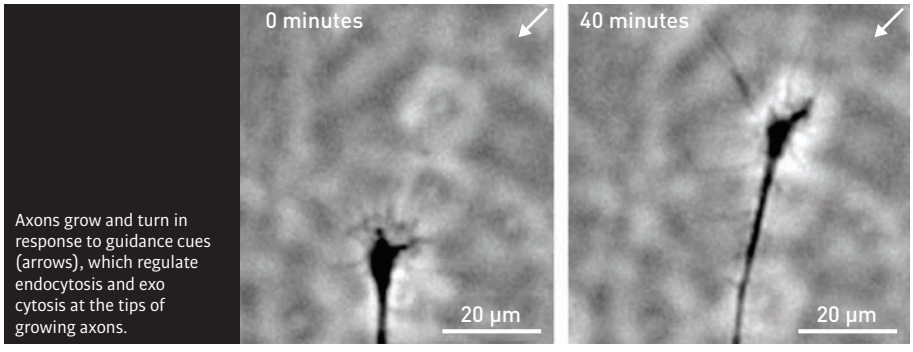
The researchers previously showed that axon-repelling cues act by inducing the removal of cell membrane—a process called endocytosis—from the side of the axon closest to the repulsive cue. The enzyme PIPKIγ90 is known to be involved in endocytosis in axons during certain types of synaptic activity, so the researchers investigated whether PIPKIγ90 also played a role in endocytosis during axon turning. By examining the developing brains of chicken embryos expressing an inactive form of PIPKIγ90, the researchers found that cues normally inducing endocytosis were no longer effective in repelling axon growth.

Cues that normally attract axons do so by driving membrane addition—exocytosis—on the side of the axon closest to the cue and also by suppressing endocytosis. Tojima's team found that axons continued to be attracted to such cues even in the absence of PIPKIγ90, suggesting that PIPKIγ90 signaling is not involved in axon attraction.

The activity of PIPKIγ90 is known to be regulated by an enzyme called CDK5, a subunit of which binds to the protein kinase CaMKII. The researchers found that by inhibiting CDK5 or CaMKII, and thereby blocking the regulation of PIPKIγ90 that is needed to suppress endocytosis, endocytosis could occur in response to attractive cues.

They also found, however, that blocking CDK5 or CaMKII did not have any effect on endocytosis if the neurons expressed a mutant version of PIPKIγ90 that was unaffected by CDK5 and CaMKII signaling. As inhibitors of CDK5 or CaMKII did not alter endocytosis in response to repulsive cues, the team's findings indicate that different signaling pathways are responsible for turning axons toward or away from guidance cues.

Additionally, Tojima and his colleagues showed that they could induce the attraction of axons toward drugs that inhibit endocytosis, suggesting that being able to control the direction of axon growth has potential therapeutic applications. "We hope our findings will aid in the development of future therapeutic strategies for rewiring neuronal networks after spinal cord injury and neurodegenerative diseases," explains Tojima. ■



Axons grow and turn in response to guidance cues (arrows), which regulate endocytosis and exo cytosis at the tips of growing axons.

Reference

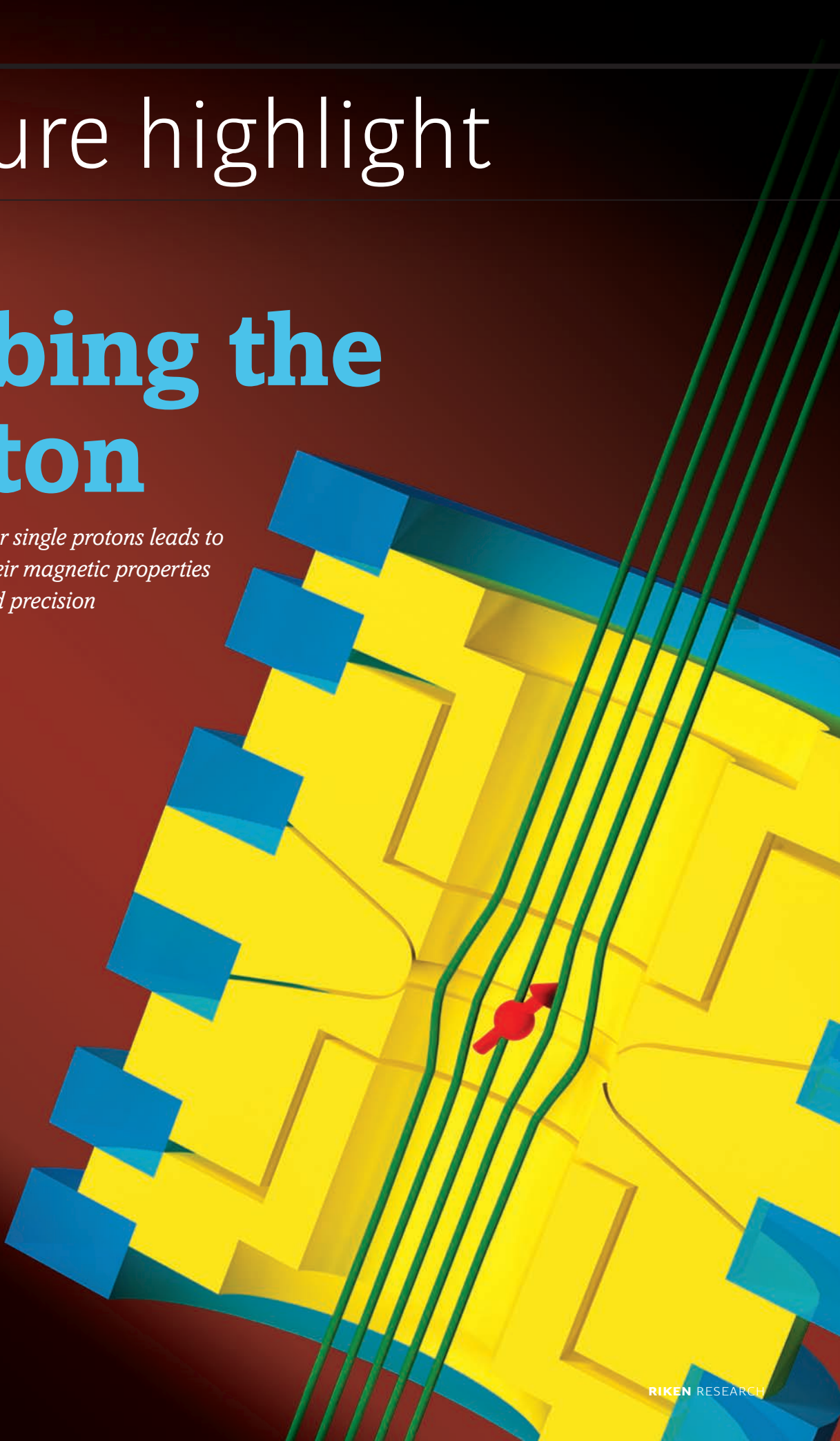
1. Tojima, T., Itofusa, R. & Kamiguchi, H. Steering neuronal growth cones by shifting the imbalance between exocytosis and endocytosis. *The Journal of Neuroscience* **34,** 7165–7178 (2014).

Feature highlight

Physics

Probing the proton

A two-stage trap for single protons leads to measurement of their magnetic properties with unprecedented precision



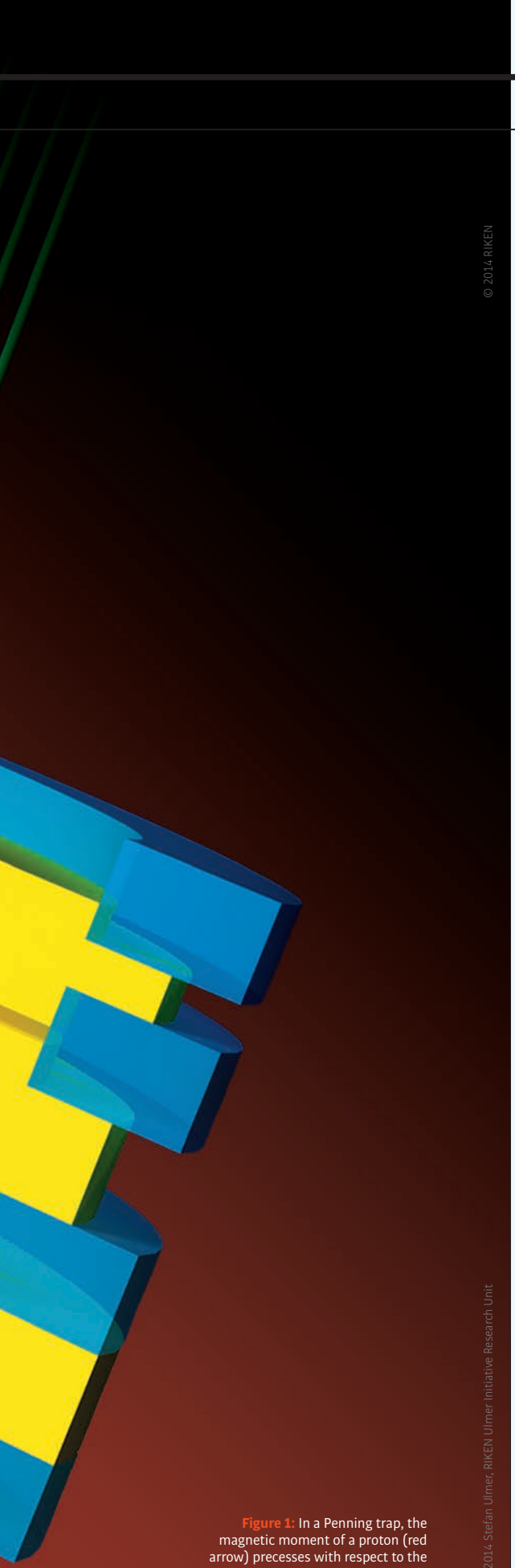


Figure 1: In a Penning trap, the magnetic moment of a proton (red arrow) precesses with respect to the magnetic field (green).

Detailed knowledge of the physical properties of the building blocks of matter is fundamental to our understanding of the Universe. These building blocks include the protons, neutrons and electrons that make up an atom, and physicists continue to strive to measure the mass, size, electric charge and magnetic properties of these subatomic particles with ever-greater precision in order to advance our understanding of the physical world.

As part of a collaboration between RIKEN and several research centers based in Germany, including the Johannes Gutenberg University Mainz, the Max Planck Institute for Nuclear Physics at Heidelberg and GSI in Darmstadt, Stefan Ulmer and colleagues from the RIKEN Ulmer Initiative Research Unit have now performed the most precise measurement of the magnetic moment of a proton to date[1].

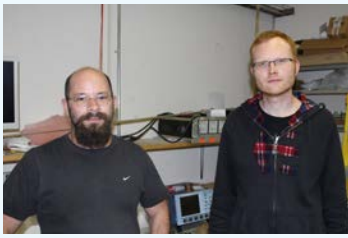
The magnetic moment of a proton defines its response to a magnetic field. The previous record for the most precise measurement of this property has stood for over 40 years. In 1972, scientists at the Massachusetts Institute of Technology in the United States investigated the microwaves emitted by hydrogen atoms under the influence of strong magnetic fields. Their experimental results, combined with theoretical corrections, made it possible to calculate the magnetic moment of the proton to an accuracy of close to ten parts in a billion.

In an attempt to surpass this record, Ulmer and his colleagues directly measured the magnetic moment of the proton using a Penning-trap technique. This approach allows individual protons to be trapped using an electric field, which creates an electrostatic well that confines the particle in one direction, while a strong magnetic field prevents it from escaping in the other direction. A single trapped proton oscillates at a characteristic frequency due to rotation, or 'precession', of the magnetic moment about an axis parallel to the magnetic field of the trap (Fig. 1). The time required to complete a single oscillation is defined by the particle's magnetic moment, mass and charge, and also the strength of the magnetic field. Measuring the frequency of the oscillation, called the cyclotron frequency, and the precession, known as the Larmor frequency, provides information about the particle's fundamental properties.

One trap or two

In Penning-trap experiments, free protons are first produced by bombarding a polyethylene target with a beam of electrons and then isolated in the trap. When sealed in an ultra-low-pressure vacuum chamber and cooled to just four degrees above absolute zero, the trap can hold a single proton for more than a year—the timeframe necessary to obtain the desired measurement precision.

Scientists have previously used Penning traps to measure the magnetic moment of electrons and



Stefan Ulmer and Andreas Mooser

Stefan Ulmer received his PhD in 2011 from Heidelberg University. He later joined a team at CERN (European Organization for Nuclear Research) as a postdoctoral fellow and contributed to the production of the first beam of antihydrogen atoms. He currently leads the RIKEN Ulmer Initiative Research Unit, and in June 2013 became the spokesperson for the Baryon Antibaryon Symmetry Experiment (BASE) collaboration at CERN, which aims to measure the magnetic moment of the antiproton with high precision. Ulmer received the 2014 IUPAP Young Scientist (Early Career) Prize in Fundamental Metrology for his efforts to measure the magnetic moments of the proton and antiproton.

