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Research article

Retroposed Elements and their Flanking Regions Resolve the Evolutionary History of Xenarthran Mammals (Armadillos, Anteaters and Sloths)

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Abstract

Armadillos, anteaters, and sloths (Order Xenarthra) comprise one of the four major clades of placental mammals. Isolated in South America from the other continental landmasses, xenarthrans diverged over a period of about 65 million years, leaving more than 200 extinct genera and only 31 living species. The presence of both ancestral and highly derived anatomical features has made morpho-anatomical analyses of the xenarthran evolutionary history difficult, and previous molecular analyses failed to resolve the relationships within armadillo subfamilies. We investigated the presence/absence patterns of retroposons from ~7400 genomic loci, identifying 35 phylogenetically informative elements, and an additional 39 informative rare genomic changes (RGC). DAS-SINE elements, previously described only in the *Dasybus novemcinctus* genome, were found in all living armadillo genera, including the previously unsampled *Chlamyphorus*, but were noticeably absent in sloths. The presence/absence patterns of the phylogenetically informative retroposed elements and other RGCs were then compared to data from the DNA sequences of the more than 12 kb flanking regions of these retroposons. Together, these data provide the first fully resolved genus tree of xenarthrans. Interestingly, multiple evidence supports the grouping of *Chaetophractus* and *Zaedyus* as a sister group to *Euphractus* within Euphractinae, an association that was not previously demonstrated. Also, flanking sequence analyses favor a close phylogenetic relationship between *Cabassous* and *Tolypeutes* within Tolypeutinae. Finally, the phylogenetic position of the subfamily Chlamyphorinae is resolved by the non-coding sequence dataset as the sister-group of Tolypeutinae. The data provide a stable phylogenetic framework for further evolutionary investigations of xenarthrans and important information for defining conservation priorities to save the diversity of one of the most curious groups of mammals.

Introduction

Sloths, anteaters, and armadillos are among the most morphologically specialized mammals. These three lineages belong to Xenarthra, a mammalian order whose monophyly is undisputed (Engelmann 1985; Van Dijk et al. 1999). On molecular grounds, xenarthrans constitute one of the four major placental clades (Madsen et al. 2001; Murphy et al. 2001a; Delsuc et al. 2002). Their evolutionary radiation began about 65 million years ago while South America was becoming isolated from other continental land masses (Patterson and Pascual 1972). Thirty-one living species of xenarthrans (21 armadillos, four anteaters and six sloths) have been described (Wetzel 1985; Vizcaíno 1995; Anderson and Handley 2001). Today's limited xenarthran species number is in sharp contrast with their past diversity, as more than 200 fossil genera are recognized (McKenna and Bell 1997). The most impressive xenarthrans, such as giant ground sloths and glyptodonts, disappeared at the end of the last Pleistocene glaciations (about 10,000 years ago; Patterson and Pascual 1972). Remnants of this ancient evolutionary radiation, most extant xenarthran species are, nevertheless, poorly studied and uncertainties remain concerning their conservation status (da Fonseca and Aguiar 2004).

As curious as xenarthrans are, so disputed is their place in the placental evolutionary tree. Whereas nuclear gene concatenations have been frustratingly inconclusive (Murphy et al. 2001b; Delsuc et al. 2002; Amrine-Madsen et al. 2003; Nikolaev et al. 2007), the classical morphology-based Epitheria hypothesis, placing Xenarthra as the sister group of all placental orders (McKenna 1975), has found some support from retroposed elements (Kriegs et al. 2006). However, Murphy et al. (2007) have recently found some rare insertion/deletion events that represent contradictory evidence in support of a sister-group relationship between Xenarthra and Afrotheria instead.

Living xenarthrans are divided into three phylogenetically distinct groups, the arboreal sloths (Folivora: Megalonychidae and Bradypodidae), the toothless anteaters (Vermilingua: Myrmecophagidae), and the shelled armadillos (Cingulata: Dasypodidae). Folivora and Vermilingua form the suborder Pilosa for which there is unequivocal support from both morphological (Engelmann 1985; Patterson et al. 1992) and molecular (Delsuc et al. 2001; Delsuc et al. 2002) data.

The phylogenetic relationships and taxonomy of the living pilosans are well resolved (Gaudin and Branham 1998; Delsuc et al. 2001; Delsuc et al. 2002). Folivora contains the two morphologically distinct tree-sloth families Megalonychidae (*Choloepus*, two-toed sloths) and Bradypodidae (*Bradypus*, three-toed sloths) (Webb 1985; Höss et al. 1996; Greenwood et al. 2001). Among Vermilingua, myological (Reiss 1997) and morphological (Gaudin and Branham 1998) studies supporting an early emergence of the pygmy anteater (*Cyclopes didactylus*) have been confirmed by molecular data (Delsuc et al. 2001; Delsuc et al. 2002). These studies therefore group together the giant anteater (*Myrmecophaga*) and tamanduas (*Tamandua*).

