geologist Gregor Eberli of the University of Miami, a co–chief scientist on Leg 166.

Drilling of Leg 166 wrapped up only last month, so complete results won't be out for years, but preliminary analysis supports the Exxon curve. "In some places we were spot on," says Eberli. "In other places, especially when you go back beyond 10 million years ago, we have a bit different times than [Exxon] has." But he notes that the global nature of the sea-level changes in earlier times gets additional support from recent data from offshore Brazil. There, Vitor Abreu and Geoffrey Haddad of Rice University, using well data provided by the Brazilian oil company Petrobras, tracked sea-level changes that correlate very well with the Florida data, Eberli says. The mismatches between his own results and Exxon's are understandable, he adds, given that the most up-to-date Exxon curve is now almost 10 years old: "We will refine their curve."

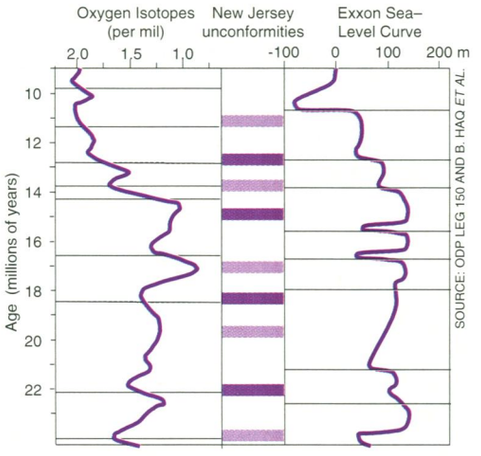
This double-barreled documentation of the curve hasn't yet swayed all doubters, though. Andrew Miall of the University of Toronto, for example, remains a staunch opponent. "I don't think this is good science at all. There are so many events in the Exxon curve and the margin of error in dating is so large that you could correlate anything with it," he says. Indeed, Miall has shown good correlations between the Exxon curve and randomly generated sets of events.

"Andrew's point is well taken," says Miller. Matching a sea-level change from one site to the Exxon curve is inevitably subjective, he notes, so there has been a tendency to make matches where none exist. But, he says, "we're nailing the timing. ... At some point, it's reasonable to say these changes are correlated and [therefore] they are causally related." Kendall agrees: "Whereas Miall is scientifically correct—it is difficult if not impossible to date all of these things perfectly—what we find is that it seems to be working."

A mysterious mechanism

Even if the Exxon curve is a faithful record of global undulations of sea level, it's likely to spark another controversy, over what's driving sea-level change. Researchers have presumed that the answer is the melting and growing of ice sheets. But the Exxon curve pushes the glacial explanation to the breaking point, for the curve rises and falls in a rapid rhythm throughout the past 250 million years—and Earth was thought to be too warm for ice sheets for much of that time.

And while researchers have been able to link the Exxon curve and ice volume during the recent past, the links peter out at earlier times. To measure past ice volume, researchers analyze the oxygen-isotope composition of carbonate sediments. As glacial ice grows



Sea changes. Some drops in sea level *(lines, left)* correlate with core unconformities *(colored bars, center)* and with rapid changes in isotopes *(lines, left)*.

at the expense of seawater or melts into the ocean, it changes the isotopic composition of seawater and the carbonate skeletons of marine plankton.

Now the Leg 155 group has correlated these changes in oxygen isotopes with their New Jersey sea-level changes and with the Exxon curve, back to 36 million years ago. And in a paper in press in *Geology*, Miller and James Browning of Rutgers extend the link between isotopic changes and the Exxon curve to at least 43 million years ago. Abreu's analysis of isotope data also shows signs of ice-driven sea-level change, up to 49 million years ago. But before that, while the world was experiencing the warmest heat wave of the past 65 million years, both groups find that the correlation falls apart, leaving no mechanism to drive sea-level changes.

Yet the evidence for rapid, global change in sea level continues to accumulate. Heather Stoll and Daniel Schrag of Princeton University have used strontium preserved in carbonates to track the exposure of continental margin sediments during the period of relative warmth 90 million to 130 million years ago, when oxygen isotope records are unreliable. When falling sea level exposes sediment to leaching by fresh water, the amount of strontium in the world ocean increases. In work presented at last fall's meeting of the American Geophysical Union, the researchers found that seawater strontium doubled in a few hundred thousand years, suggesting rapid sea-level drops of 30 to 50 meters, and the drops coincide with major falls in the Exxon curve. Stoll and Schrag also turn to a glacial explanation, suggesting that ice sheets may have temporarily grown large enough to lower sea level—a provocative idea, given signs in the fossil record of balmy, high-latitude climes.

