RIKEN RESEARCH

FEBRUARY
2011 Volume 6 Number 2

Trapping antimatter

www.rikenresearch.riken.jp

RIKEN

Antimatter atoms ready for their close-up

Controlling antihydrogen atoms using two different methods brings physicists closer to answering quantum and cosmic questions

Two international teams of physicists, including RIKEN researchers, have trapped and manipulated atoms made out of antimatter, in milestone experiments that should help to reveal why the substance is so rare in our Universe.

Since its existence was first predicted by physicist Paul Dirac in 1931, antimatter has become an increasingly common sight. The antiparticle of the electron, for example, is routinely used in positron emission tomography, a clinical imaging technique. Yet despite this routine use of isolated antimatter particles, making 'anti-atoms' is extremely difficult because matter and antimatter annihilate each other in a flash of energetic photons when they meet.

The simplest and most abundant atom in the universe—hydrogen—consists of a positive proton and an electron. Its opposite number, antihydrogen, contains a negative antiproton and a positron, and teaming the antiparticles without allowing them to touch any ordinary matter is a ticklish business.

In parallel research efforts, known as ALPHA and ASACUSA, the international teams of physicists have shown how to handle antihydrogen atoms in a way that will soon allow their properties to be investigated precisely, and compared with normal hydrogen.

Physicists are keen to make this comparison because one of the foundations of modern quantum physics—the charge, parity and time reversal symmetry theorem—states that hydrogen and antihydrogen should have identical energy levels, producing matching spectra when probed with light. But this also suggests that at the very beginning of the Universe, both matter and antimatter would have been created in equal quantities. So the fact that our Universe is almost entirely made of matter seems to contradict quantum theory, and poses a fundamental question about how the cosmos works.

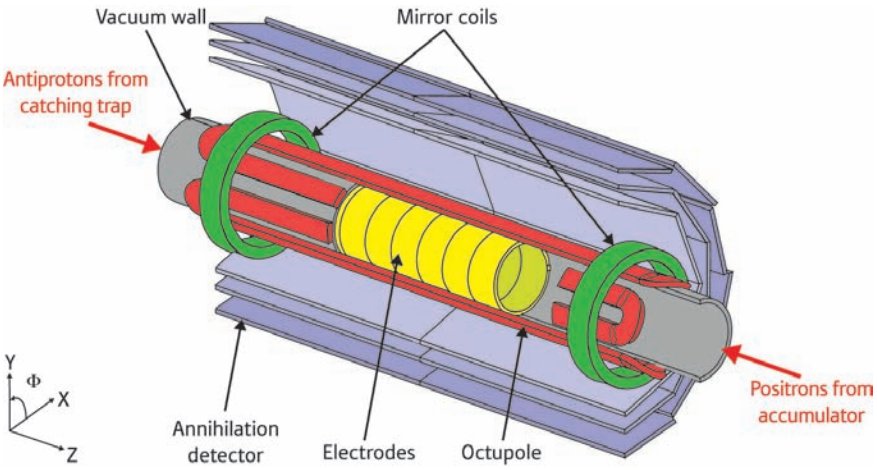


Figure 1: A drawing of the central section of the ALPHA trap for antiprotons.

Trapped in an asymmetric field

Researchers working on the ATHENA and ATRAP experiments at CERN, the European particle physics facility based in Geneva, Switzerland, first combined positrons and antiprotons to create cold antihydrogen in 2002. The ATHENA project evolved into ALPHA, which relies on electric and magnetic fields—a 'magnetic bottle', or Ioffe-Pritchard trap—to control, cool, and mix the particles, and to trap antihydrogen atoms.

"The challenge is the temperature of antihydrogen atoms," says Yasunori Yamazaki of the RIKEN Advanced Science Institute in Wako, Japan, who is involved with both the ALPHA and ASACUSA experiments. Fast-moving antiprotons as hot as 100,000 Kelvin must be chilled to less than 0.5 Kelvin to form trappable antihydrogen.

In recent experiments, the ALPHA researchers collided about 30,000 antiprotons with electrons to cool them to roughly 200 Kelvin in a cloud about 1.6 millimeters across. They cooled a separate pool of positrons by allowing the hotter particles to 'evaporate' away from the rest, leaving a 1.8 millimeter-diameter cloud of about two million particles at roughly 40 Kelvin. The strong magnetic field containing the particles was shaped so that the particles collected in the center of the trap (Fig. 1), and the researchers slowly coaxed the antiprotons towards the positrons by changing the electric field. After mixing for just a second, they removed any unreacted antiparticles from the trap.

About 0.2 seconds after the removal of antiprotons and positrons, the researchers opened the magnetic bottle to look for trapped antihydrogen atoms. Since

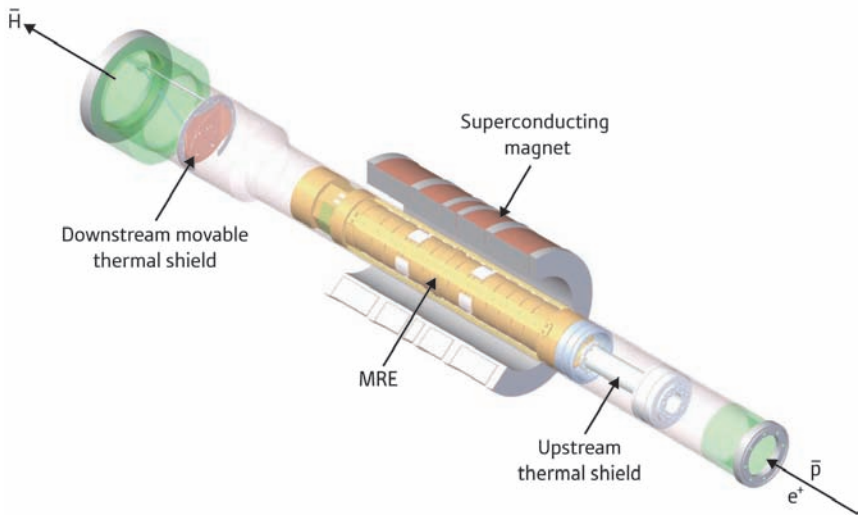


Figure 2: A drawing of the central section of the cusp trap for antiprotons used in the ASACUSA experiment.

antihydrogen atoms are neutral, any that formed were no longer controlled by the electric field. Those not cold enough to be trapped in the magnetic bottle drifted towards the sides of the trap, where they annihilated and formed exotic particles called pions, which were registered by silicon detectors. Studying the energy and the trajectory of the pions allowed the researchers to weed out any signals that had been produced by cosmic rays—high-energy particles from space. Overall, they found 38 atoms of antihydrogen from 335 experimental runs[1].

Yamazaki hopes that antihydrogen could be trapped for much longer in future experiments, which would help efforts to study its properties. But "the strong magnetic field gradient of the magnetic bottle would make real high-resolution spectroscopy not straightforward," he adds.

Synthesized in a symmetrical field

ASACUSA uses a different method of taming antihydrogen. It collects antiprotons and positrons in a cusp trap (Fig. 2), which relies on symmetrical magnetic and electric fields, unlike ALPHA's asymmetrical fields. Recent experiments show that ASACUSA researchers can use the cusp trap to combine antiprotons and positrons to produce a beam of antihydrogen atoms[2]. This approach has unique advantages, says Yamazaki.

"First of all, we can extract antihydrogen atoms as an intensified beam in a magnetic-field free region, which enables high-resolution spectroscopy. Secondly, the temperature of the antihydrogen atoms can be much higher—say 10 Kelvin—which makes it orders of magnitude more efficient to synthesize a usable number of antihydrogen atoms," explains Yamazaki. "We think we can confirm the beam next year, and if everything goes well, we can also get some spectroscopic results for the first time," he adds. ALPHA, too, is already making plans for its own laser spectroscopy measurements.

Improving supply

Both experiments could benefit from a new project at CERN, called ELENA, which can deliver lower-energy antiprotons. "We really hope this project will be approved as soon as possible," says Yamazaki. This could provide a continuous supply of much larger numbers of chilled antiprotons for ALPHA and ASACUSA, which "should have a tremendous impact on both antihydrogen projects," he notes.

Of both projects' latest results, he adds: "I feel that these two achievements are really big milestones towards realizing low-energy antimatter physics for the first time." ■

1. Andresen, G.B., Ashkezari, M.D., Baquero-Ruiz, M., Bertsche, W., Bowe, P.D., Butler, E., Cesar, C.L., Chapman, S., Charlton, M., Deller, A., *et al.* Trapped antihydrogen. *Nature* **468**, 673–676 (2010).
2. Enomoto, Y., Kuroda, N., Michishio, K., Kim, C.H., Higaki, H., Nagata, Y., Kanai, Y., Torii, H.A., Corradini, M., Leali, M., *et al.* Synthesis of cold antihydrogen in a cusp trap. *Physical Review Letters* **105**, 243401 (2010).

About the researcher

Yasunori Yamazaki was born in Osaka, Japan, in 1949. He graduated from the Department of Physics, Osaka University, in 1973, received his master degree in 1975, and obtained his doctoral degree in 1978 from the Department of Applied Physics at the same institute. He was appointed research associate of the Tokyo Institute of Technology in 1978, associate professor of The University of Tokyo in 1988, and professor at the same university in 1993. He was jointly appointed as chief scientist at RIKEN in 1997. From 2010, he has held the title of distinguished senior scientist of RIKEN and professor emeritus of The University of Tokyo. His research interests are cold antimatter science with antihydrogen atoms as well as applications of beam physics to various fields of natural science, including living cell surgery, micromodification of liquid–solid interfaces and virtual x-ray spectroscopy of relativistic highly charged heavy ions channeling through crystalline targets.