The armadillos are the oldest and most speciose lineage of xenarthrans. Their phylogeny has been difficult to reconstruct from morpho-anatomical data with incongruent results among the rare studies (Engelmann 1985; Patterson, Segall, and Turnbull 1989; Abrantes and Bergqvist 2006; Gaudin and Wible 2006). Molecular evidence (Delsuc et al. 2002; Delsuc, Stanhope, and Douzery 2003) has, nevertheless, clearly defined three major lineages compatible with the subfamilies of McKenna and Bell's (1997) classification: Dasypodinae (the single genus *Dasypus*), Tolypeutinae (genera *Tolypeutes*, *Cabassous*, and *Priodontes*), and Euphractinae (genera *Euphractus*, *Chaetophractus*, and *Zaedyus*). A close relationship between Tolypeutinae and Euphractinae was also strongly supported, with Dasypodinae emerging first within Cingulata (Delsuc et al. 2001; Delsuc et al. 2002; Delsuc,

Stanhope, and Douzery 2003). These relationships are congruent with the study of spermatozoa (Cetica et al. 1998) but contradict morphological studies (Engelmann 1985; Gaudin and Wible 2006).

However, even molecular data have failed to resolve relationships within the subfamilies Tolypeutinae and Euphractinae, with contradictory results obtained from mitochondrial versus nuclear genes suggesting that speciation events occurred very rapidly within each of these two armadillo lineages (Delsuc, Stanhope, and Douzery 2003). Within tolypeutines, a close relationship between *Cabassous* and *Priodontes* would be consistent with their classification in the tribe Priodontini based on their similar morphologies (McKenna and Bell 1997; Abrantes and Bergqvist 2006; Gaudin and Wible 2006) and a study of their spermatozoa (Cetica et al. 1998). Within euphractines, the grouping of *Euphractus* and *Chaetophractus* to the exclusion of *Zaedyus* would be congruent with a recent cladistic study of craniodental characters (Gaudin and Wible 2006) whereas another cladistic study including also postcranial characters rather supports a close relationship between *Chaetophractus* and *Zaedyus* (Abrantes and Bergqvist 2006). Uncertainty remains in morphological evidence because of the highly derived morphology of *Tolypeutes* within Tolypeutinae, and the very similar morphologies exhibited by extant members of Euphractinae.

At present, the only armadillo subfamily for which no molecular data is available is Chlamyphorinae (fairy armadillos). It includes only two living species classified in the genus *Chlamyphorus*: *Chlamyphorus truncatus* (pink fairy armadillo) and *Chlamyphorus retusus* (chacoan or greater fairy armadillo). These two species are morphologically specialized to a subterranean lifestyle with notably reduced eyes and reinforced forearms supporting enlarged digging claws. Some cladistic analyses of morphological characters including fossils have supported a close relationship of fairy armadillos with *Zaedyus* (Engelmann 1985; Gaudin and

Wible 2006). However, when only extant taxa were considered in an analysis of craniodental characters, *Chlamyphorus* grouped with Euphractinae (Gaudin and Wible 2006), a result also obtained by Abrantes and Bergqvist (2006) in their morphological study. Yet, the phylogenetic affinities of fairy armadillos have never been tested with molecular data, as both species are fairly elusive and rare in the field (Cuéllar 2001; Superina 2006).

The genomic insertion patterns of various retroposed mobile elements provide an extraordinary archive from which to elucidate the evolutionary history of organisms (Shedlock and Okada 2000). SINEs (Short INterspersed Elements) and other retroposed elements, shared by some taxa but missing from the genomes of others, are highly valuable, essentially homoplasy-free indicators of relatedness (Okada 1991; Nikaido, Rooney, and Okada 1999; Salem et al. 2003; Roos, Schmitz, and Zischler 2004; Kriegs et al. 2006; Nishihara, Hasegawa, and Okada 2006), with an extremely large possible number of basically unique character states (Steel and Penny 2005). A specific tRNA-derived retroposed SINE family, called DAS-SINEs, has been discovered in the *Dasypus novemcinctus* genome (Borodulina and Kramerov 2005; Churakov et al. 2005), with average genomic copy numbers of about 467,000 calculated from the ~71% of available genomic information (Ensembl GeneBase version 45.1c). Using a specific strategy to compare nested DAS-SINEs, distinct historical waves of activity of six DAS-SINE subfamilies were defined (Churakov et al. 2005). This information was used for the first time in the present study to screen for a maximum variety of young — and respectively old — phylogenetically informative elements to provide the first retroposon presence/absence support for terminal — and respectively deep — splits in xenarthrans.

Furthermore, low complexity, rare genomic changes (RGCs), such as random insertions or deletions (indels) provide additional capability in molecular systematics (Rokas and Holland 2000). Although simple random indels are of lower reliability than complex

retropon insertions, they have often been shown to be evolutionarily conserved and phylogenetically informative (Murphy et al. 2007). Retroposed elements with their characteristic flanking target site duplications (direct repeats – DR), diagnostic mutations, and often specific truncations are exceptionally informative RGCs (Ray et al. 2006) and, compared to simple random indels, are virtually ambiguity-free. In the present study, we combined different strategies to find phylogenetically informative retroposed elements and indels to serve as cladistic molecular markers for reconstructing the phylogeny of all xenarthran genera including the previously unsampled genus *Chlamyphorus*. Moreover, phylogenetic analyses of the flanking regions of these loci enabled us to reconstruct the evolutionary history of xenarthrans using a large data set of non-protein coding DNA. The resulting phylogenetic tree was used as a framework for mapping the presence/absence of retroposed elements and indels providing independent evidence for further resolving the phylogeny of this major placental clade.

