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Seeing molecules move in real-time

Ultrafast lasers instantaneously track a molecular twist in progress

Although chemists are experts at characterizing the products of their reactions, understanding what goes on inside the beaker—where atoms twist, bend, separate, and rejoin into new molecular units—remains a mystery on many levels.

"Watching chemical reactions in real-time has long been a dream of chemists," says Tahei Tahara of RIKEN's Advanced Science Institute in Wako. "To reach a correct understanding of chemical reactions, this 'watching' is crucial."

Now, thanks to Tahara and his colleagues, scientists are awakening to a reality where an atom can be followed along a three-dimensional path. In their latest work, Tahara and a team of international and Japanese scientists have directly observed how an organic molecule named stilbene rearranges its structure[1].

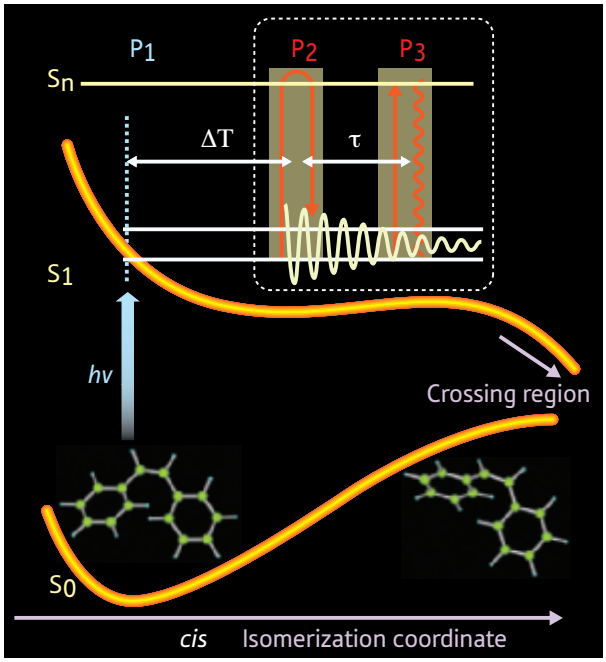

Figure 1: Schematic of the real-time detection process. An initial (P_1) pulse of laser light (*hν*) excites a *cis*-stilbene molecule from the ground to the excited state ($S_0 \rightarrow S_1$), starting a rearrangement reaction. A second laser pulse (P_2) causes the molecule to vibrate, while a third pulse (P_3) detects the vibration signal by monitoring absorption to higher excited states (S_n). Varying the time delay between pulses (ΔT, τ) reveals a series of vibrational 'snapshots', depicting motion during the chemical reaction.

Good vibrations

The best way to watch reactions in real-time is to monitor molecular vibrations. When light hits a molecule, it can interact with the chemical bonds between nuclei and cause them to vibrate periodically. These vibrational frequencies are chemically specific: for example, a carbon–carbon bond vibration is easily distinguished from a carbon–hydrogen signal. And, because very small changes to a chemical structure create easily observed shifts in vibrational frequencies, tracking these motions provides a way to follow the dynamics of a reaction.

However, tracking atoms in chemical reactions has previously seemed unrealistic, because the nuclei move so fast—movements can be complete within 1 picosecond (10^{-12} second). Polyatomic molecules like stilbene are even more challenging to visualize because scientists must account for multiple vibrations. Furthermore, some characteristic vibrations used for chemical identification often occur at low frequencies that are beyond the limits of most analytical instruments.

Probing atoms with ultrafast light

The development of lasers that emit light faster than nuclei move allowed scientists to make real-time observations of chemical reactions. Initial experiments used a 'pump–probe' technique: a first laser pulse—the pump—excited the molecule to initiate a reaction, and then the second pulse—the probe—captured the position of the nuclei. Changing the time delay between pump and probe pulses allowed pictures of the chemical reaction to emerge.

The resolution obtained with the pump–probe technique, however, is limited. In 2003, Tahara and his colleagues developed a new technique that combined pump–probe methods with Raman vibrational spectroscopy to measure the movements of short-lived, excited-state molecules[2].

The researchers then initiated a chemical reaction by exciting electrons with a laser pulse. After a short time delay, they induced the entire molecule to vibrate using 10-femtosecond (10^{-14} second) lasers. Finally, using a third laser pulse, they measured how these atoms vibrated in real time, as the reaction progressed (Fig. 1).

Tahara and his team's work allowed the low frequency motions in the excited state to be accurately resolved, which provides information not accessible by other techniques, and is crucial for understanding how a polyatomic molecule like stilbene can rearrange its structure.

Capturing a twist in progress

Stilbene is one of the most popular molecules used to study photoisomerization, the class of reactions that powers molecular switches and plays a central role in vision. The initial isomer, called *cis*-stilbene, has two benzene rings positioned close together and connected by a carbon double bond. When excited by light, this molecule twists and rearranges to *trans*-stilbene, such that the benzene rings end up far apart.

Scientists have long believed that the rearrangement of stilbene is accomplished by large vibrational movements of the benzene rings. Watching this reaction with Tahara's spectroscopic method, however, revealed that the molecule changes geometry using a completely different mechanism.

"With excitation, the central carbon double bond is weakened," explains Tahara. And then, hydrogen atoms attached to the carbon double bond move in opposite directions, initiating a twisting motion that leads to *trans*-stilbene. "That stilbene twisting is realized by hydrogen atom movement, [and] not by a large motion of benzene rings, was surprising to us," says Tahara.

Computer-aided pictures

To visualize the three-dimensional molecular motion (Fig. 2), the team combined experimental results with a high-level quantum-chemical calculation. The computation correlated the frequency changes observed in the experiment with particular molecular movements—and helped identify the exact twisting mechanism that had previously eluded researchers.

"Quantum computation was indispensable in this work," says Tahara. "However, we had to be very careful to choose the most reliable computational method because different methods provided significantly different computational results."

Fortunately, Tahara and his team's experiments provided reliable data that they could use to gauge the accuracy of theoretical calculations—a combined approach that will be useful in visualizing other molecular systems.

"Because it is dangerous to blindly believe the computation, it is crucial to check the consistency between the experimental data and computation, especially for calculations on excited polyatomic molecules," explains Tahara. "We carefully examined the reliability of different methods by comparing the computational results with the spectroscopic data of stilbene."

"In a sense, the data supplied by this type of advanced spectroscopy provides check points for the theoretical calculations that are now advancing very rapidly," he says.

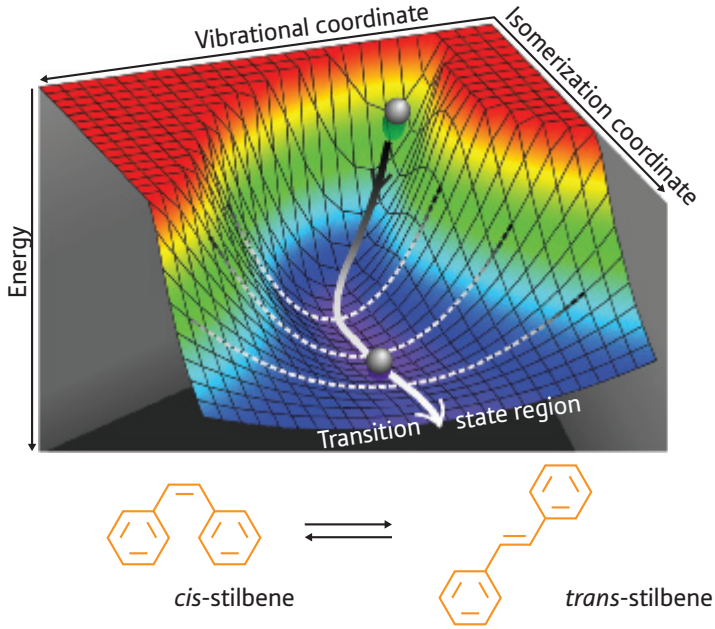

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Figure 2: Schematic of a three-dimensional potential energy map of the twisting motion taken when *cis*-stilbene converts to *trans*-stilbene.

Lasers or test tubes?

With scientists now able to observe what goes on in their beakers using ultrafast lasers, it begs the question—can they start to use those lasers to control chemical reactions in ways never seen before?

Tahara says he doesn't know how conceivable it is to control chemical reactions by light. "Nevertheless, I would like to try it on the basis of solid understanding of the potential energy of reactive molecules, which is obtainable by this type of study."

1. Takeuchi, S., Ruhman, S., Tsuneda, T., Chiba M., Taketsugu T. & Tahara, T. Spectroscopic tracking of structural evolution in ultrafast stilbene photoisomerization. *Science* **322,** 1073–1077 (2008).
2. Fujiyoshi, S., Takeuchi, S. & Tahara, T. Time-resolved impulsive stimulated Raman scattering from excited-state polyatomic molecules in solution. *Journal of Physical Chemistry A* **107,** 494–500 (2003).

About the researcher

Tahei Tahara was born in 1961 in Tokyo, Japan. He graduated from the Faculty of Science, the University of Tokyo, in 1984, and obtained his PhD degree in 1989 from the same university. He became research associate of the Department of Chemistry, Faculty of Science, the University of Tokyo in 1989, and then moved to newly founded Kanagawa Academy of Science and Technology (KAST) as research associate in 1990. In 1995, he joined Institute for Molecular Science (IMS) as associate professor and started his own research group. He was appointed to Chief Scientist of RIKEN in 2001 and, since then, he has been director of Molecular Spectroscopy Laboratory. His research interest is development and application of advanced molecular spectroscopy to study dynamics and structure of 'complicated' molecular systems in the condensed phase. He currently focuses on ultrafast spectroscopy and nonlinear spectroscopy in solutions, at interfaces, and for micro-spaces.

