Remarkable ancient divergences amongst neglected lorisiform primates

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Lorisiform primates (Primates: Strepsirrhini: Lorisiformes) represent almost 10% of the living primate species and are widely distributed in sub-Saharan Africa and South/South-East Asia; however, their taxonomy, evolutionary history, and biogeography are still poorly understood. In this study we report the largest molecular phylogeny in terms of the number of represented taxa. We sequenced the complete mitochondrial cytochrome b gene for 86 lorisiform specimens, including ~80% of all the species currently recognized. Our results support the monophyly of the Galagidae, but a common ancestry of the Lorisinae and Perodicticinae (family Lorisidae) was not recovered. These three lineages have early origins, with the Galagidae and the Lorisinae diverging in the Oligocene at about 30 Mya and the Perodicticinae emerging in the early Miocene. Our mitochondrial phylogeny agrees with recent studies based on nuclear data, and supports Euoticus as the oldest galagid lineage and the polyphyletic status of Galagoides. Moreover, we have elucidated phylogenetic relationships for several species never included before in a molecular phylogeny. The results obtained in this study suggest that lorisiform diversity remains substantially underestimated and that previously unnoticed cryptic diversity might be present within many lineages, thus urgently requiring a comprehensive taxonomic revision of this primate group.

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INTRODUCTION

Cryptic or sibling species are generally those deemed morphologically indistinguishable from their sister taxa (Mayr, 1963; Mayden, 1997; Bickford et al., 2007; Ceballos & Ehrlich, 2009). Within a broad spectrum of animal groups ranging from tropical frogs (Stuart, Inger & Voris, 2006) to rainforest butterflies (Hebert et al., 2004), deep-sea clams (Vrijenhoek et al., 1994), freshwater fish (Feulner et al., 2006) and mammals (Mayer, Dietz & Kiefer, 2007), advances in molecular methods have resulted in a dramatic increase in the description of cryptic taxa (Bickford et al., 2007). Cryptic species should be more likely to be discovered amongst species that favour mate recognition signals that are less obvious to humans and where convergent and/or parallel evolution have been strong (Mayr, 1963; Bickford et al., 2007). For instance, amongst mammals, nocturnal species may tend towards crypsis because low or poor light conditions limit opportunities for visual communication and also increase the importance of auditory and olfactory communication. In these taxa, cryptic morphology can also represent an antipredator adaptation by helping the animal hide against a background while resting during the day.

A clade that fits this description and has shown a dramatic increase in recognition of cryptic species in recent years is the nocturnal primates of Africa and Asia. This group comprises the infraorders Lemuriformes and Chiromyiformes of Madagascar, Tarsiiformes of Indonesia and the Philippines, and Lorisiformes of mainland Africa and Asia. Over the last two decades, the Malagasy lemurs have been subjected to extensive molecular and behavioural studies, resulting in an escalation in the number of species from 50 to 101 (Tattersall, 2007, 2013; Mittermeier et al., 2010; Weisrock et al., 2010; Mittermeier, Rylands & Wilson, 2013; Thiele, Razafimahatratra & Hapke, 2013). Similarly, within the Asian tarsiers the number of species has increased from three to 11, and more recently two new genera have been described (Groves & Shekelle, 2010; Shekelle, Gursky-Doyen & Richardson, 2013; Roos et al., 2014). Molecular studies have not only shown higher species diversity within nocturnal primates, but also suggested deep divergences between phenotypically nearly identical taxa. For instance, molecular estimates suggest Late Miocene origins for mouse lemurs (Microcebus spp.), dwarf lemurs (Cheirogaleus spp.), and tarsiers (Tarsius spp.) (Shekelle et al., 2010; Perelman et al., 2011; Springer et al., 2012; Thiele et al., 2013).

Almost completely neglected in terms of taxonomic research are the Lorisiformes, comprising the two families Galagidae (galagos) and Lorisidae, the latter with two distinctive subfamilies: Perodicticinae (angwantibos and pottos) and Lorisinae (lorises) (Groves, 2001; Grubb et al., 2003). The galagos, pottos, and angwantibos are restricted to Africa and range in body mass from 45–1510 g (Nekaris & Bearder, 2011; Nekaris, 2013a, b, 2014). The lorises are found in Asia and range in body mass from 85–2100 g (Nekaris & Bearder, 2011; Pimley & Bearder, 2013; Nekaris, 2013a). Galagos have one of the widest distributions, across the whole of Africa south of the Sahara, whereas pottos and angwantibos are restricted to Central Africa. Slender lorises are confined to Sri Lanka and southern India, whereas the slow lorises range from northeast India to southern China to Sundaland and the western Philippines (Fig. 1). The lorisiforms occupy a wide range of habitats, from near-desert conditions, through subtropical savannahs, woodlands, and riverine forests to dense tropical rainforests. In altitude they cover the entire range from sea level to upper-montane. Some species live allopatrically but in some areas up to six species occur in sympatry (Grubb et al., 2003; Nekaris & Bearder, 2011; Nekaris, 2013a, b).