Andreas Mooser studied physics at Johannes Gutenberg University Mainz (JGU) in Germany and the University of Bristol in the United Kingdom. He obtained his PhD from JGU in 2014, focusing his research on the first observation of single spin-flips of a single proton and measurement of the magnetic moment of the proton with high precision. Mooser recently joined the RIKEN Ulmer Initiative Research Unit as a postdoctoral fellow and is contributing to BASE to conduct experiments that stringently test CPT (charge, parity and time reversal) invariance.

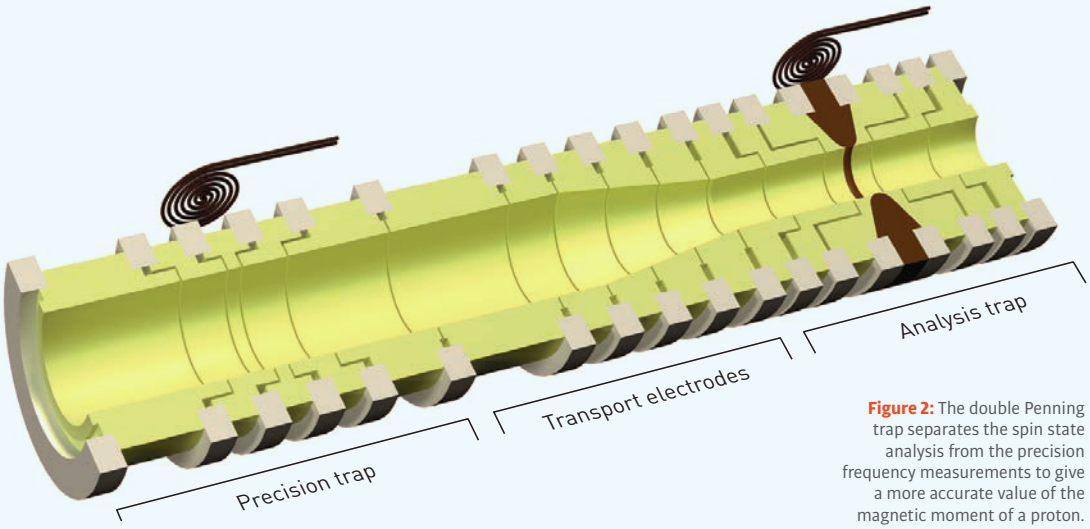


Figure 2: The double Penning trap separates the spin state analysis from the precision frequency measurements to give a more accurate value of the magnetic moment of a proton.

have achieved a precision of 3.8 parts in a trillion. The magnetic moment of a proton, however, is about 658 times smaller than that of an electron, which requires a far more sensitive experimental setup.

In the Penning trap, an aberration or 'inhomogeneity' in the longitudinal magnetic field is applied in order to couple the particle's magnetic moment —associated with its 'spin'—to its axial oscillation frequency. By measuring the resultant frequency, researchers can nondestructively detect the particle's spin state, and by taking measurements while alternately driving spin transitions with a well-characterized radiofrequency drive, they can identify the Larmor frequency. The problem with this approach, however, is that the magnetic inhomogeneity needed to make the spin-flips observable—which for protons is 2,000 times stronger than for electrons—makes it difficult to measure the oscillation frequency precisely. In fact, previous attempts to measure the proton magnetic moment using such a Penning-trap technique have resulted in poor precision of just several parts per million—far less precise than the indirect hydrogen-spectroscopy method used in 1972.

To overcome this problem, the collaborative research team built a double Penning trap (Fig. 2) consisting of an 'analysis' trap containing the magnetic inhomogeneity, and a second 'precision' trap located over four centimeters away so as to attenuate the interfering effect of the inhomogeneity. The team then fitted electrodes to shuttle the single proton between the two traps as desired. "The particle's spin state could be identified in the analysis trap, and then the particle would be shuttled to the precision trap where the cyclotron frequency could be measured and where spin-flips were driven," explains Ulmer.

A test of precision

Using the double Penning trap, Ulmer and his colleagues cycled an individual proton between the two traps several hundred times. This allowed them to measure the magnetic moment of the proton with a precision 760 times better than the 1972 result. The value of the magnetic moment they obtained was 2.792847350 times the nuclear magneton, which is a physical constant for the magnetic moment known precisely in terms of other well-defined fundamental constants. This value is in excellent agreement with the currently accepted value, known as the CODATA value, but with a higher precision of 3.3 parts per billion.

Such high-precision experiments are only valid, however, when coupled with a detailed analysis of the various sources of statistical and systematic error. These errors include the effect of the small magnetic-field inhomogeneity in the precision trap, asymmetry in the electrostatic well or the magnetic fields, as well as relativistic effects. The researchers believe that they can improve the accuracy of their measurement by a factor of ten by reducing the residual field inhomogeneity in the precision trap and by employing phase-sensitive measuring techniques. "We will next apply this technique to measuring the magnetic moment of the antiproton," says Ulmer. "This will provide a sensitive test of matter–antimatter symmetry."

Reference

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Fundamental particles such as quarks could behave very differently under the extreme conditions found at the center of stars.

A new flavor of superconductor

Powerful computer simulations show how fundamental particles can behave like electrons in a superconductor

The protons and neutrons that make up the nucleus of an atom are themselves made up of fundamental particles known as quarks. Under everyday conditions, quarks exist only in pairs or triplets called hadrons. In high-energy environments such as those at the center of neutron stars or in particle accelerators like the Large Hadron Collider, however, quarks can exist as semifree particles. Arata Yamamoto from the RIKEN Nishina Center for Accelerator-Based Science has now used supercomputer simulations to show that quarks can behave like electrons in a superconductor[1].

The existence of quarks in a semifree state under extreme conditions raises the fascinating question of whether quarks can behave like other free particles such as electrons. Electrons have a property called spin, which can be oriented either up or down. In some materials and at low temperatures, electrons with opposite spin and opposite momentum form interacting pairs called Cooper pairs, which are responsible for superconductivity. Quarks, on the other hand, are characterized by their 'flavor', which can take one of six values: up, down, charm, strange, top and bottom. Protons, for example, consist of two up quarks and a down quark.

Yamamoto investigated whether the pairing of an up and a down quark, which together form a hadron called a pion, could exhibit similar behavior to a Cooper pair. "I used computer simulations to investigate superconductivity in hadron physics," says Yamamoto.

The interaction between quarks is described by a complex theory known as quantum chromodynamics (QCD). Yamamoto performed the computationally intensive QCD simulations using the RIKEN Integrated Cluster of Clusters facility—a supercomputer comprising multiple computer clusters connected by a high-speed network.

Yamamoto started by investigating a system with a balanced number of up and down quarks, as quantified by the chemical potential, or the energy of the most excited particle in a system. The results showed that when the chemical potentials of the up and down quarks are equal in magnitude, the pions all exist in the same energy state. This 'condensate' state is a signature of a superconductor. When the chemical potentials of the two quarks were

brought out of balance, however, the condensate state disappeared. The results demonstrate that, similar to electrons, quarks can form Cooper-like pairs under certain conditions.

"This is the first implementation of such a model with a population imbalance between flavors," explains Yamamoto. "The next step is to use this same approach to see if inhomogeneity and superconductivity can exist simultaneously." ■

Reference

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Higgs versus the Big Bang

The Higgs boson, which gives elementary particles mass, could also explain the earliest expansion of the Universe

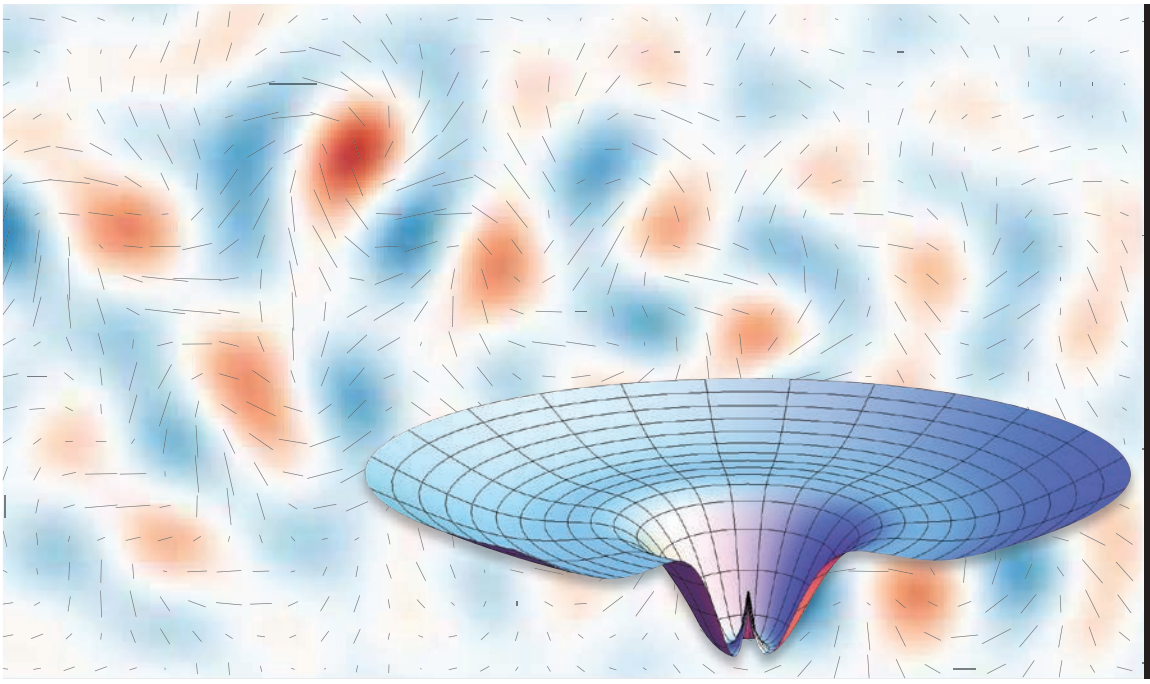
Fedor Bezrukov from the RIKEN–BNL Research Center and Mikhail Shaposhnikov from the Swiss Federal Institute of Technology in Lausanne propose that the Higgs boson, which was recently confirmed to be the origin of mass, may also be responsible for the mode of inflation and shape of the Universe shortly after the Big Bang[1]. "There is an intriguing connection between the world explored in particle accelerators today and the earliest moments of the existence of the Universe," explains Bezrukov.

The Universe started with a giant explosion known as the Big Bang, and has been expanding ever since. The expansion is balanced such that its shape is flat and not bent, which can only be the case for a very specific distribution of matter density.

The coupling between the Higgs boson and other fundamental particles provides mass. In the first moments of the Universe, however, coupling between the Higgs field and gravity accelerated the Universe's expansion. An important parameter for this coupling is the mass of the Higgs boson. Experiments at the Large Hadron Collider at CERN (European Organization for Nuclear Research) have shown that the mass of the Higgs boson is very close to a critical value that separates two possible types of Universe—the stable one we know or a potentially unstable alternate.

Bezrukov and Shaposhnikov have now studied the implications arising from the Higgs mass being near this critical boundary and the impact this has on cosmological inflation. Through theoretical arguments, they found that as the mass of the Higgs approaches the critical value, gravitational waves from the Big Bang become strongly enhanced. The Big Bang is thought to have created many gravitational waves, which act like ripples in space and time, and it is these waves that are amplified for a Higgs of near-critical mass.

Experimentally, the influence of the Higgs boson could have significant implications for the observation of gravitational waves, which had eluded physicists until recently, when analysis of data acquired by the BICEP2



The influence of the Higgs boson and its field (inset) on cosmological inflation could manifest in the observation of gravitational waves by the BICEP2 telescope (background).

telescope near the South Pole suggested the first signs of gravitational waves in the cosmic microwave background that fills the Universe (see image).