Twist and turn

Experiments with a rotating magnetic field provide new understanding on its coupling to the electric polarization of a multiferroic material

The electric polarization of a multiferroic material is linked directly to its magnetism, which allows the control of magnetism with electric fields and vice versa. Researchers at RIKEN's Advanced Science Institute in Wako, in collaboration with scientists from the University of Tokyo, have now studied how the electric polarization of multiferroic materials responds to changes in an externally applied magnetic field.

To date, the number of known multiferroic compounds is limited to a few oxide compounds. Furthermore, in most multiferroics the coupling of the magnetic field and electric polarization, or multiferroic coupling, is rather small, particularly at room temperature. However, some oxide compounds, such as $Eu_{0.55}Y_{0.45}MnO_3$, have a strong multiferroic coupling, albeit only at relatively low temperatures.

Common to this novel class of multiferroics is an arrangement of atomic magnetic moments, or spins, in the form of either a helix or a cycloid where the spins have a slightly different orientation to their neighbors. It is this cycloidal arrangement that creates an electric polarization (Fig. 1a).

As reported in *Physical Review Letters*[1], the researchers studied the influence of a rotating magnetic field on the cycloidal spins, which consequently start to follow the external rotation. They have found that in the presence of a magnetic field perpendicular to these cycloids, the atomic spins tilt towards the direction of the magnetic field, and a conical structure develops (Fig. 1b). The conical structure preserves the handedness of the cycloid structure, so as the magnetic field rotates around the cycloid axis (Fig. 1c,d), the electric polarization rotates in similar fashion.

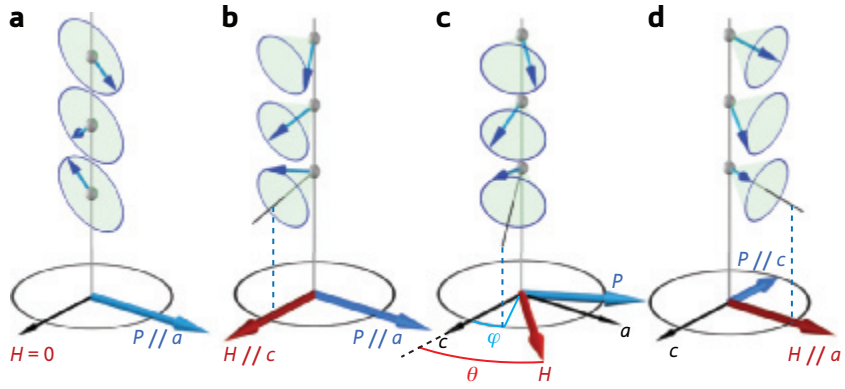


Figure 1: Response of electric polarization, *P*, to a magnetic field, *H*. (a) In the absence of a magnetic field the polarization points to the crystal axis *a*. (b) If a magnetic field is applied in *c*-direction, the cycloids evolve into a conical structure. (c) As the magnetic field is turned at an angle of θ, the polarization moves by a similar angle, ϕ. (d) As H points towards a, a complete 90° rotation is completed.

When the researchers applied the rotating external magnetic field in the direction of the cycloids, the response of the electric polarization was slightly more complex as the cycloids react slightly different to tiny variations in magnetic field. However, they noted that the electric polarization still responds very sensitively to the magnetic field.

The team studied the multiferroic material $Eu_{0.55}Y_{0.45}MnO_3$, but their results apply to all related compounds. "The electric polarization is highly sensitive to the rotation of the magnetic field, which illustrates how these multiferroics may be used as a magnetic sensor," comments team member Shintaro Ishiwata on the implications of their findings.

These findings are important to detail the dynamics of the multiferroic coupling; however the operational temperatures for these helical multiferroics are currently limited to cryogenic temperatures and this restricts their technical application. "Our ultimate goal is to find a material that works at room temperature operation," stresses Ishiwata. ■

1. Murakawa, H., Onose, Y., Kagawa, F., Ishiwata, S., Kaneko, Y. & Tokura, Y. Rotation of an electric polarization vector by rotating magnetic field in cycloidal magnet $Eu_{0.55}Y_{0.45}MnO_3$. *Physical Review Letters* **101,** 197207 (2008).

Surface patterning: Hop to it

The controlled rearrangement of surface-adsorbed molecules can be achieved by careful application of an electric field between a scanning tunneling microscope tip and a surface

On a fundamental level, the ability to assemble patterns of single molecules on a surface can provide researchers with important information on the interactions between neighboring molecules. Molecules that are adsorbed on a surface can be moved by pushing or pulling them with an STM (scanning tunneling microscope) tip. However, this can be a slow process, and can easily result in damage to both the fragile tip of STM or to the adsorbed molecule.

Writing in *Physical Review B*[1], Yousoo Kim and colleagues from the RIKEN Advanced Science Institute in Wako have reported a non-contact method for rapidly and accurately positioning single molecules. The researchers demonstrate their method by preparing patterns of methyl thiolate ions adsorbed on a copper surface. Each molecule of thiolate is adsorbed on the copper surface at a so-called hollow site—spaces that exist between the arrangement of copper atoms at the surface. When an electric field is applied between the STM tip and the surface, the molecules' vibrations are increased—the chemical bonds in the molecule can be considered as small springs—and the molecule hops to an adjacent hollow site. The researchers showed that this description of the hopping movement is correct by showing that the voltage that must be applied corresponds to the known vibrational frequency of the carbon–sulfur bond in the methyl thiolate.

This vibrational excitation has been observed before but, the electric field has always been applied directly at the center of the molecule, and the movement of the molecules was random in nature. Kim and colleagues, however, investigated the effect of applying the electric field slightly off center. They showed that they could not only cause the molecule to move to an adjacent hollow site, but they could control the direction in which it moved in a highly selective fashion. As a demonstration, the researchers used their method to arrange molecules of methyl thiolate to produce the letters 'STM' (Fig. 1).

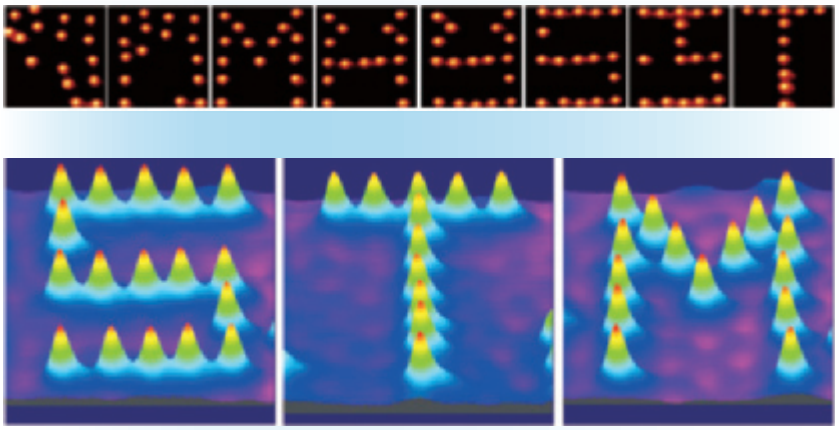


Figure 1: A group of methyl thiolate molecules adsorbed on a copper surface can be repeatedly rearranged to spell out the letters of STM.

It has been shown previously that when adsorbed on a copper surface, the methyl thiolate probably bears a negative charge. This is supported by the movement direction of the methyl thiolate. When the STM tip is negatively charged, a repulsive electrostatic force causes the molecule to hop away from the tip. Similarly, when the STM tip is positively charged, the molecules hop towards the tip. Precise positioning of molecules in this way will be important for the development of functional materials such as those used in memory devices. ■

1. Ohara, M., Kim, Y. & Kawai, M. Electric field response of a vibrationally excited molecule in an STM junction. *Physical Review B* **78**, 201405(R) (2008).

Breaking symmetry in the strong force

Supercomputers allow researchers to calculate symmetry violations in the strong interaction that holds atoms together

An international research team has reconciled two theories that explain the properties of the pion. The work is important because this subatomic particle plays a key role in the strong interaction—the fundamental force that holds atomic nuclei together.

The pion consists of a quark and an anti-quark, meaning it is classified as a hadron alongside protons and neutrons—but it has very different properties.

"One puzzle was that the pion is much lighter than other hadrons," says scientist Sinya Aoki, based at the University of Tsukuba and the RIKEN BNL Center in New York.

The unexpectedly light pion mass was first explained by Yoichiro Nambu, who received the Nobel Prize for Physics in 2008. He realized that the strong interaction usually obeys a rule called 'chiral symmetry', but in a vacuum this rule can be broken.

"A quark has spin, or self-rotation, which can be in a left-handed or right-handed direction," Aoki explains. "The chiral symmetry means that left-handed quarks and right-handed quarks never mix with each other. If this chiral symmetry is spontaneously broken, a pion appears to be massless. This, however, is not true if the quarks have mass."

In fact, pions have a tiny mass due to the small but non-zero quark mass, irrespective of the large energy scale of the strong interaction.

Effects of quark mass in the presence of spontaneous chiral symmetry breaking have been illustrated using a tool called chiral perturbation theory. However it is important to show that the symmetry breaking can occur in the fundamental theory of the strong interaction, called quantum chromodynamics (QCD), which governs the behavior of quarks and gluons.