Before the 1970s the accepted taxonomy of the Galagidae included only two genera (Galago and Euoticus) and only six species (Schwarz, 1931). Subsequent revisions expanded the number of genera to five and the number of species to 11 (Nash, Bearder & Olson, 1989; Olson, 1979), 17 (Bearder, Honess & Ambrose, 1995), 18 (Butynski, Kingdon & Kalina, 2013; Nekaris, 2013b), and 25 (Grubb et al., 2003). Bioacoustic studies have been at the forefront of galago taxonomic revision (Zimmermann, 1990; Masters, 1991; Honess, 1996; Bearder, 1999; Ambrose, 2003; Butynski et al., 2006). Taxonomic changes within galagids were also supported by examination of hand, foot, and penile morphology, and comparison of the hair structure (Anderson, 2000; Anderson et al., 2000; Perkin, 2007) and to a lesser extent, genetic research (e.g. Masters et al., 1994; Bayes, 1998).

The systematic within the Lorisidae has been long debated. Currently two subfamilies are recognized: Perodicticinae, including the two African genera Arctocebus and Perodicticus, and Lorisinae, including the two Asian genera Loris and Nycticebus. This classification was first proposed by Groves (1971) and was based on craniodental features. In contrast to this hypothesis, Schwartz & Tattersall (1985) suggested that the two robust forms, Nycticebus and Perodicticus, and the two slender forms, Loris and Arctocebus, form reciprocal monophyletic clades. Molecular studies based on both sequence data (Chatterjee et al., 2009; Fabre, Rodrigues & Douzery, 2009; Perelman et al., 2011; Springer et al., 2012; Pozzi, Disotell & Masters, 2014a) and mobile elements (Roos, Schmitz & Zischler, 2004) consistently support the former classification. These primates are difficult to trap and occur in areas where genetic sampling is difficult. Our knowledge of their taxonomic diversity has thus been restricted to
differences in behaviour, morphology, and facial markings, and limited genetic data (Schulze & Meier, 1995; Nekaris & Jayewardene, 2004; Nekaris & Jaffe, 2007; Nekaris & Munds, 2010; Munds, Nekaris & Ford, 2013). Currently there are five recognized perodicticine species and ten recognized lorises (Munds et al., 2013; Nekaris, 2013a; Roos et al., 2014).

The evolutionary relationships within lorisiforms are far from resolved (Rasmussen & Nekaris, 1998). Attempts to establish the phylogenetic relationships of the lorisiforms with molecular and morphological evidence have resulted in contradictory results (Yoder, Irwin & Payneur, 2001; Masters & Brothers, 2002; Roos et al., 2004; Masters et al., 2007). Although the standard practice is to consider the Lorisidae (Perodicticinae and Lorisinae) a monophyletic group to the exclusion of the Galagidae, most molecular studies have failed to provide strong support for this clade. No consensus has yet been reached as to whether the potto and lorises are indeed monophyletic, or if they form one of the most spectacular examples of parallel evolution amongst primates (Yoder et al., 2001; Roos et al., 2004; Masters et al., 2007; Pozzi et al., 2014a).

Recent fossil discoveries have added new vigour to debates regarding the origins of the Lorisiformes. Early evidence for lorisiform origins pointed back to the Miocene of East Africa. Intense debate characterizes the subfamilial designation of the three best-known Early Miocene forms, Mioeuoticus, Progalago, and Komba. Both cranial and postcranial features have allied these genera with either lorises or galagides (Le Gros Clark & Thomas, 1952; Walker, 1970; Gebo, 1986; McCrossin, 1992). Other authors have suggested that basal lorisiforms may have demonstrated a combination of lorisine cranial characteristics and galagide postcranial adaptations (Rasmussen & Nekaris, 1998). More recent specimens from Egypt suggest that the lorisiforms may be amongst the most ancient of the living primates, with origins extending back to the Late Eocene (Martin, 2003; Seiffert, Simons & Attia, 2003; Seiffert et al., 2005; Seiffert, 2007). A recent molecular study that included most of the lineages within the lorisiformes supported this hypothesis, suggesting a Late Eocene origin for the crown lorises and an origin for the galagids soon after the Eocene–Oligocene boundary (Pozzi et al., 2014a). True, irrefutable lorisines

Figure 1. Distribution and taxonomic abundance for lorisiforms, Perodicticinae (or African lorises), Lorisinae (or Asian lorises), and Galagidae. Images provided by Stephen Nash and used with permission from the IUCN/SSC Primate Specialist Group.
(Nycticeboides simpsoni) and galagids (Otolemur howelli) have been dated to the Late Miocene of Pakistan and Early Plio-Pleistocene of Ethiopia and Kenya (Seiffert, 2007; Harrison, 2010).