When matter and antimatter collide

The discovery that particles called antiprotons collide with molecules and atoms in different ways is contrary to theoretical expectations

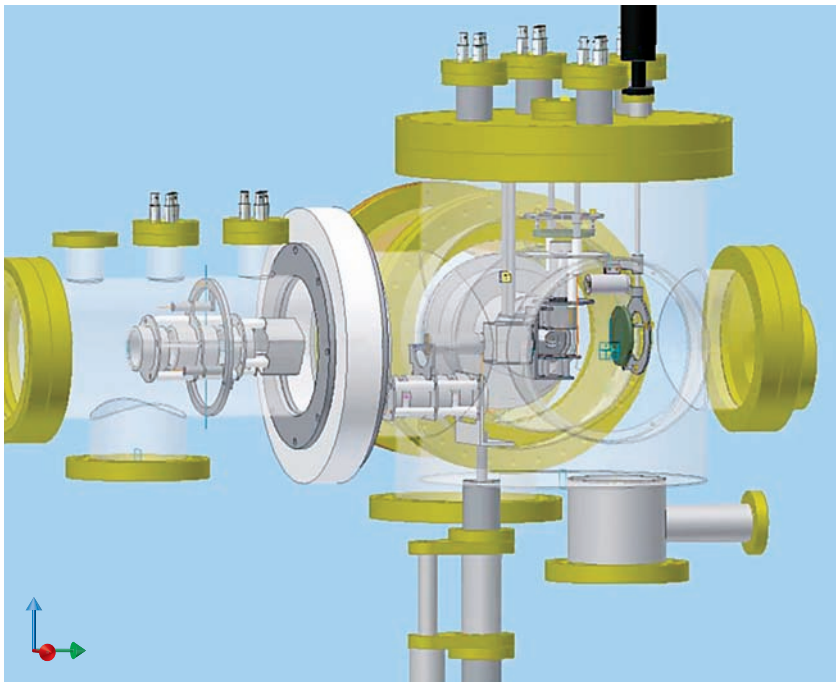


Figure 1: A schematic diagram of the antiproton decelerator at CERN that is used to smash antiprotons and molecular hydrogen molecules together so that the remaining particles can be analyzed to provide insight to their interactions.

Antimatter, a substance that often features in science fiction, is routinely created at the CERN particle physics laboratory in Geneva, Switzerland, to provide us with a better understanding of atoms and molecules. Now, RIKEN scientists, as part of a collaborative team with researchers from Denmark, Japan, the United Kingdom and Hungary, have shown that antiprotons—particles with the same mass as a proton but negatively charged—collide with molecules in a very different way from their interaction with atoms[1]. The result sets an important benchmark for testing future atomic-collision theories.

RIKEN scientist Yasunori Yamazaki explains that to assess such collisions: "We shot the simplest negatively charged particles, slow antiprotons, at the simplest molecular target, molecular hydrogen." Slow antiprotons are a unique probe of atoms and molecules because their negative charge does not attract electrons—thereby simplifying theoretical modelling. Further, slower projectile speeds mean longer-lasting, stronger interactions and avoid the need for complicated relativistic calculations.

The scientists at CERN created antiprotons by firing a beam of high-speed protons into a block of the metal iridium. Then, in a facility known as the Antiproton Decelerator, they used magnets to focus the antiprotons before applying strong electric fields to slow them down to approximately 10% of the speed of light. Yamazaki and his colleagues trapped and cooled these antiprotons to 0.01% of the velocity of light before accelerating them one by one to the desired velocity (Fig. 1). They then slammed antiprotons into a gas of molecular deuterium—a pair of bound hydrogen atoms each with a nucleus comprising one proton and one neutron—and used sensitive equipment to detect the remnants of the collision.

Yamazaki and the team found that the likelihood of the ionization of the deuterium molecules scales linearly with the antiproton velocity. This is contrary to what is expected for the atomic target, hydrogen. "This was a big surprise, and it infers that our understanding of atomic collision dynamics, even at a qualitative level, is still in its infancy," says Yamazaki. The team suggests that molecular targets provide a mechanism for suppressing the ionization process. As an antiproton approaches one of the protons in the molecule, the presence of the second proton shifts the orbiting electron cloud. The slower the antiproton, the more time the electron has to adjust, and hence the smaller the chance of ionization.

The team now hopes to investigate how ionization depends on the antiproton–target distance and the orientation at the moment of collision. ■

1. Knudsen, H., Torii, H.A., Charlton, M., Enomoto, Y., Georgescu, I., Hunniford, C.A., Kim, C.H., Kanai, Y., Kristiansen, H.-P.E., Kuroda, N., *et al.* Target structure induced suppression of the ionization cross section for very low energy antiproton–hydrogen collisions. *Physical Review Letters* **105**, 213201 (2010).

Anything goes in oxides

The interaction of electrons in an unusual oxide reveals new ways to tune electrical conductivity

Researchers in Japan have demonstrated why the material Sr_2IrO_4—a transition metal oxide—that was expected to be an electrical conductor is actually an insulator[1]. Harnessing this material's unusual conducting properties could form the basis for novel electronic devices or superconductors.

The difference between an electrical conductor and an insulator is that electrons in the latter cannot move freely through the crystal. This is because insulators have a gap in their energy spectrum that electrons cannot overcome. Hiroshi Watanabe, Tomonori Shirakawa and Seiji Yunoki from the RIKEN Advanced Science Institute in Wako and the Japan Science and Technology Agency have now uncovered how the electronic gap in Sr_2IrO_4 arises. Other RIKEN scientists had shown previously that the compound is an insulator[2].

Sr_2IrO_4 is a member of the oxygen-containing compounds based on transition metals that have high atomic numbers. In these transition metals, the electrons of elements such as nickel, copper or cobalt strongly interact with each other, which results in effects such as superconductivity or magnetism.

In compounds made from the heavier transition metals, the outermost electrons circle the atoms in the so-called '*5d* electron shell', which is relatively distant from the core. For electrons that occupy this shell there is an unusually strong interaction between their magnetic property, called spin, and the orbital motion around the atomic nucleus. The energy of this spin–orbit interaction is as large as the electron's energy of motion or the energy arising from the electrostatic interaction between the electrons. This has dramatic consequences on their electronic properties, according to Yunoki, who led the research team. "Literally anything can happen in *5d* electron systems because of the subtle balance of those three fundamental energy scales."

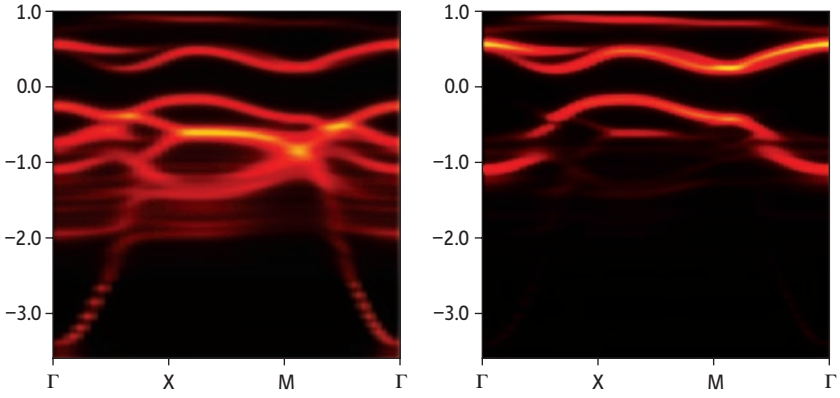


Figure 1: The energetic states of Sr_2IrO_4. The left panel shows the spectrum of all the computed electronic states. A gap in energy (y-axis) is clearly visible for electrons moving in all crystallographic directions (x-axis). The letters on the x-axis denote specific crystallographic directions. The right panel shows an isolation of the gap arising from states that form as a result of the spin-orbit interaction.

How this energetic interplay modifies the electron conducting behavior in Sr_2IrO_4 became evident from the researchers' calculations. The strong spin–orbit interaction in Sr_2IrO_4 shifts some of the electronic states to higher energies, which is sufficiently strong to create an energy gap in the electronic states (Fig. 1).

Furthermore, the calculations reveal an intriguing connection to the family of high-temperature superconductors that have a similar gap in their electronic states. In these compounds, superconductivity is achieved through a small addition of atoms introducing an electron surplus. The researchers are now investigating the possibility that this could also be the case here. "It would have an enormous impact if one can make Sr_2IrO_4 superconducting," says Yunoki. "We hope that our theoretical calculations will be of help to experimentalists." ■

1. Watanabe, H., Shirakawa, T. & Yunoki, S. Microscopic study of a spin-orbit-induced Mott insulator in Ir oxides. *Physical Review Letters* **105**, 216410 (2010).
2. Kim, B. J., Ohsumi, H., Komesu, T., Sakai, S., Morita, T., Takagi, H & Arima, T. Phase-sensitive observation of a spin-orbital Mott state in Sr_2IrO_4. *Science* **323**, 1329–1332 (2009).

Particles that are their own worst enemies

A newly proposed superconducting device could lead to the first observation of particles that are their own antiparticles

The matter that makes up the universe consists of particles such as electrons and protons, as well as their counterparts known as antiparticles. Particles and antiparticles that collide, however, annihilate each other in an intense flash of energy. Nevertheless, the Italian physicist Ettore Majorana proposed that some particles could exist that are their own antiparticles although physicists are yet to observe such particles.