If glaciers didn't drive sea level up and down, what did? The jostling of tectonic plates has been suggested; Kendall has even speculated that meteorite impacts might have done the job in torrid times, by changing tectonic stresses. But there's little evidence for such theories. "People start having problems" with the Exxon curve in earlier times, concedes Haq, "because the mechanism is still unknown." Geologists may now be willing to accept Exxon's gift, but they haven't yet unwrapped all its meanings.

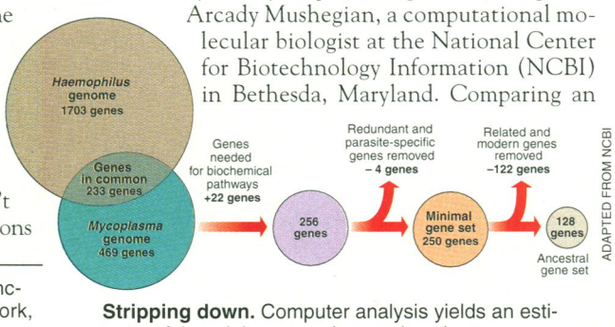
–Richard A. Kerr

GENOME MEETING

Seeking Life's Bare (Genetic) Necessities

COLD SPRING HARBOR, NEW YORK—How many genes does an organism need to survive? Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known genomes, concluded that today's organisms can be sustained with just 250 genes, and that the earliest life forms required a mere 128 genes. The other researcher mapped genes in a simple parasite and estimated that for this organism, 800 genes are plenty to do the job—but that anything short of 100 wouldn't be enough.

Although the numbers don't match precisely, those predictions "are not all that far apart," especially in comparison to the 75,000 genes in the human genome, notes Siv Andersson of Uppsala University in Sweden, who arrived at the 800 number. But coming up with a consensus answer may be more than just a genetic numbers game, particularly as more and more genomes are completely mapped and sequenced. "It may be a way of organizing any newly sequenced genome," explains Arcady Mushegian, a computational molecular biologist at the National Center for Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an



Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.

* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

organism's genome with the most basic set of genes could quickly reveal what makes the organism unique and specialized. Says Mushegian: "Any new genome can be visualized as an extension of this minimum set."

Mushegian and fellow computational molecular biologist Eugene Koonin of NCBI took the first step toward defining this minimum set by identifying the genes shared by two very different bacteria. The team used computer programs that compared the genetic sequences of two organisms whose genomes have been completely sequenced: *Haemophilus influenzae* and *Mycoplasma genitalium*. These two are quite different taxonomically (one is a gram-negative bacteria and the other is gram-positive), but as parasites, both organisms have evolved to be "stripped almost to the bare minimum," Mushegian says.

The team looked for similar stretches of DNA in these organisms and also in the common bacterium *Escherichia coli*. From the DNA sequences, they inferred the genes in those stretches and the functions of their proteins. Next, the researchers pieced together metabolic pathways implied by the proteins, checking to see if any necessary proteins were missing; they filled out their minimum genome with the corresponding genes. Finally, they removed redundant and parasite-specific genes.

This analysis resulted in 250 genes, the likely genome of the ancestor common to both gram-negative and gram-positive microorganisms, and the minimum genome for a modern organism. To estimate the genome of an ancient organism, the team excluded genetic siblings, or genes that diversified from a single, ancestral gene. Although modern organisms may rely on a whole family of genes to do a particular job, presumably the ancestral organisms needed only the ancestral gene. In addition, the researchers discarded some of the genes needed to process DNA, as many think that the very first genomes consisted of RNA. If the primordial world provided amino acids, fatty acids, purines, and pyrimidines, then the putative ancient microbe needed no more than 128 genes, they say. "These genes should be essential for the survival of any cell under all circumstances mentionable," asserts Koonin, who directs the minimum genome project.