In this study, we investigated the evolutionary relationships and divergence times for the lorisiform primates by using complete mitochondrial cytochrome b (cytb) sequences. This gene has been widely used in phylogenetic and phylogeographical studies in mammals, including primates (e.g. Roos et al., 2004; Meyer et al., 2011; Haus et al., 2013; Boubli et al., 2015). Although cytb represents only a relative small fragment of the mitochondrial genome, multiple studies have shown that it can provide good estimates of phylogeny and divergence time when compared with other mitochondrial genes (Tobe, Kitchener & Linacre, 2010; Nicolas et al., 2012). Moreover, by selecting cytb as the marker for our analyses, we were able to maximize the number of taxa included in the study for two main reasons: (1) for multiple specimens in our study, only low-quality samples (such as faecal or museum specimens) were available, making it extremely difficult to obtain longer fragments or nuclear DNA; and (2) the high number of cytb sequences already available from GenBank for other strepsirrhine primates allowed us to build a large comparative data set for our analyses. We assembled the largest data set for the lorisiforms to date in terms of the number of taxa represented: overall, 86 specimens representing 26 species (~79% of the species currently recognized) were included in the analyses.

MATERIAL AND METHODS

SAMPLING

In total, 86 specimens of Lorisiformes were analysed for this study, 37 galagids and 49 lorisids. We obtained 59 samples (hairs, tissue, faeces, DNA) from colleagues and various institutions, including both zoos and museums (see Supporting Information Table S1). Another 27 samples were collected from wild populations using Tomahawk and modified Chardonnet live traps as described in previous studies (e.g. Pozzi et al., 2014a) or by hand (cf. Rode-Margono & Nekaris, 2014). Hair and tissue samples were obtained using standard protocols. Hairs were plucked from the dorsum and ventrum and stored in clean dry envelopes; tissue samples – approximately 2 mm² ear biopsies – were taken from each individual and preserved in sterilized 2 mL tubes filled with either RNAlater buffer or 70% ethanol. All the animals were released immediately after sample collection at the exact site of capture. Sample collection was approved by the Animal Welfare Body of the German Primate Center and adhered to the American Society of Primatologists Principles for the Ethical Treatment of Non-Human Primates (see http://www.asp.org/society/resolutions/EthicalTreatmentOfNonHumanPrimates.cfm). No animals were sacrificed for this study. In addition to the above 86 samples, we included 52 cytb sequences available from GenBank (one galago – Galago matschiei – and 51 lemurs). All the sequences used in this study, including location, provider, and GenBank accession number are presented in Table S1.

DNA EXTRACTION, AMPLIFICATION, AND SEQUENCING

Total genomic DNA from tissue and faeces was extracted with the DNeasy or Stool Mini Kits from Qiagen, respectively. When hair follicle cells were used, one to five hairs were directly implemented into the PCR. Depending upon DNA quality the complete cytb gene was PCR-amplified either as a single ~1.2-kb-long fragment using the primers 5′-AATGATATGAAA AACCATCGTTGTA-3′ and 5′-AACTGCAGTCAT CTCCGGTTTACAAGAC-3′ or via two to three overlapping fragments (primers available upon request). PCR reactions were carried out in a total volume of 30 μL containing a final concentration of 0.33 μM of each primer, 3 mM MgCl2, 0166 mM deoxynucleotide triphosphates, 1x buffer, and 1 U Biotherm Taq DNA polymerase (Genecraft). PCR conditions consisted of a pre-denaturation step at 94 °C for 2 min, followed by 40–50 amplification cycles, each with denaturation at 94 °C for 1 min, annealing at 50 °C for 1 min, and extension at 72 °C for 1.5 min. At the end a final extension step at 72 °C for 5 min was added. PCR performance was checked on 1% agarose gels. PCR products were excised from the gel, cleaned with a Qiagen Gel Extraction Kit, and sequenced on an ABI 3130xl DNA sequencer using a BigDye Cycle Sequencing Kit (Applied Biosystems) and the amplification primers. Sequences were assembled and manually edited in SeaView 4.4.0 (Gouy, Guindon & Gascuel, 2010).