Researchers from the RIKEN Advanced Science Institute in Wako have now proposed a scheme where Majorana particles could be not only observed for the first time but also manipulated[1]. The observation would occur in a conventional material rather than space. "Our main aim is to find a platform where the existence of Majorana fermions can be shown," explains team member Shigeki Onoda. "And beyond that, we propose concrete steps towards the control of several Majorana particles."

In some rare materials, energetic excitations that resemble Majorana particles are predicted to exist in materials. One class of these materials is known as topological insulators on the surface of which electrons can travel almost unperturbed. In topological insulators that are also superconducting, Majorana particles are predicted to exist in the presence of magnetic fields. These Majorana particles can be imagined as electronic excitations that run around the magnetic field lines.

The device proposed by Onoda and his colleagues offers deliberate control over Majorana particles within a topological insulator that they hope will make them accessible to experiments. Their device consists of a surface of a superconducting topological insulator attached to two magnetic sections (Fig. 1). The magnetic fields of the two magnets point in opposite directions. The researchers predict that, along the interface between the magnets, a periodic chain of magnetic field lines form in the superconducting topological insulator. Each of these magnetic field lines could accommodate a Majorana particle.

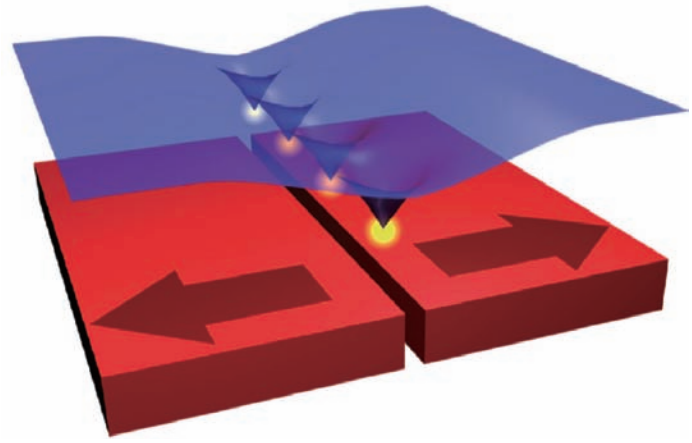


Figure 1: A schematic diagram of Majorana particles lined up in two opposing magnetic fields (red) that interact with a superconducting topological insulator (blue). At the gap between the magnets, the superconductor is weakened and magnetic field lines assemble in a periodic chain to which Majorana particles (yellow) attach.

Once their existence is proved, Majorana particles could also enable extremely stable new forms of computing based on quantum physics, says Onoda. "As long as the Majorana particles are well separated, the information encoded in these states would be robust against local perturbations."

For the time being, however, such quantum computing schemes must remain theoretical. Although widely expected to exist, superconducting topological insulators, as yet, exist only in theory. Once such a material has been found, the researchers believe that the proposed device structure will be straightforward to implement. The expected periodic arrangement of Majorana particles would then provide a convenient platform to study these elusive particles. ■

1. Neupert, T., Onoda, S. & Furusaki, A. Chain of Majorana states from superconducting Dirac fermions at a magnetic domain wall. *Physical Review Letters* **105**, 206404 (2010).

Hydrogen gas: Under pressure

Simulations have explained the peculiar nature of molecular hydrogen vibration under high pressure

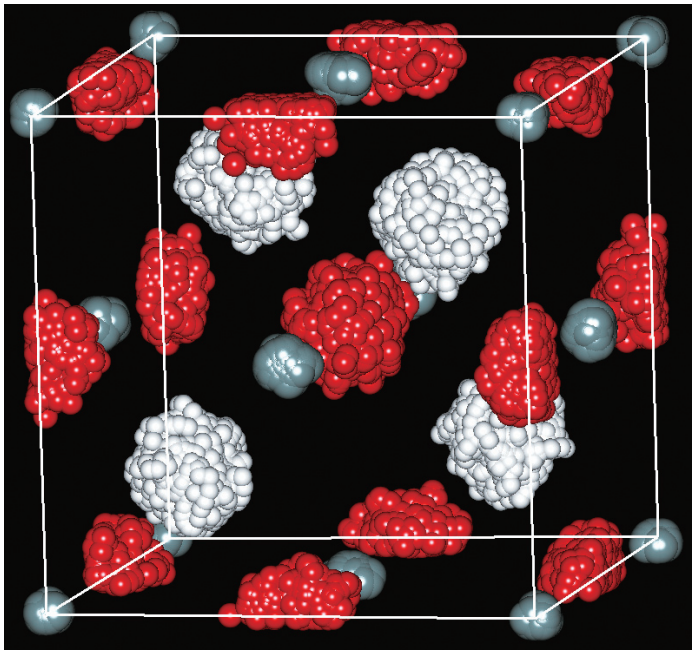


Figure 1: Traces of the positions of silane and hydrogen molecules over time at 32 GPa, obtained from molecular dynamics calculations. Hydrogen atoms at tetrahedral (white) and octahedral (red) sites are shown. Silicon atoms at so-called 'face-centered cubic' sites are shown by gray spheres.

Most of our Universe consists of hydrogen atoms, which are often found under extraordinarily high pressure as high as tens of millions of times the atmospheric pressure of Earth. Understanding the exotic physics of such a high-pressure regime will contribute to our understanding of planet formation, hydrogen storage, room temperature superconductivity and other fields, explains Toshiaki Iitaka from the RIKEN Advanced Science Institute in Wako.

Iitaka, along with colleagues from the Institute of High Performance Computing in Singapore and the University of Saskatchewan in Canada, recently uncovered the physical basis underlying a newly discovered behavior of hydrogen molecules under high pressure[1].

This behavior was observed in a complex of hydrogen molecules, and hydrogen bound to silicon, which is called silane. Silane's hydrogen atoms are under so-called 'chemical compression' by virtue of their being part of a chemical bond. In 2009, physicists found that the vibrational frequency of hydrogen molecules in silane–hydrogen complexes fell as the applied pressure rose. This anti-correlation was the opposite of previous observations of high-pressure hydrogen.

Iitaka and colleagues modeled the system using molecular dynamics simulations. They first optimized the relative arrangement of hydrogen and silane molecules inside a unit cell, finding that the hydrogen molecules tend to sit at octahedral and tetrahedral sites (Fig. 1). They then computed the vibrational frequencies of the hydrogen molecules, and found two groups of vibrational modes, one at high energy and one at low energy.

The frequencies of the lower-energy group decreased monotonically as applied pressure increased. However, the frequencies of the higher-energy group increased with pressure until about 20.1 giga Pascals (GPa), after which they fell. This reproduced the experimentally observed anti-correlation between vibrational frequency and applied pressure, indicating that the simulation was accurate.

The simulations also revealed that this rise and fall in frequencies resulted from interactions between hydrogen and silane molecules. These interactions resulted from the overlap between the filled electron orbitals of one molecule and the empty orbitals of the other molecule. This overlap stabilizes the system, and its strength depends on the distance between the molecules. This distance, in turn, depends on the applied pressure.

The simulation results are another glimpse into the exotic physics that underpins the high-pressure regime, according to Iitaka. "We have shown that there is much more interesting new physics and chemistry to be explored in the world of high pressure." ■

1. Yim, W.-L., Tse, J.S. & Iitaka, T. Pressure-induced intermolecular interactions in crystalline silane-hydrogen. *Physical Review Letters* **105**, 215501 (2010).

Better together

Twin zinc atoms can direct an important organic double-bond-forming reaction with greater efficiency than other methods

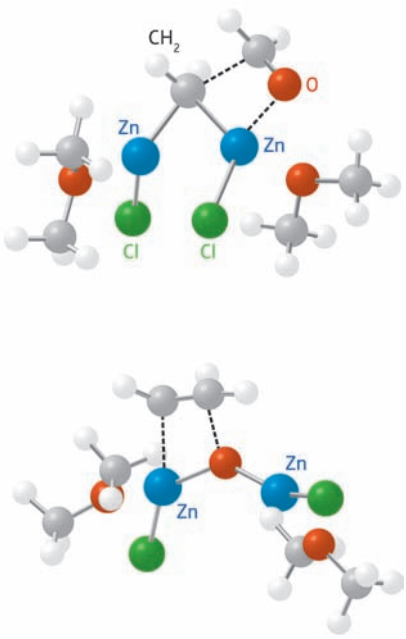


Figure 1: The ability of the *gem*-dizinc (Zn-CH_2-Zn) (top) to create carbon–carbon bonds (bottom) from carbonyl (H_2C=O) groups in two distinct steps promises to make natural product synthesis easier than ever. (O, oxygen; Zn, zinc; Cl, chlorine)

Many natural compounds found in plant and animals display potent medicinal capabilities, but their intricate chemical structures prevent large-scale manufacturing. One common difficulty is synthesizing carbon–carbon double bonds, or alkenes, on the exterior of a molecular framework—a reactive and relatively unstable location. Exposure of the exact mechanisms of an alkene-generating reagent with the moniker of *gem*-dizinc may resolve this problem, report Shinsuke Komagawa and Masanobu Uchiyama from the RIKEN Advanced Science Institute in Wako and their colleagues from Kyoto University and The University of Tokyo[1].

