MEETING AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE

Revisiting the Numbers: Human Genes and Whales

BOSTON—The annual meeting of the American Association for the Advancement of Science (publisher of *Science*), held from 15 to 19 February, included symposia across the scientific disciplines. The following is a sampling from the early sessions; more coverage will be published next week.

Human Gene Count On the Rise

When the draft human genome sequence was completed last year, a computer analysis suggested that the number of genes was shockingly small. Now, an experimental approach suggests that the number may actually be much closer to the early prediction of 70,000 genes, according to a presentation on 16 February.

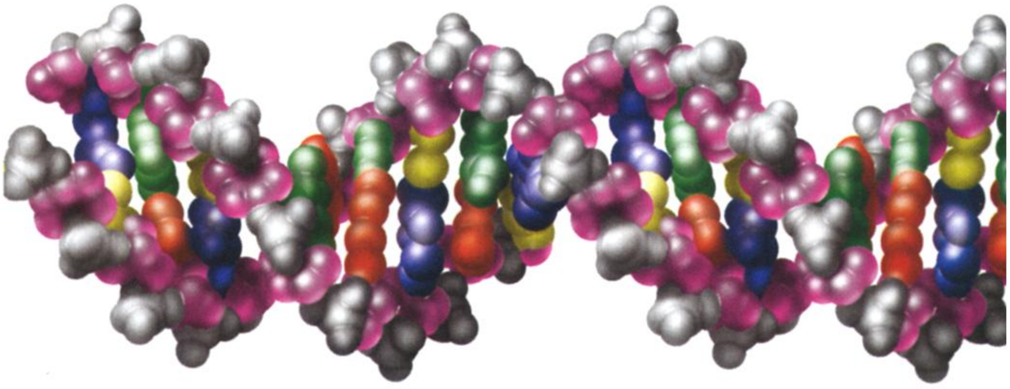
The all-day session started innocently enough. Eric Lander of the Whitehead Institute for Biomedical Research in Cambridge, Massachusetts, a leader of the Human Genome Project, told a standing-room-only audience that his best guess was still that there are about 32,000 human genes. That's based on the use of specialized computer software to identify genelike sequences in DNA.

Later in the day, Victor Velculescu mounted a small rebellion by raising the gene count. He and his colleagues, at Johns Hopkins University in Baltimore, Maryland, have gone back to the lab to look for genes that the computer programs may have missed. Their technique, called serial analysis of gene expression (SAGE), works by tracking RNA molecules back to their DNA sources. After isolating RNA from various human tissues, the researchers copy it into DNA, from which they cut out a kind of genetic bar code of 10 to 20 base pairs. The vast majority of these tags are unique to a single gene. The tags can then be compared to the human genome to find out if they match up with genes discovered by the computer algorithms. Velculescu said that only roughly half of the tags match the genes identified earlier—evidence, he says, that the human inventory of genes had been underestimated by about half.

The reason for the disparity may be that the standard computer programs were largely developed for the genomes of simple (prokaryotic) organisms, not for the more complex sequences found in the genomes of humans and other eukaryotes. "We're still not very good at predicting genes in eukaryotes," said Claire Fraser of The Institute for Genomic Research in Rockville, Maryland. It's entirely possible that there could be more than 32,000 genes, and SAGE is an important approach to finding them, she says: "You absolutely have to go back into the lab and get away from the computer terminal."

–BEN SHOUSE

Ben Shouse, a former *Science* intern, is an intern at *The Nation.*



A Whale of a Chain Reaction

Whaling decades ago may have triggered a cascade of ecological events that ultimately wiped out kelp forests off Alaska's coast, a researcher suggested here on 15 February. The idea—which runs counter to conventional wisdom—suggests that overharvesting of top marine predators can have far-reaching impacts throughout an ecosystem.

Alaskan collapse. Orcas turned to smaller prey when other whales were decimated by whaling after World War II.

Researchers have been struggling for years to explain why kelp forests have crashed along Alaska's Aleutian archipelago. Many researchers believe that overfishing or climate change drove down fish and sea lion populations, forcing orcas—the region's top predator—to prey on less desirable sea otters instead. Fewer sea otters, in turn, led to a boom in sea urchins, spiny invertebrates that then overgrazed the region's lush kelp forests, leaving behind empty "urchin barrens" (*Science*, 16 October 1998, p. 473).

But James Estes of the University of California, Santa Cruz, has put a new twist on the story. Orcas, he suggests, turned to seals and sea lions only after their original prey, the great whales, were decimated by the whaling industry after World War II. The decline of the great whales forced orcas to "fish down the food chain," shifting to smaller and smaller prey as human whalers claimed the larger animals. Estes calculates that current declines in Steller's sea lions could be explained by as few as 18 orcas eating only that species, or by a mere 1% shift in diet among all orcas.

"As this line of reasoning has developed, I've found it more and more compelling," said Elliott Norse of the Marine Conservation Biology Institute in Redmond, Washington. But not all scientists are satisfied with the hypothesis. Vincent Gallucci of the University of Washington, Seattle, suggests that a growing population of sharks precipitated the kelp decline by competing with sea lions for food or preying on pups.

–JAY WITHGOTT

Jay Withgott is a science writer in San Francisco.

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