Materials and Methods

Computational strategies

To identify phylogenetically informative presence/absence patterns of retroposed elements, we applied three different *in silico* search strategies.

Strategy 1: We downloaded all available *Dasyopus novemcinctus* sequences from the NIH Intramural Sequencing Center at <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=nucleotide> (20.1 million bases) and used the local version of RepeatMasker (Smit and Green at <http://www.repeatmasker.org>) containing a specific library comprising all DAS-SINE subfamily consensus sequences to scan for DAS-SINEs. All detected DAS-SINEs were extracted along with 250 nucleotides of their flanking sequences (2023 loci). For outgroup comparison and to construct conserved

PCR primers the selected loci were aligned against human genomic sequences using the UCSC Server (<http://genome.ucsc.edu/cgi-bin/hgBlat>). Only sequence alignments with more than 80% identity were used to generate conserved PCR primers (80 loci).

For estimating the genomic number of DAS-SINEs in *Dasybus novemcinctus* we downloaded available sequence information from <http://www.ensembl.org/info/data/download.html> (*Dasybus_novemcinctus.0.ARMA.45.dna.nonchromosomal.fa.gz*) and used our specific DAS-SINE library for a local RepeatMasker screen. We extrapolated the number of all detected elements to the expected full size of the genome.

Strategy 2: For finding markers for other xenarthran branches in which DAS-SINEs were possibly not active (deep xenarthran splits), we also searched for other retroposed elements (i.e., Long INterspersed Elements (LINEs) or retroposed small nuclear (sn) RNAs such as spliceosomal U snRNAs) in conserved regions. We downloaded all available trace sequences for *D. novemcinctus* and *Choloepus hoffmanni* from <ftp://ftp.ncbi.nih.gov/pub/TraceDB/> (4.6 gigabases for *D. novemcinctus* and 4.2 gigabases for *C. hoffmanni*) and detected 5206 potentially phylogenetic informative loci with embedded L1MB4 (2609), L1MB5 (625), L1MB7 (1891) elements that were potentially active in xenarthrans (Kriegs et al. 2006), as well as 81 snRNA retrogenes. These loci were screened using trace blast (<http://www.ncbi.nlm.nih.gov/BLAST/mmtrace>) in three different ways: (1) for the presence of retroposed elements in *C. hoffmanni* that were absent in *D. novemcinctus* in order to find potential integrations on the branch leading to sloths, (2) for the presence of elements in *D. novemcinctus* that were absent in *C. hoffmanni* in order to find potential integrations specific to Cingulata, and (3) for the presence of elements in both species in order to find potential markers indicating xenarthran monophyly. From the 5206 candidates, only 32 contained insertions meeting at least one of the above criteria. They were used to generate conserved PCR primers (12 L1MB4, four L1MB5, four L1MB7, and 12 spliceosomal RNAs).

Strategy 3: To identify randomly inserted xenarthran-specific retroposed elements, we PCR amplified 171 highly conserved mammalian loci that were previously analyzed by Kriegs et al. (2006).

Statistical analyses

To test the validity of clade hypotheses at various nodes of the phylogenetic tree we used the method of Waddell et al. (2001). Assuming the sequence-based tree reconstruction as a prior hypothesis at any given node, a minimum of three integration sites against zero for alternative branching hypotheses are required for a significance level of $p < 0.04$.

Tissue sampling

We isolated genomic DNA from tissue samples conserved in 95% ethanol from the following species using standard protocols (Sambrook, Fritsch, and Maniatis 1989): Folivora: *Bradypus tridactylus* (pale-throated three-toed sloth) and *Choloepus hoffmanni* (Hoffmann's two-toed sloth); Vermilingua: *Tamandua tetradactyla* (southern tamandua), *Myrmecophaga tridactyla* (giant anteater), *Cyclopes didactylus* (silky anteater); Dasypodinae: *Dasypus novemcinctus* (nine-banded armadillo), *Dasypus kappleri* (greater long-nosed armadillo); Euphractinae: *Euphractus sexcinctus* (six-banded armadillo), *Zaedyus pichiy* (pichi), *Chaetophractus vellerosus* (screaming hairy armadillo); Chlamyphorinae: *Chlamyphorus truncatus* (pink fairy armadillo); Tolypeutinae: *Tolypeutes tricinctus* (three-banded armadillo), *Cabassous unicinctus* (southern naked-tailed armadillo), *Priodontes maximus* (giant armadillo); and Afrotheria (outgroup): *Loxodonta africana* (African savanna elephant) and *Trichechus manatus* (Caribbean manatee).