To transform terminal carbon–oxygen double bonds, or carbonyl groups, into alkenes via a short-lived complex that connects two carbon atoms together, chemists classically turn to organophosphorus salts known as Wittig reagents. Sometimes, however, these reagents fail to react with carbonyls or give unwanted by-products, fueling a search for new substances with improved activity and better structural control.

gem-Dizinc compounds are Wittig-type reagents that can produce a wide range of terminal alkenes quickly and at room temperature. They consist of twin zinc atoms that sandwich a methylene (CH_2) unit. Despite these synthetic advantages, the use of *gem*-dizinc reagents remains limited because their structures are unstable and their modes of action controversial; some mechanistic features have eluded discovery for nearly forty years.

Komagawa, Uchiyama, and their team tackled this challenge by first using detailed spectroscopic experiments to identify the active form of the metal complex. Dizinc compounds can readily react with each other to make dimers, polymers, or cyclic structures. However, their measurements conclusively demonstrated that the single monomer was the dominant chemical species.

The researchers took this information as the starting point for sophisticated density functional theory calculations of the reaction pathways. Their simulations showed that alkene formation takes place in two steps (Fig. 1): initially, *gem*-dizinc adds to the carbonyl and forms a cyclic complex. Then, the carbon–carbon double bond is created after *gem*-dizinc swaps its methylene unit for an oxygen atom. They found that the key factor in making this process so efficient was a cooperative 'push–pull synergy' between zinc metals that drove the transformation without having to shuffle electrons between different atoms, making this process quicker than other approaches.

According to Komagawa, these results should help spur the logical design of even better complexes. "The comprehensive mechanistic knowledge acquired in this approach will drive the next stage of this chemistry—more efficient metal reagents that improve the yield and selectivity of alkene formation," he says. ■

1. Sada, M., Komagawa, S., Uchiyama, M., Kobata, M., Mizuno, T., Utimoto, K., Oshima, K. & Matsubara, S. Reaction pathway of methylenation of carbonyl compounds with bis(iodozincio)methane. *Journal of the American Chemical Society* **132**, 17452–17458 (2010).

Making light work of artificial muscles

Polymer films that unfurl in the light could be the first of a new family of functional materials

A new form of self-assembling polymer film that bends and stretches when hit by light is pointing the way to a new family of functional materials. This flexing film is the first material to have been made by coaxing complex molecules to form large-scale, highly ordered three dimensional arrays—a discovery that could change the way that many active material are made, from artificial muscles to solar cells.

Nobuhiko Hosono, Takuzo Aida and colleagues at RIKEN Advanced Science Institute in Wako and The University of Tokyo developed the self-assembly protocol. The researchers found that brush-shaped polymers would form an orderly film when hot-pressed between two sheets of Teflon[1].

They made their discovery while studying a polymer in which each side chain, or bristle, of the brush structure incorporates light-responsive azobenzenes—two benzene rings separated by a pair of nitrogen atoms. When hit by UV light, the bond between the nitrogens rearranges, contracting the side chain.

The researchers used this photoisomerization behavior to confirm the remarkable long-range order of the polymer structure. Because the side chains were all aligned, when those at the surface were hit by light they curled up in concert, bending the film. A second beam of light at a different wavelength reversed the isomerization process, and the film relaxed back to its original shape.

The trick to making the material is to heat it between two sheets of Teflon that have been drawn tight in one direction, says Hosono. This tension orients the Teflon sheets' internal structure along a single axis, which acts as a template for the molten polymer brushes sandwiched in between. The side chains of the polymer brush align with the Teflon, pulling each brush upright. As each polymer brush aligns in the same way, it forms a repeating three-dimensional array (Fig. 1).

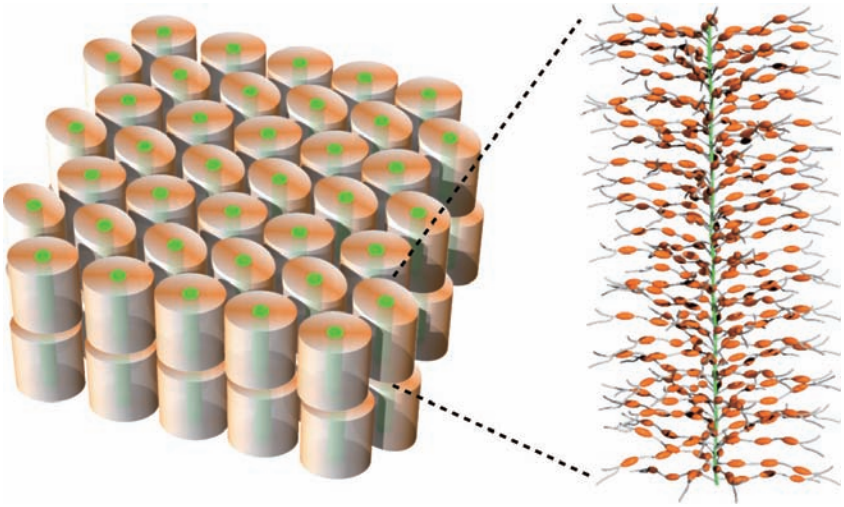


Figure 1: The light-responsive film is made up of polymer brushes (right) that have self-assembled into a two-layer, three-dimensional array (left).

Hosono, Aida and colleagues expect the technique to work for other polymer brushes with similar side chains. To improve the artificial muscle-like behavior of their polymer film, Hosono says the team will try cross-linking the polymer side chains. This will prevent the molecular structure from becoming disordered as the polymer repeatedly curls and relaxes over many cycles, giving the muscle a longer lifetime.

The team is already assessing other potential applications. The wide-area three-dimensional molecular ordering of the polymer brush has great potential for building electronic devices, says Hosono. "We now have designed a new type of polymer brush for development of highly efficient thin-layer organic solar cells." ■

1. Hosono, N., Kajitani, T., Fukushima, T., Ito, K., Sasaki, S., Takata, M. & Aida T. Large-area three-dimensional molecular ordering of a polymer brush by one-step processing. *Science* **330**, 808-811 (2010).

Twisted switches

Helical molecules that contract reversibly when oxidized pave the way to new single-molecule electrochemical switches

Figure 1: *o*-Phenylene oligomers can be envisaged as springy chairs. When oxidized (red), the molecule is contracted and less dynamic than its neutral counterparts (white).

The degree of twisting of natural helical structures, such as the DNA double-helix, plays an essential role in many important biological functions. Because of their twisted architecture, artificial helices can facilitate the separation and the synthesis of chiral compounds—asymmetric molecules that cannot be superimposed with their mirror image.

New, small spring-like polymer chains, or oligomers, from organic compounds called *o*-phenylenes have been created by Eisuke Ohta, Takanori Fukushima, Takuzo Aida and colleagues at RIKEN Advanced Science Institute in Wako[1]. These oligomers consist of benzene rings that connect to each other at a sharp angle, leading to their helical structure. The team's oligomers can change shape and become more rigid when subjected to an electrochemical signal (Fig. 1). They could soon serve as single-molecule machines for application in molecular computers.

Many researchers have investigated molecules that alter their features such as color, luminescence and mode of aggregation when exposed to external stimuli. However, the stimuli-induced change in rigidity demonstrated by the RIKEN team is unprecedented and may open the door to new types of molecular switches.

The researchers synthesized the *o*-phenylene oligomers using an iterative approach, which allowed them to gradually incorporate electrochemically sensitive units to the oligomer's backbone.

Ohta explains that while trying to generate the longest *o*-phenylene oligomers ever synthesized, they noticed that the oligomers possessed highly condensed electron clouds and exhibited a significant reversible difference in rigidity upon removal of one electron during oxidation reactions.

The helical configuration easily causes cyclization—the formation of non-helical structures— which makes the synthesis and investigation of open oligomer chains difficult. The researchers overcame this hurdle by replacing hydrogen atoms positioned at the extremities of the oligomers with so-called 'nitro functional groups'. Moreover, the octamer, which consists of eight *o*-phenylene units, was essential for extending the helices while preventing the cyclization, providing long oligomers of up to 48 *o*-phenylenes.

While purifying their products, the researchers discovered that the nitro-bearing octamer underwent a 'chiral symmetry-breaking process', which produced crystals that contained helices with either a left- or right-handed twist. Furthermore, the helices rapidly switched handedness in solution. However, during oxidation these structures contracted, which slowed the switching process between the two chiral states, enhancing their lifetime. These long-lived states resemble 0 and 1 in binary code, making them attractive for optical memory storage.

The researchers are currently examining the chemical and physical properties of these oligomers, which remain unexplored to date. "We want to unveil these properties now," says Ohta. ■

1. Ohta, E., Sato, H., Ando, S., Kosaka, A., Fukushima, T., Hashizume, D., Yamasaki, M., Hasegawa, K., Muraoka, A., Ushiyama, H., Yamashita, K. & Aida, T. Redox-responsive molecular helices with highly condensed π-clouds. *Nature Chemistry* **3**, 68–73 (2011).

A colorful combination

The ability of bacteria to change the body color of aphids has ecological consequences

A bacterium that can live symbiotically inside the pea aphid, *Acyrthosiphon pisum*, is able to change the insect's body color from red to green, a RIKEN-led team of molecular entomologists has found[1]. Because body color affects how other animals are attracted to aphids, infection with the bacterium is expected to impact on interactions with other symbiotic organisms, predators and parasites. Studies of the molecular mechanism behind the color change could lead to technologies for generating pigments more efficiently, and also for changing the appearance of some organisms, the researchers say.

