remaining three iron atoms of the cluster are bound by three cysteine amino-acid residues that occur close together in an evolutionarily conserved motif in the amino-acid sequences of the enzymes. The interaction of SAM with the iron–sulphur cluster has also been shown[5] to cause electron orbitals on the cluster to overlap with those of the positively charged sulphur atom in SAM, implying that direct overlap of orbitals is necessary for the electron transfer that initiates S–C bond cleavage.

But a puzzling question has remained: why is the S–C bond to the 5′-deoxyadenosyl group of SAM the only one to be cleaved by radical SAM enzymes? This is especially strange given that the S–C bonds to the non-methyl groups in SAM have similar strengths, and that the radicals produced by the homolytic cleavage of these bonds have comparable stability.

Zhang and colleagues' results[1] demonstrate that the S–C bond to the 5′-deoxyadenosyl group is not special in its ability to undergo homolytic cleavage. But it does raise the question of why this bond is exclusively broken by radical SAM enzymes, whereas Dph2 breaks only the S–C bond to the 3-amino-3-carboxy-propyl group. The origin of this selectivity probably lies in differences in the way SAM interacts with the iron–sulphur clusters in the enzymes. Electron transfer to SAM is likely to cause the cleavage of a particular bond if the electron enters the 'antibonding' orbital of that bond. In radical SAM enzymes, we would thus expect that the antibonding orbital corresponding to the S–C bond to the 5′-deoxyadenosyl group would overlap with the electron-donating orbital from the iron–sulphur cluster. Consistent with this idea, the crystal structures[6–10] of radical SAM enzymes in complex with SAM all reveal similar orientations of SAM relative to the iron–sulphur cluster.

But in Dph2, the antibonding orbital of the S–C bond to the 3-amino-3-carboxypropyl group should provide the necessary overlap. Unfortunately, no SAM is bound within the crystal structure of Dph2 reported by Zhang et al.[1], and so it remains to be seen whether SAM adopts an orientation in this enzyme that is consistent with this theory.

Intriguingly, Zhang et al. report that the structural fold of Dph2 that contains the iron–sulphur cluster is entirely unrelated to the analogous folds of the radical SAM enzymes whose structures have been solved to date. Furthermore, unlike the radical SAM enzymes, the amino-acid sequence of Dph2 does not contain a motif of close-lying cysteines that binds to the cluster. Instead, the three cluster-binding cysteines of Dph2 arise from three different domains of the protein, and were therefore not previously recognizable as a binding motif.

If other enzymes are identified that homolytically cleave the same S–C bond in SAM as that broken by Dph2, will they also have cluster-binding cysteines in different protein domains, in folds that resemble that of Dph2? Or will their iron–sulphur clusters be bound by the cysteine motif found in radical SAM enzymes? More excitingly, could there be other kinds of fold that also bind to clusters involved in SAM's radical chemistry? Whatever the answers, it seems evident from Zhang and colleagues' work[1] that Dph2 employs analogous reactions to those of the radical SAM enzymes in order to achieve a very different chemical outcome. ■

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SOLAR SYSTEM
Blink from a remote world

Bruno Sicardy

The use of stellar occultations to disclose unknown aspects of our Solar System is not new. But the latest such event to be reported involves an object that lies beyond the orbit of Neptune — and is a first.

Sometimes, a blink is more informative than a steady look. This is certainly the case when it comes to stellar occultations, events that occur when a planetary body hides a star as it moves across the sky. More than being a mere curiosity, such events provide a wealth of information about the occulting body — more so than direct images of it. For instance, stellar occultations have proved a powerful tool in discovering planetary rings, probing remote atmospheres at microbar pressure levels and measuring sizes at kilometric accuracies for bodies located hundreds of millions of kilometres from Earth. On page 897 of this issue, Elliot and colleagues[1] report the first detection of a stellar occultation by a small object orbiting beyond the giant planet Neptune. The object is 2002 TX$_{300}$ (also known as KBO 55636), which lurks at a distance of more than 6 billion kilometres from our planet.