KEK

Figure 1: **The supercomputer at the High Energy Accelerator Research Organization (KEK) in Tsukuba that was used to verify the small mass of the pion within the fundamental theory of quantum chromodynamics.**

Until now it has been difficult for QCD to verify the small pion mass owing to problems such as 'sea quarks'—virtual quark-antiquark pairs that pop in and out of existence in the gluon field.

In their latest work[1], Aoki and co-workers used powerful supercomputers (Fig. 1) at the High Energy Accelerator Research Organization (KEK) in Tsukuba to run QCD numerically on a lattice. They calculated exactly how the mass and decay properties of a pion depend on the quark mass.

They have shown for the first time that QCD provides the same results as chiral perturbation theory, if one assumes a small enough quark mass. Aoki is delighted with the success.

"Our results not only show that the lattice QCD and the chiral perturbation theory agree, but also prove that Nambu's chiral symmetry breaking indeed occurs in QCD."

1. Noaki, J., Aoki, S., Chiu, T.W., Fukaya, H., Hashimoto, S., Hsieh, T.H., Kaneko, T., Matsufuru, H., Onogi, T., Shintani, E. & Yamada, N. Convergence of the chiral expansion in two-flavor lattice QCD. *Physical Review Letters* **101**, 202004 (2008).

Spin lattices enter a new phase

A new ordered phase is predicted for geometrically frustrated spin systems even in the absence of magnetic order

RIKEN scientists, in collaboration with researchers at the University of Tokyo, Japan, and Sungkyunkwan University, Korea, have unveiled the possible existence of a new magnetic phase in the spatial arrangements of electron spins[1]. The new arrangement is considered to be the combination of two unconventional types of order.

Spin, in this context, is the smallest magnetic moment associated with an electron and can point in any direction. In most solid structures, the spins of electrons sitting on different atoms will tend to point in such a way that neighboring spins point in opposite, or 'anti-parallel' directions. This gives rise to the so-called antiferromagnetic phase. There are, however, some atomic structures for which this is not possible, and they are called geometrically frustrated structures. Triangular lattices, including the compounds κ-(BEDT-TTF)$_2$Cu$_2$(CN)$_3$and NiGa$_2$S$_4$, are common examples of geometrically frustrated structures.

As team-member Shigeki Onoda from the RIKEN Advanced Science Institute in Wako explains, the spins interact among themselves and with the natural vibration of the lattice. This combined interaction can give rise to unusual types of order. One example is the helical order (Fig. 1a), in which spins rotate with respect to one another, but in an ordered way. The helical order is a type of chiral order: as in all chiral systems, it cannot be superimposed on its mirror image. Another example is the nematic order (Fig. 1b) in which the orientation angle of the spins is fixed, but keep flipping their direction.

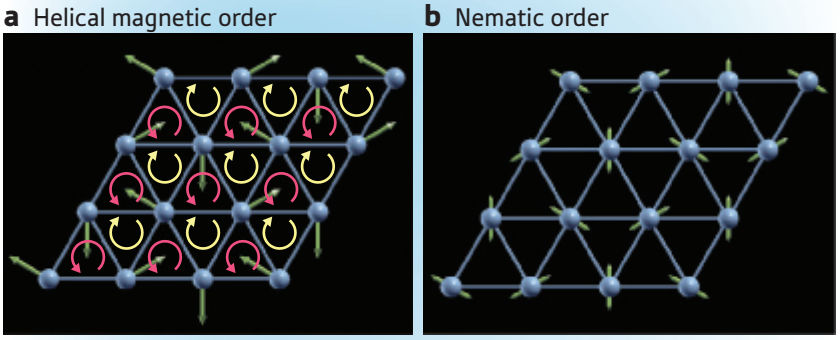


Figure 1: Schematic representation of (a) helical and (b) nematic order in a triangular spin lattice.

The researchers studied theoretically the phase diagram of a triangular lattice in which spins can point in any direction in the plane. The mutual interaction between spins has two components: one that is usually responsible for the emergence of helical order, and one that leads to nematic order. Until now, however, no-one had considered the combination of both.

The team's calculations show interesting results in the case in which the nematic component is predominant. When the temperature rises—increasing the lattice vibrations—the helical order is replaced by a new chiral phase, in which the spins flip in time, similar to the nematic case. According to Onoda, this chiral–nematic order could be used in applications. The chirality allows rotating the polarization of a transmitted laser beam. By varying the external conditions, such as external fields, pressure, or temperature, it could be possible to switch the chirality—and the polarization rotation—on and off, effectively creating a functional optical device. ■

1. Park, J.-H., Onoda, S., Nagaosa, N. & Han, J.H. Nematic and chiral order for planar spins on a triangular lattice. *Physical Review Letters* **101**, 167202 (2008).

Smashing pictures

Controlled collisions of molecules allow RIKEN scientists to visualize dual microscopic chemical reaction pathways

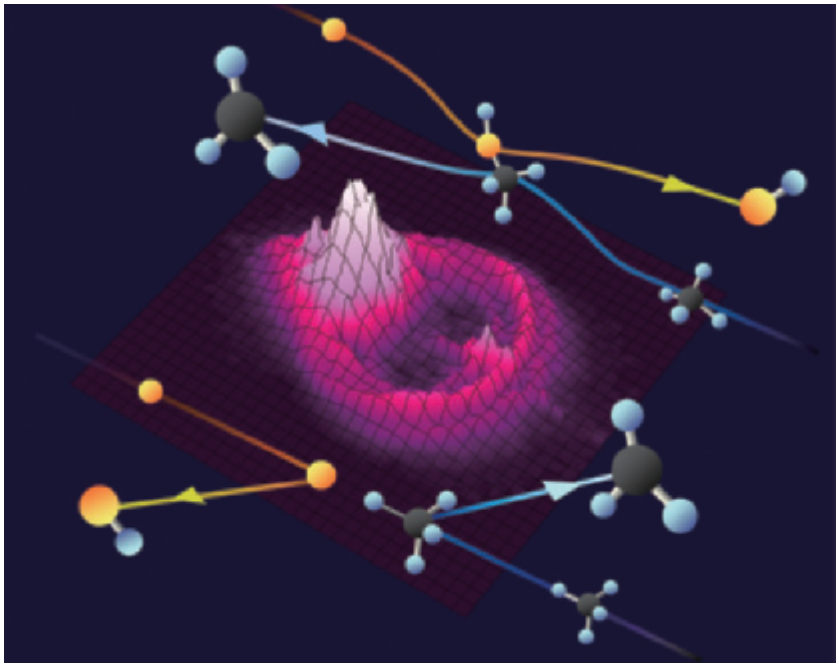


Figure 1: Three-dimensional dynamic imaging of a chemical reaction. Most excited oxygen atoms (orange spheres) undergo a glancing collision with methane molecules (black/blue spheres), producing a large, bright distribution of CH_3 in the forward direction via insertion (top). Only head-on collisions of atoms and molecules produce discreet rings of CH_3 in the backward direction via abstraction (bottom).

A research team at RIKEN's Advanced Science Institute in Wako has broken the rules of chemical reactions. Instead of using test tube sets, the researchers generated high-velocity beams of atoms and molecules. By imaging the collision process, they were able to visualize the exact reaction pathway taken during the creation of new molecular species.

The team, led by Toshinori Suzuki, is a world leader in the field of imaging molecular collisions. In recent work, the researchers tackled how electronically excited oxygen atoms (O*) react with methane (CH_4) gas[1]. This reaction is one of the most important primary processes in the stratosphere.

First, Suzuki and colleagues used a laser to generate the O* atoms needed to reproduce the reaction in the laboratory. Then, they crossed accelerated beams of methane and O* gas at right angles in a vacuum chamber, smashing the gases together. The collisions produced a large amount of the methyl radical species CH_3, which could be ionized and projected onto a phosphor screen, as in a cathode-ray TV.

The projected images showed how CH_3 scatters away from the interaction center at different velocities, and dramatically revealed the co-existence of two chemical reaction pathways (Fig. 1). The CH_3 products either scatter forward, in a large continuous distribution, or backward, as discrete concentric rings.

When the team crossed beams of O* and methane, they found that particles usually undergo a glancing collision, hitting each other's sides. This contact inserts oxygen between a carbon and hydrogen atom, forming a methanol intermediate in its ground electronic state that quickly breaks up into two products: CH_3, which continues in the same forward direction as the original methane beam, and OH, which moves in the opposite direction.

The torque from the glancing collision produces a broad distribution of forward scattered CH_3. Because energy is conserved in the collision, the continuous range of CH_3 velocities directly indicates that the other product, OH, is vibrating and rotating considerably.

Backward scattered products are much rarer, and happen when O* directly abstracts a hydrogen to produce OH and CH_3 via the excited electronic state of CH_4-O*. "For the reaction to occur, the oxygen, hydrogen, and carbon atoms must lie in a straight line, and collide head-on," explains Yoshihiro Ogi, a postdoctoral researcher in the group. "The discrete rings indicate that the OH product is vibrating, but not rotating, upon formation."

"This experimental technique will continue to reveal much about gas-phase reactions, especially those related to atmospheric chemistry," says Ogi. ■

1. Kohguchi, H., Ogi, Y., & Suzuki T. Reaction mechanism duality in $O(^1D_2) + CD_4 \rightarrow OD + CD_3$ identified from scattering distributions of rotationally state selected CD_3. *Physical Chemistry Chemical Physics* **10**, 7222–7225 (2008).