Both red and green forms of pea aphid occur in natural populations. Previous research by other workers has shown that body color is correlated with the presence or absence of a single gene, and that red is dominant. Ecologically, the balance between the colors is maintained because the most important predators, ladybug beetles, preferentially eat red aphids, while parasitoid wasps attack the green form.

While screening aphids collected in France, Tsutomu Tsuchida from the RIKEN Advanced Science Institute in Wako, together with colleagues from France, and from other Japanese research institutions, found several strains of green aphids with red young that turned green as adults.

Studies by Tsuchida and other researchers have demonstrated that symbiotic bacteria play a role in the adaptation of pea aphids to particular varieties of plants and to high temperature, as well as in the development of resistance to natural enemies. On investigating the symbiotic bacteria in Western Europe, the researchers found that about 8% of pea aphids are infected by a previously unrecognized species of *Rickettsiella* bacteria. Measurements of growth rate, body size and fecundity of infected aphids showed no negative impact on fitness.

Figure 1: The green aphid (left) and red aphid (right) have identical genetic backgrounds. The body color of the green aphid was generated by *Rickettsiella* infection of a previously red aphid.

By generating separate lines of aphids infected and uninfected by *Rickettsiella*, Tsuchida and his colleagues were able to show that uninfected red aphids always retained their color, as did all green aphids. Not all infected red aphids turned green, but the color change from red to green was always associated with *Rickettsiella* (Fig. 1). In fact, the intensity of green color depended on the level of infection. The researchers thus concluded that the color change depended on an interaction between the *Rickettsiella* and aphid genomes.

"We are now extensively analyzing the genome sequence of the symbiotic bacterium and symbiont-induced gene expression of the host aphid," Tsuchida says. "These analyses should show us the molecular and metabolic interplay that leads to the body color change." ■

1. Tsuchida, T., Koga, R., Horikawa, M., Tsunoda, T., Maoka, T., Matsumoto, S., Simon, J.-C. & Fukatsu, T. Symbiotic bacterium modifies aphid body color. *Science* **330**, 1102–1104 (2010).

Fish frozen in fear

Fear responses of zebrafish are controlled by brain structures of previously unknown function

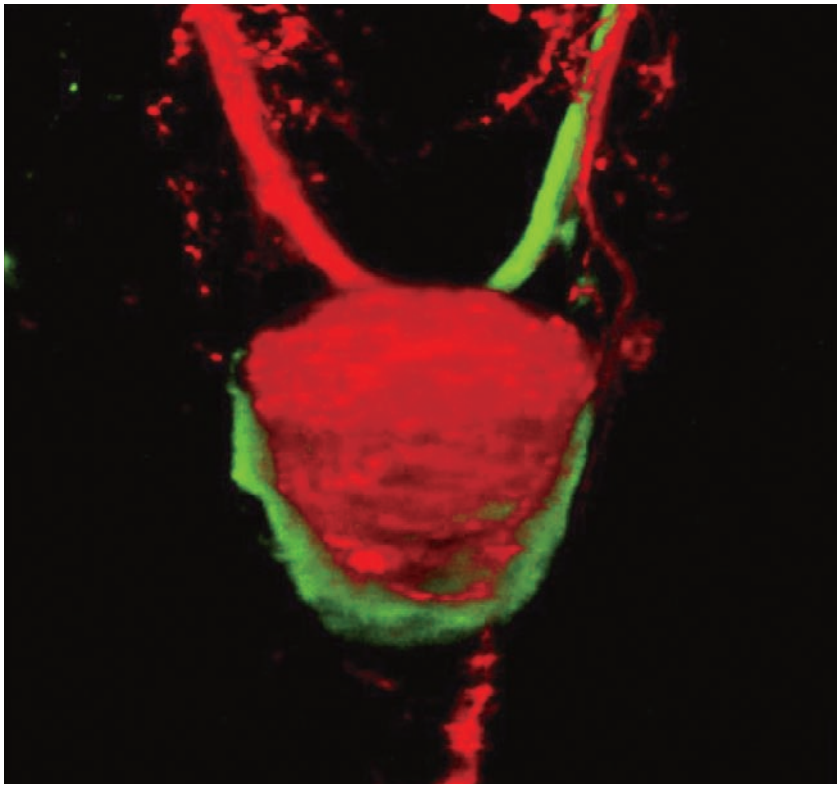


Figure 1: Confocal fluorescence micrograph of the larval zebrafish brain, showing neural pathways from the lateral (red) and medial (green) subnuclei of the dorsal habenula to the interpeduncular nucleus.

A brain structure called the habenula is crucial for modifications of fear responses in zebrafish, according to a new study by researchers from the RIKEN Brain Science Institute, Wako[1]. The zebrafish dorsal habenula is subdivided into two regions, each connected to different brain structures, but the function of each, and the significance of their connections, was unclear.

Hitoshi Okamoto and his colleagues used fluorescent dyes to trace the neural pathways from the interpeduncular nucleus (IPN), which receives connections from the dorsal habenula region (Fig. 1). They found that the dorsal IPN projects to midbrain structures called the dorsal raphe nucleus and griseum centrale. The corresponding structures in the mammalian brain have been implicated in responses to fear and stress, suggesting that the habenula–IPN pathway in zebrafish is also involved in these responses.

To investigate this, the researchers created transgenic zebrafish expressing tetanus toxin in the lateral subnucleus of the dorsal habenula. The toxin blocks neurotransmission, preventing neurons in that region from sending signals.

The transgenic fish were then subjected to an established fear conditioning task, in which a red light is repeatedly paired with an electric shock. Normally, the fish learn to associate the two stimuli, and become agitated—recognized by an increase in the frequency of turning—in the presence of the light alone. However, when the transgenic fish encountered the red light after the fear conditioning task, they froze rather than escaping. Okamoto and colleagues observed these differences between the transgenic fish and controls during the fear conditioning task. Both froze the first time they encountered the red light; the controls started to become agitated the second time, but the transgenic fish continued to freeze.

The exploratory behavior of the transgenic fish was no different from that of the controls, showing that their responses to fear conditioning were not due to abnormal sensory or motor function. Instead, the results suggest to the researchers that the transgenic fish cannot modify their fear response after new experiences. They therefore conclude that experience-dependent modifications of fear responses are controlled by the neurons in the lateral subnucleus of the dorsal habenula in the zebrafish.

"We would like to know whether the same regulation mechanism works in mammals, including humans," says Okamoto, "and would also like to extend our research to reveal the functions of the other parts of the habenula." ■

1. Agetsuma, M., Aizawa, H., Aoki, T., Nakayama, R., Takahoko, M., Goto, M., Sassa, T., Amo, R., Shiraki, T., Kawakami, K., *et al*. The habenula is crucial for experience-dependent modification of fear responses in zebrafish. *Nature Neuroscience* **13**, 1354–1356 (2010).

Keeping brain development in focus

A newly characterized protein promotes embryonic brain formation by hiding a receptor with the potential to undermine this process

Figure 1: Staining reveals the specific expression of the *Jiraiya* gene within the neuroectoderm of a developing *Xenopus embryo*.

The various bone morphogenetic protein (BMP) signaling factors play an important role in early neural development in the vertebrate embryo. However, maturation of these tissues ultimately depends on the coordinated activity of factors that suppress BMP activity within the neuroectoderm, a cell population that ultimately gives rise to the nervous system.

Yoshiki Sasai and colleagues at the RIKEN Center for Developmental Biology in Kobe have now revealed a novel regulator of BMP signaling, *Jiraiya*[1], which they originally identified in a screen for genes activated by the BMP inhibitor Chordin in the African clawed frog, *Xenopus laevis*[2]. "*Jiraiya* was intriguing as it encoded a novel membrane protein that had no homology to known proteins, and its expression was neural-specific," says Sasai.

Unexpectedly, his team determined that the Jiraiya protein acts as a specific inhibitor of BMPRII, one of two core subunits of the BMP receptor, within the neuroectoderm (Fig. 1). BMPRII chemically modifies BMPRI in response to BMP binding; BMPRI subsequently activates downstream components of the signaling cascade. Initial experiments showed that Jiraiya specifically interferes with signaling at a point between ligand binding and BMPRI activation.

When overexpressed in cultured embryonic frog cells, Jiraiya depleted BMPRII from the plasma membrane by sequestering it within complexes in the cytoplasm. Evidence suggests that this protein physically interferes with the delivery of newly synthesized receptor molecules to the cell surface.

BMPRII is part of a larger family of receptor proteins that are relatively similar to one another, but features a distinctive 'C-terminal tail domain' (TD) that contains within it the specific Jiraiya-binding motif. This enigmatic 'EVNNNG' sequence appears to be a unique feature of BMPRII, although it is closely conserved in receptor homologues from other species. Transplantation of the motif onto a different receptor, ActRIIA, was sufficient to make that protein susceptible to similar Jiraiya-mediated inhibition. "The most intriguing part is that it acts only on the type II subunit of BMPR via this tail-domain whose role in dynamic signaling modulation had not been known," says Sasai.

He and his colleagues conclude that Jiraiya appears to represent an important mechanism for the cell-specific inactivation of BMP-responsive pathways, and thereby helps define the boundaries of neural tissue development. The *Jiraiya* gene is found in a broad range of vertebrate species, although expression in the mouse embryo does not seem to follow the same neural-specific pattern of localization seen in frog embryos. Sasai hopes to further clarify its role in mammalian development in future studies. ■

1. Aramaki, T., Sasai, N., Yakura, R. & Sasai, Y. Jiraiya attenuates BMP signaling by interfering with Type II BMP receptors in neuroectodermal patterning. *Developmental Cell* **19**, 547–561 (2010).
2. Sasai, N., Mizuseki, K. & Sasai, Y. Requirement of FoxD3-class signaling for neural crest determination in *Xenopus*. *Development* **128**, 2525–2536 (2001).