PCR amplification

We initiated our screening with high-throughput PCR for all selected 283 loci, using DNA from *C. hoffmanni*, *M. tridactyla*, *D. novemcinctus*, *C. vellerosus*, *T. tricinctus*, and *T. manatus*. PCR primers for conserved, potentially informative loci were generated for amplicates not longer than 1 kb. Subsequently, we focused on 39 loci with detectable fragment size-shifts (Schmitz, Ohme, and Zischler 2001) to amplify in the full species sampling. The following conditions were used for PCR amplifications: 4 min at 94°C, 35 cycles of 30 s at 94°C, 30 s at the primer-specific annealing temperature (Supplementary table 1, Supplementary Material online) and 90 s at 72°C. PCR reactions were finished with 5 min at 72°C.

The pDrive Cloning Vector (Qiagen, Hilden, Germany) was utilized for ligation of PCR fragments purified from 1% agarose gels. TOP10 electrocompetent cells (Invitrogen, Groningen, The Netherlands) were used for electroporation. Sequencing was performed with standard M13 forward and reverse primers (Supplementary table 1, Supplementary Material online) and the Ampli Taq FS Big Dye Terminator Kit (PE Biosystems, Foster City, California).

Sequence alignment and phylogenetic analyses

All amplified sequences were manually aligned for the final 39 selected loci. For detection and classification of additional random insertions we used the RepeatMasker Server (Smit and Green, RepeatMasker at <http://www.repeatmasker.org/cgi-bin/WEBRepeatMasker>) and the CENSOR software tool (Kohany et al. 2006); <http://www.girinst.org/censor/index.php>). Newly obtained sequences were submitted to the NCBI database (NCBI accession numbers EF465537-EF466007).

The raw concatenation of the 39 alignments yielded a combined dataset of 28,869 sites for the 16 species. For phylogenetic reconstructions from these flanking regions of retroposed elements, we adopted a conservative approach. First, regions containing the retroposed elements were entirely removed from the concatenation to make subsequent phylogenetic inferences fully independent of the retroposed insertions. Then, ambiguously aligned sites and highly gapped/repeated regions were excluded, reducing the dataset to 12,488 sites of which 5,530 were variable. Alignments are available upon request.

Phylogenetic analyses were conducted using Maximum Likelihood (ML) and Bayesian approaches. The best fitting model of sequence evolution was selected using Modeltest 3.7 (Posada and Crandall 1998). Among 56 competing models, the Akaike Information Criterion (AIC; Akaike 1974) identified the transversional model (TVM) with among-site rate heterogeneity modeled by a gamma distribution with eight discrete categories (+ Γ_8) as the best fitting model for our concatenated dataset. The TVM model is a restriction of the most general, General Time Reversible (GTR) model. It allows different base compositions and different substitution rate probabilities for the four types of transversions, whereas the two types of transitions have the same rate.

The homogeneity of base composition across taxa was evaluated by the χ^2 test implemented in PAUP* 4.0b10 (Swofford 2002). This test did not reject the null hypothesis of overall base composition homogeneity ($P = 0.64$) in this A+T rich (62%) non-protein coding dataset. ML phylogenetic analyses were conducted with PAUP* through heuristic searches with Tree Bisection Reconnection (TBR) branch swapping starting from a Neighbor-Joining (NJ) tree. ML model parameters were estimated with a successive approximation approach (Sullivan et al. 2005) using three rounds of optimization, starting from a NJ topology derived from ML distances obtained from a GTR+ Γ_8 model ($\alpha = 0.5$) and followed by ML heuristic searches by TBR branch swapping under the best fitting TVM+ Γ_8 model.

Reliability of nodes was estimated by bootstrap resampling with 500 pseudo-replicate datasets generated by the program SeqBoot of the PHYLIP package (Felsenstein 2001). The 500 corresponding ML heuristic searches were performed using PAUP* with the previously estimated ML parameters, NJ starting trees, and TBR branch swapping. They were parallelized on a Beowulf-class cluster supercomputer comprising 16 processor Weon 5160 Dual Core AMD Athlon computing nodes enabling simultaneous running of up to 64 processes. ML bootstrap percentages were obtained from the majority-rule consensus tree of the 500 bootstrap-generated trees using the latest version of TreeFinder (Jobb, von Haeseler, and Strimmer 2004).

Bayesian phylogenetic analyses of the concatenated flanking sequence dataset were implemented using MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003). Two independent runs of four incrementally heated Metropolis-coupled Markov chains Monte Carlo (MCMCMC) were launched from random starting points. We used Dirichlet priors for base frequencies (1,1,1,1) and for GTR parameters (1,1,1,1,1) scaled to the G-T substitution rate, a Uniform (0.05,50.00) prior for the Γ distribution, and an Exponential (10.0) prior for branch lengths. The four MCMCMC were simultaneously run for 1,000,000 generations using the program default priors as starting values for the GTR+ Γ_8 model parameters. Parameters and trees were sampled every 100 generations and the convergence of MCMCMC was checked by monitoring values of the marginal likelihood and model parameters through generations. Bayesian Posterior Probabilities (PP) were obtained from the 50% majority rule consensus of the 2 x 9,000 trees sampled at stationarity after removing the first 1,000 trees as the “burn-in” stage.

