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Protein Sequences Indicate That Turtles Branched Off from the Amniote Tree After Mammals

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Abstract. The phylogenetic relationships among the major groups of amniote vertebrates remain a matter of controversy. Various alternatives for the position of the turtles have been proposed, branching off either before or after the mammals. To discover the phylogenetic position of turtles in relation to mammals and birds, we have determined cDNA sequences for the eye lens proteins αA- and αB-crystallin of the red-eared slider turtle (Trachemys scripta elegans). In addition, databases were searched for turtle protein sequences, for which mammalian, avian, and outgroup orthologs were available. All sequences were analyzed by three phylogenetic tree reconstruction methods (neighbor-joining, maximum parsimony, and maximum likelihood). Including the α-crystallins, 7 out of 12 proteins support a sister-group relation of turtles and birds with all 3 methods. For each of the other five proteins no topology was consistently preferred by the three approaches. Analyses of the combined amino acid data (1,695 aligned sites) also give extremely strong evidence that turtles are nearer to birds, indicating that mammals branched off before the divergence between turtles and birds occurred.

Key words: Testudines — Trachemys scripta elegans — Tetrapod phylogeny — Molecular evolution — α-crystallin

Introduction

The major groups of amniote vertebrates diverged from a common ancestor during a relatively short period at the end of the Paleozoic era, about 300–250 million years ago (Carroll 1987; Laurin and Reisz 1995). Until recently there was a broadly accepted view of the relationships between these amniote groups, based on paleontological and morphological evidence. This held, as already implied by Haeckel (1866), that mammals represent the sister group of all other extant amniotes. The turtles (Testudines) were generally considered to be the next group to have branched off, followed by Lepidosauria (tuatara, lizards, and snakes), with the final divergence occurring between crocodiles and birds (together the Archosauromorpha) (Carroll 1987).

In the past decade this view has seriously been challenged with the advent of more sophisticated cladistic analyses. The hypothesis of a sister-group relation between mammals and birds (Gardiner 1982, 1993; Løvtrup 1985), reviving the clade Haematothermia (Owen 1866), has stirred much debate. Also, the position of the turtles is controversial. Some authors unite Testudines and Archosauria, to the exclusion of Lepidosauria (Løvtrup 1977; Hennig 1983; Ax 1984). Alternatively, the turtles have been proposed to be the first to branch off from the amniotes, followed by the mammals (Gaffney 1980). This latter view has indeed been adopted in some recent text books (e.g., Chaline 1990, p 78; Ridley 1993, p 465). Various authors have, however, provided renewed support for the classical branching pattern, based on morphological characters (Carroll 1987; Gauthier et
Reamplification with the same primers was necessary to obtain enough
T[A,C,G,T]TC-3'. Hybridization temperatures were 45°C for the aA-
CACCC-3' and 5'-ATAAAGCTTACCTC[C,T]GAGAGTCCCG-
for aB-crystallin we used 5'-ATACTGCAGGATATCACCATTCA-
Total RNA was isolated from eyes.

**Materials and Methods**

Sequence Analysis of α-Crystallins. Total RNA was isolated from eyes
of three juvenile red-eared slider turtles, *Trachemys scripta elegans*, by
the lithium chloride/urea method (Auffray and Rougeon 1980). RNA
was reverse transcribed using SuperScript reverse transcriptase (Gibco
BRL/Life Technologies) and oligo(dT) primer. α-Crystallin sequences
were amplified from the resulting single-stranded cDNA by the poly-
merase chain reaction (PCR) method, using *Taq* polymerase (Gibco
BRL/Life Technologies). Degenerated oligonucleotide primers were
designed to amplify cDNA sequences coding for amino acid positions
12-160 of αA-crystallin and positions 9-61 of αB-crystallin. For α-

crystallin, the primers were as described earlier (Caspers et al. 1994);
for αB-crystallin we used 5'-ATACTGCAAGATATCACCATTCA-
CACCC-3' and 5'-ATAAAAGCTTACCTC[C,T]GAGAGTCCCG-
Τ[Α,С,Γ,Τ]ΤC3'. Hybridization temperatures were 45°C for the α-

crystallin amplification and 55°C for the αB-crystallin amplification.