Unearthing the mechanisms controlling plant size

Keiko Sugimoto

Unit Leader
Cell Function Research Unit
RIKEN Plant Science Center

Plants have been cultivated and studied from the earliest days of human civilization, yet much remains unknown about them. A good example is the mechanism by which the size of plant cells is determined. Keiko Sugimoto, leader of the Cell Function Research Unit in RIKEN's Plant Science Center, in working to elucidate this mechanism has discovered a series of genes that control cell division or cell growth, attracting the attention of researchers and companies worldwide. "Our research focuses on the cellular aspects of plants," says Sugimoto.

A garden of lilies

While a high-school student, Sugimoto noticed that a single lily that had blossomed in her garden the year before had become three lilies a year later, followed by ten the next year and as many as 100 the year after. "But what impressed me most was that all of those flowers were the same size, and had the same color and same shape every year," she says. "Although I knew that this was a manifestation of heredity, which I had learned at school, I was fascinated. I wanted to understand the mystery of plants, and this led me into research."

After completing her master's course in Japan, Sugimoto gained her PhD in plant science at the Australian National University. She then went to work at the John Innes Center in the UK—a Mecca for researchers studying plant biology—and in 2007 she set up the Cell Function Research Unit in RIKEN's Plant Science Center. "How is plant cell size controlled? We are now working to solve this difficult problem."

The aspect that had impressed Sugimoto most as a high-school student was that the sizes of flowers, leaves, seeds and other plant organs depend roughly on the species of plant. Each organ grows as its cells self-divide and increase in number, and each cell expands. However, plant organs do not continue to grow infinitely. "Flowers and leaves stop growing when they reach a certain size. Research has shown that plant hormones such as auxin and cytokinin are involved in plant growth, but we still don't know how plant hormones control cell division and cell expansion to determine ultimate organ size," says Sugimoto. "Plant size cannot be understood without knowing what is happening in cells. We are conducting research focusing on the cellular aspects of plants, which is a unique approach."

Determinants of plant growth

"Every time I cut radishes or carrots into long, thin strips for cooking, I cannot help admiring the slices for a moment," says Sugimoto with a smile. "If you look closely at a slice, you can see a finely textured portion near the tip. This is called the meristem. It is

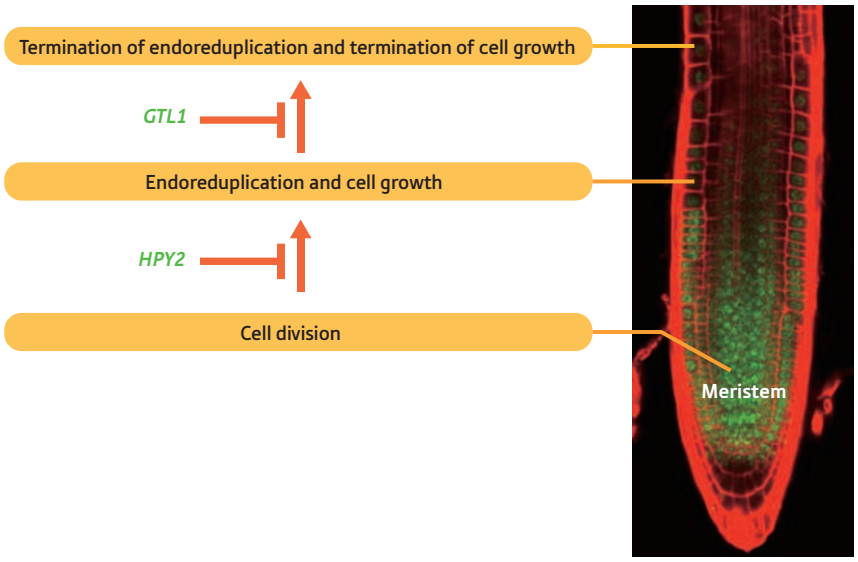


Figure 1: Mechanism underlying an increase in plant size.
Photograph showing a cross-section of *Arabidopsis* roots. Plant cells divide mainly in the meristems at the tips of roots and stems. After dividing several times, cells begin to increase their size due to endoreduplication. When the cell reaches a certain size, endoreduplication and cell growth cease. The *HPY2* gene controls the transition from cell division to endoreduplication, whereas the *GTL1* gene stops cell growth. The green fluorescence indicates the *HPY2* expression.

dividing tissue where the cells self-divide. Try taking a look next time you're preparing a meal."

In plants, meristems (Fig. 1) are found only in the tips of roots and stems. Plant growth is the result of cell division and proliferation at the meristem, which is followed by cell expansion. "There are two key time points in plant growth. One is a turning point when cell division switches to cell expansion. Once a cell begins expanding, it cannot return to the stage of proliferation by division. The other is the point when cell growth stops and cells no longer expand. Plants cannot grow normally unless these two points are strictly controlled." Sugimoto and her colleagues have attracted global attention for their discovery of the genes that control these two growth points.

Genes control cell division and endoreduplication

Sugimoto used a new technique to discover genes that control the point at which cells stop dividing and begin increasing in size. "Many researchers have tried to look for genes that control cell size, but most of them were trying to find mutants with altered cell size. Mutants have been identified merely based on the appearance of cells. We developed a method to accurately measure nuclear DNA content and isolate mutants with altered DNA levels."

The cells of *Arabidopsis*, a commonly used experimental material in plant science, just like human cells, have two sets of chromosomes, one from the mother and the other from the father. The DNA of a cell having two sets of chromosomes is denoted 2C. When a 2C cell divides, its DNA is first replicated to produce 4C, which is then equally distributed into the next two dividing cells, resulting in two 2C daughter cells. In *Arabidopsis*, however, 2C and 4C cells are not the only cell types to be found. Gametes (pollen, ovules) that have undergone meiosis, a special process of cell division that results in half the number of chromosomes as found in somatic cells, are 1C cells, but there are also 8C, 16C and 32C cells (Fig. 2). "In plant cells, DNA replication is sometimes followed by doubling in DNA without mitosis," says Sugimoto. "This phenomenon is called endoreduplication, which results in 8C, 16C and 32C cells. The nuclear DNA and cell size are correlated; cells expand as their nuclear DNA increases."

Together with Takashi Ishida, a postdoc in her lab, Sugimoto examined the nuclear DNA content of *Arabidopsis* cells and discovered a mutant having fewer 2C and 4C cells and more 32C, 64C and 128C cells (Fig. 3). "Usually in plants, 2C and 4C cells in meristems continue to divide at a constant rate. We assume that in the mutant we discovered, these meristematic cells have undergone endoreduplication and switched into cell expansion prematurely. A more detailed investigation revealed that this mutant had lost the function of the *HPY2* gene. Hence, *HPY2* plays a role in controlling the point of switching to endoreduplication, where cells stop dividing and instead grow in size."

This achievement was announced in August 2009, drawing attention not

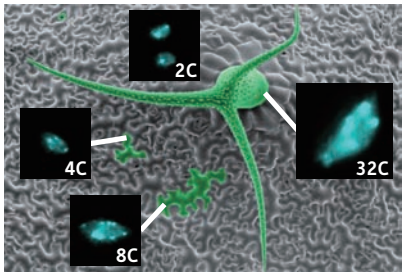


Figure 2: Endoreduplication and cell size in *Arabidopsis*.
A scanning electron microscopy image of the surface of an *Arabidopsis* leaf showing a trichome. Most cells have 2C nuclear DNA content, but some cells have increased nuclear DNA contents of 4C, 8C and 32C due to endoreduplication. The four insets show the correlation between cell size and the amount of nuclear DNA. The trichome has a nuclear DNA content of 32C.

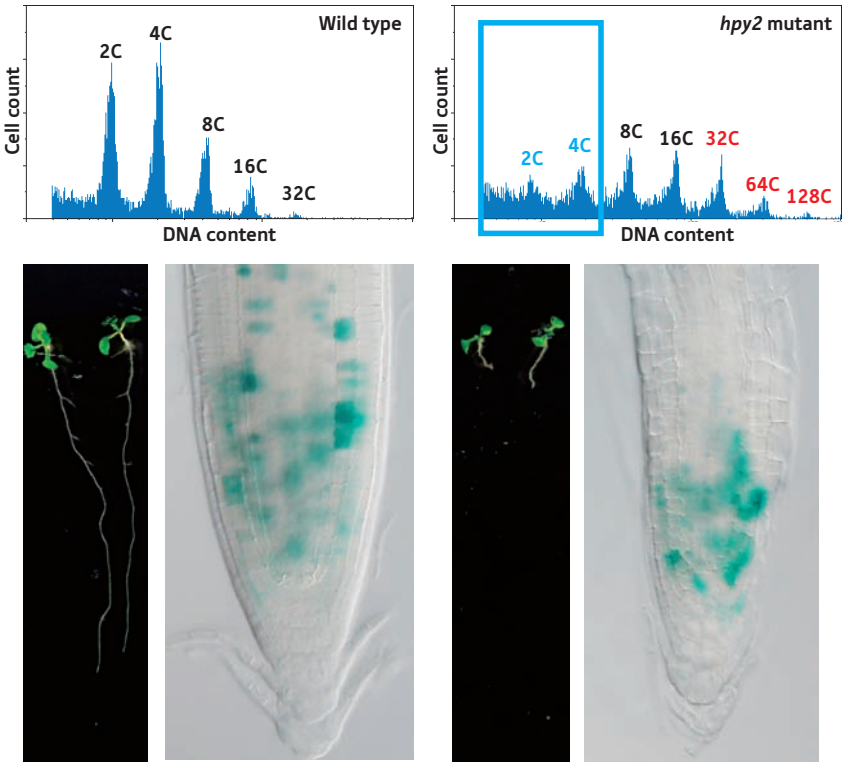


Figure 3: Regulation of cell division by the *HPY2* gene.
(Upper) Nuclear DNA content of a cell population. The *hpy2* mutant has lower ratios of 2C and 4C and higher ratios of 32C, 64C and 128C compared to the wild-type control. (Lower) Photographs of wild-type (left) and *hpy2*-mutant (right) plants ten days after germination. The mutant has very small roots and leaves. The Blue staining indicates defective cell division in the mutant.

only from plant biologists, but also from researchers studying a wide variety of other organisms. "This is because *HPY2* is involved in the function of a small peptide known as SUMO, a small ubiquitin-like modifier. SUMO is found in a broad range of species, from humans to plants and yeasts. It binds to other proteins to enhance or weaken their functions, and to regulate the diverse functions of cells. The reason why my result attracted so much attention is that researchers studying diverse ranges of organisms have been interested in SUMO."

