Exotic nuclear decay detected

A detector that was designed to probe dark matter, the ‘missing’ mass in the Universe, has seen an elusive nuclear decay called two-neutrino double electron capture — with implications for nuclear and particle physics. See Letter p.532

For half a century, our view of the world has been based on the standard model of particle physics. However, this view has been challenged by theories† that can overcome some of the limitations of the standard model. These theories allow neutrinos to be Majorana particles (that is, they are indistinguishable from their own antiparticles) and predict the existence of weakly interacting massive particles (WIMPs) as the constituents of invisible ‘dark matter’ in the Universe. Majorana neutrinos mediate a type of nuclear decay called neutrinoless double-β decay, an example of which is neutrinoless double electron capture. A crucial step towards observing this decay is to detect its standard-model equivalent: two-neutrino double electron capture. On page 532, the XENON Collaboration reports the first direct observation of this process in xenon-124 nuclei, using a detector that was built to detect WIMPs.

All known interactions in the Universe are mediated by one of four forces: electromagnetic, gravitational, strong or weak. The electromagnetic force and gravitational force, which we encounter in daily life, are long-range and can act over large distances. The strong force acts over short distances and binds together elementary particles known as quarks to form nucleons (protons and neutrons) on the femtometre scale (1 fm is 10−15 m). The weaker long-range residue of the strong force, in turn, binds nucleons into atomic nuclei. For example, this residue binds together the 124 nucleons (54 protons and 70 neutrons) of a xenon-124 nucleus. Last, the weak force is extremely short-range and causes atomic nuclei to disintegrate through a process called nuclear β-decay.

One type of β-decay is located under the Gran Sasso massif in the Gran Sasso National Laboratory, which captures are registered one by one, and for experiments in geochemical studies. Moreover, the researchers’ use of a detector, the authors achieved the first direct observation of two-neutrino double electron capture in xenon-124 nuclei. They measured the half-life of this process to be 1.8 × 1022 years — about one trillion times the age of the Universe.

The XENON Collaboration looked for the decay of xenon-124 to tellurium-124, which occurs through two-neutrino double electron capture, using the XENON1T dark-matter detector. This instrument contains about 3 tonnes of ultra-pure liquid xenon and was designed to search for the scattering of WIMPs off xenon nuclei. The detector is at the Gran Sasso National Laboratory, which is located under the Gran Sasso massif in central Italy, roughly 120 km from Rome. The researchers carried out a direct counting experiment in which emissions of X-rays and Auger electrons were measured to pin down the rare decay. The data were collected over one year (between 2017 and 2018) as part of the hunt for WIMPs.

Thanks to the huge amount of xenon in the detector, the authors achieved the first direct observation of two-neutrino double electron capture in xenon-124 nuclei. They measured the half-life of the process to be 1.8 × 1022 years, which is about one trillion times the age of the Universe. The successful measurement of this half-life lays the foundations for experiments that aim to detect these rare decays in other nuclei. Moreover, the researchers’ use of a
 suite of protein targets are needed to develop new anticancer drug-based treatments. Writing in Nature, Behan et al. 1 (page 511) and Chan et al. 2 (page 551), and, in eLife, Lieb et al. 3, report that certain tumours that have deficiencies in a type of DNA-repair process require an enzyme called Werner syndrome ATP-dependent helicase (WRN) for their survival. If inhibitors of WRN are found, such molecules might be promising drug candidates for further testing.

Imagine a scenario in which scientists could perform an experiment that reveals how almost every gene in the human genome is dysregulated in cancer. Even better, what if such an investigation also offered a road map for how to select a target when trying to develop treatments that take aim at cancer cells, but are not-toxic to normal cells? A type of gene-editing technology called CRISPR–Cas9 enables just that in an approach termed functional genomics. Using this technique, the function of almost every gene in cell-based models of cancer (comprising human cells grown in vitro or in vivo animal models) can be perturbed, and the effect of each perturbation on cancer-cell survival can be measured.

CRISPR can be used to mutate, repress or activate any targeted human gene 4-7. In functional genomics, gene function is assessed in a single experiment by growing a large number of cells and then perturbing one gene in each of the cells. The approach is aided by measuring the concentration in each sample of the DNA sequence that encodes an engineered RNA molecule (termed a single-guide RNA; sgRNA) that is needed for the CRISPR gene-editing process. When the DNA that encodes a particular sgRNA is present in a sample of cancer cells in such an experiment, this means that the gene that the sgRNA targets is not required for cell survival. However, if the sgRNA-encoding DNA sequence is not detected, this indicates that the gene targeted by the sgRNA is required for cancer-cell viability, and those cells containing it died, thereby eliminating the sgRNA-encoding sequence from the sample. This approach offers the possibility of systematically searching for genes that are crucial to tumour-cell survival in large collections of cancer cells that are representative of the diversity of tumour types in humans.

Behan et al. report their development of an online database that they call Project Score. It is a platform for cancer researchers that amalgamates Behan and colleagues’ large-scale data for genome-wide gene editing by CRISPR with previously published genomics information about the cancer models used. The resource consists of data for more than 5 million CRISPR-mediated perturbations undertaken to prevent the expression of individual genes (generating what are known as gene knockouts) in 324 cell-based models of cancer, representing 30 types of cancer in humans. This systematic effort has enabled the identification of genes on which cancer cells depend for survival, as well as those that drive cancer-cell proliferation.

In the database, the authors’ integrated analysis of this functional-genomics data is provided together with other data about the field of nuclear-structure theory. The measured two-neutrino double electron capture will help to test the various nuclear models 8 that are used to calculate rates of double-β decay. Moreover, the acquired half-life data will enable model parameters to be fine-tuned, allowing scientists to more accurately predict the values of the nuclear matrix elements that are associated with neutrinoless double electron capture, as well as neutrinoless double-β decays in general. Finally, all of these factors will contribute to the accurate extraction of neutrino parameters from the data gathered by present and future neutrino experiments.