**Results**

α-Crystallin Sequences

α-Crystallins belong to the small heat-shock protein family
(Caspers et al. 1995). They occur in the vertebrate eye
lens as multimeric complexes composed of two types of
homologous subunits, αA- and αB-crystallin (Groenen et
al. 1994). Both subunits are encoded by single-copy
genes (King and Piatigorsky 1983; Quax-Jeukem et
al. 1985), which avoids the problem of paralogy in
comparative studies. αA-Crystallin protein sequences have
already contributed to resolving the relationships be-
 tween mammals, lizards, crocodiles, and birds (Stapel et
corresponding sequences of α-crystallins from other species, selected cDNAs (positions 12-160 and 9-61, respectively) were aligned with sequences of turtle αA-crystallins (A) and αB-crystallins (B) (Fig. 1).

Hedges (1994). αB-Crystallin has only recently been used for almost the entire length of this 173-residue polypeptide. Residues 9-61 of αB-crystallin represent the largest portion of the protein-coding information in the first exon of the αB-crystallin gene. These turtle αA- and αB-crystallin sequences in Fig. 1B reveals that position 53 is for mammalian monophyly. Comparison of the αB-crystallin data set with that from other proteins available in the databases, exhaustive searches were performed for turtle sequences that might indicate where residues are identical to the turtle sequences; dashes denote deletions. Species names and database accession numbers are given in the legends of Fig. 2 and Table 1.

Fig. 1. Comparison of variable sites in turtle and other vertebrate αA-crystallins (A) and αB-crystallins (B). Dotted amino acid sequences of turtle Trachemys scripta elegans αA- and αB-crystallin cDNAs (positions 12-160 and 9-61, respectively) were aligned with corresponding sequences of α-crystallins from other species, selected to cover the variety within extant vertebrates. Only those positions are shown at which different residues occur in these data sets. Amino acid position numbers are those of the complete α-crystallin chains. Dots indicate where residues are identical to the turtle sequences; dashes denote deletions. Species names and database accession numbers are given in the legends of Fig. 2 and Table 1.

The nucleotide sequences corresponding to amino acid residues 12-160 of αA-crystallin and to residues 9–61 of αB-crystallin of the red-eared slider turtle (Trachemys scripta elegans) were determined. The deduced amino acid sequence of αA-crystallin accounts for almost the entire length of this 173-residue polypeptide. Residues 9–61 of αB-crystallin represent the largest part of the protein-coding information in the first exon of the αB-crystallin gene. These turtle αA- and αB-crystallin sequences are aligned in Fig. 1A with corresponding sequences of representative other vertebrate α-crystallins.

The neighbor-joining tree based on this αA-crystallin data set clearly includes the turtle in a turtle–lizards–archosaurian clade (bootstrap value of 93%) (Fig. 2A). Also the maximum likelihood tree and the most parsimonious tree for these αA-crystallin sequences support such a clade—in the case of the parsimony tree, with a bootstrap value of 92% (not shown). With all three tree construction methods the turtle is the first to branch off within this clade. However, the statistical support for the resulting lepidosaurian–archosaurian clade is very weak (bootstrap value of 45% in the neighbor-joining and 42% in the parsimony tree). This data set also strongly groups the placentals mammals together, as well as the two marsupials, but gives only poor support for mammalian monophyly. Comparison of the αB-crystallin sequences in Fig. 1B reveals that position 53 probably represents a synapomorphous insertion of one amino acid in the mammalian lineage. However, the character state at this position is not known in lepidosaurs and crocodiles. Analysis of the αB-crystallin data set supports a turtle–bird relationship with all three tree construction methods (Table 1, see below).

