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# Matter and antimatter scrutinized

A search for differences in the charge-to-mass ratio of protons and antiprotons, conducted at unprecedented levels of precision, results in stringent limits to the validity of fundamental physical symmetries. [SEE LETTER P.196](#)

KLAUS P. JUNG MANN

The standard model<sup>1</sup> of particle physics is considered to be the best physical theory that we have. It is built on symmetries and can describe all the experiments and observations concerning the known subatomic particles. However, the model includes some 30 free parameters and is not fully explanatory. For example, it cannot explain a profound mystery of physics and cosmology<sup>2</sup>, the fact that there is no antimatter in the Universe. When matter and antimatter mutually annihilated each other following the Big Bang, any pre-existing symmetry between them was broken. Matter but no antimatter was left behind, and we lack a satisfactory explanation as to how this occurred<sup>3</sup>. Research on the fundamental differences between particles and antiparticles may provide an answer. In this vein, Ulmer *et al.*<sup>4</sup> (page 196) perform a high-precision, comparative study of the properties of protons and antiprotons.

The authors used negatively charged

hydrogen atoms (which represent protons for technical reasons) and individual antiprotons, the latter generated by the antiproton decelerator facility at CERN, Europe's particle-physics laboratory near Geneva, Switzerland. These species were stored in a sophisticated device known as a Penning trap, which consists of metal electrodes placed at defined electric potentials inside a strong and stable magnetic field (Fig. 1). In the trap, which has a diameter of just a few millimetres, the motion of electrically charged particles is similar to that in an accelerator such as the Large Hadron Collider at CERN, but the energies attained are  $10^{15}$  times smaller.

A particle's cyclical motion in the Penning trap has a characteristic frequency (known as the cyclotron frequency), which is proportional to the magnetic field strength and the particle's charge-to-mass ratio. Ulmer *et al.* determined the cyclotron-frequency ratio for the antiproton and the negative hydrogen ion, alternately recycling the same individual particles at intervals of a few minutes from each

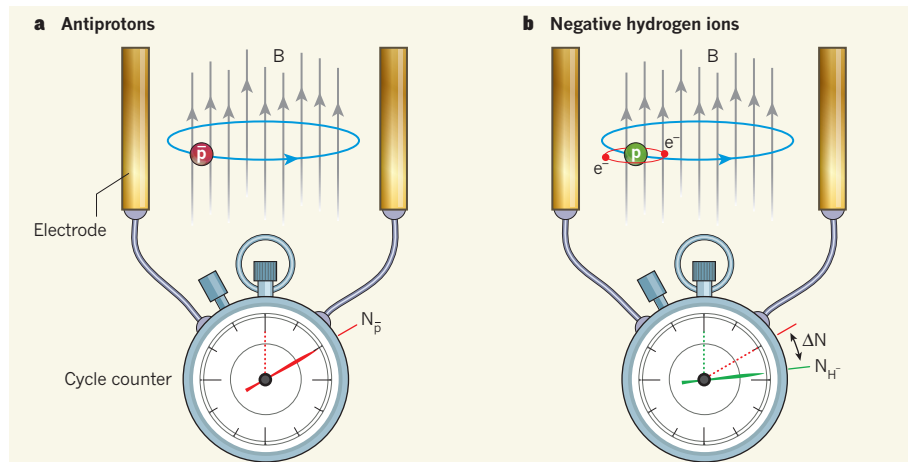
other in the same experiment. The authors repeated this procedure 6,500 times within 35 days and scrutinized the results for systematic errors. Finally, they found that the charge-to-mass ratios of protons and antiprotons are equal to within 69 parts per trillion.

This result is four times more accurate than previous measurements<sup>5</sup> of these ratios, and has implications for the validity of fundamental physical symmetries and theories that have been proposed to address unexplained aspects of the standard model. Symmetries have a central role in physics. A symmetry that holds across the Universe is an indication that a conservation law is at work. For example, adjusting a clock by an arbitrary time interval leaves all physical processes completely unaffected. A consequence of this is that energy can neither be created nor destroyed. But, when a symmetry is violated or a quantity is not conserved, a symmetry-breaking process must be at work.