PHYLOGENETIC ANALYSES

A total of 138 cytb sequences was aligned using MUSCLE (Edgar, 2004) and the final alignment consisted of 1140 bp. Phylogenetic analyses were conducted using both maximum likelihood and Bayesian algorithms. The data set was partitioned in three different ways: (1) no partition scheme, (2) two-partition scheme, with first and second codon positions together and third separate, and (3) three-partition scheme, with each codon position codified as an independent partition. The optimal substitution model for each partition was selected using the Bayesian information criterion as implemented in jModeltest 2.1.4 (Guindon & Gascuel, 2003; Darriba et al., 2012). Maximum likelihood analyses were run using a randomized accelerated maximum likelihood model in RAxML v. 7.2.6
RESULTS

We sequenced cytb sequences for 86 lorisiform specimens, comprising 26 different species. By combining the 86 newly generated sequences with 52 additional strepsirrhine sequences, the data set represents all seven strepsirrhine families, 23 of the 24 recognized genera (95.8%), and 76 of the 134 currently recognized species (56.7%) (Butynski et al., 2013; Mittermeier et al., 2013; Nekaris, 2013a, b; Roos et al., 2014).

All phylogenetic analyses (RAxML, MrBayes, and BEAST) supported very similar topologies (Figs 2, 3). Within the lorisiformes, Perodicticinae, Lorisinae, and Galagidae were strongly supported (posterior probability or PP > 0.95 and bootstrap support or BP > 0.70) as monophyletic, but the family Lorisidae was recovered as paraphyletic, with the African lorisids (Perodicticus and Arctocebus) more closely related to the galagids than to the Asian lorisids (Loris and Nycticebus) (BP = 85%) and PP = 1.00). All alternative topologies for this node, including the monophyly of Lorisidae, could not be rejected by either the Kishino–Hasegawa (Kishino & Hasegawa, 1989) or Shimodaira–Hasegawa (Shimodaira & Hasegawa, 1989) tests (Table S2).

Within the galagids, all the analyses strongly supported the basal position of the genus Euoticus as sister taxon of all the other galagids. The genus Galagoides was not monophyletic: the clade including Galagoides demidoff and Galagoidea thomasi is the sister group to all the remaining galagids, whereas the Eastern clade, including Galagoides orinus, Galagoides rondoensis, and the Zanzibar complex (Galagoides zanzibaricus, Galagoides granti, and Galagoides cocos), is the sister group to Galago. The latter relationship however was only weakly supported by the RAxML (BP = 66%) and MrBayes analyses (PP = 0.94). The genus Otolémur was strongly inferred as sister taxon to the genus Sciurocheirus, and this clade was recovered to be sister group to the clade including Galago and the Eastern Galagoides species.

Within the eastern African clade of Galagoides, the Zanzibar complex, including G. granti, G. zanzibaricus, and G. cocos, was strongly inferred as monophyletic. However, the relationships between this species complex and the other two members of this clade (G. orinus and G. rondoensis) were only weakly supported. All of the analyses suggested a sister relationship between the montane dwarf galago (G. orinus) and the Zanzibar complex, to the exclusion of the Rondo dwarf galago (G. rondoensis). However, the support values for this node were very low in both maximum likelihood (BP = 47%) and Bayesian analyses (PP = 0.70).

Within the lorisis phylogenetic relationships were consistent across analyses. Within Nycticebus, the most diverse lorisid genus, all species were inferred to be monophyletic. Nycticebus pygmaeus was recovered as
Figure 2. Phylogenetic tree inferred from maximum likelihood (RAxML) and Bayesian (MrBayes) analyses. Specific values for those nodes that were weakly supported in the analyses (bootstrap support < 70% and/or posterior probability < 0.95) are reported in the tree. Scale bar represents substitutions per nucleotide site. Images provided by Stephen Nash and used with permission from the IUCN/SSC Primate Specialist Group.

Figure 3. Estimated divergence ages with 95% highest probability densities (HPDs, blue bars). A geological time scale is given below and above the tree (values are millions of years ago). For detailed information on estimated divergence ages see Table S3. Numbers in the tree refer to the major nodes mentioned in Table S3. Plio, Pliocene; Ple, Pleistocene; K-Pg, Cretaceous–Paleogene; E-O, Eocene-Oligocene. Images provided by Stephen Nash and used with permission from the IUCN/SSC Primate Specialist Group. *The family Cheirogaleidae was not recovered as monophyletic in our analyses.

a relative old lineage (>10 Mya), and the sister taxon to all the other slow lorises. Within *Perodicticus*, *Perodicticus potto* is basal in the genus, and *Perodicticus edwardsi* and *Perodicticus ibernus* are sister taxa.