Sugimoto's group demonstrated that the protein produced by *HPY2* mediates the binding of SUMO to other proteins, resulting in the regulation of cell division. This was the first report of SUMO being associated with the regulation of cell division in multicellular organisms. "I never thought that my studies on the mechanism of plant cell size control would lead to SUMO. Research is fascinating because it can lead to unexpected results."

Sugimoto has also discovered three other genes that control the switch into endoreduplication like *HPY2*. Her next task is to clarify the differences in their functions.

A gene terminating cell growth

In September 2009, following the discovery of *HPY2*, Sugimoto's group discovered a gene involved in the second point—when plant cells stop growing in size. "It began with the discovery of a mutant having very large trichomes by Christian Breuer, a posdoc in my lab, who was searching for mutants with abnormal cell size."

Trichomes are hair-like outgrowths that cover the surfaces of *Arabidopsis* leaves to protect them from insects, pathogens and even ultraviolet radiation (Fig. 4). "Each trichome comprises a single epidermal cell in *Arabidopsis*. It is large enough to be seen macroscopically." While even a normal-sized trichome is 500 times larger than an ordinary cell, the mutant discovered by Breuer has trichomes that are more than twice this size.

The mutant was found to have the *GTL1* gene partially modified and expressed in excess. When the function of *GTL1* was artificially suppressed, the mutant's trichomes became more than twice the size of wild-type trichomes. Based on these experiments, Sugimoto's group hypothesized that *GTL1*

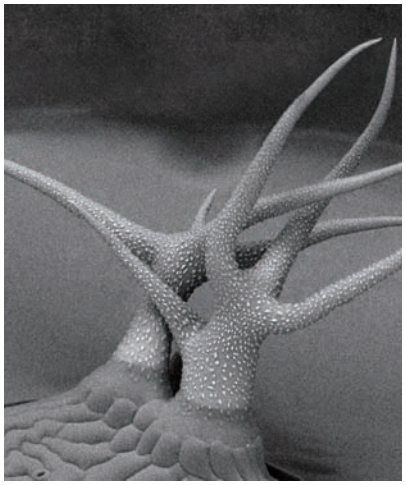


Figure 4: *Arabidopsis* trichomes.
Trichomes are hair-like outgrowth at the plant leaf surface, each comprising a single cell. These cells protect plants against insects and pathogens, and trichomes in some species produce useful secondary metabolites such as aspirin. Sugimoto's group examined *Arabidopsis* mutants with abnormally expanded trichomes and discovered *GTL1*, a gene that terminates cell growth. The photograph shows a mutant having an increased number of trichome branches. A normal trichome has three branches.

functions to terminate cell growth. To test the hypothesis, they examined when and where *GTL1* is expressed. It was found not to be expressed in smaller trichomes in the early stage of growth or trichomes that had stopped growing, but to be expressed only in trichomes that have just expanded to maximum size (Fig. 5).

Previously, it had been thought that cell growth ceases when the supply of cellulose and other components of the cell wall is stopped, or when water absorption in vacuoles ceases. However, the discovery of *GTL1* shows that plants have an intrinsic mechanism for actively stopping cell growth. The discovery is groundbreaking, overturning the traditional concept of plant growth.

Trichomes are cells undergoing endoreduplication, which is known to cease at 32C. Sugimoto's group is conducting research on the hypothesis that *GTL1* may control endoreduplication. It is already known that the function of the gene necessary for endoreduplication is activated in mutants lacking the function of *GTL1*. "*GTL1* produces a protein known as a transcription factor, which binds to the DNA of a certain gene to promote or suppress its transcription to RNA. In the future, I want to clarify how *GTL1* controls transcription and of which genes, and to discover the mechanism of endoreduplication."

Figure 5: Trichome size and *GTL1* expression.
Photograph (left) and fluorescence image (right) of wild-type and *GTL1*-lacking mutants. *GTL1* (labeled with green fluorescent protein) is expressed only in trichomes that have just grown to maximum sizes, and not in younger or older trichomes.

Giant prospects

Since the announcement of the discovery of *GTL1*, Sugimoto has received a flood of offers for joint research, including many inquiries from industry, who have great expectations for creating larger fruits and vegetables by suppressing the function of *GTL1*.

Some cultivars are already available with increased yields thanks to artificial duplication of nuclear DNA with chemical agents. However, this chemical treatment unavoidably duplicates the nuclear DNA in all cells constituting the plant body, which in turn makes the plant unable to produce seeds. "Advanced research on *GTL1* may allow us to promote endoreduplication at desirable portions of plants, such as fruits, flowers and leaves, or whenever needed, to change their sizes without preventing seed production," says Sugimoto, who is keen to conduct joint research with industry.

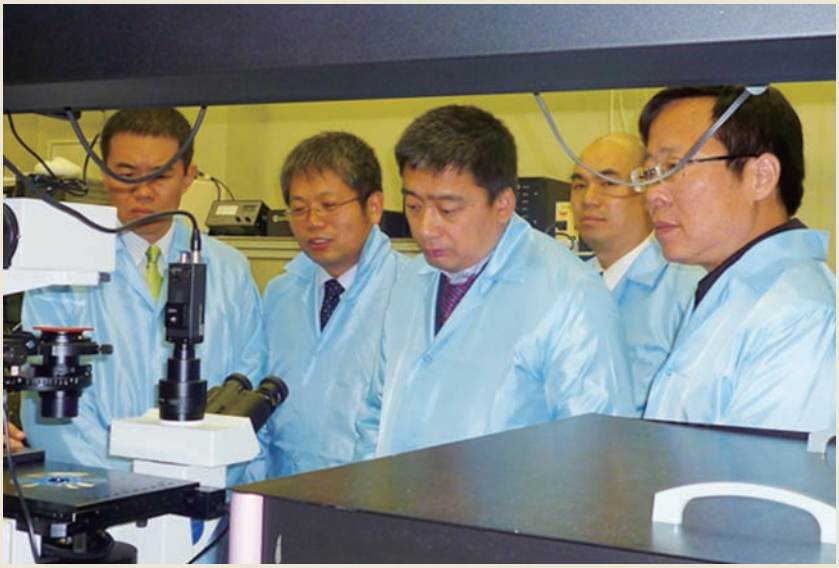
"Now is the most enjoyable time in my academic career," declares Sugimoto. However, she is not satisfied with just discovering the genes that control plant growth. Further extensive investigation of the functions of individual genes is needed. It is also necessary to identify the targets of *HPY2* and *GTL1* to determine on which genes and proteins they act. She is also interested in the relationship between *HPY2* and *GTL1*, and their association with plant hormones. "Much remains to be done, and I have not found the answer to my question about lilies when I was a high school student. In the plant kingdom, there are so many unanswered questions. This is why I am fascinated by plant research." ■

Keiko Sugimoto

Keiko Sugimoto was born in Hiroshima, Japan, in 1971. She graduated from Osaka University in 1995, and obtained her PhD in 2000 from the Australian National University. After five years of postdoctoral training at the Department of Cell and Developmental Biology, John Innes Center (JIC), UK, she became group leader at the JIC. In 2007, she moved to Japan to take up a position of group leader at the RIKEN Plant Science Center. Her research focuses on the molecular and cellular mechanisms of plant size control.

