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 three approaches. 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 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
An amalgamation and 55°C for the otB-crystallin amplification.  

CACCC-3' and 5'-ATAAAGCTTACCTC[C,T]GAGAGTCCCG-  

Materials and Methods  

and 5'-phosphorylated with Klenow DNA polymerase and T4 poly­

merase chain reaction (PCR) method, using  

was amplified from the resulting single-stranded cDNA by the poly­

were reverse transcribed using SuperScript reverse transcriptase (Gibco  

If available, multiple outgroups were used. Species names and database accession numbers are given in  

Data Base Searches. The SwissProt (version 31.0), PIR (version 44.0), EMBL (version 42.0), and GenBank (version 83.0) databases were searched for amino acid sequences and protein-coding nucleic acid sequences from turtle species. Only sequences for which at least a mammalian, avian, and outgroup homolog were available were used. Sequences suspected not to obey the orthology criterion (i.e., resulting from a gene duplication rather than a speciation event) were excluded (e.g., gastrin/cholecystokinin, parvalbumin, and ribonuclease). However, as long as we found no evidence against the hypothesis that homologous sequences diverged from one another close in time to the ancestral divergence of their species lineages, they were treated as orthologs (Goodman et al. 1987); in cases where two different protein sequences of one species were available (β-hemoglobin, insulin), both were included in the analyses. Where several turtle sequences were known, species from all available families were included. If available, the mammalian sequences used were human, bovine, mouse, and a marsupial. For birds, chicken, and, if available, another species, preferably a paleognath, were used. When possible, multiple outgroups were used. Species names and database accession numbers are given in the legends of Fig. 2 and Table 1.  

Phylogenetic Analyses. Because of the divergence times dealt with in this study, we used amino acid rather than nucleotide sequences for phylogenetic analyses. Sequences were aligned with PILEUP from the GCG package (Devereux et al. 1984). Phylogenetic analyses were performed with maximum parsimony (PROTPARS), neighbor-joining (Saitou and Nei 1987) (PROTDIST and NEIGHBOR, or TREECON) using Kimura distances (Kimura 1983), and maximum-likelihood methods (Felsenstein 1981) (PROTML) based on the JTT model (Jones et al. 1992). The programs PROTPARS, PROTDIST, and NEIGHBOR are from the PHYLIP package (Felsenstein 1993), TREECON has been written by Van de Peer and De Wachter (1994) and PROTML by Adachi and Hasegawa (1992). Confidence in the maximum-parsimony and neighbor-joining methods was assessed by bootstrap sampling (Felsenstein 1983) (SEQBOOT and CONSENSE (Felsenstein 1993) for the programs from the PHYLIP package). Confidence in the maximum-likelihood method was assessed by the differences in log-likelihood from the highest-likelihood tree (Bishop and Friday 1985).  

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-Jeuk et al. 1985), which avoids the problem of paralogy in comparative studies. αA-Crystallin protein sequences have already contributed to resolving the relationships between 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

Fig. 1. Comparison of variable sites in turtle and other vertebrate

Hedges 1994). αB-Crystallin has only recently been used to cover the variety within extant vertebrates. Only those positions are probably represents a synapomorphous insertion of one bor-joining and 42% in the parsimony tree). This data set

crystallin sequences in Fig. 1B reveals that position 53 for mammalian monophyly. Comparison of the αB-
crystallin sequences are aligned in Fig. 1 with corre-
sponding sequences of turtle sequences; dashes denote deletions. Species names and database accession numbers are given in the legends of Fig. 2 and Table 1.

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(T,B)) topology with two of the methods, while cytochrome b, myoglobin, and somatotropin support a (T(B,M)) 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).
Fig. 2. Amniote relationships inferred from (A) αA-crystallin amino acid sequences (see Fig. 1A), and (B) the 12 combined protein sequences from Table 1. Neighbor-joining trees are shown, constructed with TREECON (Van de Peer and De Wachter 1994) using Kimura distances, with bootstrap values from 1,000 replications. Distance is proportional in the minimum number of mutations per residue. With the combined protein sequences, the fact that branch lengths in the reptile—bird lineage are considerably shorter than the branches leading to the mammalian species, also observed in the maximum-likelihood tree (not shown), is not due to a general acceleration in the evolutionary rate in the mammalian lineage but rather to particular more divergent sequences (mouse insulin and human cytochrome c and somatotropin).