The BICEP2 result, however, is far from unequivocal, with continued debate as to whether the incredibly faint signal of gravitational waves could really be detected in this way. The effects of a near-critical Higgs mass could put such debate to rest. "The Higgs mass at the critical boundary could explain the BICEP2 result," Bezrukov explains. ■

Reference

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A stellar odd couple that takes it slow

An x-ray investigation of a slowly rotating neutron star paired with a red-giant star reveals properties that conflict with existing theory

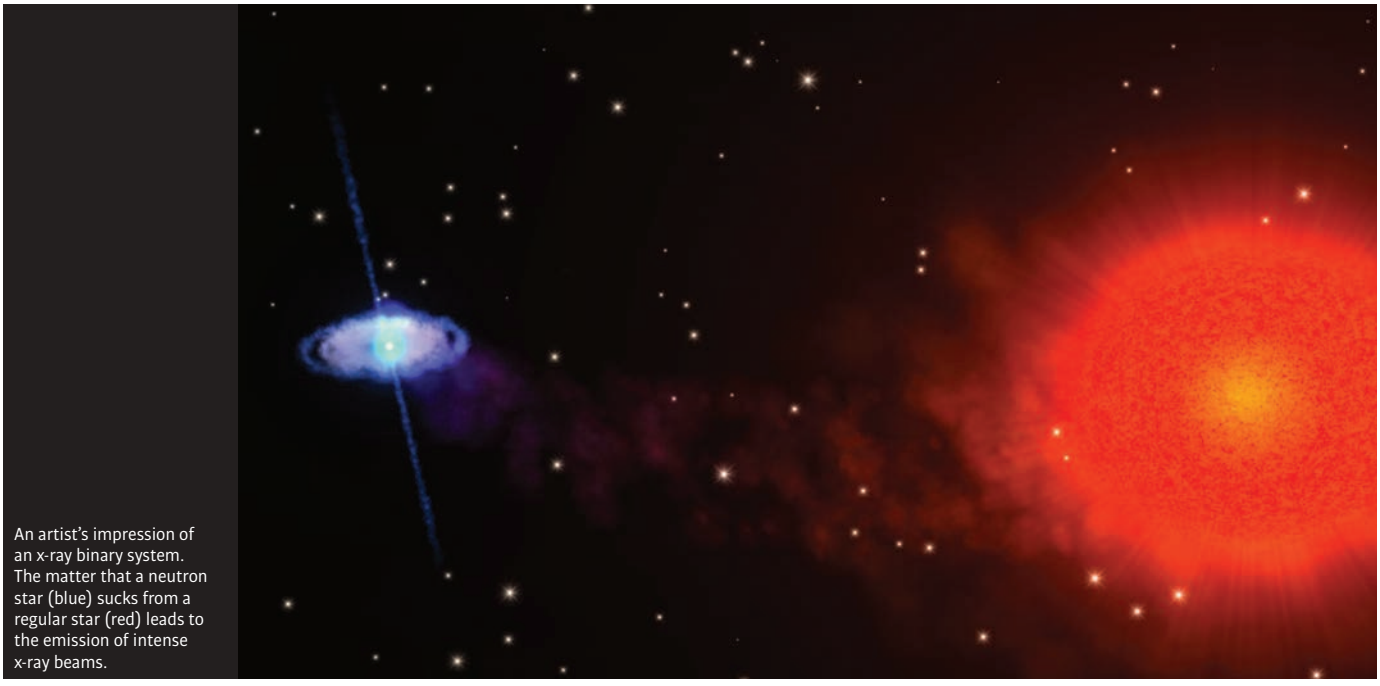
Neutron stars are amongst the most exotic astrophysical objects in the Universe. Born from the supernova explosion of massive stars, neutron stars are so densely compacted by their own gravity that a sphere just 20 kilometers in diameter has more mass than our Sun. In rare circumstances, neutron stars can become paired with regular stars to form 'binaries' that emit intense pulses of x-rays (see image).

Teruaki Enoto and colleagues from the High Energy Astrophysics Laboratory at the RIKEN Nishina Center for Accelerator-Based Science have led research that has now uncovered properties of a rare symbiotic x-ray binary (SyXB) that challenge our understanding of these extraordinary astronomical objects[1].

In the recently discovered SyXB class of binaries, the neutron star is paired with an M-type red giant with a similar mass to our Sun. As with all binaries, the influence of the red giant leads to periodic intensity changes and complex patterns in the wavelength of the x-rays emitted from the neutron star.

Enoto's team, in collaboration with co-workers from institutions in Japan, the United States and Germany, studied an SyXB with the slowest known rotating neutron star, a system known as 4U 1954+319. Whereas neutron stars usually have rotation periods of hundreds of seconds or shorter, the 4U 1954+319 system is unusual in that the rotation period of the neutron star is about 5.4 hours.

As the small size of neutron stars makes them impossible to study using telescopes, scientists have to extract information from the x-rays that they emit. In the case of 4U 1954+319, the powerful instruments on the Japanese satellite Suzaku made it possible to study the x-ray emissions over a wide energy band. Computer modeling of the data



An artist's impression of an x-ray binary system. The matter that a neutron star (blue) sucks from a regular star (red) leads to the emission of intense x-ray beams.

Image courtesy of NASA

revealed that the magnetic field around the neutron star is very strong in comparison to other neutron stars, but at the same time not as intense as assumed to explain some of its features based on conventional theories. Amongst other seemingly contradictory properties, this places SyXB into a binary-star category of its own.

"In our galaxy, nearly 2,000 neutron stars have been discovered and have revealed a large variety of types, whose diversity, evolution and physical behavior remains poorly understood," comments Enoto. The results therefore unearth new questions on the birth and evolution of systems such as 4U 1954+319. "For example," says Enoto, "why does such a high-magnetic-field neutron star exist with a comparatively old star as a companion?" ■

Reference

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Measuring a magnetic halo

Precise data on the magnetic interaction between the nucleus and electrons in beryllium-11 could help to pin down its unusual nuclear shape

Atomic nuclei come in a range of shapes and sizes, from spherical to pear-shaped, and many behave as if they were blobs of an incompressible fluid. A few nuclei are different—beryllium-11, for example, has an inner core of protons and neutrons with an outer 'halo' neutron, which makes the effective nuclear radius of this isotope much larger than predicted by simple models.

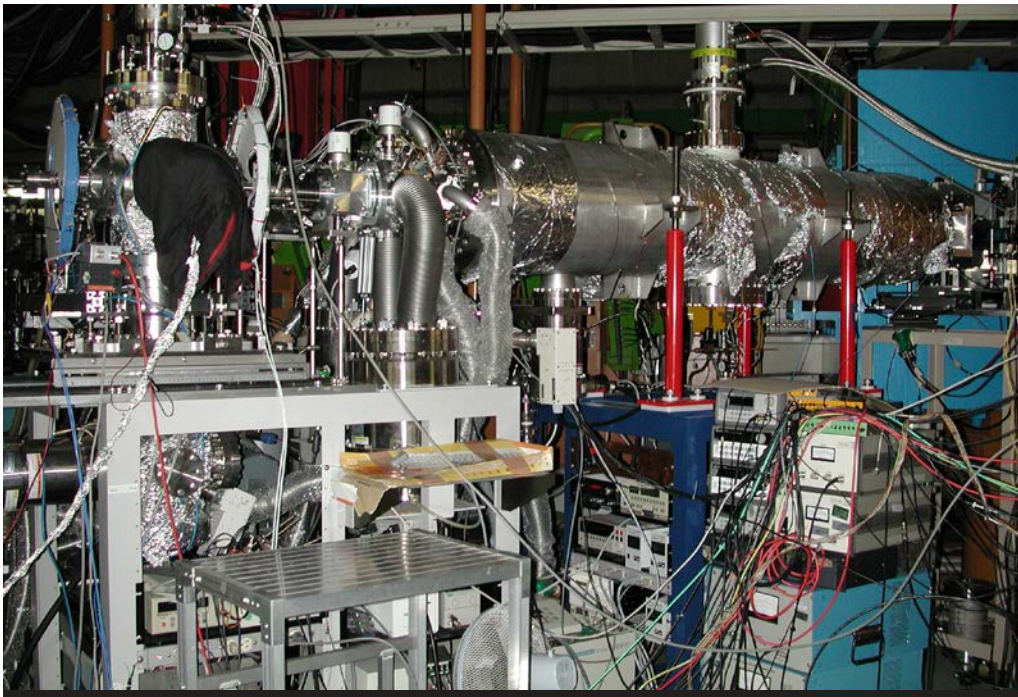
A team led by Michiharu Wada at the RIKEN Nishina Center for Accelerator-Based Science has now made some high-precision measurements that could help determine the magnetic radius of the beryllium-11 nucleus[1].

The characteristic spectrum of light frequencies absorbed and emitted by an atom is shaped by electromagnetic interactions between its nucleus and electrons. Each frequency can consist of a double signal, known as a splitting or hyperfine structure, stemming from the way that the electron energies are populated. The gap between these hyperfine energy levels is influenced by the magnetization distribution of the nucleus—a phenomenon called the Bohr–Weisskopf effect. "The magnetization of beryllium-11 is mainly carried by the single halo neutron," says Wada. "If the halo neutron has an extended distribution, the Bohr–Weisskopf effect should be large."

Using the prototype slow radioactive nuclear ion beam facility (SLOWRI) (see image), the researchers bombarded a beryllium-9 target with a beam of carbon-13 atoms to create high-energy beryllium-11 ions. These were cooled and trapped in batches of about 110 ions, which have a half-life of less than 14 seconds.

The team then irradiated the trapped beryllium-11 ions with laser light at a slightly lower energy than the ions' resonant wavelength, which caused them to emit millions of photons per second, and then cooled them to temperatures very near absolute zero. Exposure to microwave radiation then induced transitions between different hyperfine energy levels, drastically changing the intensity of the observed fluorescence. From this change, the researchers could determine the hyperfine transition energy.

The data yielded the most precise measurements obtained to date for the magnetic hyperfine structure constant for beryllium-11. This constant quantifies the interaction energy between the nuclear magnetization and the electrons. To calculate the Bohr–Weisskopf effect itself, Wada's team now needs to measure the magnetic moment of the nucleus with comparable precision.



The prototype slow radioactive nuclear ion beam facility (SLOWRI) can create, cool and trap ions of short-lived ions such as beryllium-11.

"We tested such measurements for stable beryllium-9 isotopes many years ago, but experiments on unstable isotopes such as beryllium-11 are totally different," says Wada. Further work on SLOWRI will enable the precision spectroscopy needed to make the crucial measurements on beryllium-11 and many other nuclei. ■

Reference

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A solitary superconductor emerges under pressure

The first single-component molecular superconductor yields new insights into the principles behind perfectly efficient electrical transport

Three decades ago, researchers discovered that certain organic molecules become superconducting at low temperatures. This finding sparked numerous investigations into the properties of these lightweight, low-cost and easy-to-modify materials. Despite much recent progress, chemists remain puzzled by one aspect of these compounds: all known molecular superconductors need the cooperative action of two or more different molecular species to move electrons without resistance.

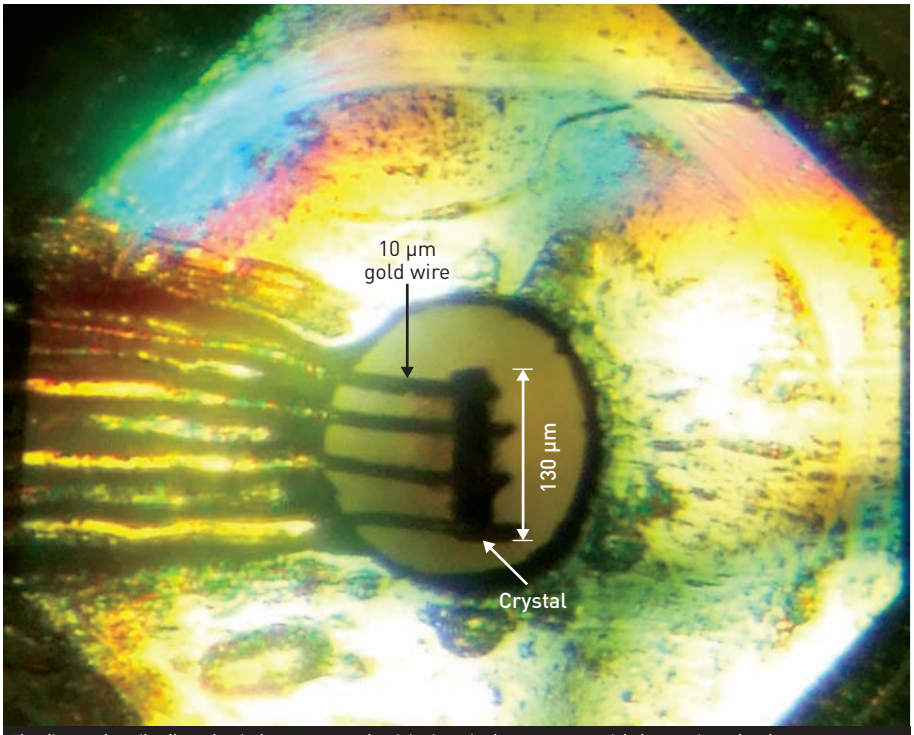
HengBo Cui and Reizo Kato from the RIKEN Condensed Molecular Materials Laboratory, in collaboration with Hayao Kobayashi and Akiko Kobayashi from Nihon University, have now realized a crucial goal in the search for metal-like organic molecules by uncovering the first molecular superconductor containing only one component[1].

Superconducting organic crystals are designed around the principle of charge-transfer complexes, where strong interactions between distinct 'donor' and 'acceptor' components move electrons through normally insulating carbon bonds. By squeezing the charge-transfer structures together using diamond anvil cells—tools that allow crystals to be compressed at pressures of up to millions of atmospheres—resistance-free electrical transport can occur at temperatures near absolute zero.

The electron donors and acceptors in molecular superconductors are normally individual ionic compounds. However, Kobayashi's team has recently spearheaded investigations into metal–dithiolate complexes that contain a complete charge-transfer system in a single molecule. These crystals, in which a central gold or nickel acceptor atom is flanked on two sides by extended aromatic donor rings infused with sulfur atoms, have a high intrinsic conductivity and exhibit metallic behavior at low temperatures.

The researchers partnered with Masaaki Sasa from Fujitsu to explore numerous metal–dithiolate synthetic derivatives. They eventually found a promising compound, nickel bis(trifluoromethyl) tetrathiafulvalenedithiolate ($Ni(hfdt)_2$). This molecule has bulky fluorinated end-groups on its dithiolate rings that trigger two-dimensional layer stacking in the crystal state—a highly favorable arrangement for metal-like conductivity.

After carefully manipulating the tiny, submillimeter-sized $Ni(hfdt)_2$ crystals into their diamond anvil cell device (see image),



The diamond anvil cell used to induce superconductivity in a single-component nickel–organic molecule.

