Laser-matter interactions

It takes two electrons to tango

Keith Burnett

Understanding the behaviour of electrons is fundamental to the science of matter and its properties. It usually relies on individual electrons adopting their own paths or 'orbitals', and explains the periodic table of the elements. But electrons are not always so aloof, and when they dance together they give rise to many intriguing physical phenomena, such as superconductivity. On page 658 of this issue, Weber *et al.*[1] provide a clearer picture of a two-electron dance in a different domain — when matter is exposed to an intense laser field. In so doing they have cleared up a controversy about how electron coupling occurs in such systems.

The interaction of matter with intense laser fields crops up in many areas, from laser surgery to ignition of nuclear fusion. Single-electron processes in atoms are fairly well understood, in both weak and strong fields. Systems of many electrons (which covers most of physics and chemistry) are much more complex, and there are fundamental questions to be answered. The study of matter in intense laser fields has been driven by developments in laser technology that make it possible to expose atoms to electric fields that rise to extraordinarily high values in a few femtoseconds (10^{-15} seconds). The peak field is as strong as that produced by the nucleus, and the electrons are ripped off the nucleus in short order. The way in which this apparently simple process — called ionization — actually happens has been challenging scientists in the fields of atomic, molecular and optical physics for some time.

Workers in these areas are now looking at multi-electron effects in atomic ions and clusters. One of the most intriguing of these is the 'double ionization' of helium in an intense laser field — that is, when both helium electrons are emitted at the same time. For certain values of the laser field the independent-electron picture fails spectacularly[2]: pairs of electrons are produced much more copiously than expected on the basis of the behaviour of independent electrons.

Theories put forward to explain the data give radically different pictures of what is going on. One of the most popular models proposes a mechanism known as 'rescattering', in which one electron is first accelerated away and then driven back towards the atom by the laser field, where it can collide with the remaining electron[3–5]. Electrons emitted in this way would be expected to have highly correlated motion. Another model suggests that the second electron is shocked out of its orbit by the disappearance of the first electron[6]. In this case the motion of one is not expected to depend on the motion of the other.

This controversy arose because the theory of strongly correlated electrons is such a tricky business. In terms of static properties of atoms, powerful techniques have given us a good picture of the correlated motion of electrons. In the case of intense laser fields, the problem is much harder. The system is evolving in time and the laser field destroys any simplification due to atomic symmetry. This means that the dynamics of even a single electron in an intense laser field is a serious computational problem. The availability of high-speed computers has made this an easier, but still not routine, task. More recently, the advent of massively parallel machines has made it possible to tackle the more difficult problem involving two electrons[7]. In that study, the emitted electrons appear on the same side of the atom, with correlated motion.

So the scene was set for an experiment to decide between the theories. The experiment of Weber *et al.*[1] has confirmed that electron correlation is responsible for the anomalous production of electron pairs in an intense laser field. To see this, the authors have developed a technique that maps the distribution of electrons ripped out of an atom by an ultra-strong laser pulse. This enables the authors to determine the distribution of both single- and double-ionization events. The results clearly show a strong correlation between the momentum of the electrons. They also show that correlations dominate at particular laser intensities, which supports the rescattering mechanism of double ionization. This is a reminder that we have to get inside the complexities of the two-electron dance if we want to understand matter in intense fields.

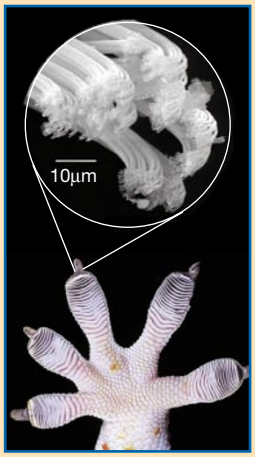
This work has given us a clearer picture of how multi-electron systems behave in strong laser fields. It should also give a great boost to their study in other systems, such as clusters of atoms or atomic surfaces. We now want to find out how electrons are correlated during the intense-field ionization and heating of atomic clusters. In particular, clusters can be rapidly heated by a laser field to produce small nuclear fusion bursts. Future experiments will challenge our theoretical understanding of interacting electrons in large assemblies of atoms (currently handled through density functional theory). The

Biomechanics

Gripping feat

Humid nights in cheap hotels in the tropics are not complete without a gecko scuttling up the walls or across the ceiling. The adhesive properties of the feet of these fleet lizards are proverbial, yet decades of investigation have still not revealed exactly how they do it. In their report elsewhere in this issue (*Nature* **405,** 681–685; 2000), Autumn *et al.* come the closest yet. Their force measurements on adhesive setae (foot-hairs) from the Tokay gecko, *Gekko gecko*, are consistent with the rapid formation and breaking of intermolecular bonds — van der Waals forces.