Results

From ~7400 investigated loci, 283 were selected for high-throughput PCRs in representatives of all major xenarthran branches and an afrotherian outgroup (Materials and Methods). 244 loci did not contain xenarthran-specific RGCs or were not amplifiable in all representative lineages. For the remaining 39 informative loci, we extended PCR screening and sequencing of retroposed elements and their flanking regions including all available species (Materials and Methods). These 39 informative loci contained 35 phylogenetically informative retroposed element markers, 14 autapomorphic retroposon insertions, and 39 phylogenetically informative indels other than retroposons (fig. 1; Supplementary table 2, Supplementary Material online). For most of the diagnostic retroposed elements, including spliceosomal U snRNAs (retropseudogenes generated by a variant L1 retroposition mechanism (Schmitz et al. 2004)), we also detected the short direct repeats (DR) and the singular target sites at orthologous positions in species devoid of the retroposons. Moreover, examination of the phylogenetically conserved random indels occurring in flanking regions was restricted to those with a minimum length of three nucleotides.

The ML tree reconstructed from the concatenated 12,488 sites of retroposon flanking sequences resulted in a well-resolved phylogeny (fig. 2). All but four nodes were supported by Bootstrap Probabilities (BPs) of 100 and PPs of 1.0. This ML topology strongly supported xenarthran monophyly and their division into the three major groups Folivora (sloths), Vermilingua (anteaters), and Cingulata (armadillos). Anteaters and sloths were firmly grouped together into Pilosa (BP = 99; PP = 1.0). Within anteaters, *Myrmecophaga* and *Tamandua* were sister-groups (BP = 100; PP = 1.0) to the exclusion of the early diverging *Cyclopes*.

Within armadillos, phylogenetic analyses unambiguously supported (BP = 100; PP = 1.0) the respective monophyly of the three previously identified subfamilies: Dasypodinae,

Euphractinae and Tolypeutinae. Among Euphractinae, the sister group of *Zaedyus* and *Chaetophractus* was strongly supported (BP = 99; PP = 1.0), whereas relationships were less clear within Tolypeutinae, where *Tolypeutes* and *Cabassous* are sister-groups (BP = 81; PP = 0.99). Finally, *Chlamyphorus*, representing the previously unsampled subfamily Chlamyphorinae, showed clear phylogenetic affinities with the clade Tolypeutinae (BP = 93; PP = 1.0).

In the 39 informative presence/absence loci examined, we found independent support for ten internal branches of the ML tree (fig. 3): [1] Xenarthra: Five independent insertions of retroposed elements (U6, U5-L1MB2-L1MB4-chimer, L1MB4, L1MB5, L1ME3A) confirm the monophyly of xenarthrans. The corresponding elements were clearly absent in Afrotherian outgroup species. [2] Pilosa: One LINE element (L1MC2) and two indels were present in all five representative species of Bradypodidae, Megalonychidae and Myrmecophagidae and were absent in all species of Dasypodidae, thus providing evidence for the monophyly of Pilosans. [3] Folivora: A diagnostic 27 nt deletion was detected in the Bradypodidae and Megalonychidae species that was not present in other Pilosa. [4] Myrmecophagidae (Vermilingua): We found one LINE element (L1MB8) and a 24 nt deletion in all three representatives of Myrmecophagidae. [5] Myrmecophaginae: Four indels present in *Myrmecophaga* and *Tamandua* indicate a common ancestry of these species to the exclusion of *Cyclopes*. [6] Dasypodidae (Cingulata): Seventeen diagnostic retroposons (10× DAS-Ia, 3× DAS-IIa, 2× DAS-IIb, U2, L1-like element) and three indels were found in the Dasypodidae that were absent in all pilosans. [7] Dasypodinae: Eight retroposons (3× DAS-Ia, 2× DAS-IIa, DAS-III1b, U2, L1MB2) and 16 indels were present in only the two investigated *Dasypus* species. [8] Euphractinae + Chlamyphorinae + Tolypeutinae: We detected one DAS-IIb element and three indels in the Euphractinae, Chlamyphorinae and Tolypeutinae species that were not present in Dasypodinae. [9] Euphractinae: One DAS-IIb insertion and seven indels

were present only in the Euphractinae species. [10] *Chaetophractus vellerosus* + *Zaedyus pichi*: A DAS-III3b element insertion and a 19 nt diagnostic deletion support the grouping of *Chaetophractus* and *Zaedyus*.

Discussion

SINE activity in xenarthran genomes

Of the retroposed elements, 36 were Cingulata-specific DAS-SINEs. As our search strategies were based predominantly on available sequence information from *D. novemcinctus*, most diagnostic insertions were found in the lineage leading to this species. Diagnostic insertions on other xenarthran branches were found as additional insertions in the investigated loci. Unfortunately sufficient sequence data to enable similar searches are not yet available for other xenarthran species. This is expressed in the limited significant phylogenetic support from discrete retroposon data (fig. 2b). The generation of large-scale genomic sequence information (e.g., by BAC or Whole Genome Shotgun (WGS) libraries) will provide a multidirectional source for additional lineage-specific informative loci in the future. The DAS-SINEs preferentially investigated in this study spread in characteristic waves of activity that correspond to the evolutionary scenario proposed by Churakov et al. (2005). Simple monomeric DAS-SINEs like DAS-Ia were active in ancient armadillo lineages and complex elements like DAS-III3b were active in species of some terminal branches.