Cui measured how its electrical behavior changed with pressure and temperature. At a pressure of about 8.1 gigapascals, he found that the resistivity suddenly plunged to zero at a temperature of 5.5 kelvin—clear evidence that they had discovered a single-component molecular superconductor. High-level theoretical calculations confirmed these experimental findings by revealing the critical point at which pressure converts $Ni(hfdt)_2$ from an insulator to a superconductor.

"This simple, single-component compound not only has the potential to bring about breakthroughs in organic solid-state devices, but will also help in the design of new superconducting systems," says Cui. ■

Reference

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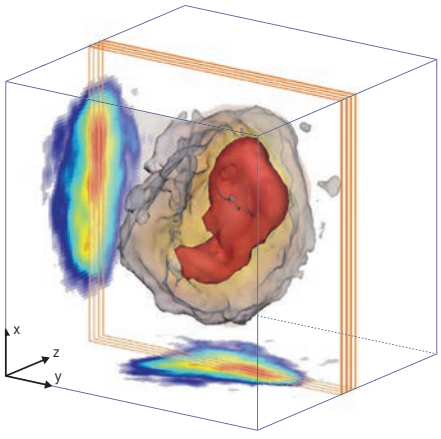
X-ray imaging reveals a complex core

A novel structural analysis scheme using multiple x-ray techniques probes the internal three-dimensional structure of macromolecular complexes

Macromolecular complexes composed of self-assembling proteins and nucleic acids hold promise for a wide range of applications, including drug delivery, sensing and molecular electronics. Scientists have developed a broad array of x-ray scattering techniques for characterizing the shape and surface morphology of these complexes, but probing their internal structure remains a challenge.

Changyong Song and colleagues from the RIKEN SPring-8 Center and RIKEN Advanced Institute for Computational Science have now devised a structural analysis scheme based on complementary advanced x-ray techniques that has allowed them to peer inside an RNA macromolecular complex for the first time[1].



The complete three-dimensional structure of an RNA interference (RNAi) microsponge.

Although knowledge of their shape and morphology is useful, it is the internal structure of macromolecular complexes that holds the secret to their formation and disassembly. RNA interference (RNAi) microsponges, for example, are self-assembled from small interfering RNA molecules to form macromolecular complexes that are capable of silencing gene expression.

The researchers set out to explore the internal structure of RNAi microsponges using a combination of x-ray techniques at the SPring-8 synchrotron radiation facility. They first performed nondestructive diffraction imaging experiments using a coherent x-ray beam. The experiments yielded high-resolution diffraction patterns that the researchers used to reconstruct projection images of RNAi microsponges (see image). The results suggest that all RNAi microsponges have a high-density core that occupies approximately 15 per cent of the projected area.

The team then performed single-shot imaging experiments using femtosecond x-ray pulses produced by the SACLA x-ray free electron laser (XFEL) facility at SPring-8. The use of intense, extremely short x-ray pulses helped compensate for the weak scattering from the RNAi microsponges. The studies revealed that irrespective of their size, all of the microsponges shared almost the same electron density distribution, suggesting that the high-density core evolves gradually through a dynamic compaction of RNA strands.

Finally, the researchers conducted small-angle scattering experiments using the XFEL. The results further confirmed that the core–shell structure is a generic feature of RNAi microsponges.

The x-ray structural analysis scheme is nondestructive, providing deeper penetration into target materials and enhanced resolution limited only by the wavelength of x-rays used. The scheme is also highly versatile because, unlike many other analysis schemes, no prior information about the sample is required to complete the structural analysis.

"X-ray diffraction is a versatile technique for understanding atomic structures, and with XFELs the technique has become even more dexterous," says Song. "Multimodal imaging combining both the SPring-8 and SACLA facilities now provides a route to the atomic world." ■

Reference

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Hitoshi Sakakibara and colleagues at the RIKEN Center for Sustainable Resource Science are studying a wild-rice cultivar, which grows vigorously and produces high biomass, to improve agricultural productivity.

Sustainable resource science

Cultivating a renewable future

As humanity's material needs continue to grow, developing smarter strategies for making efficient use of available resources is becoming ever more critical. Scientists at RIKEN are drawing on lessons from natural and artificial systems to maximize agricultural productivity, remove harmful pollutants from the environment and create new 'green' materials and manufacturing processes.

Kazuo Shinozaki is director of the RIKEN Center for Sustainable Resource Science
Since joining RIKEN as a chief scientist in 1989, Shinozaki has conducted research into molecular biology and functional genomics, with specific emphasis on plant response and tolerance to environmental stresses. More recently, his interests have also focused on the application of basic research for the sustainable production of food, biomass and energy.

Our society enjoys steadily improving technological capabilities and quality of life, but these advances could come at a severe cost unless we plan for the well-being and security of future generations. We now recognize the dangers associated with unfettered use of fossil fuels such as coal and oil, which have powered civilization for nearly two centuries. Scientists have gathered powerful evidence that atmospheric accumulation of waste products from fossil fuel consumption—most notably carbon dioxide—is actively driving climate change. Although the full consequences of this shift remain to be seen, indicators such as abnormal weather patterns and accelerating polar ice melt demonstrate the seriousness of our situation.

In parallel with these climatic risks, the demands of a steadily growing population threaten to exceed the finite supply of raw materials. Ensuring food security must be a priority; this will require developing crops with improved productivity that are suited to a changing global environment. Food, however, is not the only limited resource. Businesses and households depend on goods manufactured from plastics and metals—often produced in ways that are inefficient, environmentally destructive or dependent on scarce materials.

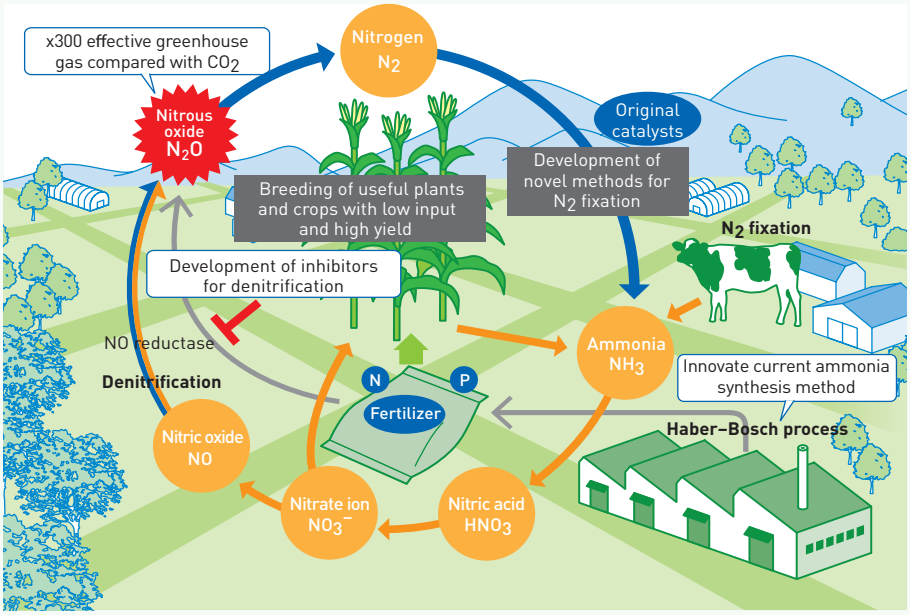


Figure 1: Researchers involved in the interdisciplinary Nitrogen Project at the RIKEN Center for Sustainable Resource Science are improving methods for efficient fertilizer production, developing techniques to reduce nitrous oxide emissions and breeding low-input, high-productivity plants and crops that can tolerate environmental stresses.

Productive plants, clever chemicals

Given these many challenges, sustainable resource science must be a top research priority in the years ahead. The goal of this field is to develop technologies that will enable society to progress on a foundation of maximized efficiency and reusability, so that communities and economies will continue to flourish while the environment is protected.

Scientists at RIKEN have been actively engaged in solving these problems for years. Since 2000, the RIKEN Plant Science Center (PSC) in Yokohama, which recently became integrated into the RIKEN Center for Sustainable Resource Science (CSRS), has explored the molecular foundations of plant physiology.

Every plant produces a diverse set of chemical compounds, known collectively as its 'metabolome', which contributes to development, disease resistance and other essential processes. The composition of the metabolome is determined both by instructions encoded within the genome and in response to shifting environmental circumstances.

Initially, the PSC focused on understanding genomic features that contribute to growth and survival in different conditions, as well as the chemical compounds that act as intermediaries. Subsequent efforts focused on identifying strategies to manipulate the genome and metabolome of key crops to maximize their durability and productivity, even in adverse conditions such as drought or extreme heat.

These discoveries demonstrated the potential of harnessing the innate adaptability of nature to build more robust agricultural systems. Importantly, they also raised the intriguing possibility that insights from plant biology could address other challenges in sustainability, including environmental remediation and ecofriendly manufacturing.

Exploring these avenues of research requires a broad interdisciplinary effort. For this reason, in 2013, key scientists from the RIKEN Advanced Science Institute joined researchers from the PSC to form the CSRS. Together they are pursuing a singular mission of 'green innovation' through the careful modification of biological systems and the construction of novel materials that could benefit agriculture, energy production and the manufacturing industry.

The valuable expertise in chemistry, chemical biology and materials science that the Advanced Science Institute brings to the collaboration promises to dramatically accelerate the molecular-scale dissection and engineering of biological processes. Over the past five years, these researchers have developed sophisticated metal catalysts that can be used to accelerate useful chemical reactions and have accumulated a wealth of knowledge about the intersection between chemistry and biology. Among their many other achievements, scientists at the institute have also built a massive collection of naturally occurring, biologically active molecules known as the 'Natural Products Depository'.

The big picture

Within the CSRS, every laboratory pursues a 'core' research program while also collaborating on three broader interdisciplinary initiatives. Each initiative revolves around a different aspect of sustainable resource production, encompassing research challenges too great for any one field to tackle alone.

The first initiative centers on carbon management. During photosynthesis,

plants use biochemical reactions powered by light to incorporate water and carbon dioxide into their living structure. Given that carbon dioxide is also a primary waste product of burning fossil fuels, one could envision manipulating the photosynthetic machinery to accelerate the removal of this greenhouse gas from the atmosphere.

In parallel, chemists and materials scientists are seeking compounds that could act as synthetic catalysts to help pluck carbon dioxide out of the atmosphere. The ultimate goal would be to use the carbon recovered in either scenario as a resource to be 'recycled' into more useful materials.

Nitrogen management is the second initiative. Plants require nitrogen but cannot obtain it directly from the atmosphere; instead, they make use of nitrogen that has been chemically 'fixed' into ammonia within the soil (Fig. 1). Naturally occurring ammonia is insufficient to support large-scale agriculture, so farmers rely on ammonia manufactured via the Haber–Bosch process. This technique requires high temperatures and pressures and consumes a considerable amount of fossil fuel. Potential ways to mitigate the use of this nitrogen source include engineering crop variants that require less fertilizer or novel chemical catalysts that reduce—or even eliminate—the need for fossil fuels in ammonia production.

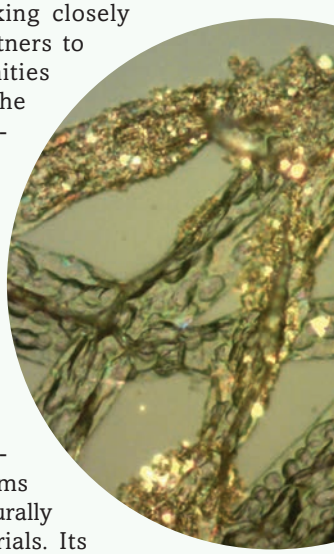
Many of the metals most valuable to industry are also the rarest, and Japan in particular suffers from limited mineral resources. The third initiative of the CSRS is therefore to develop innovative strategies for overcoming this scarcity. One possibility is replacement; for example, hydrogen fuel cells depend on costly platinum or palladium catalysts and alternatives based on more abundant materials could help make this 'green' power source more widely available.

Many roads to sustainability

CSRS scientists have already made important early strides in these areas. Zhaomin Hou and colleagues, for example, recently developed a titanium-based catalyst that can convert nitrogen into ammonia at room temperature[1] (Fig. 2, left). Meanwhile, the biodiversity found in nature is providing RIKEN scientists with a valuable arsenal of tools. Researchers led by Hitoshi Sakakibara have learned a great deal about how the chemical structure of plant hormones contributes to their ability to promote shoot growth[2]—knowledge that could be exploited to improve crop productivity. Sakakibara and his colleagues are also working with mosses that possess an innate capacity to absorb gold and lead, a promising natural solution for recovering mineral resources or improving the health of soil and water supplies (Fig. 2, right).

These are only starting points, and the CSRS is actively developing technologies that can accelerate the dissection and manipulation of biological systems. A robust 'metabolomics platform' previously developed by scientists at the PSC can accurately measure quantities of various chemical components from a particular plant or microbe, and it has already proved invaluable as a discovery tool. The platform can be combined with the Natural Products Depository to explore how different compounds affect the metabolic activity of organisms, a key step towards modifying existing biological processes or even engineering entirely new ones.

