Studies on the Phylogenetic Position of the Ctenodactylidae (Rodentia)\textsuperscript{1}

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More than half of all mammalian species belong to the order of the rodents. Although many phylogenetic relationships among rodents have been established beyond doubt, others are not yet established. The phylogenetic position of the Ctenodactylidae (gundis) was discussed in several contributions to a symposium in Paris in 1984 (Luckett and Hartenberger 1985). This is a small rodent family with only four species living in the border regions of the Sahara Desert in Africa. This taxon has been grouped either with the hystricognathous rodents or as a separate branch, as a very early offshoot from the rodent stem: Luckett (1985), Bugge (1985), and George (1985) concluded, from different sets of data, that the Ctenodactylidae share with the hystricognathous rodents a number of derived traits and that the Ctenodactylidae should be considered as an early offshoot of the latter. Wood (1985) discussed the phylogenetic position of several sciurognathous hystricomorph families, including the Ctenodactylidae. These families are also restricted to Africa and have often been associated with the hystricognathous rodents. However, in Wood's opinion there are no indications for these relationships, the similarities being the result of conservation of ancestral features or of convergence. Hartenberger (1985) concluded from the fossil evidence that the Ctenodactylidae are one of the oldest recognized rodent families, diverging from all other rodent taxa in the Lower Eocene. With additional molecular data, it may be possible to shed more light on this controversy and to learn more about the origin of the rodents.

No molecular evidence is yet available on the phylogenetic position of the Ctenodactylidae. Therefore, several tissues and blood of gundis were collected, and a number of proteins were isolated and investigated.

Gundi myoglobin was isolated, and its amino acid sequence was determined (Beintema et al. 1990). Only four other rodent myoglobin sequences have been determined so far: mouse (\textit{Mus musculus}) (Harris et al. 1985), casiragua (\textit{Proechimys guairae}) (Harris et al. 1985), viscacha (\textit{Lagostomus maximus}) (Gurnett et al. 1984)), and mole rat (\textit{Spalax ehrenbergi}) (Gurnett et al. 1984). The gundi amino acid myoglobin sequence was compared with the 73 other known vertebrate myoglobin amino acid sequences by using computer procedures, described by Czelusniak et al. (1990), that search for the tree or set of trees with shortest nucleotide substitution length. The shortest trees for the 74 myoglobin sequences found in this search failed to represent rodents, primates, and artiodactyls as monophyletic orders. In these shortest trees, the gundi joins the hystricognath (casiragua/viscacha) branch, which is rather widely separated from the mouse/mole rat branch. If the four other rodents are forced together, which requires four additional nucleotide substitutions, the branch to the gundi still joins the two hystricognaths, or, for the same score, the gundi branches off before the divergence of the other four rodent sequences.

The amino acid sequences of the \(\alpha\) and \(\beta\) hemoglobin chains of gundi were

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determined (Beintema et al. 1990) and compared with the α and β hemoglobin sequences from 134 vertebrate species—α sequences by themselves, β chains by themselves, and tandemly combined α and β chains. Parsimony procedures were used to find the shortest tree. When the β sequences are used, the gundi groups with the tree shrew, and the common branch of those two joins lemur and then joins a branch with nine rodents and pig. When the α sequences are used, gundi groups with squirrel, but this branch does not join the other rodents. However, when tandemly combined α and β sequences are used, a monophyletic tree of the rodents is obtained, with the first intrarodent divergence separating gundi from all the other rodents (fig. 1). Joining gundi with the hystricognath guinea pig results in a tree with two more substitutions. This is a low number compared with the branch lengths connecting gundi and guinea pig to the rest of the rodent stem.

Studies of other proteins provide little additional evidence about the phylogenetic position of the Ctenodactylidae. Gundi αA-crystallin shares a replacement with two hystricognath species that separates these taxa from other rodents (Hendriks et al. 1987). Immunological studies of serum proteins indicate no special affinity between

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mouse
roof rat
muskrat
hamster
mole rat
ground squirrel
souslik
marmot
guinea pig
gundi
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Fig. 1.—Most parsimonious tree of tandemly combined α and β sequences of rodent hemoglobins. Numbers above the lines indicate nucleotide replacements. Species and literature references are as follows: mouse, *Mus musculus* (Popp 1967; Konkel et al. 1979; Nishioka and Leder 1979); roof rat, *Rattus norvegicus* (Chua et al. 1975; Garrick et al. 1975, 1978); muskrat, *Ondatra zibethica* (Bieber and Braunitzer 1983); hamster, *Mesocricetus auratus* (Braunitzer et al. 1980); mole rat, *Spalax ehrenbergi* (Kleinschmidt et al. 1985a); ground squirrel, *Spermophilus townsendi* (Kleinschmidt et al. 1985b); souslik, *Citellus citellus* (Soskic et al. 1986); marmot, *Marmota marmota* (Sgouros et al. 1986); guinea pig, *Cavia porcellus* (Braunitzer et al. 1979).
gundi and any other investigated rodent species (Sarich 1985, and personal communication).

The molecular data summarized in this letter confirm that both the Ctenodactylidae and the hystricognathous rodents are early offshoots in the order of the rodents, but—as in classical phylogeny—it is impossible yet to decide whether they share a common ancestor or are located on separate branches.

Sequence Availability

The amino acid sequences of gundi myoglobin, α hemoglobin chain, and β hemoglobin chain have been deposited in the NBER Data Library under accession numbers A33082, B33082, and C33082, respectively.

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LITERATURE CITED


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