

Tiny isotopic difference tests the standard model

Gerald Gwinner & Roshani Silwal

A high-precision comparison of the magnetic moments of two isotopically different neon ions opens a path to the search for elusive particles that could explain the unexpectedly low observed mass of the Higgs boson. **See p.479**

The co-inventor of the laser, Arthur Schawlow, famously suggested that one should never measure anything but frequency, because time is by far the most accurately measurable quantity. A corollary to this adage might be: if you have to determine the difference between two very similar frequencies, devise a method that measures this difference directly. Easier said than done, perhaps, but this is precisely what Sailer *et al.*¹ have accomplished, as they report on page 479. In an experimental tour de force, they measured a tiny frequency difference, then used the result to extract the difference between the magnetic moments of two ions of distinct neon isotopes. And they did this with a remarkable fractional precision of half a trillionth the value of the moments themselves, representing a 100-fold improvement over existing methods. In doing so, they have provided a possible way of proving the existence of exotic interactions between electrons and nucleons (protons and neutrons).

The electron's magnetic moment (picture it as a tiny bar magnet) has played a distinguished part in uncovering the secrets of the atomic and subatomic world over the past century. It can be expressed as a proportionality, known as the *g* factor, relative to the Bohr magneton, which is the basic unit of quantum-mechanical magnetic moment. In 1928, English physicist Paul Dirac incorporated the ideas of the special theory of relativity into quantum mechanics and came up with a relativistic equation for the electron², which suggested that the *g* factor is equal to two – a result that was in agreement with observations.

Two decades later, US physicist Julian Schwinger revised this figure to approximately 2.0023 in a celebrated calculation that heralded the advent of quantum electrodynamics, the theory that describes how light and matter interact³. Since then, the *g* factor of a free electron (free as in isolated from other matter) has been predicted and measured to 12 digits – the most accurately verified prediction of any kind^{4,5}. But when the electron is bound to a nucleus, the presence of

the nucleus subtly modifies the *g* factor. At around the ninth decimal place of the value of the *g* factor, the size of the nucleus starts to become apparent. And at even higher precision, hypothetical interactions between the electron and the nucleons could enter the picture. However, corrections arising from quantum electrodynamics limit the theory to around the tenth decimal place, making it impossible to identify such effects in the data.

Sailer and colleagues' conceptual breakthrough was the realization that these contributions from quantum electrodynamics are identical for ions of different isotopes, and will therefore cancel in a relative measurement between them. Furthermore, by probing two ions simultaneously in the same device for storing charged particles, known as a Penning trap, the authors ensured that the ions were subjected to almost identical

conditions, which drastically reduced the experimental uncertainties. They combined two well-tested techniques: their own measurement apparatus, featuring a pair of Penning traps⁶, previously used to determine *g* factors of single ions, and a balance that was designed to measure the ratio of masses of two ions to ultrahigh precision⁷.

A Penning trap uses a combination of magnetic and electric fields to confine charged particles to an orbit within the device. In Sailer and co-workers' experiment, electrons of the neon-20 and neon-22 isotopes were removed sequentially, so that only a single bound electron remained in each ion. Two ions (one of each type) were prepared in a Penning trap, called the analysis trap, so that their moments were aligned with the magnetic field. They were then transferred to a second trap, the precision trap, and placed in the same orbit, thus sampling the same magnetic field (Fig. 1). A precisely timed pulse of microwave radiation was applied to effectively rotate the moments into the plane perpendicular to the field. Because the two isotopes have different numbers of neutrons in their nuclei, their *g* factors are not identical, so their magnetic moments rotate rapidly, but with slightly different frequencies (known as their Larmor frequencies) in this plane. This difference made the moments oscillate in time between pointing in the same direction and in opposite directions.

After a short delay, a second identical pulse rotated the moments back along the direction of the field. If the moments were pointing in the same direction immediately before the second pulse, they ended up pointing in

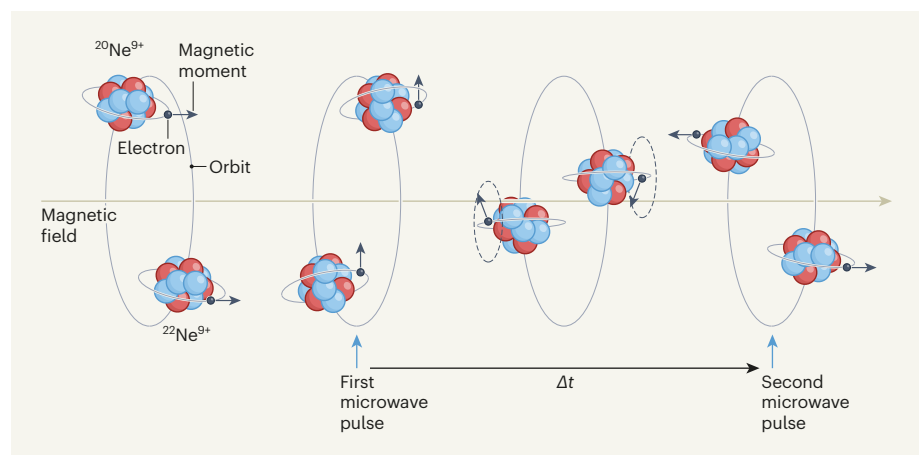


Figure 1 | An ultraprecise comparison of isotopic ions. Sailer *et al.*¹ measured the difference in the magnetic moments associated with the single electrons of ions of neon isotopes (²⁰Ne⁹⁺ and ²²Ne⁹⁺), whose nuclei differ by only two neutrons. The ions were trapped in an orbit in a device called a Penning trap (not shown), and their moments were aligned with a magnetic field. A pulse of microwave radiation rotated the moments to a direction perpendicular to that of the field, after which they rotated around this direction with frequencies that differed due to the effects of the two neutrons. This difference made the moments oscillate in time between pointing in the same direction and in opposite directions. A second pulse rotated them back to the plane of the field, preserving their direction relative to each other. By repeating this cycle many times and varying the time Δt between the two pulses, Sailer *et al.* measured the difference between the moments with a precision that was around 100 times higher than previously possible.