Suction and friction — two other hypotheses — have been ruled out, as gecko feet can work in a vacuum, and the lizards are quite content on surfaces as smooth as polished glass. Electrostatic attraction is also unlikely, as the feet can still adhere in ionized air. And there aren't any gland cells that might produce some kind of glue. The role of adsorbed water, however, has yet to be studied. Nevertheless, the observation that geckos get stickier with increasing surface energy of the substrate suggests that they are tapping directly into the molecular structure of the surfaces they walk on.



MARK MOFFETT

Viewed through a microscope, the foot of a gecko is densely packed with fine setae, shown here in the inset. There are around 5,000 per square millimetre — around half a million on each foot. The end of each seta is further subdivided into between 400 and 1,000 structures called spatulae. The setae tend to point towards the heel: as the gecko takes a step, driving the sole into the substrate and pushing it backwards, the setae become maximally engaged. If all the setae were simultaneously stuck to the surface, the feet of a gecko could produce an adhesive force equivalent to ten atmospheres. The gecko releases each foot by 'peeling' off the setae at a critical angle, rather like peeling adhesive tape. Engineering a structure as exquisite as the foot of the gecko is probably beyond human technology, say Autumn *et al.*, but the principles on which it operates could inspire the design of new kinds of dry adhesive. **Henry Gee**

present studies of electron correlation provide a benchmark for the development of methods that are used in many areas of physics and chemistry. ■

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1. Weber, Th. *et al. Nature* **405,** 658–661 (2000).
2. Walker, B. *et al. Phys. Rev. Lett.* **73,** 1227–1231 (1994).
3. Corkum, P. *Phys. Rev. Lett.* **71,** 1994–1997 (1993).
4. Becker, A. & Faisal, F. H. M. *J. Phys. B* **29,** L197–L202 (1996).
5. Watson, J. B. *et al. Phys. Rev. Lett.* **78,** 1884–1887 (1997).
6. Sheehy, B. *et al. Phys. Rev. A* **58,** 3942–3952 (1998).
7. Taylor, K. T. *et al. Laser Phys.* **9,** 98–104 (1999).

Structural biology

Pumping ions

David H. MacLennan and N. Michael Green

Calcium activates a variety of cellular responses when it enters the cytoplasm of a cell by means of transmembrane channels. But, to be effective as a signal, its concentration must be returned to submicromolar levels by ATP-driven pumps. The Ca^{2+} pump is a membrane-bound, Ca^{2+}-activated ATPase[1,2], similar to the Na^+/K^+ pump that controls ion balance and membrane potential in all animal cells[3]. These pumps belong to a superfamily of ATPases known as 'P-type', because they depend on the autophosphorylation — using ATP — of a conserved aspartic acid residue.

On page 647 of this issue, Toyoshima *et al.*[4] describe the first high-resolution structure of any member of this family — the sarco(endo)plasmic reticulum Ca^{2+}-ATPase (SERCA1a). This important structure illuminates past investigations and reveals a model for the structural changes that underlie the activity of this pump.

In the forty years since its discovery, ingenious experiments have revealed much about how the Ca^{2+}-ATPase works. Kinetic studies[5] showed that this pump transports Ca^{2+} by a reversible cycle (Fig. 1), but this vectorial transport can be understood only in a structural context. After the initial topology of the Ca^{2+} pump was deduced[6,7] and refined[8], electron microscopy[9] provided a map of the molecule at a resolution of 8 Å. The structure of a homologous enzyme, haloacid dehalogenase, was recently modelled into the map[10] to give a picture of the cytosolic phosphorylation domain that forms the catalytic heart of the Ca^{2+} pump. The two Ca^{2+}-binding sites were proposed to lie side by side near the centre of four transmembrane helices, and to be formed by the appropriate juxtaposition of acidic and oxygen-containing amino acids in a region of the protein that is sensitive to mutation[11–13]. So, small changes in these helices could lead to disruption of the Ca^{2+}-binding sites and to alterations in the movement of ions to the cytosol or to lumenal spaces. These studies made clear that the Ca^{2+}-binding sites in the membrane domain and the phosphorylated aspartic acid residue in the cytosolic domain are separated by 40–50 Å, raising the question of how these long-distance interactions are mediated[8].