Surprise shift

A first-of-a-kind switch in chemical bonding by a zirconium atom spotted by scientists

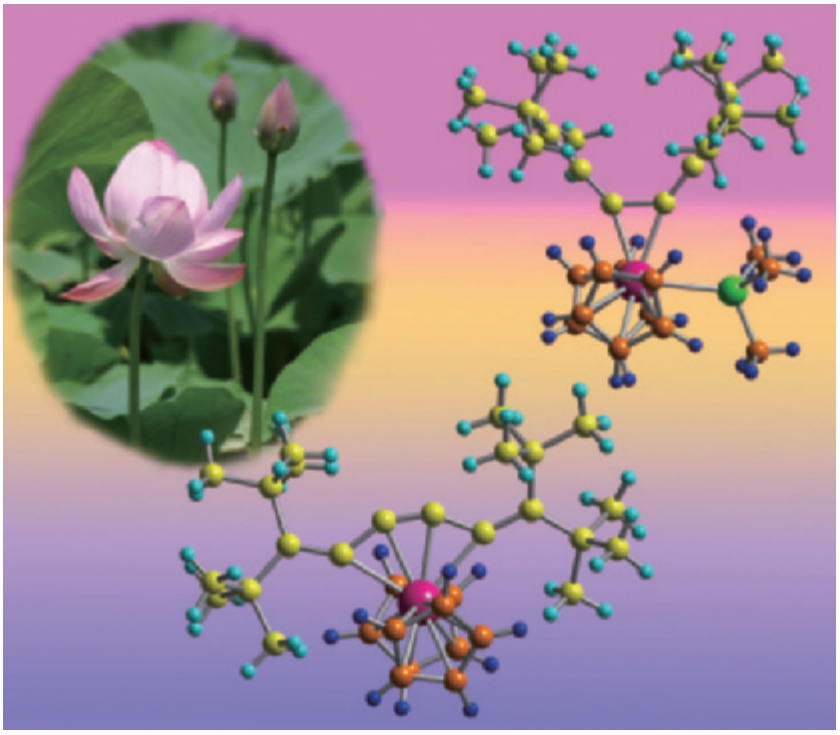


Figure 1: Schematic showing that adding or removing an extra chemical group (green) to the zirconium atom (pink) can open and close the structure of the molecule like the petals of a lotus flower.

A zirconium atom can switch easily between two different bonding patterns in an unusual molecule created by Japanese scientists.

The molecule's odd behavior is the first example of this particular type of chemical bonding shift, according to Noriyuki Suzuki of RIKEN's Advanced Science Institute in Wako, now at Sophia University, and his colleagues at Saitama University and Saitama Institute of Technology. "These complexes have very unique structures and show interesting movement," says Suzuki. An example is shown in Figure 1.

The team discovered the phenomenon when they were experimenting with a molecule (hexapentaene) made from a chain of six carbon atoms, all doubly bonded to each other. The chain is surrounded by a long cloud of delocalized electrons, which can bond with a zirconium-based compound to create a new complex.

Once the new complex has formed, the zirconium atom normally tends to bridge between carbon atoms in different parts of the chain, creating a five-membered ring. But when very bulky groups were added to each end of the chain, the zirconium switches its allegiance so that it sticks to just the central carbon–carbon double bond.

The complex could be toggled between its two bonding modes by adding or removing other chemical groups such as phosphines around the zirconium atom. Further experiments showed that this sort of shift was the first step in a reaction the scientists had previously studied, where adding an isocyanide chemical to the zirconium complex created a compound with a small ring of four carbon atoms at its heart.

This switching behavior is well known in certain ring-shaped organic molecules, but is much rarer in these molecular chains, and is unprecedented with this particular compound. "It suggests the possibility of a molecular motion like scissors or tongs," says Suzuki. The research is published in the *Journal of the American Chemical Society*[1].

Suzuki's team has spent several years investigating a range of such zirconium complexes, which were long assumed to be too unstable to isolate[2,3].

Although there are no immediate applications for this family of complexes, Suzuki suggests that it may be possible to use the scissoring action identified in their latest research to capture another molecule or ion. "We might be able to achieve a molecular machine that catches a certain target," says Suzuki. ■

1. Suzuki, N., Hashizume, D., Yoshida, H., Tezuka, M., Ida, K., Nagashima, S. & Chihara, T. Reversible haptotropic shift in zirconocene–hexapentaene complexes. *Journal of the American Chemical Society* **131,** 2050-2051(2009).
2. Suzuki, N., Nishiura, M. & Wakatsuki, Y. Isolation and structural characterization of 1-zirconacyclopent-3-yne, five-membered cyclic alkynes. *Science* **295,** 660–663 (2002).
3. Suzuki, N., Hashizume, D., Koshino, H. & Chihara, T. Transformation of a 1-zirconacyclopent-3-yne, a five-membered cycloalkyne, into a 1-zirconacyclopent-3-ene and formal "1-zirconacyclopenta-2,3-dienes". *Angewandte Chemie International Edition* **47,** 5198–5202 (2008).

Partners in crime

A genomic study reveals important details about how microbes dwelling in the termite gut help their insect hosts to wreak havoc

Figure 1: A partial look at the termite gut ecosystem. One of the most important protists in the gut of the *C. formosanus* termite (left) is *P. grassii* (top right), and each *P. grassii* cell is in turn dependent on the presence of thousands of CfPt1-2 endosymbionts (bottom right) for its survival.

Just as any shovelful of dirt may contain within it a thriving ecosystem of interdependent organisms, many animal species contain within their gut an equally active community of microorganisms, all collaborating to promote host survival. For the Formosan subterranean termite, *Coptotermes formosanus,* and its relatives, this means facilitating these insects' destructive appetites and assisting them in extracting sustenance from wood—a challenging and relatively nutrient-poor food source.

Scientists have confidently fingered one protist, *Pseudotrichonympha grassii,* as this termite's primary accomplice. "*C. formosanus* cannot survive without *P. grassii,* even when other protist species remain abundant," explains Yuichi Hongoh of the RIKEN Advanced Science Institute in Wako. The picture gets more complicated, however, as this microbe is itself a haven for numerous tiny bacteria known as endosymbionts, which also make vital contributions to the gut ecosystem (Fig. 1).

Termite gut flora have proven difficult to cultivate, making it challenging to understand how they contribute to termite survival. However, powerful new DNA sequencing methods have now enabled Hongoh and his colleagues to fully decode the genome of an essential bacterium from *C. formosanus,* yielding valuable insights into the 'black box' of termite wood digestion[1].

They targeted the endosymbiont CfPt1-2, which resides within *P. grassii* and is the most abundant bacterium in the *C. formosanus* gut. From a single *P. grassii* cell, they extracted thousands of CfPt1-2 bacteria, obtaining enough genetic material by whole-genome amplification to derive its complete genomic sequence. These data providsed valuable details about how CfPt1-2 facilitates termite survival, revealing genes that convert dinitrogen in the air into essential amino acids that are otherwise scarce in the termite diet.

Equally importantly, CfPt1-2 appears to assist *P. grassii* host cells by recycling nitrogenous wastes such as ammonia into more useful compounds for biosynthesis. This bacterium also has the apparent capacity to produce energy from hydrogen waste generated during the wood digestion process.

On the other hand, the evolutionary streamlining of this endosymbiont's genome has resulted in the loss of other essential functions that make it equally dependent upon *P. grassii* for survival. "The CfPt1-2 bacterium has evolved like an organelle, which cannot live outside the host cell," explains Hongoh. "Long-term evolution has established this elaborate, multi-layered symbiosis."

Hongoh believes further exploration of the *P. grassii*-CfPt1-2 partnership will not only yield valuable insights about how they sustain their termite hosts, but may even facilitate development of effective strategies for extracting energy from wood-based biofuels. ■

1. Hongoh, Y., Sharma, V.K., Prakash, T., Noda, S., Toh, H., Taylor, T.D., Kudo, T., Sakaki, Y., Toyoda, A., Hattori, M. & Ohkuma, M. Genome of an endosymbiont coupling N2 fixation to cellulolysis within protist cells in termite gut. *Science* **322**, 1108–1109 (2008).

Finding an opening

A detailed structural analysis reveals new insights into the operating mechanism of a protein pore

Many newly synthesized proteins will pass their lives within the confines of the cell, but many others end up secreted or embedded in the cellular membrane. Such proteins are labeled by specific 'tags' encoded in their sequences, which get recognized by proteins that escort them to the pore-like translocon protein complex. In bacteria, translocons are situated in the inner cell membrane. They remain effectively closed until they interact with an escorted protein, at which point the pore opens and allows the protein to pass through the membrane.

The central pore complex of the bacterial translocon is formed by a trio of proteins: SecY, SecE and SecG. Pore opening is initiated via interaction of the SecYEG complex with an additional protein, SecA, although many mechanistic details of this process remain unclear. Now, new work from a multi-institutional research team, led by Osamu Nureki of the University of Tokyo and Koreaki Ito of Kyoto University, and including RIKEN scientists Naoshi Dohmae and Yuji Sugita of the Advanced Science Institute in Wako, has yielded valuable new insights into this process[1].

The team generated crystals of the SecYE complex from the bacterium *Thermus thermophilus*, assisted by the inclusion of an antibody fragment that helped to stabilize the complex, and then compared this structure against a previously determined structure of the 'closed' translocon from a primitive bacterial species that lacks SecA[2]. This comparison revealed the existence of an opening absent from the closed structure, suggesting that the SecYE-antibody complex had assumed a transitional 'pre-open' state.