Sequences from Databases

To combine the phylogenetic information from these newly determined α-crystallin sequences with that from other proteins available in the databases, exhaustive searches were performed for turtle sequences that might enable the resolution of the turtle–mammal–bird relationship. Amino acid sequences from ten additional sets of orthologous genes were found to be suitable for this purpose (Table 1). Selection criteria are described in Materials and Methods.

Each data set was subjected to maximum parsimony, neighbor-joining, and maximum-likelihood analyses. The support for the three alternative branching orders of mammals (M), turtles (T), and birds (B) with respect to outgroup sequences is summarized in Table 1. This table overwhelmingly demonstrates the evidence for a (M(T,B)) topology. Seven out of 12 protein sequences support a sister-group relation of turtle and birds in all analyses. Prolactin and nicotinamide adenine dinucleotide dehydrogenase subunit 2 (ND2) support a (M(B,T)) topology with maximum parsimony and maximum likelihood. In the case of prolactin the likelihood support is equal for all three topologies.

Combining all proteins in a single analysis provides the strongest measure for the resolution of the four-taxon case under investigation. To that end a composite outgroup sequence was constructed from the phylogenetically nearest outgroups (see footnote f of Table 1). For the ingroups, a turtle, chicken, human, and mouse were the only taxa available for all proteins. The combined analyses of all amino acid sequences (1,695 aligned sites) supports the sister-group relationship of turtle and birds almost at the highest possible levels (Table 1, Fig. 2B).
Species names and database accession numbers for αA-crystallins are: chicken Gallus gallus (P02504), tinamou Eudromia elegans (L25850), alligator Alligator mississippiensis (P06904), tegu lizard Tupinambis teguixin (P02506), human Homo sapiens (P02489 with minor correction according to L25781), elephant Loxodonta africana (P02498), mouse Mus musculus (P02490), bovine Bos taurus (P02470), sloth Choloepus hoffmanni (P02486), opossum Didelphis virginiana (P02503), kangaroo Macropus rufus (P02502), frog Rana esculenta (up to amino acid position 70)/? temporaria (from position 71 onward) (P02507 and P02508), and bullfrog R. catesbeiana (X85205). For species names and database accession numbers used in the combined protein analysis, see legend of Table 1.

**Discussion**

Previous studies of protein and nucleic acid sequences failed to give conclusive evidence about the position of turtles among the amniotes. 18S rRNA placed turtles outside a bird–mammal clade (Hedges et al. 1990; Eernisse and Kluge 1993), although weighting the nucleotide positions generated the classical amniote tree (Van de Peer et al. 1993), or nearly so (Marshall 1992). 28S rRNA sequences, which had earlier been inconclusive (Hedges et al. 1990), did group turtles within a bird–reptile clade, but as sister group to crocodiles, while salamanders were also included in the bird–reptile clade in this analysis (Eernisse and Kluge 1993). Studies of turtle insulin (Cascone et al. 1991), prolactin (Yasuda et al. 1990), and tyrosinase (Yamamoto et al. 1992; Morrison et al. 1994) noted that these proteins were closer to avian than to mammalian orthologs. α- and β-hemoglobin sequences, and a combined analysis of α- and β-hemoglobin, myoglobin, and cytochrome c placed turtles in a clade with crocodiles and birds, excluding a mammal–lepidosaur clade (Eernisse and Kluge 1993). In earlier studies, β-hemoglobin and myoglobin grouped birds with mammals, both in maximum-parsimony (Goodman et al. 1987; Hedges et al. 1990) and in maximum-likelihood analyses (Bishop and Friday 1988). However, different taxonomic sampling may have played a role in these deviating results. Finally, mitochondrial tRNA sequences contained little phylogenetic information for inferring the position of turtles among the amniotes, while flanking protein-coding sequences (ND2) supported a placement of turtles as a sister group to a bird–crocodile clade (Seutin et al. 1994).