the same direction when they aligned with the field. If they were pointing in opposite directions, they stayed that way after the pulse. Sailer *et al.* detected this difference by moving the ions back into the analysis trap. By repeating this cycle and varying the delay between pulses, the difference in Larmor frequencies and hence the *g* factors could be directly mapped out. Amazingly, the authors were able to follow the process over several seconds, during which the moments revolved 100 billion times.

Assuming that no exotic new physics was involved, the measurement yielded the difference in the nuclear size of the two isotopes with an uncertainty of 0.0001 of the radius. This agrees with existing data, but is ten times more accurate. Importantly, the approach is radically different from other methods, and can provide powerful systematic checks. Because the effect of nuclear size on the *g* factor grows rapidly with nuclear charge, there is considerable potential for applying the method to elements that are heavier than neon.

The authors arrived at an intriguing interpretation by incorporating an independently measured value for the nuclear size difference in their analysis⁸. By doing so, they ensured that all known physics was accounted for, which allowed them to set upper bounds on unknown physics, such as particles that might mediate a hypothetical interaction between electrons and nucleons. Neon-22 has two more neutrons than neon-20, so an interaction between the electron and these two neutrons would be evident in the team's difference measurements.

One such interaction might arise through the exchange of a massive particle, dubbed the relaxion, that was proposed in 2015 as a possible solution to a puzzle known as the hierarchy problem⁹. This puzzle essentially concerns the fact that the observed mass of the Higgs boson is considered unexpectedly low in the context of the standard model of particle physics, and evidence for new physics that could explain the situation has not yet been discovered in experiments at the Large Hadron Collider at CERN, Europe's particle-physics laboratory near Geneva, Switzerland. But the relaxion couples to the Higgs boson, influencing its mass, and as the early Universe expanded, the expansion would have weakened this coupling, thereby 'relaxing' the Higgs mass down to its currently observed value.

Constraints have been placed on the parameter values that could feasibly verify the existence of this particle in the past five years¹⁰. But in some of the methods used previously to pin down these values, the signature of the relaxion competed directly with effects caused by features of the nuclear structure, which are difficult to track^{11,12}. Sailer and colleagues' interpretation is quite straightforward, and a welcome addition to the tool

chest for searches for new physics. Ultimately, combined use of these diverse methods will ensure that a robust and coherent picture emerges. There are already plans to take this to the next level by evaluating combinations of *g* factors and the lowest (ground-state) energies of electrons for pairs of isotopes¹³.

Finally, one cannot discuss methods for precise measurements of ions without considering how they can be applied to antimatter. This question looms large in particle-physics research, because the Universe seems to be made almost entirely of matter, but the Big Bang is thought to have created just as much antimatter. And, indeed, Sailer *et al.* conclude their report by outlining ideas for comparing the *g* factors of protons and antiprotons using their method in search of an answer. Relaxion or not, there is work to be done; no time to relax.

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The authors declare no competing interests.

Genetics

The road to accurate and complete human genomes

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Sequences of the human genome have typically included gaps in repetitive regions of DNA. A combination of state-of-the-art technologies has now enabled researchers to generate the first complete human genome sequence.

The telomere-to-telomere (T2T) consortium has just taken a massive step forwards in human genomics. Writing in *Science*¹, the group describes the first essentially complete sequence of a human genome, called the T2T-CHM13 assembly. This landmark resource, which contains regions of the genome that had not previously been represented in a reference assembly, provides an alternative sequence to the existing human reference genome^{2–4}. Along with the sophisticated methods that enabled its construction, the assembly opens up a path to the generation of many diverse human genomes.

The Human Genome Project was launched in 1990 with the goal of obtaining a highly accurate sequence of most of the human genome. A draft was published² in 2001, and a finished genome three years later³. This reference sequence was a momentous achievement by scientists from 20 institutions in 6 countries, at an estimated cost of more than US\$2 billion ([see go.nature.com/3seOwie](https://go.nature.com/3seOwie)). It has enabled

some of the most important biological discoveries of the past two decades. Nonetheless, technological limitations left some regions of the genome unresolved.

The strategy for sequencing the existing human reference genome was a clone-based approach, in which individual genomic regions (clones) were ordered and oriented across each chromosome, then sequenced. Each clone was 'finished' by an experienced scientist who manually fixed any sequence misassemblies and carried out post-hoc sequencing reactions to fill in gaps. The finished clones were pieced together to construct the final genome assembly. But accurately placing clones was not always possible in repetitive regions of the genome, resulting in some large gaps in regions around these areas (Fig. 1), including around structures called centromeres at the chromosome centre and the sub-telomeric regions close to the chromosome ends.

These limitations were further exacerbated by the fact that the original human genome