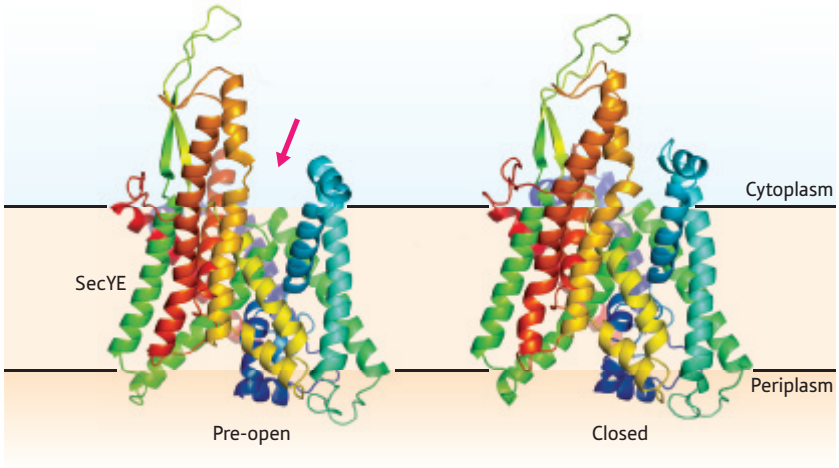


Figure 1: Model of the transition of the Sec translocon between the pre-open and closed forms. When SecA associates with SecYE, the complex rearranges into a 'pre-open' state, which features an opening—indicated here by a pink arrow—through which proteins can be delivered. This opening is absent in the pore's 'closed' state.

Follow-up analysis yielded multiple lines of evidence that the antibody interaction with SecYE mirrors the association of this complex with SecA, suggesting that the structure seen here is a true intermediate in the translocon opening process, and that SecA binding induces formation of an entry point in SecYE for translocation-ready proteins (Fig. 1). This transition of SecYE into the pre-open state also appears to induce major conformational changes in SecA, which enable it to act as a motor for facilitating protein transit through the translocon pore.

Dohmae and Sugita are continuing to collaborate in the further examination of this mechanism, using chemical analysis techniques and computational simulations to confirm that the model developed based on these findings reflects the reality of how these proteins interact in the cell, but both researchers are pleased with these initial structural insights. "This crystal structure is useful to understand the early process of polypeptide translocation through Sec channels," says Sugita. ■

1. Tsukazaki, T., Mori, H., Fukai, S., Ishitani, R., Mori, T., Dohmae, N., Perederina, A., Sugita, Y., Vassylyev, D.G., Ito, K. & Nureki, O. Conformational transition of Sec machinery inferred from bacterial SecYE structures. *Nature* **455,** 988–991 (2008).
2. Van den Berg, B., Clemons, W.M., Collinson, I., Modis, Y., Hartmann, E., Harrison, S.C. & Rapoport, T.A. X-ray structure of a protein-conducting channel. *Nature* **427,** 36–44 (2004).

From robotics to animal motor-control systems

Multiple timescales of neural activities are important to motor-control systems in animals, according to research using robots

Programmers of robots have long been challenged by the difficulty of implementing some of the simplest of human activities, such as walking up stairs or digging a ditch. This is partially due to the versatility of human motor behavior in varying situations. Such robustness can be achieved with a functional hierarchy: a division of labor that allows complex motor behaviors to arise from simpler tasks that are connected at a higher level.

Previously, researchers had theorized that a connection of reusable sub-movements called motor primitives would be represented by spatially localized networks in the brain. Now, Yuichi Yamashita and Jun Tani from the RIKEN Brain Science Institute, Wako, have shown that the temporal characteristics of neurons in these motor networks may be just as critical to their functional hierarchy[1].

Yamashita and Tani took a synthetic approach to test their hypothesis that multiple timescales of activity could mediate motor organization. To this end, the scientists trained a robot to complete a set of distinct, but related, tasks. These motor behaviors included picking up a block to shake it side to side (Fig. 1), picking up a block to shake it up and down, and touching the top of a block with one hand.

"It is generally thought that diverse behavior of an animal results from a functional hierarchy of the motor-control system," explains Yamashita, where "motor primitives are flexibly integrated." For example, the robot's tasks could be executed by mixing and matching such primitives as making contact with an object, lifting it, and shaking it.

Figure 1: A humanoid robot executes one of its tasks, which involves picking up an object, shaking it side to side three times, and setting it back down. Use of the robot was made possible through a collaboration with SONY Corporation.

The key distinction in Yamashita and Tani's work was that the hierarchical organization arose from multiple timescales in the network activity, rather than through spatial connections. The spatially based networks of previous studies consisted of isolated modules responding to each primitive in the lower levels, and gates to select and switch between primitives in the higher levels.

By contrast, the neural network of Yamashita and Tani's robot comprised fast units, which could respond quickly to changing inputs, and slow units, which tended to avoid rapid fluctuations by relying on previous states. Based on the network activity, it appeared that the fast units had spontaneously organized to represent motor primitives, whereas the slow units resembled gates that ordered and activated the primitives. This discovery helps to explain the puzzling discrepancy between previous theories of spatially based motor organization and the elusive evidence of such spatial organization in the animal brain. ■

1. Yamashita, Y. & Tani, J. Emergence of functional hierarchy in a multiple timescale neural network model: A humanoid robot experiment. *PLoS Computational Biology* **4**, e1000220 (2008).

Unearthing the diversity of plant chemicals

Determining the molecular workings of plant cells is now possible using a newly developed method

Molecular biologists from RIKEN's Plant Science Center in Yokohama have published a systematic method for linking the detectable working molecules or metabolites in plant cells to their biological functions.

The technique was developed to assist studies of the diversity of plant chemicals and deliberately avoids targeting particular compounds. "The wide variety of plant chemicals [is] a good source of natural medicines, spices, and toxins," says first author, Fumio Matsuda.

The method provides enough structural information to allow chains of reactions or pathways to be mapped, compounds to be linked to genes, and the molecular consequences of mutations to be studied. Cells from different tissues can be compared to determine which metabolites are specific to particular species or parts of plants.

The researchers created a library of all the metabolites of a particular cell tissue and labeled them with spectral tags—data on two or more fragments of the same compound that can be used to identify its presence in mass spectrometer information. The compounds were separated by means of liquid chromatography and the tags generated using tandem mass spectrometry. The tags themselves provide data on parts of the molecule which can be used to deduce its structure directly, or can be matched by software with spectral information on standard compounds.

The researchers tested their method using extracts from shoot and flower tissues of the plant genetics model organism *Arabidopsis* (Fig. 1). They were able to detect more than 1,000 compounds, and about half were tagged. Of these, 95 were identified and annotated with at least some information on their structure and function. The details have been published in a recent paper in *The Plant Journal*[1].

Figure 1: The model plant *Arabidopsis thaliana* is being used in research to determine the biological functions of various plant chemicals found in different tissues.

Among the annotated compounds were some which, on the basis of their tags, appeared structurally related. These could be used as the basis of hypotheses about metabolic pathways. The researchers also compared the occurrences of 44 annotated compounds in four different plant tissues. They found several of them to be tissue-dependent, and in some cases were even able to trace unusual metabolites back to the genes coding for them. When the researchers deliberately inserted mutant genes into plants, they found they could track differences in the metabolites the cells produced.

"We showed our technique could be useful for investigating metabolic functions in plants," Matsuda says. "We are now making a detailed catalogue of phytochemicals in various plant species such as rice, wheat, soybean and tomato."

1. Matsuda, F., Yonekura-Sakakibara, K., Niida, R., Kuromori, T., Shinozaki, K. & Saito, K. MS/MS spectral tag-based annotation of non-targeted profile of plant secondary metabolites. *The Plant Journal* **57,** 555–577 (2008).

Chemical genetics—providing insights on life's mysteries and developments in drug discovery

Minoru Yoshida

Group Director
Chemical Genomics Research Group
Chemical Biology Department
RIKEN Advanced Science Institute

In chemical biology, researchers use chemistry to explore and understand life. Chemical genetics is an area of chemical biology in which scientists make compounds, such as microbial metabolites, act on cells so they can investigate affected proteins and any changes that occur as a result. In this way, they establish the relationship between genes and their functions. There is a good possibility that chemical genetics will enable scientists to explain complex phenomena associated with life, and discover potential new therapeutic agents derived from compounds produced by microorganisms. At RIKEN, scientists have started a full study of chemical genomics, a large-scale chemical genetic study that targets the whole genome. As described in this article, RIKEN's scientists are at the forefront of chemical genetics and chemical genomics, which are currently hot topics in the areas of both fundamental and applied research.

Figure 1 : **Microbe mound.**

From dropout to successful researcher

Microorganisms can produce a variety of useful substances. Japanese breakfast foods such as *natto,* a traditional fermented soybean food, and *miso* soup and western foods such as bread and yogurt, for example, are all produced by microbial fermentation. Soy sauce, cheese, pickles, alcoholic beverages, penicillin (an antibiotic) and mitomycin (an anticancer drug) are other examples. Microorganisms are so useful that a stone monument named 'Microbe Mound' has been built to express thanks to them," says Minoru Yoshida, the Group Director of the RIKEN Chemical Genomics Research Group.

Microbe Mound is in the holy precinct of the Manshuin Temple in Kyoto (Fig. 1). The title on the stone monument was engraved by Kin-ichiro Sakaguchi, a professor emeritus at the University of Tokyo, a world authority on applied microbiology and the first vice-president of RIKEN when it was a government-affiliated company. He was also known as 'Doctor *Sake*'.