The armadillo-specific distribution of DAS-SINEs was confirmed by screening all available genomic sequences of *C. hoffmanni* using a DAS-SINE specific library (RepeatMasker). Not a single copy of DAS-like sequences was detected. Interestingly, we found no other lineage-specific SINE elements for other xenarthrans than those for Cingulata. A more elaborated search (e.g., for SINE specific promoter boxes) will be necessary to fill

this gap. However, we did find lineage-specific L1-like and L1MB2 elements in Cingulata and L1MC2 and L1MB8 elements in Pilosa.

Improved resolution of xenarthran phylogeny

Reconstructing phylogenetic relationships among living xenarthran genera has been the subject of previous molecular studies using a combination of three nuclear and two mitochondrial genes (Delsuc et al. 2002; Delsuc, Stanhope, and Douzery 2003). These studies, including all extant genera except *Chlamyphorus*, resulted in a comprehensive phylogenetic framework with only two remaining uncertainties within armadillos. The present study represents the first ever evidence from retroposed elements for resolving xenarthran phylogeny. Also, the concatenation of flanking sequences offered the first large-scale, non-protein coding dataset from which the evolutionary history of all living xenarthran genera could be inferred. The results from the present work independently corroborated previous studies and provided strong additional support for most internal branches within Xenarthra including the areas of uncertainty.

Indeed, previous molecular data failed to resolve relationships within the subfamilies Tolypeutinae and Euphractinae. Contradictory results were obtained from mitochondrial versus nuclear genes resulting in low statistical support values when analyzing their concatenation (Delsuc, Stanhope, and Douzery 2003). These difficult-to-resolve trifurcations were interpreted as evidence for the occurrence of two radiation events possibly triggered by environmental changes (Delsuc, Vizcaíno, and Douzery 2004). Consensus network analyses of the phylogenetically conflicting signals present in the combination of two mitochondrial and three nuclear genes (Delsuc and Douzery *in press*) revealed that two of the three competing hypotheses coexisted with almost equal support within each subfamily:

Chaetophractus + *Euphractus* versus *Chaetophractus* + *Zaedyus* within Euphractinae and *Cabassous* + *Priodontes* versus *Cabassous* + *Tolypeutes* within Tolypeutinae.

Phylogenetic analyses of the more than 12 kb dataset of non-protein coding DNA provided unambiguous support for the grouping of the genera *Chaetophractus* and *Zaedyus* within Euphractinae (fig. 2a). Furthermore, *C. vellerosus* and *Z. pichiy* shared a diagnostic DAS-III3b element insertion and a 19 nucleotide-long deletion providing independent evidence for their direct common ancestry to the exclusion of *E. sexcinctus* (fig. 3) (Supplementary figure 1, Supplementary Material online). This result is in contradiction to a cladistic study of craniodental characters favoring a sister-group relationship between *Chaetophractus* and *Euphractus* supported by 5 synapomorphies (Gaudin and Wible 2006), but it agrees with the relationships proposed by Abrantes and Bergqvist (2006) based on additional postcranial evidence.

Our results appeared less clear-cut for the relationships within Tolypeutinae, as no diagnostic retroposed element insertions or indel events were found (fig. 3). Sequence-based phylogenetic analyses, nevertheless, favor the monophyly of *Cabassous* and *Tolypeutes* to the exclusion of *Priodontes* (fig. 2a). This is also in contrast to the morphological evidence for grouping *Cabassous* with *Priodontes* (Abrantes and Bergqvist 2006; Gaudin and Wible 2006). However, in this case it is possible that morphologically based cladistic reconstructions might have been confounded by the highly derived morphology of *Tolypeutes* relative to other members of Tolypeutinae. Obviously, more work is needed to understand the reasons of these discrepancies between molecular and morphological characters.

The present work provides the first molecular data to resolve the phylogenetic position of the armadillo subfamily Chlamyphorinae (fairy armadillos) within Cingulata. In contrast with cladistic analyses of morphological characters (Abrantes and Bergqvist 2006; Gaudin and Wible 2006), the probabilistic phylogenetic analyses of the flanking region dataset

strongly supported a close relationship of *C. truncatus* with Tolypeutinae instead of Euphractinae (fig. 2a). However, no diagnostic RGC was found to confirm this unexpected result (fig. 3). Future extensive wet-bench approaches focusing on retroposons in these and other lineages will help to strengthen the sequence-based relationships and balance biased *in silico* methods that depend on available sequence sources. However, for the present work only very little tissue was available from the rare species. This constrained our analyses to preferentially *in silico* methods instead of the tissue intensive wet-bench approaches. The inclusion of the second, morphologically divergent, species of fairy armadillo (*C. retusus*) in future sequence-based phylogenetic analyses might also help to confirm the position of Chlamyphorinae within the xenarthran tree by breaking up the branch leading to *C. truncatus*.