The discoveries made by these research programs will have value only if they can be rapidly disseminated. For this reason, the CSRS is working closely with industry partners to identify opportunities for accelerating the commercial development of sustainably derived resources. The center's Biomass Engineering Program offers a model for such collaboration. The goal of this program is to devise bioengineered systems for producing naturally synthesized materials. Its scientists are currently working closely with the Japanese manufacturer Kaneka Corporation to develop improved biopolymers that can be assembled into plastics suitable for a wide range of applications.



This pragmatic approach, focused on existing needs and clear-cut contemporary problems, will maximize the immediate impact of the center's sustainability research efforts. The challenges are great, but so is the reward: a society whose present needs can be comfortably and affordably fulfilled, without jeopardizing the well-being of our descendants or our environment.

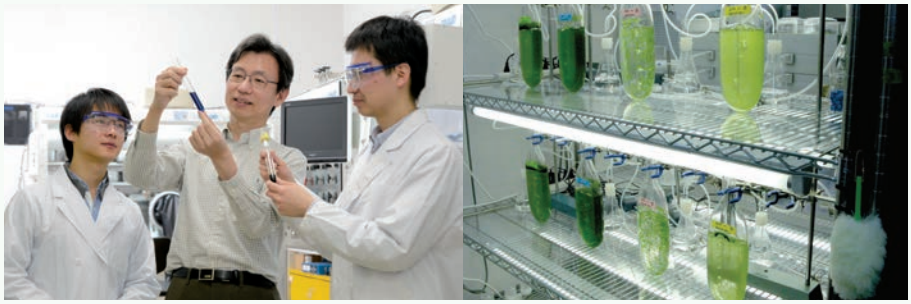


Figure 2: New catalysts developed by Zhaomin Hou can convert nitrogen into ammonia at room temperature (left). Meanwhile, Hitoshi Sakakibara is working with the moss *Funaria hygrometrica*, which absorbs gold and lead (flasks: right; and microscope image: top right), enabling the recovery of heavy metals from the environment.

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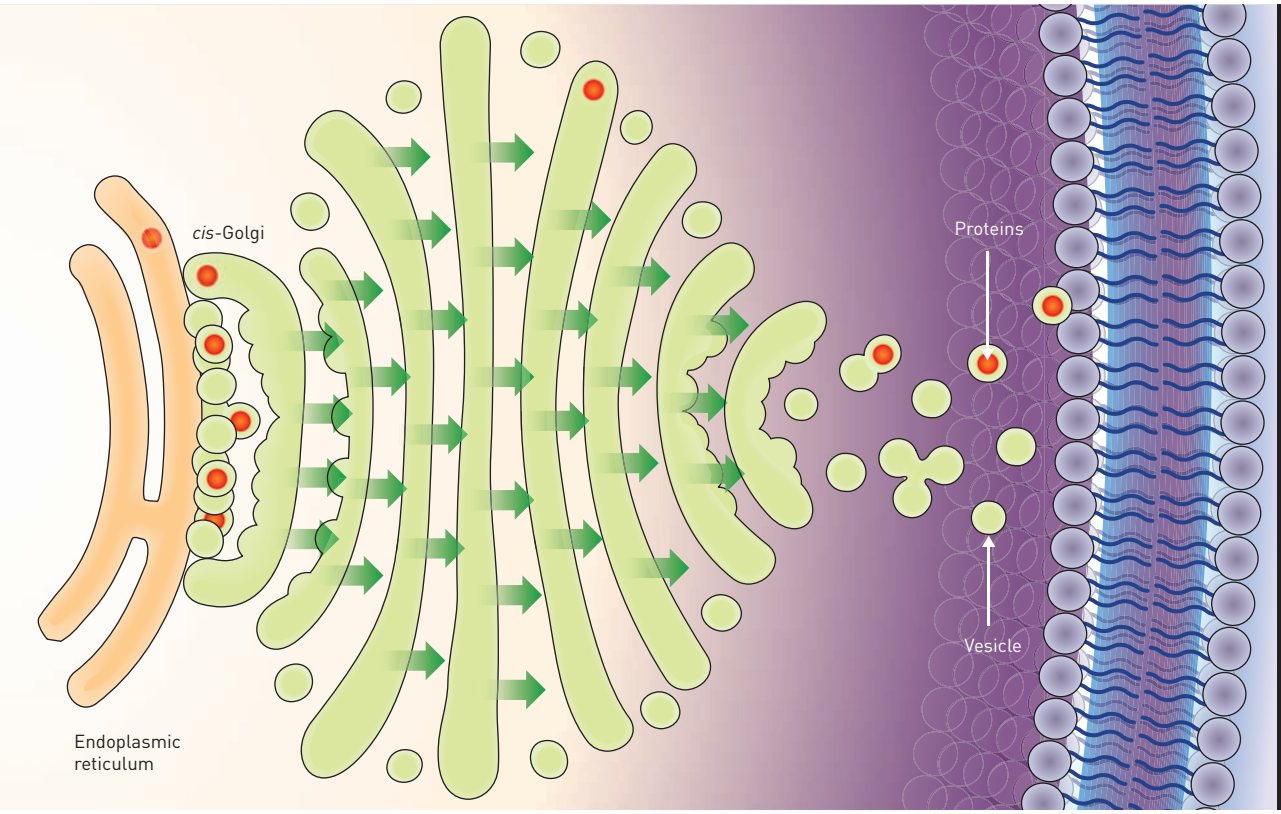

Whereas transport of proteins from the endoplasmic reticulum (ER) was previously thought to occur by the release of vesicles from the ER, new observations suggest that the *cis*-Golgi extends to make contact with the ER to capture newly produced vesicles.

Protein transport by 'hug-and-kiss'

The first direct observation of a key molecular transport mechanism in cells challenges previous models of the process

Eukaryotic cells contain a number of compartments, each surrounded by a membrane that water-soluble molecules are unable to cross. This means that dedicated transport mechanisms are needed to move molecules such as proteins between compartments. Kazuo Kurokawa and colleagues from the Live Cell Molecular Imaging Research Team at the RIKEN Center for Advanced Photonics have now revealed a previously unknown mechanism that facilitates one crucial transport step[1].

About one third of all proteins are manufactured in a cellular compartment called the endoplasmic reticulum (ER). From the ER, they are passed to the Golgi apparatus—a series of membrane-bound compartments through which proteins pass as they are sorted for delivery to their final location in the cell. The entry point for proteins into the Golgi is called the *cis*-Golgi, and Kurokawa's work focused on the mechanism that transports proteins to this location from the ER.

Researchers previously assumed that the mechanism involved the release of small sacs or 'vesicles' containing the proteins from the ER. These vesicles diffuse across the gap to fuse with the *cis*-Golgi membrane and release the proteins inside. However, this mechanism includes no way to ensure that the vesicles reach the *cis*-Golgi efficiently. Furthermore, some proteins are too big to be packaged into normal vesicles, and the existence of so-far unobserved, oversized vesicles has been proposed to facilitate their transportation.

Kurokawa's team looked in more detail at this transport step in yeast cells. They fluorescently labeled a structural protein of vesicles called COPII at release sites in the ER, as well as proteins in the *cis*-Golgi membrane. Sophisticated microscopy techniques then allowed them to watch the transport process directly.

"Our microscope system has extremely high speed and high resolution," explains Kurokawa. "The images collected contain a massive amount of precise information, which makes it possible to use mathematical processing to localize fluorescence sources with very high accuracy."

The team found that vesicles were not released from the ER. Instead, the *cis*-Golgi membrane extended to come into direct

contact with vesicles while still on the ER—a process the researchers called 'hug-and-kiss' (see image). Their experiments showed that the newly manufactured proteins are passed between the compartments during this contact.

"Our findings suggest that vesicles are not necessarily released, but are instead captured by the *cis*-Golgi before release," explains Kurokawa. "This mechanism appears to be much safer than forming many free vesicles. If our proposed mechanism is correct, the release of oversized vesicles containing large proteins may not be needed."

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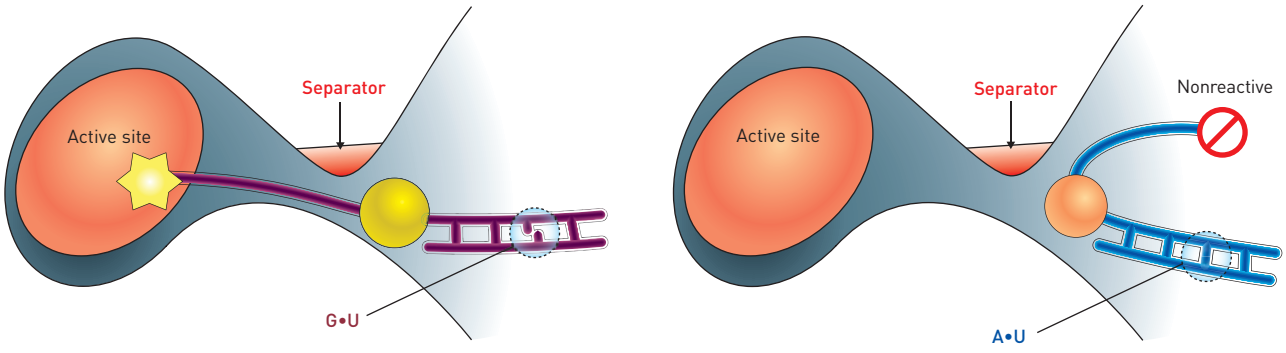
Deflecting protein production

Insights into the mechanistic details of protein synthesis could inform efforts to manipulate the genetic code

The recipe for any given protein is written out as a series of 'codons', each of which encodes a particular amino acid. These amino acids are delivered via transfer RNA (tRNA) molecules, which feature an 'anticodon' element that recognizes a particular codon. For this system to function properly, every tRNA must be linked to the correct amino acid—a process that is mediated by a family of enzymes called aminoacyl-tRNA synthetases. A research team led by Shigeyuki Yokoyama from the RIKEN Structural Biology Laboratory and Paul Schimmel of The Scripps Research Institute in the United States has now learned how one such enzyme achieves such selective coupling[1].

Decades ago, Schimmel discovered a single base pair within the tRNA associated with the amino acid alanine ($tRNA^{Ala}$) that serves as an 'identity set' critical for recognition and processing by its associated aminoacyl-tRNA synthetase enzyme. Strangely, this base pair resides far from the active site of the enzyme that actually attaches alanine to the tRNA. "It was a complete mystery how these nucleotides indirectly affect the active site of the enzyme," says Yokoyama. "Furthermore, it seemed almost impossible that a tRNA could depend so strictly on a single base-pair interaction."

Yokoyama therefore set about analyzing the structure of complexes formed by two different versions of $tRNA^{Ala}$ and its aminoacyl-tRNA synthetase. In general, the nucleobase adenine preferentially pairs with the nucleobase uracil. However, the $tRNA^{Ala}$ identity set consists of a less common 'wobble pairing' between the nucleobases uracil and guanine. The introduction of a mutation that changed this naturally occurring guanine–uracil pairing to adenine–uracil had subtle but important consequences. The nucleobases in each pairing bind with different geometries, and the mutation introduces a curvature in the tRNA structure (see image). The curvature deflects the acceptor region of the tRNA away from the active site of the enzyme such that the nucleotides that would normally be joined to alanine are instead physically masked by a 'separator' segment of the enzyme. This single mutation



In the naturally occurring guanine–uracil 'identity set' pairing (left), the tRNA acceptor region (yellow) is properly positioned at the enzyme's active site for chemical modification with the amino acid alanine. In the adenine–uracil mutant (right), the tRNA is deflected away from the active site and alanine addition is blocked.

was sufficient to dramatically reduce the efficiency of this enzyme-mediated reaction.

Yokoyama's group is actively engaged in manipulating the interactions between tRNAs and synthetase enzymes as a means of producing proteins that incorporate novel amino acids with distinctive functional properties, and Yokoyama now hopes to learn whether similar principles apply in other tRNA–aminoacyl-tRNA synthetase pairings. "These findings could open the door for dramatic developments in the expansion of the genetic code," he says.

Reference

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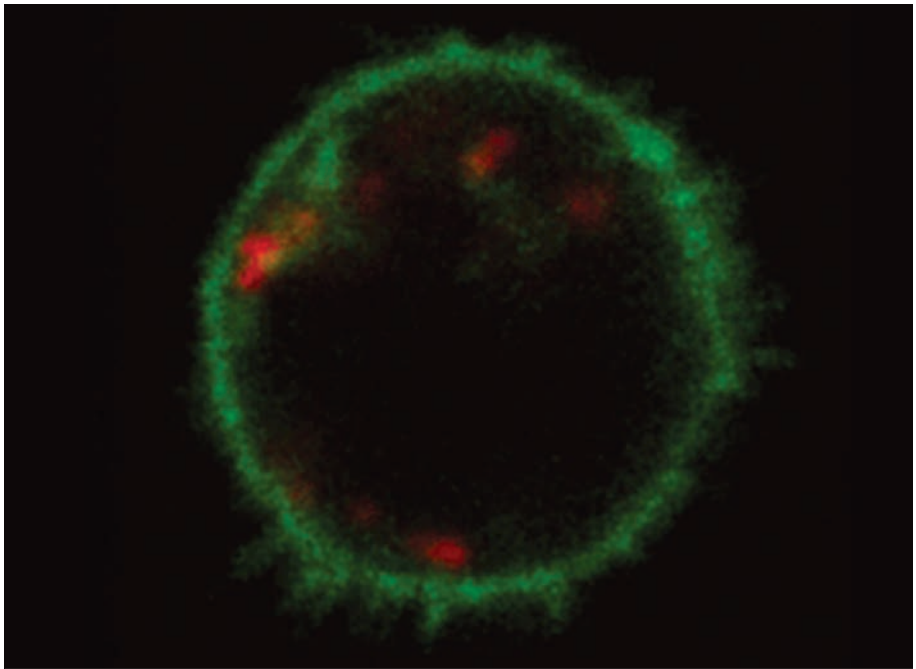
Dying cells trigger immunity

The release of nucleic acids from dying cells induces the maturation of a type of immune cell that fights parasites and drives allergic reactions

The immune system produces various types of immune cells—some are pre-programmed to target pathogens that the immune system has previously encountered, while others are 'naive' and retain the ability to mature or differentiate into specific cell types to target new invaders. Some of the triggers of this differentiation, however, remain poorly understood.