Yoshida studied at the Laboratory of Fermentation and Microbiology under the supervision of Sakaguchi at the Department of Agricultural Chemistry in the Faculty of Agriculture at the University of Tokyo. "I started my studies as a natural products chemist trying to find new compounds produced by microorganisms."

While studying for his doctorate, Yoshida discovered the compound trichostatin A in a culture of the microorganism known as actinomycete. "Investigation showed that it was a known substance. In natural products chemistry, much importance was placed on finding new products," explains Yoshida. "Therefore most researchers do not turn to known substances. However, I was so interested in trichostatin A that I could not bring myself to look for other new compounds. I was a dropout as a natural products chemist," he says with a smile, looking back on those days.

First of all, natural products chemists investigate the structure of compounds, or their 'faces'. "In most cases, we can determine whether or not a newly discovered compound has useful

functions by comparing its structure with that of known compounds." While Yoshida was investigating trichostatin A, he realized that it has a very unusual structure. Trichostatin A was administered to mouse leukemia cells, and surprisingly the cells changed to normal erythrocytic, or red blood, cells. It was also proved that trichostatin A is effective at a concentration of only 10 nM. "We decided to use what is now called 'chemical genetics' to investigate which proteins trichostatin A acts on, and how it works on them," Yoshida explains.

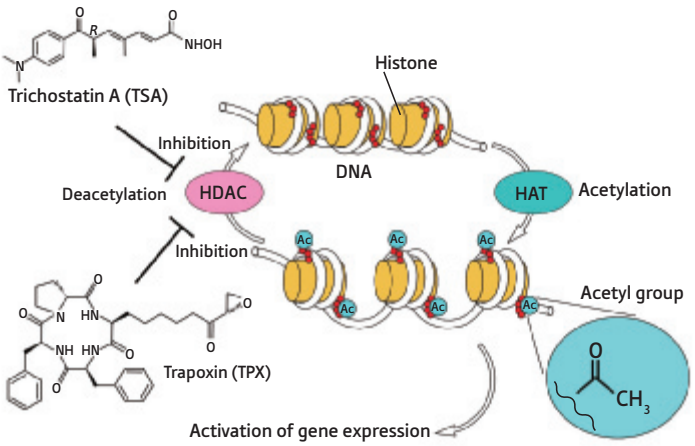


Figure 2: Inhibition of histone deacetylation by trichostatin A.
A strand of DNA winds around histone proteins. When histones are acetylated by a protein called histone acetyltransferase (HAT), the strand begins to loosen, which allows gene expression. After a short time, the histones are commonly deacetylated by HDAC, which causes the gene expression to stop. Trichostatin A binds to HDAC and inhibits its function. As a result, the histones remain acetylated and gene expression is activated. Trapoxin works in the same way as trichostatin A.

What is chemical genetics?

Genetics is a study that relates genes to phenotypes, which are observed as forms or characteristics of organisms. In genetics, scientists search for mutant strains that are variations of phenotypes and identify the genes responsible. Recently 'reverse genetics' has become very popular. Researchers select interesting genes from among those whose base sequence, encoding the genetic information, has been determined, and cause them to mutate so that they can investigate how the associated phenotypes change. Phenotypes of higher organisms such as human beings, however, may not change because they have multiple genes with the same functions; one gene can therefore compensate for another if one of the genes mutates.

Chemical genetics offers a way of overcoming this problem. "When compounds are administered, they bind to some special proteins and inhibit their functions, even when they are produced from different genes with the same function. This induces similar phenotypic changes to those caused when genes are mutated," explains Yoshida. "Thus, chemical genetics is a study that takes advantage of compounds to clarify the relationship between genes and phenotypes."

Genes with sequences of the same kind can produce proteins of the same kind. Because compounds can act on all proteins of the same kind, no functions are complemented by different gene products with the same function. In this way, phenotypic changes can be investigated. In addition, the changes occur only when compounds are being administered, and they are easily observed because phenotypes return to their original state when the compounds are removed. Unfortunately it was difficult for researchers to investigate the functions of essential genes using conventional methods based on genetics because the methods destroy genes essential for survival and stop embryonic development. In contrast, the use of compounds can provide a method for investigating essential genes.

Chemical genetics is attracting greater attention as a new area of genetics. "This is because the approach based on compounds could lead to the discovery of many interesting and unpredictable phenomena, and it is hoped that the compounds will lead directly to therapeutic agents," says Yoshida.

Towards therapeutic drugs for cancer and neurodegenerative diseases

The application of chemical genetics to trichostatin A, which was what Yoshida was really interested in, revealed that it binds to a protein known as histone deacetylase (HDAC) (Fig. 2).

Histones are proteins around which a strand of DNA is wound, and HDAC can remove acetyl groups from the histones. Trichostatin A binds to HDAC proteins and thereby inhibits histone deacetylation, producing a stable condition in which genes are easily expressed.

The discovery of a specific histone deacetylation inhibitor is amazing because no such inhibitors had previously been discovered. "I do not know why, but when trichostatin A inhibits the function of HDAC, the expression of genes that serve to cure diseases is activated, not the expression of genes that cause diseases," says Yoshida, flagging another surprise. At present, besides trichostatin A and trapoxin, many compounds that inhibit the function of HDAC have been discovered or synthesized. About ten of these have been clinically tested as anticancer drugs. "In addition to anticancer drugs, HDAC inhibitors are attracting increasing attention because they are reported to be effective in treating nerve-cell diseases such as Huntington's disease and Alzheimer's disease," Yoshida notes.

Splicing inhibitors aimed at anticancer drugs

Recently, Yoshida has focused his work on FR901464, a compound known to have anticancer activity against colon- and lung-cancer cells. He conducted an experiment using spliceostatin A,

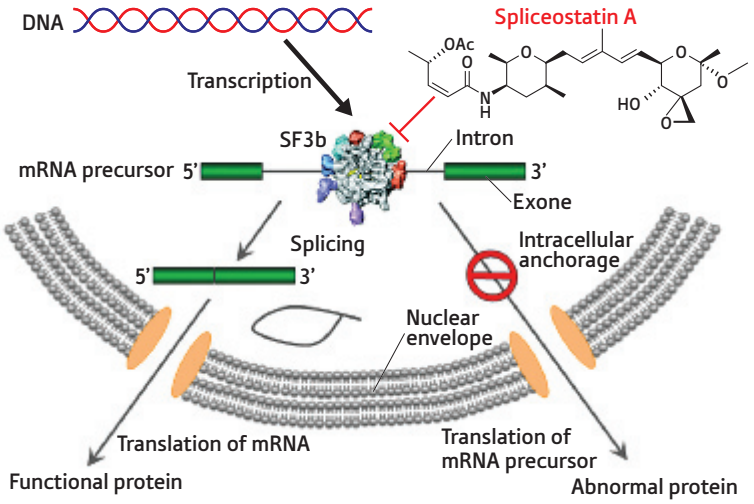


Figure 3: Spliceostatin A and the function of its target SF3b.
Spliceostatin A inhibits splicing by binding to protein complexes called SF3b. As a result, intron-containing immature mRNAs accumulate in the nucleus. Some immature mRNAs also move out of the nucleus and are then translated into abnormal proteins. It has been shown that SF3b is not only essential for splicing, but also has the function of keeping immature mRNAs within the nucleus by binding directly to the introns.

which is a variation of FR901464 that has been slightly modified in structure for stabilization. "I thought that spliceostatin A would bind to HDAC to inhibit histone deacetylation in the same way as trichostatin A," Yoshida explains. "To our surprise, however, we found that spliceostatin A binds to SF3b, a protein complex necessary for splicing, not to HDAC (Fig. 3). In other words, spliceostatin A is a splicing inhibitor."

Splicing is an essential process in the production of normal proteins: it removes the non-coding 'introns' from the RNA that is transcribed from a DNA sequence, and correctly joins the remaining coding 'exons'.

While Yoshida was completing this work, Eisai Co. Ltd., a pharmaceutical company, found another compound that binds to SF3b and inhibits splicing, demonstrating that it could serve as an anticancer drug. "It is natural to think that if splicing is inhibited, no normal proteins will be produced, and therefore normal cells will die," Yoshida points out. Why cancer cells die selectively is a mystery. "In the future, we will collaborate with Eisai to figure out what is behind this unexplained phenomenon," he says. "Therapeutic agents that can inhibit DNA duplication, transcription in, and translation into, proteins have been developed, but no splicing inhibitors. We hope that our study will lead to the development of anticancer drugs that work on a new mechanism."

Additionally, Yoshida found that when splicing is inhibited, some immature RNAs accumulate in the nucleus, while others move out of the nucleus. The immature mRNAs with introns are then translated into abnormal proteins, although under normal circumstances the introns would be removed. "SF3b is not only essential for splicing, but it also keeps immature mRNAs within the nucleus by directly binding to the introns of mRNAs." The intron has recently become an important subject of life science research.