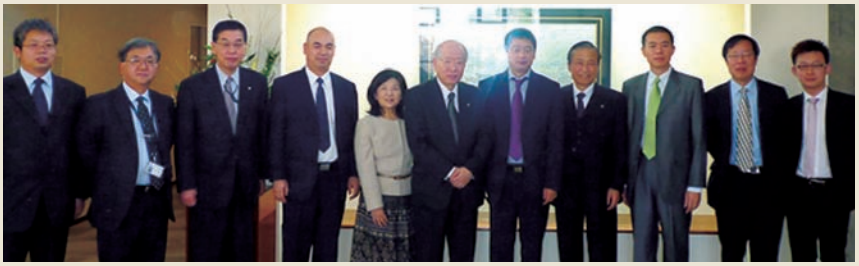
RIKEN hosts delegates from China's Ministry of Science and Technology

On 6 January 2011, RIKEN welcomed to the Wako campus visitors from the Chinese Ministry of Science and Technology, including Deputy Director General Xu Chaoqian from the Department of International Cooperation, Directors Xu Jie and Jiang Xiaoping of the Division of Asia and Africa, Wu Xiang Lei (interpreter), along with Li Ying (counselor) and Miao Yun (attaché) from the Chinese embassy in Tokyo. This is the first visit to RIKEN by a high-ranking official of China's Ministry of Science and Technology. The delegation was welcomed by RIKEN President Ryoji Noyori and RIKEN's executive directors who explained RIKEN's management and evaluation systems as well as its human resources development programs. The presentations were followed by lively discussion on the potential for collaboration and joint research programs between RIKEN and China's leading universities. The delegation was next taken on a tour of the Radioactive Isotope Beam Factory, including visits to the Metamaterials Laboratory headed by Takuo Tanaka and the Organometallic Chemistry Laboratory headed by Zhaomin Hou, both of which are involved in joint Japan–China science and technology research projects. Throughout the visit, there was friendly discourse on the possibilities for long-term cooperation between RIKEN and the Chinese Ministry of Science and Technology.



High-ranking delegates from the Chinese Ministry of Science and Technology made their first visit to RIKEN in January 2011.

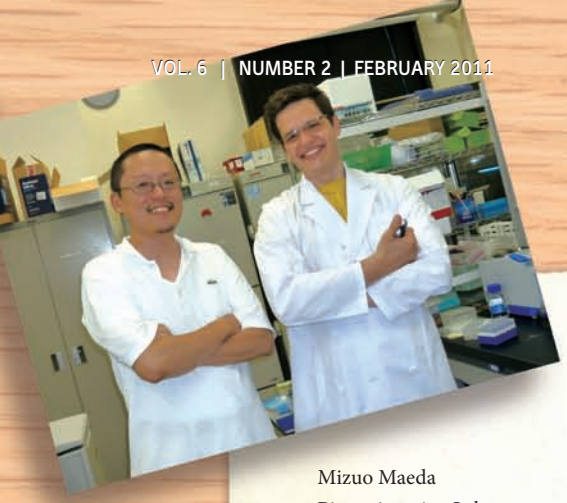
RIKEN's ties with China are steadily growing in importance. Since it first entered into a general memorandum on research collaboration with the Chinese Academy of Sciences in 1982, RIKEN has been actively involved in personnel exchange, joint research, joint symposiums and other such collaborations with a variety of Chinese partners ranging from the Chinese Academy of Sciences headquarters and the Institute of Modern Physics, to institutions such as the universities of Peking, Tsinghua, Shanghai Jiao Tong, Xi'an Jiaotong and Zhejiang. RIKEN also has more than 200 Chinese scientists working at its campuses, accounting for roughly 20 percent of RIKEN's foreign researcher population.

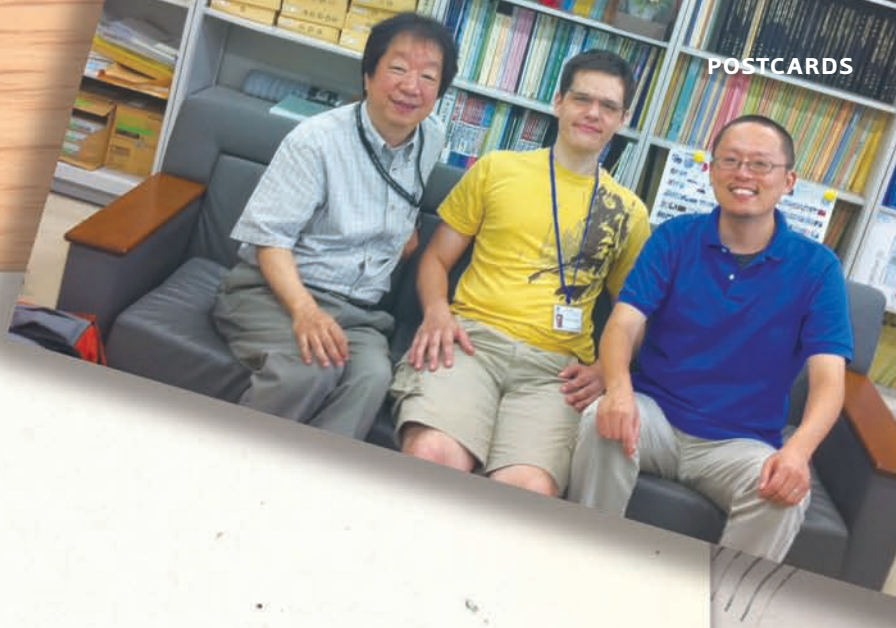


To further reinforce its commitment to China, RIKEN sent a representative to China in September 2006 to apply for permission to establish a RIKEN China office. While awaiting this permission, RIKEN held information meetings for Chinese scientists, sent delegations to visit Chinese universities, research institutions and corporations, and created a researcher alumni network. RIKEN President Noyori also visited China to present special lectures.

All these efforts have borne fruit. RIKEN now has formal collaborative agreements with the universities of Peking, Shanghai Jiao Tong, Xi'an Jiaotong, and Zhejiang, and is already pursuing joint research with these Chinese partners. Most recently, on December 2010, permission was granted by the Chinese Ministry of Science and Technology for RIKEN to open an office in China.

Moving forward, the new RIKEN Beijing Representative Office will act as the focal point for even more active research collaboration and exchange between RIKEN and China. ■





Mizuo Maeda
Bioengineering Laboratory
RIKEN Advanced Science Institute
Wako, Saitama, Japan

Dear Prof. Maeda,

It has been three months since I left RIKEN and I am now putting together my thesis for my PhD. I remember boarding an ANA flight to Narita airport in June last year, my stomach tingling slightly from nerves but mostly from excitement. It is a feeling that I always get when I travel long distance and I absolutely love it. My mind was filled with images of Japan that I had seen in museums, movies and in popular culture from back in London.

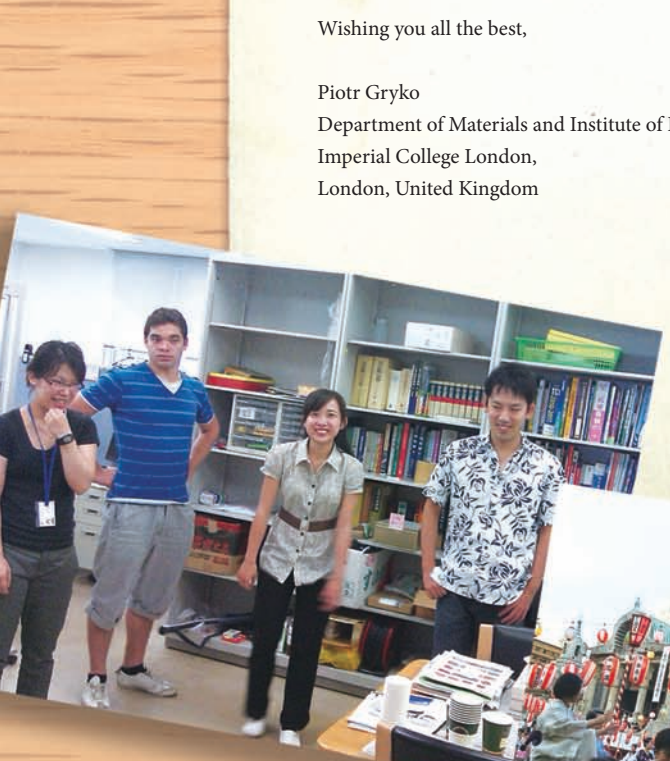
I was fortunate enough to be accepted by both your research group and the Japan Society for the Promotion of Science (JSPS), and when I arrived I attended a week-long course on Japanese culture and language organized by the JSPS. The course was held at the Shonan Village Center with the support of the Sokendai Graduate University for Advanced Studies. We were taught Japanese customs and provided with a crash course in 'survival' Japanese. While Japanese is a beautiful but complicated language, it is difficult to master while recovering from jet lag.

When I finally arrived at RIKEN, I was impressed by your group's great laboratory facilities and the expertise of your research staff. Doctor Zako and other members of your group provided me with extensive support on a daily basis, greatly aiding me with my work. I was kindly invited to see a Japanese drum performance played by Dr Zako's wife. The performance was electrifying, I have never seen five people play in an energetic choreographed synchronized manner for over an hour.

I would like to thank you for placing me in contact with a research group at Kyushu University and arranging for me to visit them. I was able to meet gifted researchers at Kyushu University and have meaningful discussions with them. I also want to thank you and your research team for making my stay at RIKEN amazing. I will miss the Japanese food (*sushi*), warm weather and excellent company.

Wishing you all the best,

Piotr Gryko
Department of Materials and Institute of Biomedical Engineering,
Imperial College London,
London, United Kingdom



www.riken.jp

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. Initially established as a private research foundation in Tokyo in 1917, RIKEN became an independent administrative institution in 2003.

RIKEN RESEARCH is a website (www.rikenresearch.riken.jp) and print publication intended to highlight the best research being published by RIKEN (www.riken.jp). It is written for a broad scientific audience and policy makers interested in science and aims to raise global awareness of RIKEN and its research.

For further information on the research presented in this publication or to arrange an interview with a researcher, please contact
RIKEN Global Relations Office
2-1, Hirosawa, Wako, Saitama, 351-0198, Japan
TEL: +81 48 462 1225
FAX: +81 48 463 3687
E-Mail: rikenresearch@riken.jp

www.rikenresearch.riken.jp