

THE DISCOVERY OF THE HIGGS BOSON

NO RECENT SCIENTIFIC ADVANCE HAS generated more hoopla than this one. On 4 July, researchers working with the world's biggest atom smasher—the Large Hadron Collider (LHC) in Switzerland—announced that they had spotted a particle that appears to be the long-sought Higgs boson, the last missing piece in physicists' standard model of fundamental particles and forces. The seminar at which the results were presented turned into a media circus, and the news captured the imagination of people around the world. “[H]appy ‘god particle’ day,” tweeted will.i.am, the singer for pop group The Black Eyed Peas, to his 4 million Twitter followers.

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Yet, for all the hype, the discovery of the Higgs boson easily merits recognition as the breakthrough of the year. Hypothesized more than 40 years ago, the Higgs boson is the key to physicists' explanation of how other fundamental particles get their mass. Its observation completes the standard model, perhaps the most elaborate and precise theory in all of science. In fact, the only big question hanging over the advance is whether it marks the beginning of a new age of discovery in particle physics or the last hurrah for a field that has run its course.

The Higgs solves a basic problem in the standard model. The theory describes the particles that make up ordinary matter: the electrons that whiz around in atoms, the up quarks and down quarks that make up the protons and neutrons in atomic nuclei, the neutrinos that are emitted in a type of radioactivity, and two sets of heavier cousins of these particles that emerge in particle collisions. These particles inter-

Pieced together. In this particle collision, it appears that a Higgs boson decays into two electrons and two positrons (red).

act by exchanging other particles that convey three forces: the electromagnetic force; the weak nuclear force, which spawns neutrinos; and the strong nuclear, which binds quarks.

But there's a catch. At first blush, the standard model appears to be a theory of massless particles. That's because simply assigning masses to the particles makes the theory go haywire mathematically. So mass must somehow emerge from interactions of the otherwise massless particles themselves.

That's where the Higgs comes in. Physicists assume that empty space is filled with a “Higgs field,” which is a bit like an electric field. Particles interact with the Higgs field to acquire energy and, hence, mass, thanks to Albert Einstein's famous equivalence of the two, encapsulated in the equation $E = mc^2$. Just as an electric field consists of particles called photons, the Higgs field consists of Higgs bosons woven into the vacuum. Physicists have now blasted them out of the vacuum and into brief existence.

That feat marks an intellectual, technological, and organizational triumph. To produce the

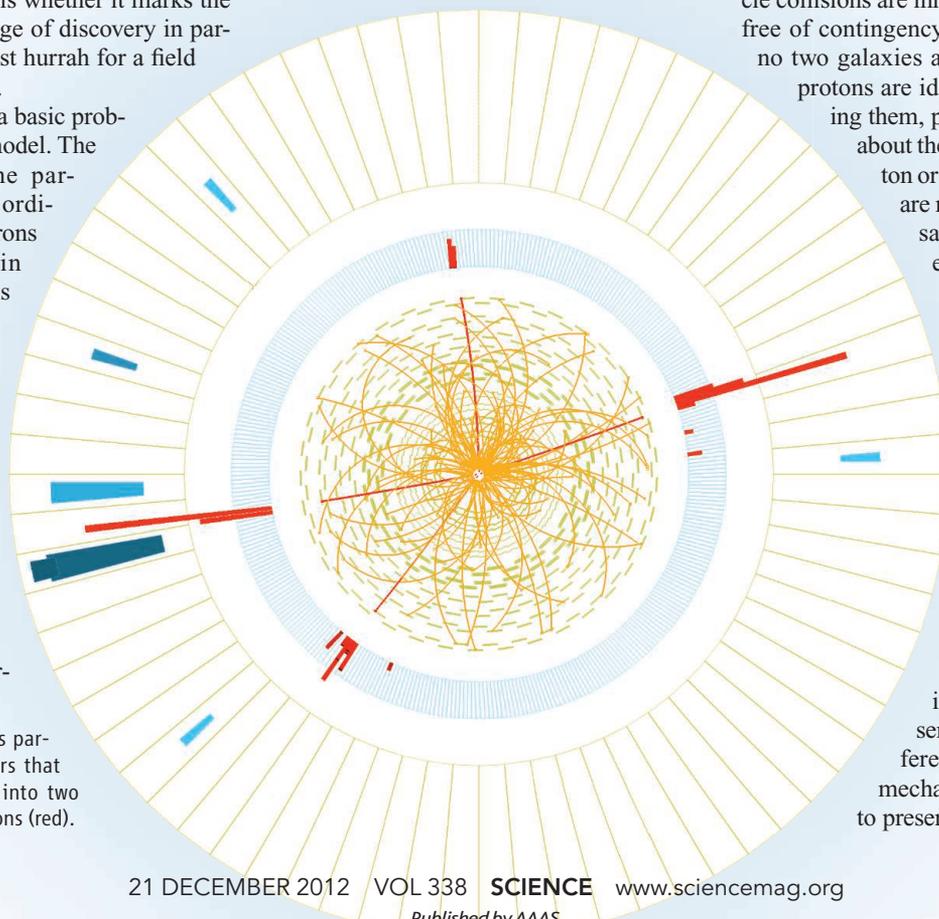
Higgs, researchers at the European particle physics laboratory, CERN, near Geneva, built the \$5.5 billion, 27-kilometer-long LHC. To spot the Higgs, they built gargantuan particle detectors—ATLAS, which is 25 meters tall and 45 meters long, and CMS, which weighs 12,500 tonnes. The ATLAS and CMS teams

boast 3000 members each. More than 100 nations have a hand in the LHC.

