PARTICLE PHYSICS

Physicists Find the Last of the Mesons

Physicists say they have finally unearthed the last of a set of subatomic particles called mesons. The discovery of the B_c meson, announced on 5 March at the Fermi National Accelerator Laboratory (Fermilab) in Batavia, Illinois, places the capstone on a pile of discoveries going back 50 years and inks the final entry in the "periodic table" for these particles. Physicists expect that the new meson's mass and lifetime will also sharpen their understanding of the force binding atomic nuclei.

Buried inside the protons and neutrons that form the nucleus are building blocks called quarks. A proton, for instance, harbors three quarks—two "up" and one "down"—bound by the so-called strong force. The same force can also hitch quarks together in pairs to make short-lived mesons.

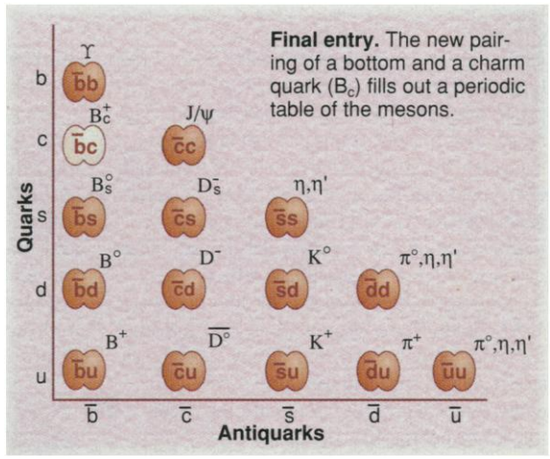
Over the years, physicists studying the debris from particle accelerators have found 14 of the 15 possible mesons formed by different combinations of five kinds of quarks. (A sixth quark, the celebrated "top" discovered 4 years ago at Fermilab, is so massive and unstable that it decays before it can pair up and form a meson.) But no experiment had produced enough B_c mesons (which contain a "bottom" quark and a "charm" quark) for them to be observed. Because these quarks are relatively heavy, they are difficult to create alone, much less in a mixed pair.

This year, because of a recent detector and accelerator upgrade, the roughly 450 physicists at the Collider Detector at Fermilab (CDF) experiment finally had enough data to corner this rare beast. Helping wade through data from trillions of collisions between high-energy protons, two students—Prem Singh of the University of Pittsburgh and Jun-Ichi Suzuki of Tsukuba University in Japan—found what looked like the tracks of about 20 B_c's: a lighter meson and another particle from the B_c's decay. "They were pretty excited at the beginning," says Fermilab physicist Jonathan Lewis, but after 2 years of refining their work, "they were pretty beleaguered."

The data allowed the researchers to measure some of the newborn's vital statistics, including its lifetime. At a half a trillionth of a second, it may be shorter than some theories predicted. One theory, for example, suggested that the charm quark would be so tightly bound that the meson would be slow to decay. A precise measurement of the meson's lifetime and mass, Lewis says, will help physicists settle that question.

However, the small number of observations has also left some room for doubt about the reality of the new meson. "I'm skeptical," says Sheldon Stone of Syracuse University in New York, who recalls "discovering" what turned out to be a mirage in a small data sample. But CDF puts the odds against the finding's being a random fluctuation at a million to one. "That's the same chance as being hit by lightning," Lewis says, "which is my personal definition of an acceptable risk."

–David Kestenbaum



Final entry. The new pairing of a bottom and a charm quark (B_c) fills out a periodic table of the mesons.

ILLUSTRATION: E. CARROLL SOURCE: *FERMI NEWS*

POPULATION BIOLOGY

Inbreeding's Kiss of Death

The hemophilia that plagued Europe's royal families in the 1800s is a clear example of how mating with first cousins and other close kin can cripple a gene pool by allowing recessive genes to emerge from hiding. Less accepted, however, is the notion that inbreeding can drive a small, isolated population of animals or plants to extinction. Many biologists have thought that natural events—widespread flooding from an El Niño, for example, or disease outbreaks—would swamp any genetic effects.

MARIO MAIER

Genetically challenged. Inbreeding helped do in some populations.

But a report in this week's issue of *Nature* suggests that inbreeding may be a more potent force than previously reckoned. After studying fragmented populations of a single butterfly species, a team led by population biologists Ilik Saccheri and Ilkka Hanski of the University of Helsinki has found a strong correlation between a population's genetic diversity and whether it went extinct. This link held up after ecological factors that also influence extinction, such as weather and population size, were taken into account. "Our study demonstrates that inbreeding *can* contribute to extinction in a natural population," says Saccheri. The finding, he adds, bolsters the idea that genetic diversity must be considered when drawing up plans to protect endangered species.

The issue of whether a meager gene pool can lead to extinction in already fragmented populations has provoked "a hell of a lot of controversy," says Richard Frankham of Macquarie University in Australia. Although some biologists have argued for the power of inbreeding, a persuasive argument of late, he says, has been that climatic events and random fluctuations in population size are far more important in the wild.

But that's not the conclusion suggested by new data from Finland's Åland islands, home to a large Glanville fritillary butterfly "metapopulation"—many small, fragmented populations transiently connected when individuals fly between them. To see whether genetic diversity plays a role in extinction, the Finnish team in 1996 collected adult females from 42 populations and analyzed seven of their enzymes and one genomic DNA section for variants, or polymorphisms. After watching seven populations wink out in the last year, the team found that those populations had at least 28% less genetic variation than the survivors. Using a statistical model they had developed to predict extinction risk, which incorporates factors such as a population's size and isolation and habitat size, the researchers found that inbreeding accounted for as much as 26% of the differences from population to population in extinction rates.

The study is "as close as you'll get to direct evidence" that inbreeding figures in extinction, Frankham says. The findings, he and others say, suggest that wildlife managers should focus scarce resources on those threatened populations with larger gene pools within a species. Says Frankham, "This is going to be absolutely critical as we deal with fragmented populations."

–Jocelyn Kaiser