In the process known as nuclear  $\beta$ -decay, for instance, a neutron is transformed into a proton, an electron and an antineutrino, but only antineutrinos of 'right-handed' nature appear. As a consequence, the electron is emitted into a preferred direction with respect to the neutron spin. This asymmetry is an example of parity (P) violation<sup>6</sup>, which means that  $\beta$ -decay would not proceed in exactly the same way in a mirrored version of the world. Similar symmetry violations are observed only in some processes that involve the weak force. They can appear if the signs of electric charges are reversed (charge conjugation, C), or if the arrow of time changes direction (time reversal, T). Symmetry violations also occur when the combination of C and P symmetries (CP symmetry) breaks down; these become evident for physical processes that occur differently when the signs of charges and handedness are changed simultaneously.

The physicist Andrei Sakharov offered<sup>7</sup> an explanation for the observed dominance of matter, based on such a CP-symmetry violation. However, all the known CP-violating processes cannot sufficiently explain the preponderance of matter over antimatter. Furthermore, at current levels of precision, no physical process has been found to violate the combination of C, P and T symmetries (CPT symmetry), which relates to fundamental physical principles. In quantum mechanics, for example, this combined symmetry ensures that particle spins take only integer and half-integer values. Moreover, the invariance of physical laws in different moving frames of reference (known as the Lorentz invariance) implies CPT symmetry<sup>8,9</sup>.

Physicist Alan Kostelecký and colleagues have suggested that a violation of this symmetry might provide an alternative explanation for the missing antimatter<sup>10</sup>. Unlike Sakharov's model, which requires the disappearance of antimatter in the early, thermally unstable Universe, the latter model does not



**Figure 1 | Particle and antiparticle motion.** Ulmer *et al.*<sup>4</sup> used a device known as a Penning trap to measure, under identical conditions, the characteristic cycling frequency of **a**, antiprotons ( $\bar{p}$ ) and **b**, negatively charged hydrogen ions ( $H^-$ , in lieu of protons; represented as a proton (p) and two electrons ( $e^-$ )) undergoing circular motion in a magnetic field of strength  $B$  (grey arrows), set perpendicular to the direction of motion. From the cycling frequency, which is the number of cycles ( $N_p$  and  $N_{H^-}$ ) that each particle type completed per unit of time, the charge-to-mass ratios of pairs of individual antiprotons and negatively charged hydrogen ions were determined. The number of cycles was measured from signals registered by the trap's electrodes. After correcting for the difference ( $\Delta N$ ) between  $N_p$  and  $N_{H^-}$  to take into account the binding energies and the masses of the two electrons in  $H^-$  that render it different from a proton, the authors found that the charge-to-mass ratios of protons and antiprotons are identical with an accuracy of 69 parts per trillion.

have this additional stringent condition. Under CPT symmetry, particles and antiparticles are strictly identical except for the sign of their charge. Ulmer and colleagues' measurements of the proton and antiproton charge-to-mass-ratios place limits on the differences between the properties of particles and antiparticles and establish a tighter boundary on a possible CPT-symmetry violation.

The charge-to-mass ratios measured by the authors do not vary by more than 720 parts per trillion during a sidereal day, which is the duration of a day with respect to the fixed positions of stars rather than to the Sun. Therefore, this level of accuracy excludes a violation of the CPT symmetry or of the related Lorentz invariance that could be attributed to a preferred frame of reference, such as the one provided by the cosmological microwave background (the Big Bang's relic radiation). It should also be noted that because the cyclotron frequency measurements took place in Earth's gravitational field, any difference in the way that protons and antiprotons interact with gravity would modify their respective frequencies<sup>11</sup>. However, the authors found no such difference larger than 870 parts per billion. This means that the weak equivalence principle — which states that all bodies in a given gravitational field undergo the same acceleration independently of their properties — holds at this level of accuracy.

Ulmer and colleagues' experiment has improved our understanding of fundamental physical principles by placing important limits on several processes. This experiment is a highlight of research on the central question of the prevailing matter–antimatter asymmetry, which the researchers approach by a promising route. Apart from the authors' tests of the CPT-symmetry invariance, there are other experiments<sup>12</sup> that have searched for violations of the CP and T symmetries. The search for the former typically involved precise measurements of particle properties, including antiprotonic systems. The hunt for the latter included searches for the elusive permanent electric dipole moments of particles, and research on the correlations in the parameters of  $\beta$ -decaying nuclei and their decay products, such as neutrinos, electrons and daughter nuclei.