Perhaps most impressive is the fact that theorists predicted the existence of the new particle and laid out its properties, right down to the rates at which it should decay into various combinations of other particles. (To test whether the particle really is the Higgs, researchers are measuring those rates now.) Physicists have made such predictions before. In 1970, when only three types of quarks were known, theorists predicted the existence of a fourth, which was discovered 4 years later. In 1967, they predicted the existence of particles that convey the weak force, the W and Z bosons, which were found in 1983.

Particle theorists offer various explanations of their knack for prognostication. Particle collisions are inherently reproducible and free of contingency, theorists say. Whereas no two galaxies are exactly the same, all protons are identical. So when smashing them, physicists need not worry about the peculiarities of this proton or that proton because there are none. Moreover, theorists say, in spite of its mathematical complexity, the standard model is conceptually simple—a claim that nonphysicists might not buy.

The standard model ultimately owes its predictive power to the fact that the theory is based on the notion of mathematical symmetry, some theorists say. Each of the three forces in the standard model is related to and, in some sense, necessitated by a different symmetry. The Higgs mechanism itself was invented to preserve such symmetry while



giving mass to force-carrying particles like the W and the Z. Simply put, symmetry arguments are powerful predictive tools.

No matter the reason for particle physicists' predictive prowess, with the Higgs boson apparently in the bag, they have no similar prediction to test next. They have plenty of reason to think the standard model is not the final word on fundamental physics. The

theory is obviously incomplete, as it doesn't incorporate the force of gravity. And the theory itself suggests that interactions between the Higgs and other particles ought to make the Higgs hugely heavy. So physicists suspect that new particles lurking in the vacuum may counteract that effect. But those arguments aren't nearly as precise as the one necessitating the Higgs boson.

In fact, scientists have no guarantee that any new physics lies within the reach of the LHC or any conceivable collider. The standard model could be all of the inner workings of the universe that nature is willing to reveal. The discovery of the Higgs is a breakthrough. Will particle physicists ever score a similar breakthrough again?

—ADRIAN CHO

A HOME RUN FOR ANCIENT DNA

Two years ago, paleogeneticists made our short list for Breakthrough of the Year for publishing the complete sequence of the nuclear genome of the Neandertals. In 2011, the same lab shared our spotlight for piecing together the genome of the Denisovans, an archaic human that lived in Siberia at least 50,000 years ago. But those ancient DNA sequences and others were blurry snapshots next to the high-resolution genomes that researchers can now sequence from living people. Much of the fragile DNA from fossils is degraded into single strands that automatic sequencers can't copy. Researchers were resigned to deciphering only parts of the code of ancient genomes, whether from archaic humans, animals, or pathogens.

This year, however, a persistent postdoc developed a remarkable new method that enabled his team to revisit the Denisovan DNA and sequence it 31 times over. The resulting genome, of a girl who lived in Siberia's Denisova Cave, reveals her genetic material in the same sharp, rich detail that researchers typically get from the DNA of living people. This technological feat promises to give a major boost to the field of ancient DNA, as researchers begin to apply the method to other samples and species.

Ancient DNA researchers typically have adapted the tools used to sequence DNA from living humans, which start with samples of double-stranded DNA. But ancient DNA usually breaks into single strands. So postdoc Matthias Meyer at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, set out to sequence single-stranded ancient DNA from scratch. He failed at first, but then managed to bind special molecules to the ends of a single DNA strand, holding it in place for sequencing. As a result, using only 6 milligrams of bone from the Siberian girl's pinky finger, Meyer and colleagues were able to copy 99.9% of her genome at least once and 92%



Single-minded. Postdoc Matthias Meyer (*above*) developed a new method to prepare single strands of ancient DNA; the technique gave researchers an unprecedented view of an ancient girl's genome.

of the genome 20 times—the benchmark for reliably identifying nucleotide positions.

The results confirmed that Denisovans interbred with the ancestors of some living humans; people living in parts of island Southeast Asia have inherited about 3% of their nuclear DNA from Denisovans. The genome literally offers a glimpse of the girl, suggesting that she had brown eyes, brown hair, and brown skin. It also allowed the team to use DNA to estimate that the girl died between 74,000 and 82,000 years ago—the first time researchers had used genomic information to date an archaic human. The high quality of the genome gives researchers a powerful new tool to fish for genes that have recently

evolved, providing a “near-complete” catalog of the handful of genetic changes that separate us from Denisovans, who were close kin to Neandertals.

These details are all the more remarkable because the Denisovans are so poorly known from fossils: Only a tiny scrap of finger bone and two molars have been reliably assigned to them so far. In contrast, the Neandertals are known from hundreds of fossils but from a much less complete genome.

Neandertal experts may catch up soon. Meyer and colleagues have been trying “Matthias's method” on fossil samples that previously failed to yield much DNA. A detailed Neandertal genome comparable to the Denisovan one is expected in 2013.



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