Species names and database accession numbers for αα-crystallins are: chicken Gallus gallus (P02504), tinamou Eudromia elegans (L25850), alligator Alligator mississippiensis (P08904), tegu lizard Tupinambis teguixin (P02506), human Homo sapiens (P02489 with minor correction according to K25781), elephant Loxodonta africana (P02498), mouse Mus musculus (P02490), bovine Bos taurus (P02470), sloth Choloepus hoffmanni (P02486), opossum Didelphis virginiana (P02506), kangaroo Macropus nufus (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 rRNA 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-
Table 1. Protein sequence evidence for the branching order of mammals (M), turtles (T), and birds (B), with respect to outgroup sequences, as 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>Bootstrap support for alternative sister-group relationships in maximum parsimony analyses</th>
<th>Differences in log-likelihood from best trees for alternative sister-group relationships in maximum likelihood analyses</th>
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<tr>
<td></td>
<td>(T(M),T(B))</td>
<td>(T(B),M)</td>
<td>(B(T),M)</td>
<td></td>
</tr>
<tr>
<td>Protein</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α-A-Crystallin*</td>
<td>97</td>
<td>3</td>
<td>&lt;1</td>
<td></td>
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<tr>
<td>αB-Crystallin*</td>
<td>99</td>
<td>&lt;1</td>
<td>ML</td>
<td>-1.9 ± 2.2</td>
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<tr>
<td>Cytochrome b</td>
<td>24</td>
<td>29</td>
<td>36</td>
<td>ML</td>
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<tr>
<td>Cytochrome c*</td>
<td>44</td>
<td>42</td>
<td>7</td>
<td>ML</td>
</tr>
<tr>
<td>α-Hemoglobin*</td>
<td>94</td>
<td>4</td>
<td>9</td>
<td>ML</td>
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<tr>
<td>β-Hemoglobin*</td>
<td>87</td>
<td>9</td>
<td>1</td>
<td>ML</td>
</tr>
<tr>
<td>Insulin*</td>
<td>100</td>
<td>&lt;1</td>
<td>ML</td>
<td>-32.5 ± 1.6</td>
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<tr>
<td>Myoglobin</td>
<td>50</td>
<td>50</td>
<td>&lt;1</td>
<td>ML</td>
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<tr>
<td>ND2</td>
<td>20</td>
<td>42</td>
<td>23</td>
<td>ML</td>
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<tr>
<td>Prolactin</td>
<td>85</td>
<td>3</td>
<td>12</td>
<td>ML</td>
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<tr>
<td>Somatotropin</td>
<td>71</td>
<td>19</td>
<td>10</td>
<td>ML</td>
</tr>
<tr>
<td>Tyrosinase*</td>
<td>50</td>
<td>22</td>
<td>29</td>
<td>ML</td>
</tr>
<tr>
<td>Combined proteins</td>
<td>99</td>
<td>1</td>
<td>&lt;1</td>
<td></td>
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</table>

Values in boldface type emphasize the typology supported by the three different methods of tree construction. Asterisks (*) indicate the proteins that support a sister-group relationship of turtle and bird in all analyses.

Bootstrap values in % (1,000 replications) that support the respective branching orders are given, followed (in parentheses) by the number 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 values in % (1,000 replications) that support the respective branching orders are given.

The highest likelihood trees are indicated by ML. The differences of log-likelihoods, with their SEs, are given for the alternative topologies that support a sister-group relationship of turtle and bird in all analyses.

Differences in log-likelihood from best trees for alternative sister-group relationships in maximum likelihood analyses.

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 aA-crystallin trees is very weakly supported. Other proteins grouped lepidosaurs from the Netherlands Organization for Scientific Research (NWO).

The present analysis further refutes the Haematothermia 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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