Takashi Saito, Takayuki Imanishi and colleagues from the Laboratory for Cell Signaling at the RIKEN Center for Integrative Medical Sciences have now led an international team of researchers that has found that nucleic acids, such as DNA and RNA, released from dying cells can trigger naive immune T cells to differentiate into T helper type 2 (Th2) cells[1].



DNA (red) is taken up inside naive T cells (green), leading to their activation and differentiation into T helper type 2 (Th2) cells.

The researchers performed a series of experiments where naive T cells were cultured with different kinds of nucleic acid species to induce T-cell activation. They found that certain classes of nucleic acids that tended to interact with other nucleic acids were more effective at activating T cells (see image), suggesting that these structural interactions enhance nucleic acid stability and uptake. Nucleic acids bound to various antimicrobial peptides and proteins —typical of the nucleic acids released by dying cells—also tended to promote T-cell activation, indicating that activation occurs at sites of inflammation or infection.

"Nucleic acids have previously been shown to be recognized by innate immune cells that present antigens to stimulate T cells," explains Saito, "but this study clarifies that T cells are directly activated by the nucleic acids themselves."

In many types of immune cells, nucleic acids bind to a class of proteins called Toll-like receptors (TLRs, which sense pathogen-associated molecular patterns to initiate innate responses and help regulate T cell-mediated adaptive immune responses. The researchers were surprised to find that TLRs did not seem to play a role in nucleic-acid-driven T-cell differentiation.

Instead, the researchers found that exposure to nucleic acids induced in the naive T cells the expression of a transcription factor that is known to specifically drive Th2 maturation. This was evidenced by the secretion of proteins characteristic of Th2 cells when naive T cells were cultured with nucleic acids.

Th2 cells drive the immune response against parasitic worms and serve a key role in triggering allergic reactions. The findings therefore suggest that blocking the ability of nucleic acids to induce Th2 maturation could be a promising possible therapeutic approach to reducing the severity of allergies in humans.

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Bioinspired catalyst splits water

Pyridine chemicals make manganese oxide more effective at neutral pH

Plants use photosynthesis to convert carbon dioxide and water into sugars and oxygen. The process starts in a cluster of manganese, calcium and oxygen atoms at the heart of a protein complex called photosystem II, which splits water to form oxygen gas, protons and electrons.

Researchers have attempted to develop synthetic catalysts that mimic this cluster, using light or electricity to convert water into fuels such as hydrogen gas. Unlike plants, however, these artificial catalysts can only split alkaline water, which makes the process less sustainable.

Ryuhei Nakamura and colleagues at the RIKEN Center for Sustainable Resource Science have now developed a manganese oxide-based catalyst system that can split water efficiently at neutral pH[1]. "Nature utilizes a safe, clean and abundant form of water to make fuels, thereby realizing sustainable ecosystems in the true sense," says Nakamura. "Catalysts that utilize water at a neutral pH as a resource for renewable energy would become the foundation for sustainable human societies."

In photosystem II, charged manganese (Mn) ions gradually give up electrons as they tear protons away from water molecules. This causes manganese in the 2+ and 3+ valence states to become oxidized, resulting in Mn^{4+} ions. Although the less-oxidized Mn^{3+} ions are quite stable in photosystem II, Nakamura and his colleagues previously found that they are unstable in synthetic manganese oxide catalysts at neutral pH.

To overcome this instability, the researchers sped up the regeneration of Mn^{3+} ions, which usually occurs when a water–Mn^{2+} complex loses a proton and an electron in two separate steps. Nakamura's team realized that ring-shaped organic molecules called pyridines could help those steps to happen at the same time—a process likely promoted by amino acids in photosystem II. They found that the manganese oxide catalyst produced 15 times more oxygen at neutral pH when used in conjunction with a pyridine called 2,4,6-trimethylpyridine.

The team also tested the reaction in deuterated water, which contains a heavier isotope of hydrogen than normal water. The catalyst generated oxygen much more slowly in the presence of 2,4,6-trimethylpyridine, suggesting that removal of a proton from the water–Mn^{2+} complex is the key step that determines the overall rate of the water-splitting reaction.

As pyridines would not be suitable for large-scale water splitting because they are potential environmental pollutants, the team now hopes to identify safer alternative proton-removing molecules that could be immobilized onto the surface of the manganese oxide catalyst to enhance its activity.

Reference

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Catalysts based on manganese (black substance) can mimic the splitting of water into oxygen and hydrogen that occurs in plants inside the photosystem II protein cluster responsible for photosynthesis.

Places

RIKEN BNL Research Center

Revisiting the early Universe

Researchers at the RIKEN BNL Research Center are studying high-speed collisions of atoms to gain a better understanding of our cosmic beginnings

Contact information

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In the first fleeting milliseconds after the Big Bang, the Universe consisted of a superdense soup of quarks and gluons that were hundreds of thousands of times hotter than the Sun. Over the next 14 billion years, the Universe stretched and cooled, leaving traces of the original brew trapped inside the protons and neutrons of atoms. Scientists at the RIKEN BNL Research Center are smashing atoms together at high speeds to liberate and observe these remnants of the early Universe and gain a better understanding of our cosmic beginnings.

The center was established in 1997 at the Brookhaven National Laboratory (BNL) in the United States. Theoretical, experimental and computational physicists at the center take advantage of some of the world's most advanced facilities. Among them are the Relativistic Heavy Ion Collider (RHIC), the first of only two accelerators in the world capable of melting heavy ions, the large PHENIX (Pioneering High Energy Nuclear Interaction eXperiment) detector with its dozens of subdetectors, as well as the QCDOC (Quantum ChromoDynamics On a Chip), a supercomputer situated at RIKEN's Wako campus that achieves 10 tera floating point operations per second (FLOPS)—soon to be replaced by an even speedier successor.

The PHENIX detector (opposite page) at the Relativistic Heavy Ion Collider (above) precisely measures particles that emerge from the collisions of beams of heavy gold ions traveling close to the speed of light.

A golden opportunity

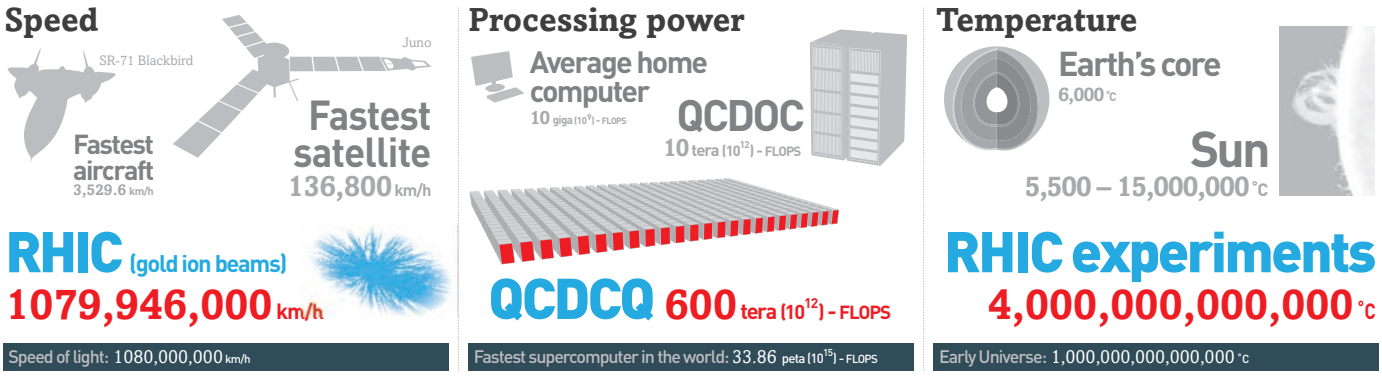
In a typical experiment at the RHIC, beams of heavy gold ions are accelerated around a 4-kilometer ring until they near the speed of light, before being smashed against each other. Producing temperatures in the trillions of degrees Celsius, the collisions frizzle protons and neutrons to free quarks and gluons for billionths of a second. Their momentary appearance is recorded by the PHENIX detector, one of four detectors at the RHIC. PHENIX precisely measures the momentum, energy and type of particles that emerge early in the collisions. The hundreds of megabytes of data generated by PHENIX every second are then processed by the QCDOC supercomputer, which was specifically designed to solve problems of a quantum physical nature.

Since the center's establishment, researchers have observed a new form of hot, dense matter with characteristics similar to the quark–gluon plasma of the early Universe. Achieving plasmas with temperatures of over 4 trillion degrees Celsius, the scientists have identified that the plasma behaves more like a perfectly flowing liquid than a gas. The researchers have also determined—to their surprise—that gluons barely contribute to the spin of protons, adding renewed perplexity to the origins of proton spin.

Connections and engagement

The RIKEN BNL Research Center emphasizes nurturing talented young physicists from around the world. In 2000, a Physics Fellow Program was introduced that offers young researchers a position at the center and a tenure-track placement at a university in the United States, Canada or Japan.

In 2012, RIKEN and the BNL extended their partnership through to 2018. The renewed agreement will enable the RIKEN BNL Research Center to collaborate in exciting plans to add an Electron-Ion Collider ring to the RHIC and to take a closer look at the relationship between gluons and proton spin. For researchers at the center, revisiting the early aftermath of the Big Bang is only a collision away.



Experiments at the RHIC achieve extreme speeds and temperatures to observe the early Universe.

The Madden–Julian Oscillation is associated with patterns of rain, thunderstorms and drought in tropical regions.

A tropical weather phenomenon meets its match

The might of Japan's most powerful supercomputer makes it possible to predict the evolution of the large-scale atmospheric circulation that dominates rain and storm patterns in the tropics

To accurately predict weather and climate, scientists need to simulate the large-scale patterns that exist in global atmospheric circulation. One of the largest circulation patterns, the Madden–Julian Oscillation (MJO), is associated with heavy rainfall and drought across the tropics. Due to the sheer size and complexity of the MJO, however, researchers have so far struggled to perform sufficiently detailed simulations over a broad enough area to accurately predict this oscillation.

Hirofumi Tomita and co-workers at the RIKEN Advanced Institute for Computational Science, in collaboration with researchers from the Japan Agency for Marine-Earth Science and Technology and the University of Tokyo, have now exploited the power of Japan's K computer—currently the fourth most powerful supercomputer in the world—to perform a series of MJO simulations with unprecedented resolution[1].

The MJO develops as a result of coupling between atmospheric circulation and warm, rising air in the tropics. It typically appears as a band of enhanced convection that progresses eastward across the Indian and Pacific oceans. The movement of the MJO results in 30- to 60-day cycles of enhanced wet and dry phases in tropical regions.

This interaction between global-scale movement and localized effects is difficult to resolve in global climate models because of the limitations of available computing power, which means that simulations need to be run on only small scales or with large geographic cell-sizes and simplified cloud modeling schemes in order to obtain results with realistic timeframes.

To resolve the MJO in more detail, Tomita and his colleagues used a modeling scheme called

the Nonhydrostatic Icosahedral Atmospheric Model (NICAM), which can explicitly resolve clouds on the fine scales needed to reproduce the MJO, in combination with the K computer. They ran the simulations 54 times using a 14-kilometer mesh, resolving cloud systems as small as 20 kilometers in size.

"Detailed MJO simulations have been possible since 2007, but only for small case studies," explains Tomita. "Using the K computer, we acquired many simulation results, meaning we can discuss the statistical aspects of NICAM's potential and the extended predictability of the MJO."

The research team estimates that the NICAM can predict the evolution of the MJO over an impressive 27 days, matching measured solar radiation, rain, humidity and wind data obtained during an intensive ground-based, airborne and shipborne weather observation campaign in the Indian Ocean. The results demonstrate the power of the NICAM for detailed MJO studies. "Our approach shows great potential for numerical weather forecasting," says Tomita. ■

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Solving the salty problem of protein stability

Advanced spectroscopy of molecular interactions helps resolve the century-old mystery of how aqueous ions affect proteins in solution

In the late 1800s, Czech chemist Franz Hofmeister discovered that the relative ability of ions to either dissolve or precipitate proteins in water followed a curious order. Instead of obeying accepted chemical principles, this sequence seemed to occur almost arbitrarily. Although researchers have successfully exploited the 'Hofmeister series' to develop stable, biomolecular-based pharmaceuticals, confusion over the microscopic mechanisms behind this phenomenon prevents accurate prediction of how novel pharmaceutical molecules might affect protein aggregation in water.

