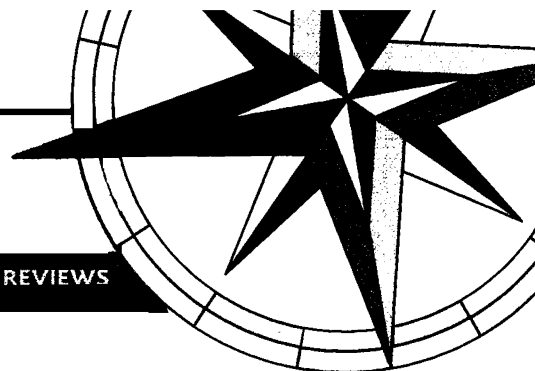




A Family Tree for Heavyweights

A CLOSE KINSHIP OF WHALES TO HOOFED mammals, and to hippopotamuses in particular, is discussed in two articles in the issue of 21 Sept., "The ancestry of whales," a Perspective by K. D. Rose (p. 2216), and a Report, "Origin of whales from early artiodactyls: hands and feet of Eocene Protocetidae from Pakistan" by P. D. Gingerich, M. ul Haq, I. S. Zalmout, I. Hussain Khan, and M. Sadiq Malkani (p. 2239). This is not a new idea. Rather, it is a vindication of the earliest explicitly phylogenetic classification of mammals. In 1866, the pioneering evolutionary biologist Ernst Haeckel classified the order Cetacea (in which he also included the sireni-ans) and the order Ungulata (with Artiodactyla and Perissodactyla as suborders) together under his legion Pycnoderma (1). In his formal classification, the hippos were placed as family Obesa, which, along with the pigs, anthracotheres, and their close allies, comprised section Choeromorpha under the suborder Artiodactyla. However, in his phylogenetic tree of the Mammalia (Plate VIII), he depicts the Cetacea and the Obesa as sister taxa; this whale-hippo clade was, in turn, the sister taxon to the clade containing the pigs and anthracotheres.

Later, Haeckel abandoned this phylogeny and considered the origin of whales questionable (2). Most subsequent cetologists

dismissed or ignored the possibility of a relationship between whales and ungulates until the idea was revived by molecular biologists in the late 20th century.

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Ernst Haeckel and friend Allens (Italy, 1862).

Did Human Hunting Cause Mass Extinction?

JOHN ALROY'S SIMULATION OF NORTH American terminal Pleistocene mammalian extinctions (Reports, "A multispecies overkill simulation of the end-Pleistocene megafaunal mass extinction," 8 June, p. 1893) leads him to conclude that people caused the loss of 41 species of mammals. However, the overkill argument is confronted by overwhelming empirical problems, two of which I mention here.

In Alroy's model, the median age of the extinction event falls 1229 years after the initial human invasion. Using a date of 13,400 yr B.P. for the appearance of Clovis

and 12,260 yr B.P. for the youngest extinctions, he obtains a close match between his prediction and the empirical data he uses. However, of the 35 genera of mammals that were lost toward the end of the Pleistocene in North America, only 15 can be shown to have survived into Clovis times (1). One can assume that the remaining 20 genera must also have been lost during those times, but assuming that all the extinctions occurred specifically during Clovis times, and then using Clovis to explain them, is problematic.

Alroy correctly observes that "humans are known to have hunted extinct megafauna" in North America, but mammoth is the only extinct mammal to have been found in secure kill association in North America. This is unlikely to be the result of sampling error, since mammoth account for only about 20% of the known late Pleistocene occurrences of extinct noncarnivores in the comprehensive FAUNMAP database (2).

Overkill is confronted by other significant problems (1, 3), but these suffice to make the point. There is little in the empirical record to support the argument that the initial human colonization of North America led inexorably and rapidly to massive extinction.

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2. FAUNMAP Working Group, *Ill. State Mus. Sci. Paps.* **25**, nos. 1, 2 (1994).
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Response

GRAYSON OVERLOOKS THE MODEL'S KEY predictions concerning overall extinction rates, extinction outcomes, human population densities, and human diet, and just as importantly, its robust logic and parameterization. The model correctly predicts that terminal megafaunal dates should be no younger than Clovis interval, but Grayson demands that no apparent terminal dates should be older than Clovis. The data are sufficient to test the for-

Letters to the Editor

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