Researchers are now starting to say that introns have unique functions although, previously, they were considered redundant areas, according to Yoshida. "Normally, introns are not stable in a nucleus. However, their functions can be investigated by using SF3b inhibitors, which make introns accumulate within the nucleus in large quantities. These findings may be the beginning of 'intron biology', in which

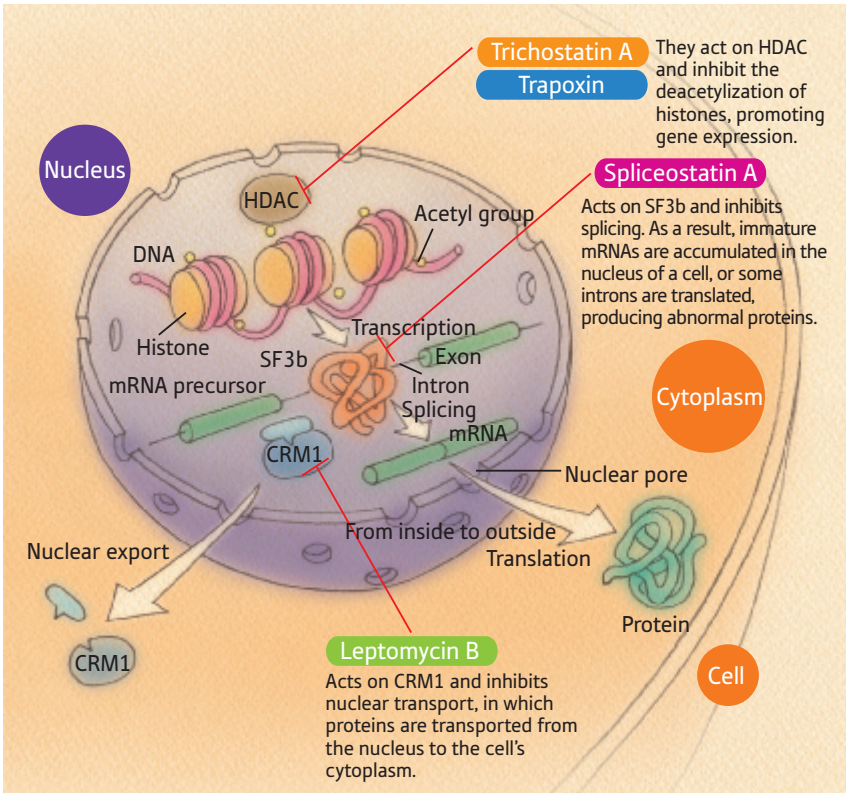


Figure 4: Control mechanism of a cell, which has been clarified by chemical genomics.
Yoshida has used compounds produced by microorganisms and modified versions of the compounds to identify target proteins. As a result, important cellular mechanisms such as gene expression and transport of proteins have been clarified one by one. The figure illustrates the normal functions of a cell. Each compound binds to a particular protein, inhibiting normal cell functions.

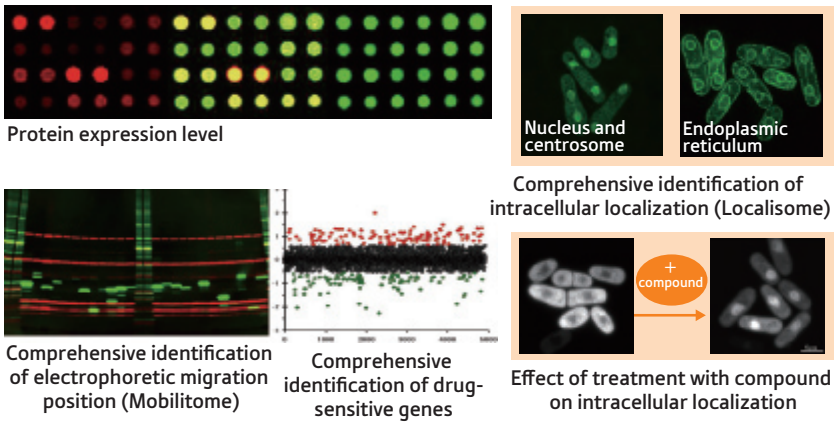


Figure 5: Comprehensive analysis of fission yeasts that serves as a basis of chemical genomics. The RIKEN Chemical Genomics Research Group has successfully cloned about 99% of all the genes that produce proteins of fission yeasts, and is now establishing a system that can exhaustively analyze the cloned genes. Using the Localisome and 'Mobilitome' databases, it is easy to tell which proteins change their gene expression levels (top left), mobility in gel electrophoresis (bottom left), or intracellular localization (top and bottom right) when compounds are administered. The Mobilitome database is related to the electrophoretic migration positions of proteins.

intron functions are explored."

In addition to trichostatin A and trapoxin, which inhibit histone deacetylation, and spliceostatin A, which inhibits splicing, Yoshida discovered leptomycin B, which inhibits the nuclear export process in which proteins are transported from a nucleus to the cell's cytoplasm. He is advancing his own research using these newly discovered compounds (Fig. 4). All of them are expected to lead to the development of therapeutic agents such as anticancer drugs.

Infrastructure development for chemical genomics

Unexpectedly discovered compounds that cause interesting phenotypic changes have been the focus of conventional chemical genetics. According to Yoshida, however, the way of the future is 'chemical genomics', a large-scale version of chemical genetics targeting the whole genome to find both useful compounds and their targets. Chemical genomics, however, requires sophistication with regard to both chemistry and biology. The current situation is that chemical genomics is not expanding as expected because of a shortage of researchers who have a good knowledge of both chemistry and biology. "We are establishing a special system, called the 'Localisome' database (Fig. 5), using fission yeasts so that every researcher can study chemical genomics," says Yoshida (Fig. 5).

Fission yeast is a model eukaryotic organism that has many genes in common with humans. The complete genome of this organism was decoded in 2002, in which 4,948 protein-producing genes were found. Yoshida extracted 4,910 genes from the yeast (about 99%), and successfully produced proteins. He also tried to attach fluorescent labels to proteins so that he could establish the Localisome database and show where particular proteins are located in fission yeast. When a compound is administered, it changes the localization of proteins. Then, by comparing it with data in the Localisome, the protein related to the compound can be identified without special knowledge. The establishment of the Localisome database was a six-year project. "If our purpose had been limited to the establishment of the database, we would never have engaged in such laborious work. We pushed hard because we were seeing the future direction of the contribution to drug discovery," he says.

A chemical genomics project started in the US in 2004, mainly at the National Institutes of Health (NIH) Chemical Genomics Center. In Europe and China, researchers are developing the infrastructure for chemical genomics studies. In the past, natural products chemistry was known as 'Japan's specialty'. However, Japan now lags behind in the field of chemical genomics. Therefore, in April 2008, a new Chemical Biology Department was established at the RIKEN Advanced Science Institute. "Unique compounds are a starting point for both chemical biology and chemical genomics. No further progress can be made without them," notes Yoshida. "We are trying to enhance the research infrastructure by focusing on the chemical bank that Hiroyuki Osada, Director of the Chemical Biology Department, is promoting." Thus, RIKEN's researchers are advancing with a view to contributing to drug discovery.

Yoshida asserts that he is most interested in epigenetics—the study of heritable changes in gene function that occur without changes in the DNA sequence. "Regulation of gene function by the process of histone deacetylation (Fig. 2) is a perfect example of epigenetics. Thus, I think I will continue to be involved in the study of trichostatin A in the future," Yoshida says. The study is likely to lead to the development of therapeutic agents for the treatment of cancer and neurogenerative disorders, such as Alzheimer's disease.

About the researcher

Minoru Yoshida was born in Tokyo in 1957. He graduated from the Faculty of Agriculture, the University of Tokyo, in 1981. After receiving his PhD in 1986 from the same university, he then became an assistant professor there, and started his career in chemical biology. He was promoted to associate professor in 1995. In 2002, he moved to RIKEN as a chief scientist. Since then he has been the director of his laboratory. He also organized the Chemical Genomics Research Group in 2008. His research focuses on identifying the cellular targets of natural products and developing methodologies for efficient drug and target discovery based on genomics and proteomics.

BRC begins distribution of human iPS and human ES cells

RIKEN BioResource Center (BRC) in collaboration with Kyoto University has started a service to provide human induced pluripotent stem (iPS) cells and human embryonic stem (ES) cells to nonprofit research organizations.

Pluripotent stem cells are capable of producing various kinds of body cells. As such, iPS cells have exciting potential in the development of medical treatments for a wide range of diseases that are currently untreatable. They can also be used to treat damage to the brain, spinal cord, skeletal muscles and heart. Kyoto University started providing stem cells to commercial enterprises in July 2008. After receiving cell lines from Kyoto University and organizing the distribution system, RIKEN BRC started provision to nonprofit academic research institutions for teaching and research purposes, on March 25.

Two lines of human iPS cells were deposited at RIKEN BRC by Shinya Yamanaka, head of the Center for iPS Cell Research and Application at the Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University. One was generated using four transcription factors, namely Oct3/4, Sox2, Klf4 and c-Myc. The other was generated using these factors except for c-Myc, which is known to cause cancer.

To receive the iPS cells, the researcher wishing to use them and his or her institution's authorized representative must submit a Material Transfer Agreement to Kyoto University and RIKEN BRC. The MTAs are available from the following websites:
www.saci.kyoto-u.ac.jp/ips/ips_index_e.html
www.brc.riken.jp/lab/cell/english/

RIKEN BRC provides the iPS cells for free, but charges a transmittal fee of Y28,000 per sample to cover preparation, handling and distribution costs.