Of all the retroposed elements and indels identified, only one indel (#25') contradicted our ML tree. This 19 nt deletion was found in *C. truncatus* and *C. unicinctus* and not in other species. It is nevertheless worth noting that in this region two species of *Dasypus* also contained a 57 nt deletion encompassing the one shared by *Chlamyphorus* and *Cabassous*. The occurrence of two embedded deletions in the same region casts doubt on the potential phylogenetic significance of these deletion events that might be homoplastic. We also cannot fully exclude neither lineage sorting nor paralogy effects, but the probability of comparing paralogs is very low with respect to the highly conserved regions compared (this conservation encompasses xenarthrans and afrotherians up to human) and the definitively singular fragments in PCRs of all compared species. The contradiction presented by this random indel emphasizes the necessity to search for additional support by more reliable retroposon insertions using experimental lineage-specific search strategies as outlined in Endoh and Okada (1986) or by random sequencing and subsequent Zoo-PCR.

The inclusion of the second, morphologically divergent, species of fairy armadillo (*C. retusus*) in future molecular phylogenetic analyses might help to confirm the position of Chlamyphorinae within the xenarthran tree by breaking up the branch leading to *C. truncatus*.

The results of the present study make Xenarthra the first major placental group to have its phylogenetic history fully resolved at the genus level by using multiple independent molecular and genomic evidences. These results provide a robust phylogenetic framework for future evolutionary studies of comparative genomics, taxonomy, cytology, and development in this mammalian order. It might also be useful for defining conservation priorities for its most endangered species (da Fonseca and Aguiar 2004).

Supplementary Material

Supplementary tables 1 - 2 and supplementary figure 1 are available at *Molecular Biology and Evolution* online (<http://www.mbe.oxfordjournals.org>).

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Figure legends

Fig. 1

Presence/absence of retroposed elements in the 39 investigated loci. Small letters denote more than one diagnostic RGC per locus. (a) Retroposon presence/absence matrix. DAS-SINEs are highlighted in gray. (+) indicates the presence of a retroposed element, (-) indicates its absence, and (?) denotes that PCR amplification did not work. (b) Indel (insertions or deletions) markers in the 39 investigated loci. Insertions are marked with black, deletions with white boxes. (1) indicates the presence of an indel, (0) the original locus without the indel. (?) denotes that the PCR amplification failed. For outgroup comparisons we selected the afrotherians *Loxodonta africana* or *Trichechus manatus*.

Fig. 2

Sequence and retroposon based phylogenetic trees. (a) Maximum likelihood phylogram based on 12,488 concatenated sites from flanking sequence of the 39 Rare Genomic Changes (RGCs) containing loci under the TVM+ Γ_8 model. Maximum likelihood (ML) estimates of model parameters were: A=0.32, C=0.19, G=0.19, T=0.30; A \leftrightarrow C=0.96, A \leftrightarrow G=3.46, A \leftrightarrow T=0.77, C \leftrightarrow G=1.18, C \leftrightarrow T=3.46, G \leftrightarrow T=1.00; α =1.73. Values at nodes represent bootstrap percentages / Bayesian posterior probabilities, respectively. (b) Phylogenetic tree based on discrete retroposon insertions. Filled circles mark the insertion of DAS-SINEs; open circles mark the insertion of other retroposed elements such as LINEs or small nuclear RNAs (snRNAs). All identifying numbers refer to those used in figures 1 and 3 and Supplementary tables 1 and 2 (Supplementary Material online). The monophyly of Xenarthra, Cingulata, and Dasypodinae are significantly supported.