At the meeting, Mushegian's presentation provoked lively discussion, and not everyone agreed that the genes held in common are those that are sufficient for life. But pinpointing these fundamental genes provides a very testable hypothesis, Koonin points out. Now experimentalists can begin to knock out all but these essential genes, and see whether the computer and its programmers guessed right. Yeast geneticist Philip Hieter from Johns Hopkins University agrees that this is a good start: "You know there *will* be an answer to the question of the minimum number of genes, eventually."

Instead of trying to answer that question by inferring the genes of a hypothetical microbe, Andersson studies present-day parasites to identify the point at which an organism has too few genes to survive on its own. The extreme case is mitochondria, cells' energy-producing organelles. Many researchers think mitochondria, which have their own small set of genes, are the remnants of intracellular parasites that eventually became an integral part of the cell. Because parasites reduce their genomes as they depend more on their hosts, the mitochondria can be seen as parasites that lost too many genes—and so lost their independence. "We're interested in what has been thrown out [of these small genomes] and what has been retained," explains Andersson.

To backtrack through mitochondrial evolution, Andersson is examining the genome of the mitochrondria's closest relative, an intracellular parasite called *Rickettsia prowazekii*. Just 1.2 million bases long, the genome of this parasite, which causes typhus, has lost some but not all of the DNA that the mitochondria did. Andersson's team sequenced some 200,000 bases in this genome and estimated the number of genes in that stretch of the genome. They then extrapolated to the whole organism, coming up with 800 genes.

Whether the minimum numbers of genes proves to be 128, 800, or some other number, these researchers have at least begun to get a handle on life's crucial genetic components, something not possible a decade ago, says David Bentley of the Sanger Center in Cambridge, England. He, for one, applauds these fledgling efforts to identify a bare-bones genome: "It's a lovely idea, however messy or arguable [the analysis] might be."

–Elizabeth Pennisi

GENOME MEETING

Studly Sheep By Non-Mendelian Means

COLD SPRING HARBOR, NEW YORK—More than a decade ago, a sheep farmer in Oklahoma noticed that some of his livestock were beefier than the rest of the flock. He and his fellow breeders saw dollar signs in the sheep's bulging hindquarters and well-sculpted muscles, but creating whole flocks of these woolly Schwarzeneggers turned out to be harder than anyone expected. Now, new work presented at a recent genome meeting here suggests that these burly sheep offer a rare and useful example of how phenotype—what an organism looks like—doesn't always match up with its genotype.

TRACY SHAY

Why not me? Normal-looking ram with two copies of the "beautiful buttocks" gene looks at his bulky offspring.

The researchers, led by Noelle Cockett of Utah State University in Logan and Michel Georges of the University of Liège in Belgium, found that a peculiar combination of non-Mendelian genetics governs which sheep bulk up and which don't. And the underlying mechanisms may one day help explain the odd patterns of inheritance seen in certain genetic diseases in humans, says Aravinda Chakravarti, a human geneticist at Case Western Reserve University in Cleveland. "There clearly are disorders where lots of individuals carry a mutation but are clinically unaffected. I think there will be all kinds of exceptions to Mendelian inheritance," he notes.

Cockett and her colleagues got their first clues to this odd sheep mutation in 1994, when, by using genetic markers from cows, they were able to map the mutated gene to sheep chromosome 18. They named the gene *callipyge*, Greek for "beautiful buttocks." Lambs normally seem to add muscle to their bodies when young and accumulate fat as they get older, but the mutant gene apparently lengthens the period of muscle addition and delays fat accumulation, explains Cockett. *Callipyge* newborns are indistinguishable from other lambs, but the adult sheep wind up with 7.8% less fat and 32% more muscle—in their rear end and hind legs.

Cockett and others assumed that the mutant form of *callipyge* was a typical dominant allele, for hefty rams mated with normal females produced bulky offspring. But breeders complained that the gene's inheritance was unpredictable. And in a poster presentation, Georges and his colleagues showed that *callipyge* actually exhibits a rare and complex pattern of inheritance. First, they found through systematic breeding experiments that this butt-building trait is evident only when passed on paternally. Lambs born to *callipyge* females mated with normal males grow up looking normal, like their dads. Such a seemingly one-sided inheritance pattern is usually a sign of imprinting, a genetic phenomenon in which the gene contributed by one parent is shut down somehow, leaving the other parent's gene as the only functional copy. About 16