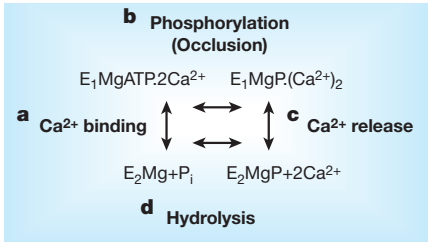

Figure 1 **Conformational states of the Ca^{2+}-ATPase. During the cycle of ATP-dependent Ca^{2+} transport, at least four interconvertible phosphorylated and unphosphorylated conformations have been defined.** a, **A rise in Ca^{2+} on the cytoplasmic side of the membrane saturates the two high-affinity Ca^{2+}-binding sites to form $E_1MgATP.2Ca^{2+}$.** b, **This activates formation of a phosphoenzyme with MgATP, occluding Ca^{2+} within the protein to form the high-energy intermediate $E_1MgP.(Ca^{2+})_2$.** c, **In a rate-limiting step to generate E_2MgP, the phosphoenzyme loses both its ability to re-phosphorylate ADP and its high affinity for Ca^{2+}, and opens its gate to lumenal spaces.** d, **Water enters the catalytic site and hydrolyses the phosphorylated aspartic acid residue to regenerate the ATPase (E_2).**

The Ca^{2+}-bound structure described by Toyoshima *et al.*[4] offers many more insights into the mechanism of action of Ca^{2+}-ATPase (Fig. 2, overleaf).The authors identify new ligands, particularly mutation-sensitive backbone carbonyl groups on transmembrane helix M4, and a single water molecule, in the Ca^{2+}-binding site, together with possible entry and exit pathways for Ca^{2+} that are lined by oxygen atoms. A striking feature of this region is the disruption of the M4 and M6 helices to form a Ca^{2+}-binding cavity. This was anticipated from earlier NMR studies of helix M6 (ref. 14), and means that structural changes in the carboxy termini of M4 and M6 may be the key to creating or closing off access to the Ca^{2+}-binding cavity.

Of the three cytosolic domains, the phosphorylation (P) and nucleotide-binding (N) domains form the catalytic site, whereas the actuator (A) domain (formerly called the transducer or beta domain) appears to be involved in the transmission of major conformational changes. Toyoshima *et al.*[4] confirm the structural similarity of the P domain to the catalytic domain of haloacid dehalogenase[10]. Note particularly that the positions of important catalytic residues (Fig. 2) are conserved.

The N domain, which is inserted, as predicted, after the first strand of the P domain (Fig. 2), forms an open cap over the catalytic site. In the Ca^{2+}-bound conformation[4], the P and N domains appear as an open jaw, so the binding site for the ATP homologue TNP-AMP in the N domain is more than 25 Å from the critical aspartic acid, Asp 351, in the P domain. This implies that Ca^{2+} binding alone is insufficient to produce a phosphorylatable conformation of this protein. But the closure of the N and P domains must occur to bring ATP close to Asp 351, and possibly to exclude water and stabilize the phosphorylated enzyme. A cautious interpretation is required, however, as TNP-AMP differs from closer analogues of ATP, which cause conformational changes and disrupt crystals of the Ca^{2+}-bound enzyme. TNP-AMP also binds at some distance from a site previously assigned to another ATP analogue, CrATP[15].

Studies of the activation of transport by non-nucleotide phosphates such as acetyl phosphate imply that domain closure to form the phosphorylated enzyme does not require occupation of the nucleotide-binding site. What we need now is a structure for $E_1Mg^{2+}P.(Ca^{2+})_2$ (Fig. 1) — the phosphoenzyme with Ca^{2+} occluded between the cytoplasm and the lumen. Experiments with glutaraldehyde, which links Lys 492 near TNP-AMP to Arg 678 near the site of phosphorylation of Asp 351 (Fig. 2), have shown that this species is probably the most tightly closed[7].

In the Ca^{2+}-bound conformation[4], the A domain is almost dissociated from the main structure, as previously observed[16]. This implies that Ca^{2+}, in the absence of nucleotide, loosens interactions between all three domains. To look for possible domain movements, Toyoshima *et al.* rotated the cytoplasmic domains to match the density of the more compact, 8-Å structure of a decavanadate-containing variant of the Ca^{2+}-free conformation of the same pump[9]. The consequent 20° rotation of domain N partially closes the gap between the N and P domains, but still leaves 15–20 Å between the nucleotide and its target — complete closure is prevented by a density ascribed to decavanadate. The 90° rotation required for the A domain brings its highly conserved and mutation-sensitive TGES loop into the site of phosphorylation. The angular relations between helices M4 and M5 and the P domain are also changed.

We can now predict that at least three conformational changes occur during ATP-