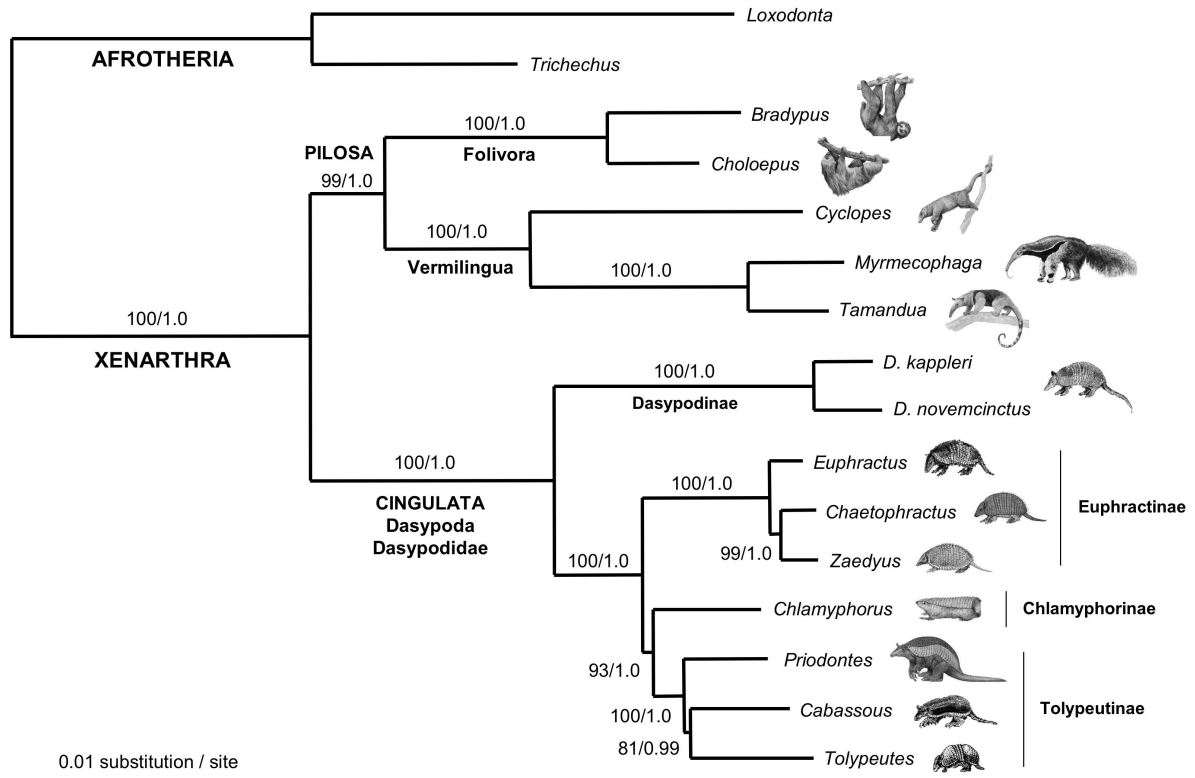
Fig. 3

Independent phylogenetic evidence from retroposon insertion and indel events mapped on the Maximum likelihood (ML) tree of Xenarthra inferred from flanking sequences.

Filled circles mark the insertion of DAS-SINES; open circles mark the insertion of other retroposed elements such as LINEs or small nuclear RNAs. Triangles mark the presence of diagnostic indels. All insertions of retroposed elements and indels are assigned identifying number and letter codes that are used in figure 1 and 2*b* and Supplementary tables 1 and 2 (Supplementary Material online). Indel #25' (right parenthesis) contradicts our ML tree in merging *Chlamyphorus truncatus* and *Cabassous unicinctus*. However this indel occurs in a variable region (see text for details).

Figure 2

(a)



(b)

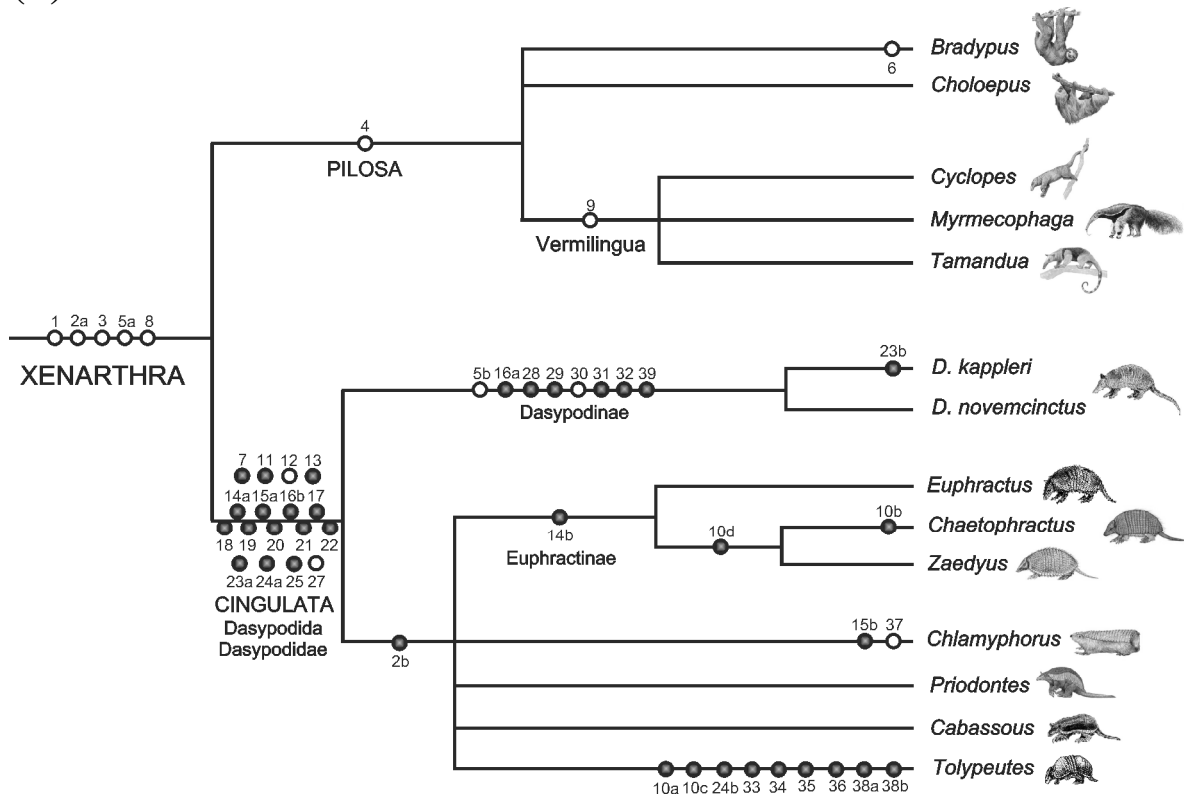


Figure 3