The 'trans-neptunian objects', also known as Edgeworth–Kuiper belt objects (or simply KBOs), constitute a population of small planetary bodies orbiting beyond Neptune, in a vast region extending to the outskirts of our Solar System[2]. These objects are observed at
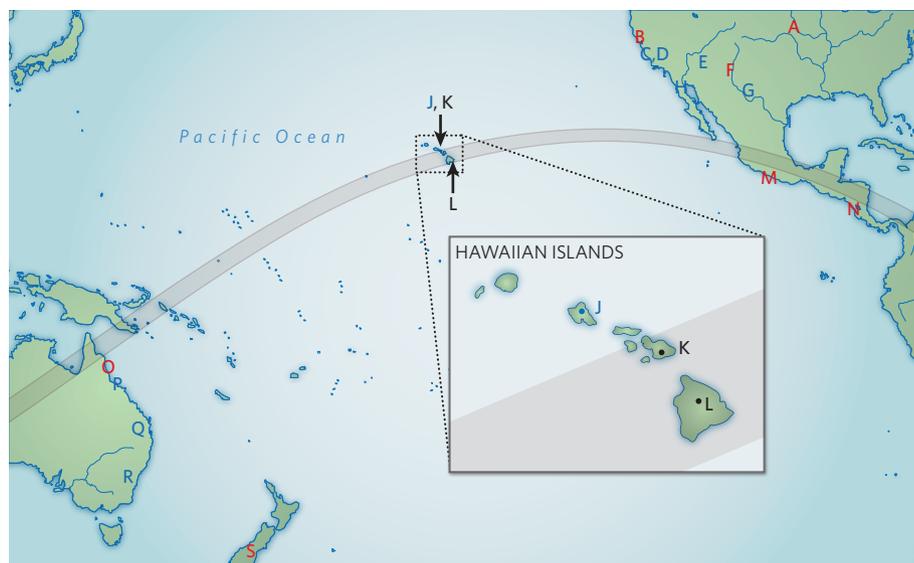

Figure 1 | Observing a stellar occultation by KBO 55636. The band shows the path of the shadow of trans-neptunian object KBO 55636 that swept across Earth's surface during the stellar occultation of 9 October 2009, reported by Elliot and colleagues[1]. It took about five minutes for the shadow to cross the Pacific Ocean from right to left. Only the two stations denoted in black, located in the Hawaiian Islands and inside this band, successfully detected the stellar occultation. The stations denoted in blue made successful observations but did not detect the occultation, and the stations represented in red could not make observations because of weather conditions.

distances as far as 50–70 astronomical units (AU) from the Sun (1 AU is the average distance from Earth to the Sun). The dwarf planet Pluto was discovered in 1930 and now ranks among the largest known KBOs. But it hasn't been a smooth ride for KBO hunters, because these objects are extremely faint and so are difficult to detect. It was only with the advent of modern charge-coupled-device light detectors, some 60 years after Pluto was spotted, that other KBOs could be discovered[3]. Now, after almost two decades of intense observations, more than 1,000 KBOs have been identified.

The Edgeworth–Kuiper belt is thought to be the relic of the primordial proto-planetary disk from which the planets emerged. Far from being a quiet, remote place, this region exhibits a surprising dynamic complexity[2], betraying a perturbed history — one that involved gravitational stirring from the giant planets during the early ages of the Solar System[4]. Although a general picture of the Edgeworth–Kuiper belt has slowly been emerging, many questions have remained unanswered. The size distribution of the KBOs remains uncertain, and knowledge of basic information about their surface properties, bulk density and internal structure is poor. Yet these physical parameters are essential for assessing the present mass of the belt, and retrieving its history.

The stellar occultation described by Elliot et al.[1] provides constraints on the size of KBO 55636. The two positive detections of this event, made on 9 October 2009 with telescopes in Hawaii (Fig. 1), indicate that, if spherical, the object must have a radius of 143 ± 5 km. If other shapes — ellipsoids, for example — are considered, smaller surface areas are obtained than would be produced by a sphere of such a radius. But all estimated surface areas, regardless of the shape considered, are significantly smaller than that made by a previous, indirect estimation[5] that combined visible and infrared measurements and yielded an upper limit of 210 km for the radius of the body.