For the first time in Japan, RIKEN BRC has also started providing KhES-1, an ES cell line, which was established by Norio Nakatsuji of Kyoto University. Both iPS and ES cells are attracting attention as multifunctional stem cells with some common features, and basic research into these cells is crucial for the progress of biological and medical research. ■

RIKEN Culture day: innovation and tradition

One of five initiatives put forth by RIKEN President Ryoji Noyori was to strive toward a RIKEN "that contributes to culture", and it was in the spirit of realizing this goal that RIKEN Culture Day was established. Every year on this day, prominent cultural figures are invited to RIKEN to give talks on their respective areas of expertise, bridging the world of science with the world of culture. This year RIKEN invited to the Culture Day event ceramicist Imaemon Imaizumi the 14th, who gave a talk at RIKEN's Wako campus on March 27th. The 14th in a long line of traditional craftsmen, the Imaizumi blends the old and the new in his work; while practicing a traditional technique of multicolored porcelain ceramics referred to as 'polychrome Nabeshima ware' passed down through generations in his family, he also experiments with modern new techniques.

The 14th Imaizumi explained in his talk that ceramic artwork was first imported into Japan in the early 17th century from places such as China and South Korea; porcelain was then discovered in the ground of Kyushu and Arita, and it was from this time that Japan's unique technique of polychrome Nabeshima ware was developed. Starting from the latter half of the 17th century, pottery from Arita was subsequently exported to Europe, exerting a strong influence on European ceramic artwork. The practice of traditional Japanese ceramic sculpture has itself also been shaped by contemporary world affairs and trends of the times.

In his speech, Imaemon Imaizumi the 14th drew a connection between traditional Japanese ceramics and the practice of scientific discovery. It is often said, he pointed out, that scientific creativity emerges through daily perseverance with experiments, combined with the repetitive practice of trial and error. "It is the same in the world of traditional handicrafts," he said. "Most important of all is the creativity that comes from the accumulation of everyday experiences."

The meaning of "tradition", he went on to explain, also bears a similarity to science: what a single generation can achieve on its own may be small, but traditions are made up of techniques developed over tens or hundreds of years, passed down through the generations in a continuous line. In this sense, he said, tradition shares much in common with scientific research.

The audience of 120 people, researchers among them, who crowded into the hall on Culture Day to see the 14th Imaizumi share his thoughts about traditions, and about science, listened intently to his every word. ■

Construction complete on building to house machines at XFEL facility

Construction of a building to house linear accelerators, undulators and other equipment for use in the X-ray Free Electron Laser (XFEL) facility was completed in March, 2009, at the SPring-8 campus of the RIKEN Harima Institute.

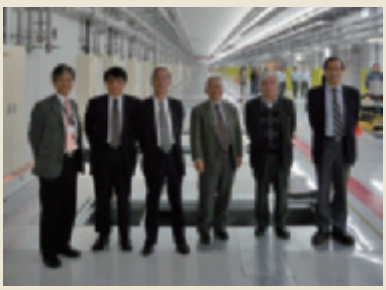
The building has a long narrow structure measuring 650m in length, and was constructed under a unique set of challenging constraints: flooring is aligned precisely to within several micrometers, and walls encasing the accelerator are a full two meters thick.

Producing light with a shortness of pulse and wavelength never before explored, the XFEL facility will illuminate worlds less than a tenth of a nanometer (one billionth of a meter) in size, on a time scale of only a femtosecond (one quadrillionth of a second). XFEL projects are being developed not only in Japan, but also in the U.S. and in Europe.

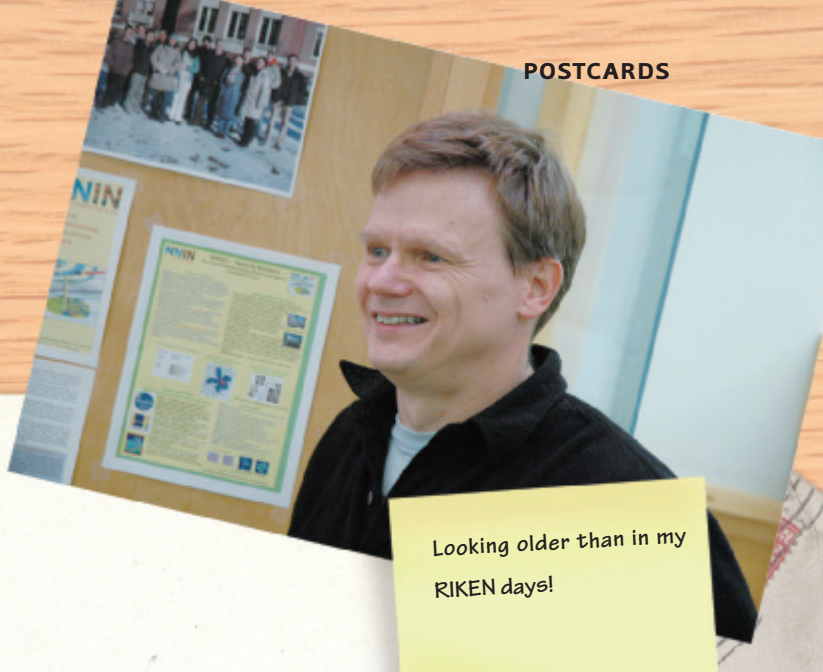
With completion of the building, installation of equipment such as accelerators and undulators, as well as configuration of temperature control systems, can now begin. Construction on buildings to be used for future experiments will also get under way.

Lasing of the XFEL is set to commence by 2010. Starting from 2011, XFEL will serve as a common-use facility for researchers from Japan and from overseas, enabling them to carry out a wide range of new cutting-edge experiments.

Preliminary experiments are already underway at a prototype XFEL (an EUV laser source with 1/32th the electron energy of the actual facility) for use in research following completion of the actual XFEL facility. ■



Celebrating completion of the facility.



Looking older than in my RIKEN days!

Dr. Koji Ishibashi
Advanced Device Laboratory
RIKEN Advanced Science Institute
2-1 Hirosawa, Wako-City, Saitama, 351-0198
JAPAN

Dear Dr. Ishibashi,

It's with great pleasure that I send you a 'postcard' from my latest location, the Center for Nanoscale Systems at Harvard University in Cambridge, Massachusetts! I have many fond memories of my days at RIKEN and I recently had the opportunity to relive some of those memories when I visited RIKEN last August. Indeed, along with my friend Toshi Iitaka and other RIKEN dignitaries such as Franco Nori and Koji Kaya, we are attempting to build a bridge of collaboration between RIKEN and Harvard University in computation and nanoscience.

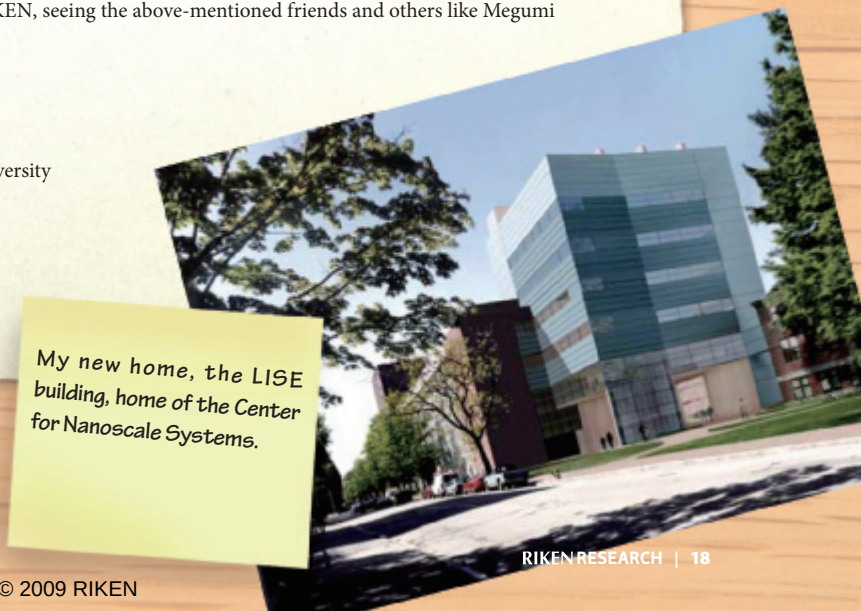
When I started at RIKEN in 1992, the Wako campus and Wako itself were dramatically different than they are now. There was no Brain Science Institute and the (new) Frontier Research Institute, which is now part of the Advanced Science Institute, was located in two buildings. Most of our group, the nanoelectronics research group, was involved in research that complemented the Solid State Group headed by my friend: Yoshinobu Aoyagi. Jon Bird and I were the spearhead in the study of a new class of devices falling in the category of 'single electronics'. Our research efforts have now metamorphosed into your laboratory. Congratulations Ishibashi-san!

During my time at RIKEN, I lived nearby and was able to ride my 50 cc bike to work every day in just five minutes. Given that I now drive for almost an hour to work every day, I really miss that bike! I also recall running in a loop around the RIKEN campus just about every night. I hated the bats and I am not surprised to find that they are still haunting the campus!

Currently I am working on problems in computational nanoscience. In particular I retain an interest in nanoelectronics and quantum dots, but I have branched out a bit into areas like photosynthesis and surface-enhanced Raman spectroscopy—all with a theoretical approach. In my recent visit to RIKEN, I had the opportunity to begin some collaborative efforts with RIKEN chemist Toshi Takada, who is a specialist on photosynthesis. I have also had the privilege of being a member of the RIKEN Supercomputer Center. At Harvard we are very interested in establishing further relations with RIKEN's computer experts.

I always look forward to coming back to RIKEN, seeing the above-mentioned friends and others like Megumi Kobayashi and remembering the old days.

All the best,
Michael Stopa
Center for Nanoscale Systems, Harvard University
Cambridge, MA, USA



My new home, the LISE building, home of the Center for Nanoscale Systems.

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