In research that could help explain the inscrutable ordering patterns of the Hofmeister series, Tahei Tahara and colleagues from the Molecular Spectroscopy Laboratory at RIKEN have now resolved the molecular structure of water around ions in charged solutions[1].

The Hofmeister series is difficult to understand because ions can influence both water and proteins in complex ways. For example, since the surface tension of pure salt solutions follows Hofmeister-series ordering, scientists long believed that ion-induced changes to bulk water were responsible for 'salting' proteins in or out of solution. However, this theory fails to match thermodynamic evidence, and researchers are now investigating the role of direct interactions between macromolecules and aqueous ions.

Tahara and his colleagues reasoned that Hofmeister-series ordering could be clarified through precise measurements of water molecules participating in macromolecule–ion interactions. Signals from water involved in such interactions are difficult to quantify because they are obscured by the much larger signals from bulk water. Fortunately, the team has spearheaded the development of a

Ultrafast laser experiments reveal that hydrogen bonding interactions between water molecules surrounding biomolecules help determine the stability of biomolecules in salt solutions.

technique called heterodyne-detected vibrational sum frequency generation (HD-VSFG) that is able to detect the infinitesimal vibrational signals of interfacial water through their nonlinear response to ultrashort laser bursts.

The researchers studied water structures at the interfaces of cetyltrimethylammonium (CTA^+) and dodecyl sulfate (DS^-) surfactants—two oppositely charged model materials that obey the Hofmeister series. By comparing the HD-VSFG signals of the pure surfactants to those containing ionic salts, they identified multiple mechanisms at play in this system. For the positively charged CTA^+ surfactant, the Hofmeister ordering is related to the ability of anions to displace water at the interface. For cations associated with the negatively charged DS^- interfaces, however, the order correlates with changes in the hydrogen-bond strength of interfacial water—a fundamental discovery made possible only through use of the ultrasensitive HD-VSFG technique.

"This work provides molecular-level views of interactions between proteins and ions, as well as water–protein interactions," says Tahara. "It provides an important basis for research into biomimetic polymers suitable for medical use." ■

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Boron takes both sides

A chemical synthesis method that allows boron atoms to be added to opposing sides of an alkyne molecule opens up new possibilities for drug and materials development

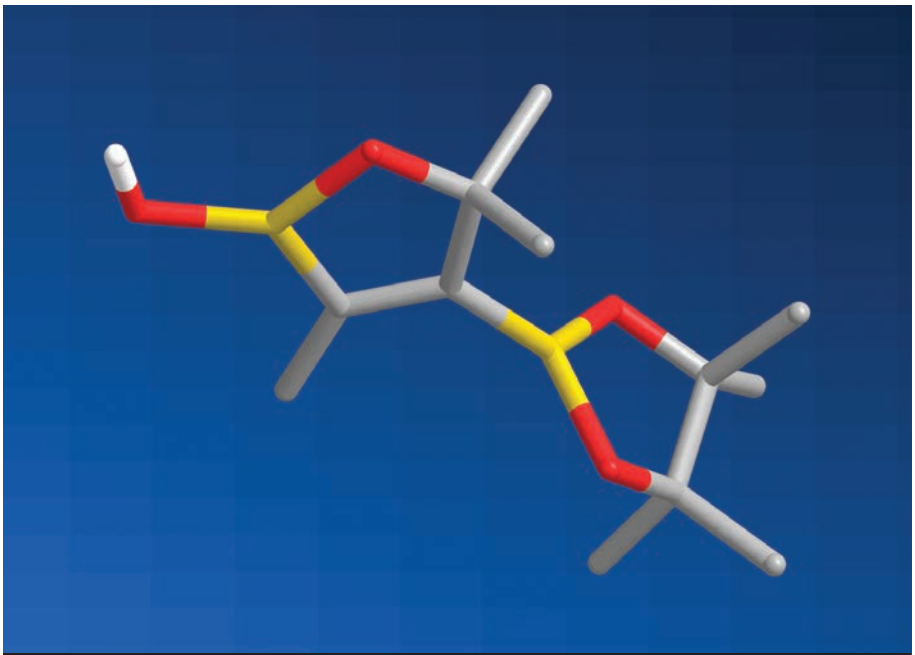
The development of new methods for preparing organic compounds is a fundamental aspect of research on new drugs and advanced materials. In many cases, the three-dimensional spatial arrangement of atoms in the synthesized molecules has a pronounced effect on functionality and reactivity, so methods that can form new types of bonds with structural selectivity often prove to be groundbreaking. Masanobu Uchiyama and Ryo Takita from the RIKEN Center for Sustainable Resource Science and researchers from the University of Tokyo have now devised a method for selectively adding boron atoms to opposite sides of an alkyne molecule[1].

When additional atomic groups are added to an organic compound such as an alkyne, which has two carbon–carbon triple bond sites, the added groups can attach to the triple bond sites such that they are oriented to one side of the molecule to form what is known as a *cis* configuration, or oriented in opposite directions to afford a *trans* structure. Uchiyama's team investigated whether diboron—two boron atoms—could be selectively added to an alkyne to form a *trans* arrangement (see image).

"Methods to form two carbon–boron bonds on the same side of an alkyne, a procedure called *cis*-diborylation, have been described previously," explains Uchiyama, "but *trans*-diborylation has not been possible. Tamoxifen, a breast cancer treatment, is an example of a compound whose synthesis might be improved by such a new method."

Uchiyama and his team started by performing computational analyses of their proposed reaction. The calculations showed that although the reaction should be possible, a large energy barrier would need to be overcome to initiate the process. Through extensive experimentation, they instead found a way to sidestep the energy barrier by using an additional reagent to help 'tie' the diboron group to the alkyne.

The formation of carbon–boron bonds is particularly attractive because reactions using



The three-dimensional structure of *trans*-diborylated alkyne, showing the position of boron (yellow), oxygen (red), carbon (gray) and hydrogen (white) atoms.

compounds bearing these bonds have been widely studied. "We have been trying to find reaction conditions that allow us to couple two different groups to the diboronated product of this reaction," says Uchiyama, "so that we can prepare compounds like Tamoxifen in a structurally selective fashion."

Ultimately, Uchiyama's team plans to develop similar reactions using alkenes, which contain two carbon–carbon double bonds, as well as 'downstream' reactions that use the carbon–boron bonds selectively. "With this method in hand, we hope to explore the properties of functional molecules that were previously difficult to access," says Uchiyama. ■

Reference

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The shape of spins to come

Electron holography reveals the startling beauty of nanoscale magnetic vortices targeted for future spintronic data storage systems

Nanoscale magnetic swirls known as skyrmions can form in certain materials such as thin magnetic films. These tiny vortices pack into dense lattices that are more stable than conventional magnetic domains and can be transported and manipulated with minimal electrical power—features that hold great promise for future information storage applications. To exploit skyrmions in such memory technologies, however, scientists need a deeper understanding of their fundamental properties.

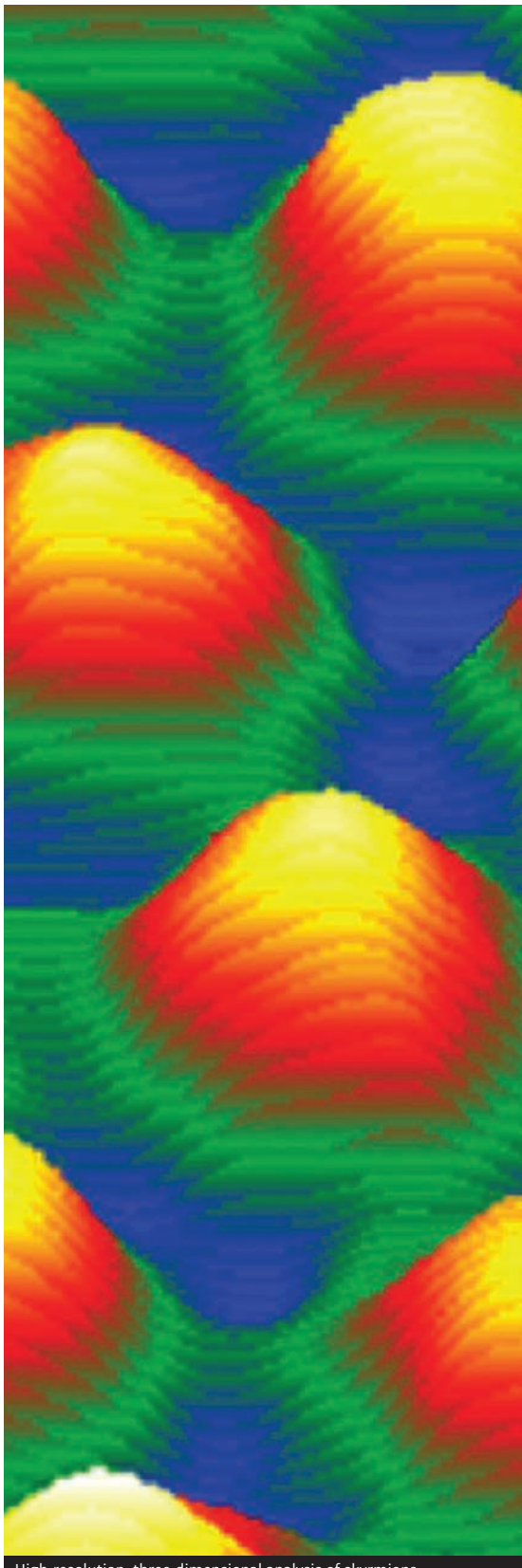
Hyun Soon Park, Toshiaki Tanigaki and colleagues from the RIKEN Center for Emergent Matter Science, in partnership with industrial and academic researchers from across Japan, have now made major progress in this area by conducting the first three-dimensional analysis of skyrmion lattices using an electron holography microscope[1].

The RIKEN-led team has pioneered techniques to view skyrmions in two dimensions using techniques that include Lorentz transmission electron microscopy. However, the magnetic structure of skyrmions—defined by the orientation of electron spins—is not flat, and instead involves a three-dimensional distribution of spin orientations to form a true vortex. Analyzing this structure in quantitative detail is difficult because the features are beyond the resolution limit of Lorentz microscopy and can be obscured by the inherent roughness of the film's surface.

Electron holography, a technique for generating three-dimensional visualizations from interfering electron waves, can be used to resolve magnetic structures with unprecedented detail. Through collaboration with the group of the late Akira Tonomura—a forefather of electron holography—at Hitachi, Ltd, the researchers constructed a high-voltage electron holography microscope with sufficient power to resolve the skyrmion structure.

Using their holographic microscope, the researchers imaged the magnetic structure of a thin iron–cobalt–silicon film while applying a magnetic field. As the magnetic field intensity was increased, they observed a change in the electron spin arrangement from a helical structure to the swirling skyrmion structure. The three-dimensional images revealed that the skyrmions adopt a distinct cylindrical shape with an eerily beautiful interior pattern (see image). Intriguingly, this magnetic vortex switches from right- to left-handed as the direction of the applied magnetic field is changed.

Park notes that skyrmions with cylindrical spin configurations can be expected to provide



High-resolution, three-dimensional analysis of skyrmions reveals a remarkably detailed magnetic structure.

more effective spin transfer torque—a critical factor in transporting skyrmions for data storage applications. He is also confident that high-voltage electron holography has enormous potential to resolve many of the uncertainties associated with spintronic devices. "Seeing complex magnetic structures with high precision or in three dimensions is key to understanding these systems," he notes.