For a given brightness, the smaller an object is, the higher its geometric albedo — a quantity used to measure, roughly speaking, the percentage of incoming solar light reflected by the object. In the case of KBO 55636, the authors deduced an albedo ranging from 82% to more than 100%, making it one of the most reflective objects in the Solar System. This is a surprising result. KBO 55636 is thought to be part of the trans-neptunian Haumea collisional family[6]; members of a collisional family are thought to be produced during a common catastrophic collision. Estimates for the age of this family[7,8] indicate that KBO 55636 is the aftermath of a collision that occurred more than one billion years ago. But if that is the case, the expectation would be for the object to have a lower albedo than that deduced by Elliot and colleagues, because space weathering, which includes processes such as bombardment by cosmic rays, can darken KBO surfaces in less than a tenth of that time. Physical processes such as cryovolcanism,

condensation of fresh ices caused by a putative atmosphere, or recent collisions can keep a surface shiny. But none of these processes is very appealing as an explanation for the estimated high albedo of KBO 55636, owing to its small size and to the fact that collisions are rare today among KBOs. The implication is that our understanding of space weathering or of the Edgeworth–Kuiper belt's dynamic history — or both — must be revised at some point.

Elliot and colleagues' observation[1] represents the beginning of a long journey, because a dozen among the largest KBOs known are now listed as candidates for stellar occultations. Predictions of such events are difficult: the angular diameter spanned by KBO 55636 on the sky is equivalent to looking at a €1 coin from a distance of 500 km. Thus, the success of observations depends on accurate predictions made by experienced teams. The merit of this observation[1] is to show that such predictions are now possible. But scientific returns may go well beyond size determinations. For instance, atmospheres with pressures as low as a few nanobars can be detected using stellar occultations. Furthermore, for KBOs with satellites, the objects' masses can be derived from the law of gravity. In those cases,

accurate size determination also means accurate density derivation, an important parameter for constraining internal structure.

Finally, it should be noted that the observations presented by Elliot et al. were made using modest telescopes (with main mirrors of diameter 2.0 and 0.34 metres), and by a team of both professional and amateur astronomers. Being at the right place at the right moment is therefore more important than using big instruments — an unusual situation in physics, where the race for larger and larger detectors has become the rule. ∎

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GENOMICS

The tale of our other genome

Liping Zhao

The groundwork for analysing the human microbiome — sequencing the collective genome of all our resident microorganisms — is now done. This work is of significance for understanding both human health and disease.

Did you know that humans have two genomes? Indeed, although most people appreciate that humans inherit a genome, many fail to realize that the collective genetic information encoded in all the microorganisms acquired from the environment, which are collectively known as the microbiome and generally live harmoniously with us, constitutes a second genome. Reporting in Science, a team from the International Human Microbiome Consortium (Nelson et al.[1]) discloses the consortium's second offering: an initial reference-genome sequencing of 178 bacterial species from the human microbiome. The first instalment was published by Qin et al.[2] a few months ago.

One might argue that just because microorganisms have colonized the human body, their collective genome — a 'metagenome' — shouldn't be given the status of a second genome. But the contribution made by microorganisms is truly impressive. Some 1.5 kilograms of bacteria colonize the human gut, with others inhabiting the external and internal surfaces of the body. In fact, only 10% of the total number of cells in the human body consists of human cells, with the rest coming from symbiotic bacterial cells[3].

As for their contribution to health and disease, molecules produced by the gut bacteria can enter the bloodstream via either a normal anatomical route called the enterohepatic circulation or through a partially damaged gut barrier. Beneficial gut bacteria can produce anti-inflammatory factors, pain-relieving compounds, antioxidants and vitamins to protect and nurture the body. Conversely, harmful bacteria may deregulate genes mediating energy metabolism, and can produce toxins that mutate DNA, affecting the nervous and immune systems. The outcome is various forms of chronic disease, including obesity, diabetes and even cancers[4–6]. This close and specific contact with human cells, exchanging nutrients and metabolic wastes, makes symbiotic bacteria essentially a human organ and their collective genomes our second genome.

It is estimated that the human gut microbiome contains around 1,000 bacterial species. Qin et al.[2] used next-generation sequencing technology — which in a single run can generate millions of short DNA reads — to create a catalogue of 3.3 million genes from 124 European faecal samples collected as part of the