It might be expected that, like in the case of the avian sister-group controversy (Hedges 1994), an extended set of various proteins will enable a more convincing resolution of the branching order of turtles, mammals, and birds within the amniotes. We therefore determined sequences of two additional turtle proteins, αA- and αB-crystallin. Database searches yielded a further ten proteins suitable for our purpose. We analyzed these se-
Inferred by maximum-parsimony, neighbor-joining, and maximum-likelihood analyses.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Number of sites</th>
<th>Bootstrap support for alternative sister-group relationships in neighbor-joining analyses</th>
<th>Differences in log-likelihood from best trees for alternative sister-group relationships in maximum parsimony analyses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein</td>
<td>(M(T,B))</td>
<td>(T(B,M))</td>
<td>(B(T,M))</td>
</tr>
<tr>
<td>α-A-Crystallin*</td>
<td>97</td>
<td>3</td>
<td>&lt;1</td>
</tr>
<tr>
<td>α-B-Crystallin*</td>
<td>99</td>
<td>&lt;1</td>
<td></td>
</tr>
<tr>
<td>Cytochrome b</td>
<td>24</td>
<td>29</td>
<td>36</td>
</tr>
<tr>
<td>Cytochrome c*</td>
<td>44</td>
<td>42</td>
<td>7</td>
</tr>
<tr>
<td>α-Hemoglobin*</td>
<td>94</td>
<td>4</td>
<td>&lt;1</td>
</tr>
<tr>
<td>β-Hemoglobin*</td>
<td>87</td>
<td>9</td>
<td>&lt;1</td>
</tr>
<tr>
<td>Insulin*</td>
<td>100</td>
<td>&lt;1</td>
<td></td>
</tr>
<tr>
<td>Myoglobin</td>
<td>50</td>
<td>50</td>
<td>&lt;1</td>
</tr>
<tr>
<td>ND2</td>
<td>20</td>
<td>42</td>
<td>23</td>
</tr>
<tr>
<td>Prolactin</td>
<td>85</td>
<td>3</td>
<td>12</td>
</tr>
<tr>
<td>Somatrotropin</td>
<td>71</td>
<td>19</td>
<td>10</td>
</tr>
<tr>
<td>Tyrosinase*</td>
<td>50</td>
<td>22</td>
<td>29</td>
</tr>
<tr>
<td>Combined proteinsf</td>
<td>99</td>
<td>1</td>
<td>&lt;1</td>
</tr>
</tbody>
</table>


d The highest likelihood trees are indicated by ML. The differences of steps in the majority-rule consensus parsimony tree or the number of extra steps required for the alternative sister-group relationships. These are not necessarily the numbers of steps in the actual most parsimonious trees. The numbers of informative sites refer to the branching orders of mammals, turtles, and birds, not to branching orders within any of these clades.

Bootstrap support in % (1,000 replications) that support the respective branching orders are given.

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It is clear from Table 1 that a sister-group relation of turtles and birds, to the exclusion of mammals, is extremely well supported, especially when the sequences are combined. Unfortunately, the presently available protein data sets are not yet sufficient to completely resolve the branching order of the amniotes. The position of the lepidosaur sequence in the α-A-crystallin trees is very weakly supported. Other proteins grouped lepidosaurs with mammals, which does not correspond to any morphological and paleontological evidence. The sister-group relationship of crocodiles and birds (Hedges 1994). The present analysis further refutes the Haematobertheria hypothesis and restores the position of the turtles as having branched off after mammals. It is quite likely that additional molecular data will further confirm the classical view of amniote phylogeny as based on morphological and paleontological evidence.

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References


Felsenstein J (1993) PHYLP: phylogeny inference package, version 3.5c. Distributed by the author, Department of Genetics, University of Washington, Seattle, WA


Haeckel E (1866) Generelle Morphologie der Organismen. G Reimer, Berlin, Tafel XII


Jones DT, Taylor WR, Thornton JM (1992) The rapid generation of
586

mutation data matrices from protein sequences. Comput Appl Biosci 8:275–282


Philippe H, Douzery E (1994) The pitfalls of molecular phylogeny based on four species, as illustrated by the Cetacea/Artiodactyla relationships. J Mamm Evol 2:133–152