Highly precise experiments at low energies, such as this, are complementary to searches for evidence of fundamental symmetry violations in high-energy particle colliders. There is still no indication whether CPT- or CP-symmetry violations may be responsible for the matter–antimatter asymmetry and for any possible, but as yet unknown, differences between particles and antiparticles. Scientists therefore look forward to improved results from ongoing, well-motivated precision experiments<sup>3</sup>, involving antiprotons in particular<sup>13</sup>, which sustain the attack on one of the most intriguing questions in physics. ■

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## MOLECULAR BIOLOGY

# It takes two to untangle

**Yeast require the enzyme Hsp104 to untangle protein aggregates, which arise in stressed or aged cells. Animals lack Hsp104, but it emerges that proteins of the DNAJ family of molecular chaperones can fulfil this role. SEE LETTER P.251**

HARM H. KAMPINGA

The intracellular protein quality-control network ensures that proteins fold properly or are soon degraded when damaged or no longer needed<sup>1</sup>. When the quality control fails, proteins can clump together in aggregates — a phenomenon associated with stress and ageing, and with many neurodegenerative diseases, several cardiac- and skeletal-muscle diseases and diabetes type II (ref. 2). In yeast, a molecular chaperone called heat-shock protein 104 (Hsp104) mediates disaggregation<sup>3</sup>, thus maintaining cellular health. But although several observational studies have suggested that animals have the potential to disaggregate proteins<sup>4</sup>, they lack a functional Hsp104 equivalent. Furthermore, *in vitro* disaggregation using human molecular chaperones has proved inefficient<sup>5</sup>. On page 251 of this issue, Nillegoda *et al.*<sup>6</sup> show that protein disaggregation in animals is mediated by synergistic cooperation between different members of another class of molecular chaperone, the DNAJ proteins.

In both yeast and animals, Hsps prevent the formation of aggregates by binding to hydrophobic stretches of amino acids. Small Hsps, together with DNAJ proteins, capture unfolded or misfolded proteins and maintain them in a soluble state. These captured clients can then be transferred to proteins of the Hsp70 family, which mediate refolding or degradation, thus preventing aggregation<sup>1</sup>. DNAJ proteins — the largest group of molecular chaperones, with 22 members in yeast and more than 50 in humans — are thought to play their part in this process by directing Hsp70 to specific clients<sup>7</sup>. In addition, individual DNAJ family members assist Hsp70 in Hsp104-dependent

protein disaggregation in yeast. However, the role of DNAJ proteins in the solubilization of aggregates in animals has been enigmatic.

DNAJ proteins are divided into A, B and C classes, of which DNAJA and DNAJB in particular have been implicated in protein quality control after stress<sup>7</sup>. The two classes are thought to interact with the Hsp70 machine separately from each other, chaperoning different types of client<sup>7</sup>. But if, and how, a combination of proteins of different DNAJ classes might act in tandem had not previously been addressed.

Using preformed, heat-aggregated model proteins, Nillegoda *et al.* show that DNAJAs and DNAJBs accelerate protein disaggregation synergistically through a mechanism that is distinct from their classical role in protein folding. In a series of experiments, the authors demonstrated that, rather than acting sequentially, the different DNAJ classes act in parallel with one another, and together with Hsp70, to mediate disaggregation.

DNAJ proteins are known<sup>7</sup> to interact with Hsp70 through their evolutionarily conserved J-domains, and with their targets through variable carboxy-terminal domains (CTDs). Intriguingly, the authors report that the synergistic relationship between DNAJA and DNAJB during disaggregation depends on interactions between the J-domain of one protein and the CTD of the other (Fig. 1). This interaction is independent of the motif called HPD, through which DNAJ interacts with Hsp70, but is instead mediated by conserved, differently charged regions in the J-domain and CTD in each protein. Most DNAJ proteins studied so far act as homodimers (pairs of the same protein)<sup>7</sup>, and Nillegoda and colleagues propose that, in the disaggregation complex, a DNAJA homodimer binds a DNAJB