goes, Laitman minces no words: "A single bone tells us absolutely nothing about any ancestor's vocal tract." He adds: "Using the exact same measurements, I can show you that pigs' hyoids in many ways are more similar to modern humans."

Where does this leave the field? "To be quite honest, I don't see how a dispassionate observer can make a choice" between the pro-Neandertal-speech and anti-Neandertal-speech camps, says University of Pennsylvania Neandertal expert Alan Mann. "I think a lot of people are in bystander mode," agrees Ian Tattersall of the American Museum of Natural History. In the end, this controversy underscores a central problem in paleoanthropology: how difficult it is to reconstruct behavior (including linguistic behavior) from the remains in the fossil record. Unless there are some remarkable, unforeseen technological breakthroughs in interpreting fossils, the punchline of the old nonjoke about what one Neandertal said to the other may just be lost forever.

–Ann Gibbons

EVOLUTIONARY BIOLOGY

Is "Flying Primate" Hypothesis Headed for a Crash Landing?

He heralded it as the "flying primate" hypothesis—the idea that a certain suborder of bats was more closely related to primates than to other bats—but lately Australian neuroscientist John Pettigrew has been feeling somewhat batted about. "I know that when five studies in a row show molecular data against the hypothesis, I can't claim I'm in a strong position," he says. Then again, the University of Queensland neuroscientist isn't quite ready to cave in.

Six years ago, Pettigrew proposed in *Science* that the so-called megabats, or flying foxes, were descended from primates, whereas the microbats were not. That flew in the face of the classical view that the two types of bats were in the same order—or "monophyletic." Since then, the issue has been up in the air, but now it looks like Pettigrew's "diphyletic" hypothesis may have come crashing to earth. In this issue of *Science*, Morris Goodman and his colleagues of Wayne State University publish the latest in a string of molecular results showing that systematists haven't really been blind as bats all this time: Microbats and megabats are closely related in evolutionary terms, they conclude, and megabats aren't really flying primates at all.

Combined with classic morphological work comparing the wings, ears, hind limbs, and other features of both types of bats, the growing body of molecular evidence "blows apart the hypothesis that megabats really are primates," Goodman argues. That hypothesis came to Pettigrew, an expert on the brain's system for processing visual information, when he looked at megabat brain tissue under a microscope for the first time. In the microscope, Pettigrew found visual pathway traits in the megabat cortex that were thought to be unique to primates (*Science*, 14 March 1986, p. 1304). The similarity was so remarkable that he proposed that megabats (*Megachiroptera*) were descended from an ancestor they shared with the primates. Microbats (*Microchiroptera*) didn't show those same neural pathways—and Pettigrew proposed that the two suborders of bats evolved from two different ancestors. The theory had the stunning implication that all the striking features of bats would have to have evolved twice.

The idea that flight evolved twice in mammals in exactly the same way was labeled as, well, batty by specialists in evolution. Classical morphologists found it hard to discount the vast number of physical similarities between megabats and microbats. The debate also created a rare opportunity for molecular evolutionists to wield their new molecular and computing tools to help settle the question. In the past couple of years, molecular evolutionists have set about sequencing the nuclear and mitochondrial DNA and amino acids from bat tissue. The first molecular studies were inconclusive, but new work on both mitochondrial and nuclear genes is much stronger, and it all reaches the same conclusion: Megabats and microbats hang from the same branch of the family tree.

In the study published in this issue, Goodman and graduate student Wendy Bailey used a 1.2-kilobase region of nuclear DNA that includes a large part of the epsilon-globin gene that codes for embryonic hemoglobin (although most of the sequence is noncoding). By examining this DNA sequence in 17 species, Goodman's group built a phylogenetic tree that puts the two suborders of bats squarely in the same order. Unpublished work on the sequence of a gene that codes for the interphotoreceptor retinoid binding protein (part of the visual system) by Michael Stanhope, a research associate in Goodman's lab, reaches the same conclusion. Both studies put the bats at some distance from primates. This work follows two other studies published recently in the *Proceedings of the National Academy of Sciences* that found similarity in the bats' mitochondrial genes—one by Ronald Adkins and Rodney Honeycutt of Texas A&M, who sequenced the mitochondrial gene for the enzyme cytochrome oxidase II, and another by David Mindell of the University of Cincinnatti, who sequenced the mitochondrial genes that code for the 12S ribosomal RNA and for the enzyme cytochrome oxidase I.

Pettigrew, however, says he has yet to be convinced that the molecular methods are infallible. "At the moment there is tremendous hubris about molecular data," says Pettigrew. "These groups think they have the answer, but we have to be cautious." There is a possibility, albeit a remote one, he argues, that the similarities in the genomes of megabats and microbats could be the result of convergent evolution—that, by chance, the different species ended up with random mutations in the same sites of the genome. An interesting idea, no doubt, but most experts in the field are betting that it won't fly.

– Ann Gibbons

Flight of fancy? Much recent evidence suggests that the hypothesis that megabats are closely related to primates may be as fanciful as this creature from the "Wizard of Oz."

ARCHIVE PHOTOS