

## f25 The genetic test of species relationships

< gorilla or pan and humans >

... willed down, waited for, in place at last and for good.

—Seamus Heaney, *Beowulf, A Verse Translation*.<sup>1</sup>

An example of convergence is an identical change in the sequence of the prion-protein gene in both cattle and hominoids and unique to them. David C. Krakauer, who reported on this in 1996,<sup>2</sup> also made the case (**Figure f25.1**) that state-of-the-art analysis of gene sequences do result in gene tree relationships that suggest rethinking of traditional phenome-homologies species trees (**Footnote f25.1**). Item: Of the more than 13,000 genes that make up the coffee genome, almost all have counterparts that perform the same function in tomato as well as in other of the ~1500 species of the genus *Solanum* (family Solanaceae) that includes potato, aubergine (eggplant), pepper and petunia.<sup>3</sup>

Most of the genome of organisms is of noncoding DNA. Coding DNA (genes) are sequences of nucleotides in the chromosomes that specify amino acids. Amino acids coded for are changed by nonsynonymous nucleotide substitutions (Ka) in coding DNA and are not changed by synonymous substitutions (Ks) in coding DNA. Wen-Hsiung Li in 1993 explains that a Ka/Ks ratio less than one indicates that a gene is experiencing the effects of purifying selection (selection for the current gene sequence) whereas greater than one indicates that a gene is undergoing the effects of positive Darwinian selection (selection for a new gene sequence).<sup>4</sup>

Of coding DNA in humans and chimpanzees, Derek E. Wildman, Lawrence I. Grossman and Morris Goodman in 2003 find that most is experiencing the effects of purifying selection (Ka/Ks value of 0.59) and this likely to change little as, for these, most mutations in their coding are deleterious presently. However, some genes with Ka/Ks values of approximately 1.6 are considered to be unambiguously undergoing positive selection. Working with these, phylogenetic relationships that can be inferred “support the hypothesis that humans and chimpanzees are sister taxa to the exclusion of gorillas and orangutans. Gorillas are the closest relatives of humans & chimpanzees given the current data, concurring with the fossil and other evidence that suggests that these three taxa evolved in Africa. Orangutans that live in Asia are the least closely related great ape.”<sup>5</sup> □

**Figure f25.1**<sup>2</sup> Phylogenetic relationships among the prion protein genes of 33 species of vertebrates (in the analysis, a bird, the chicken *Gallus gallus*, was used as the outgroup). The gene tree shown does not agree with the currently accepted species tree which comparative anatomy studies have suggested. For example, in the gene tree the Old World and New World monkeys are sister groups, whereas in the species tree the Old World monkeys and the hominoids are sister taxa. *Homo* is a sister group of *Gorilla* in the gene tree, whereas in the species tree, *Homo* is the sister species of *Pan*. Sequences from 97 active genes common to humans and chimpanzees are 99.4 percent the same (Morris Goodman, 2003).<sup>6</sup>

The genomes of the chimpanzee (published September, 2005) and of humans (published in 1995) can be directly compared to reveal that 40 million evolutionary events separate them from us. E. Culotta and E. Pennisi, summarize: “We differ by only about 1% in the nucleotide bases that can be aligned between our two species, and the average protein differs by less than two amino acids. But a surprisingly large chunk of noncoding material is either inserted or deleted in the chimp as compared to the human, bringing the total difference in DNA between our two species to about 4%.”<sup>7</sup> For classification’s grouping this is close but, in reality, is a huge difference indicating evolution from a common ancestor which can be estimated to have lived between 5 and 6 million years ago.