Reference

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Joining the dots for quantum computing

Arrays of electrons trapped in nanoscale circuitry could form the basis for future scalable quantum computers

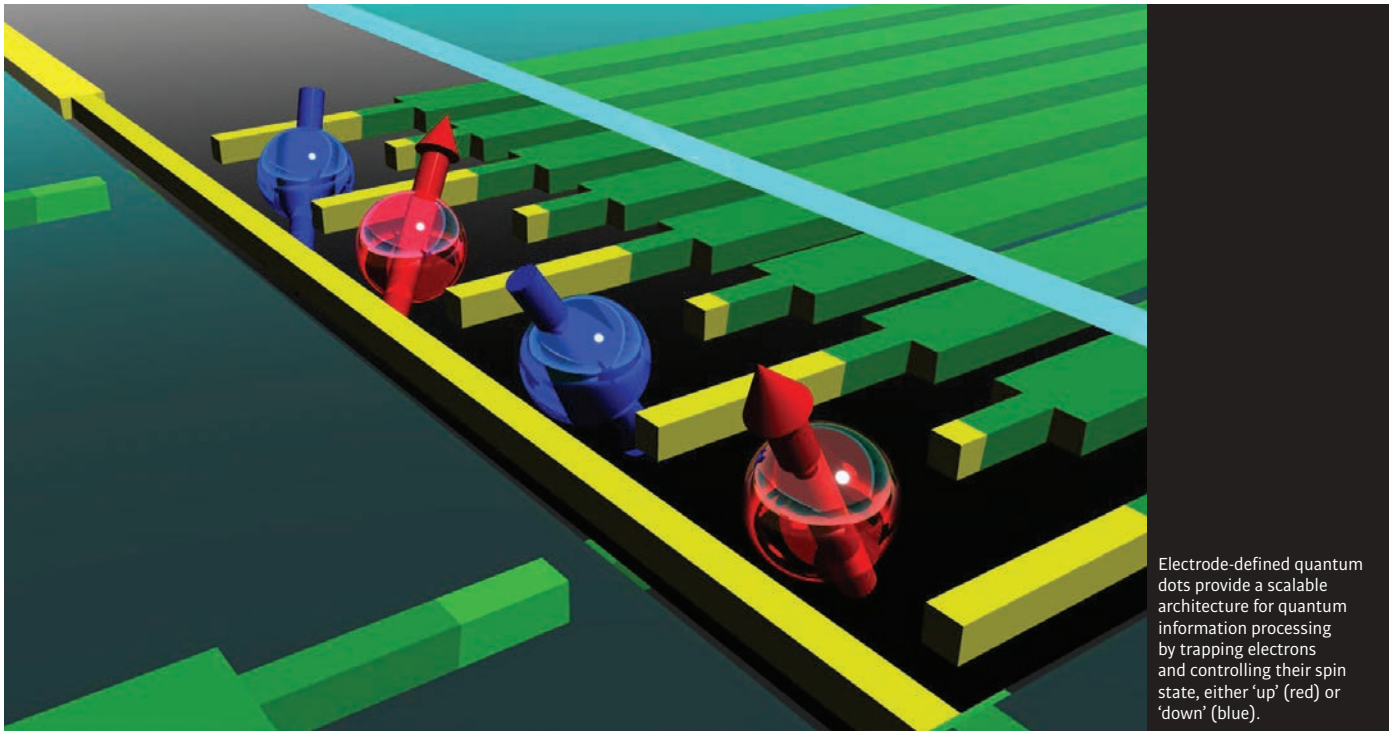
A single electron trapped in a semiconductor nanostructure can form the most basic of building blocks for a quantum computer. Before practical quantum computers can be realized, however, scientists need to develop a scalable architecture that allows full control over individual electrons in computational arrays.

Matthieu Delbecq and colleagues from the RIKEN Center for Emergent Matter Science, in collaboration with researchers from Purdue University in the United States, have now demonstrated the scalability of quantum dot architectures by trapping and controlling four electrons in a single device[1].

Electrons have a property known as spin that can be either 'up' or 'down'. This is the same binary coding as used in conventional computing, but electrons can also be linked at the quantum level to form quantum bits, or 'qubits', that can have many more usable states, providing dramatic improvements in computational performance.

Circuits of quantum dots are one of the most promising practical routes to harnessing this potential. A quantum dot creates an electric field 'well' that is too deep for the electron to escape, allowing individual electrons to be confined to a space just a few nanometers across. Scientists have fabricated two- and three-dot devices in the past, but a real processor would need many more. Delbecq and his colleagues have now used a similar approach to create a four-quantum-dot structure, proving the scalability of this architecture.

"The number of manipulated electrons is increased only by one with respect to previous structures," explains Delbecq, "but even a



Electrode-defined quantum dots provide a scalable architecture for quantum information processing by trapping electrons and controlling their spin state, either 'up' (red) or 'down' (blue).

small increase in the number of electrons significantly increases the complexity of device manipulation."

Each of the dots in the device created by Delbecq's team was formed by three nanoscale metallic electrodes on a semiconductor substrate (see image). The capacitance between each dot couples the electron in one dot to that in the next, and the researchers could tune the strength of this coupling by adjusting the voltages applied to the electrodes. All this was achieved at extremely low temperatures, just a fraction above absolute zero.

The researchers demonstrated a scheme for both controlling the electrons in the four quantum dots and measuring or 'reading out' the spin state of the electrons. "The next step is to form four spin qubits with this architecture and use them to actually perform computations," says Delbecq. The results demonstrate that quantum dot architecture has the potential to be scaled up to the number of qubits needed to realize a fully functional quantum computer. ■

Reference

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X-ray studies without the damage

A non-damaging x-ray technique makes it possible to investigate the detailed structure of large biomolecules, leading to a better understanding of their biological functions

Biological molecules such as proteins can contain hundreds of thousands of atoms, which makes it very difficult to understand their function in detail. Identifying the exact atomic structure of these complex molecules is essential for biological studies and drug discovery, but the high-intensity x-ray beams needed to study them inevitably cause significant radiation damage to the molecules being investigated.

Hideo Ago and colleagues from the RIKEN SPring-8 Center, along with researchers from other institutions in Japan, have now developed an x-ray technique that allows one of the most powerful modern x-ray machines, the x-ray free electron laser (XFEL) at the SPring-8 synchrotron facility, to be used to study large, complex molecules without radiation damage[1].

X-ray diffraction experiments involve measuring the scatter of x-rays from atoms in a crystal. Since the atoms in a crystal are ordered in periodically repeating arrangements, the reflected x-rays form regular patterns that can be traced back to the arrangement of the atoms in the crystal, allowing the molecular structure to be determined.

"The dilemma of conventional x-ray protein crystallography, however, is that the x-ray intensities required for a precise structure determination also cause severe radiation damage to the protein molecules," explains Ago.

The XFEL at the SPring-8 facility offers a solution. The ultra-intense, femtosecond x-ray pulses generated by the XFEL are so short that they do not interact with proteins long enough to cause structural changes. Although the individual interactions are weak, if the crystals are thick enough, the pulses have sufficient cumulative interaction to give clear x-ray diffraction patterns and resolve the details of even highly complex molecules.

To avoid damage from successive pulses hitting the same spot in the crystal, the

Using ultrashort x-ray pulses generated by the x-ray free electron laser (XFEL) at the SPring-8 synchrotron facility allows the structure of complex biomolecules to be investigated without radiation damage.

x-ray spot size is made very small and successive measurements are taken at different locations in the crystal. Averaging the x-ray patterns obtained from various locations then allows the optimized crystal structure to be determined.

As an example, the researchers successfully studied the oxygen reaction center in the bovine enzyme cytochrome *c* oxidase, which is particularly susceptible to radiation damage and had therefore defied previous attempts at precise structural characterization.

In future, this method could be employed for the study of a number of important molecules, particularly in biology, says Ago. "Our system is very useful for studying the catalytic function of enzymes and proteins. Famous examples include the proteins involved in photosynthesis, and we would like to study the exact mechanism behind their amazingly efficient light-harvesting ability."

Reference

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Boosting microelectronics with a little liquid logic

The combination of ferroelectric crystal and ionic liquid could lead to a new class of transistor for fast, low-power memory and logic devices

Certain titanium-based metal oxides can form a crystal structure known as perovskite that results in a subtle internal imbalance of electric charges. This imbalance gives the material the ability to flip between two 'ferroelectric' states in response to an electric field—a promising recipe for fast, ultra-low-energy storage of digital data.

Masashi Kawasaki and colleagues from the RIKEN Center for Emergent Matter Science, in collaboration with Yusuke Kozuka and coworkers from the University of Tokyo, have now discovered a way to sweep away the stray charges that typically degrade the performance of ferroelectric materials by using an ionic liquid[1].

Silicon-based field-effect transistors are the basis of modern electronics. In these devices, current flow through the transistor junction is controlled by altering the electronic state of a semiconducting 'gate' between the input 'source' and output 'drain'. Current can only flow in such devices when a voltage is applied to the semiconductor. In contrast, the switchable electronic properties of ferroelectric crystals could make it possible to permanently set the polarization of the channel between source and drain terminals, allowing current to flow in the 'on' state without a constant voltage on the channel. This strategy could prove very useful for non-volatile memory applications and logic circuits.

However, ferroelectric transistors naturally attract charged adsorbents, which counteract the crystal's internal ferroelectric properties. To resolve this issue, the research team switched from a conventional gate oxide to one based on an ionic liquid—a molten organic salt that can store charge by a mechanism known as electric double-layer capacitance (see image). Applying a voltage or 'bias' to the ionic-liquid gate produced a large accumulation of ions that squeezed out the adsorbed impurities. "This cleaning function under biasing indicates that ionic liquids are an ideal medium for ferroelectric materials," says Kozuka.

The next challenge facing the researchers was to optimize the ferroelectric material, in this case barium titanate. Comparing two devices, one made by growing a crystalline layer of the ferroelectric material as a thin 'epitaxial' film and the other based on a commercial bulk crystal, they found that the thin-film transistor showed surprisingly small resistance in its 'on' state, passing 10,000 times more current than in its 'off' position. The bulk-crystal device, on the other hand, displayed an abrupt increase in resistance due to a structural phase transition, preventing transistor operation. This result, the team notes, verifies that epitaxial films are an effective way to maintain the near-metallic behavior of ferroelectric crystals.

Reference

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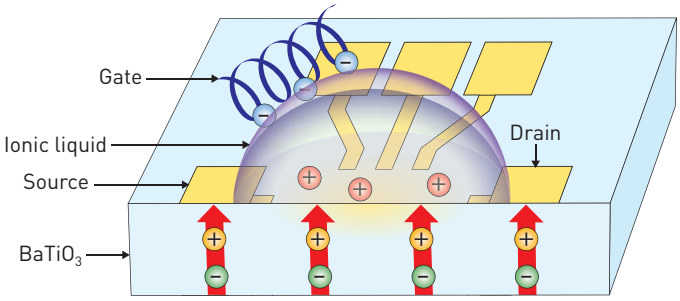

Schematic of an electric double-layer transistor featuring a ferroelectric barium titanate ($BaTiO_3$) channel and an ionic liquid 'gate' that removes impurities for improved device performance.

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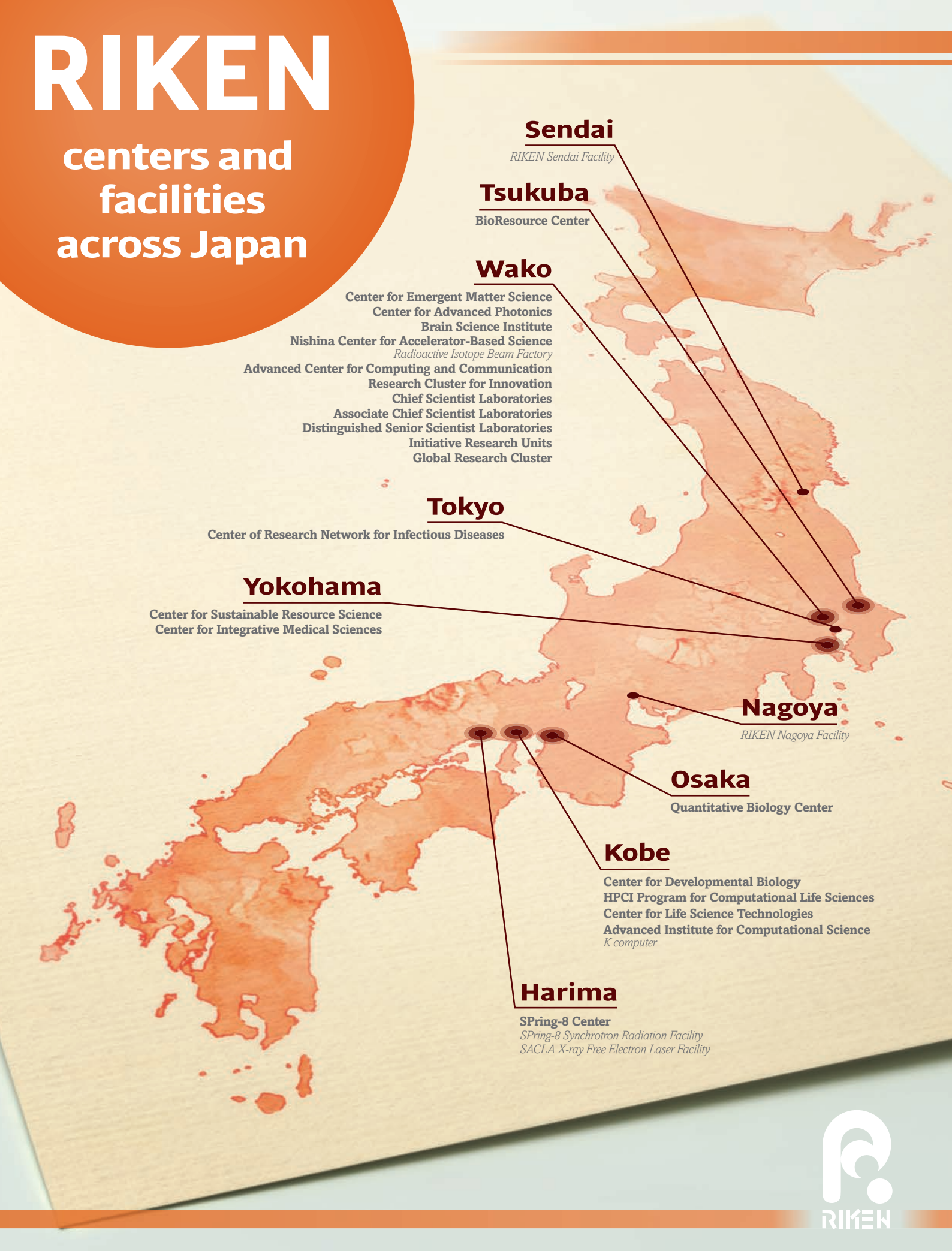

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