As the monophyly of the Lorisiidae was not statistically rejected (P > 0.05), divergence ages were also estimated based on an a priori constrained monophyly of the Lorisiidae as suggested by retroposon integrations and morphological studies (Yoder et al., 2001; Masters & Brothers, 2002; Roos et al., 2004). The estimates from unconstrained and constrained analyses did not differ significantly (see Table S3); therefore, here we report only the dates for the constrained topology. Age estimates for all the main nodes in the tree are reported in Table S3 and Figure 3. Divergence times within the Lorishiformes are ancient, with the divergence between the two families (Galagidae and Lorisiidae) at around 39 Mya (39.70 Mya; HPD = 35.71–43.56), followed by split between the African and Asian lorisids at 37.85 Mya (HPD = 32.96–42.40). Both the most recent common ancestors (MRCA) for the Galagidae and the Lorisiidae were dated to about 30 Mya (Galagidae: 29.83 Mya; HPD: 23.96–35.55; Lorisiidae: 29.32 Mya; HPD = 23.08–35.52), whereas the common ancestor for the subfamily Perodictinae was estimated to be more recent, about 23 Mya (HPD = 17.39–28.87).

Whereas the MRCA for *Nycticebus* was quite old (10.91 Mya; HPD = 7.62–14.46), the one for *Loris* was recent (2 Mya; HPD = 1.21–2.85). Similarly, within African lorisids, *Perodicticus* emerged about 8 Mya (8.25 Mya; HPD = 5.59–10.54), whereas *Arctocebus* diverged only less than 1 Mya (0.77 Mya; HPD = 0.37–1.21). Within the Galagidae, *Eutricus* was the first lineage to emerge in the Early Oligocene (29.83 Mya; 23.96–35.55), whereas the MRCA for all the other genera was dated in the Early Miocene at 21.58 Mya (HPD = 16.92–26.3). Most of the genera within the galagos emerged in the Late Miocene (6–11 Mya), with the only exception being *Sciurocheirus*, for which the MRCA was dated to within the Pliocene, at about 3 Mya (2.93 Mya; HPD = 1.70–4.29).

**DISCUSSION**

Our study based on cyt b data for most of the recognized species of Lorishiformes provided well-resolved phylogenetic relationships and predominantly strong support for most of the nodes. In general, the results obtained herein agree with some recent molecular studies (Springer et al., 2012; Pozzi et al., 2014a). Within galagos, *Eutricus* represents the deepest split, estimated at 30 Mya. This estimate is only slightly younger than the one obtained from nuclear data by Pozzi et al. (2014a), and further supports an origin of the living galagos soon after the Eocene–Oligocene boundary. Both the phylogenetic relationships and the age estimates within the galagos are concordant with the study conducted by Pozzi et al. (2014a). The genus *Galagoidea* was not inferred as monophyletic, but it comprises two independent clades, one including *G. demidoff* and *G. thomasi* (Western clade) and one including all the species distributed in eastern Africa (*G. cocos, G. zanzibaricus, G. granti, G. rondoensis*, and *G. orinus*; Eastern clade). This Eastern clade was inferred to be the sister group to the genus *Galago*, but the support values were relatively low in most analyses. This result is generally concordant with nuclear data, where a relatively high level of tree discordance was found across independent loci (Pozzi et al., 2014a). In fact, despite the sister-group relationship between *Galago* and Eastern *Galagoidea* being the most favoured topology, alternative relationships were also recovered, including a sister-group relationship between *Otolemur* and *Galago* and between *Otolemur* and Eastern *Galagoidea* (Pozzi et al., 2014a). It is likely that the relatively small amount of time that passed between the emergence of these three lineages, and the consequent small level of phylogenetic signal, are the main cause of gene tree heterogeneity at this node. Within the Eastern clade of *Galagoidea*, the Zanzibar complex was strongly recovered as a monophyletic group. Our phylogenetic analyses suggested an origin for this group in the Late Miocene (~5.8 Mya) and a sister-group relationship between *Galagoidea cocos* and *Galagoidea zanzibaricus*, to the exclusion of *Galagoidea granti*. Despite the high level of morphological crypsis, species within this complex clearly differ based on species-specific advertising calls (Grubb et al., 2003; Butynski et al., 2006) and penile morphology (Perkin, 2007). This study provides for the first time genetic evidence supporting the taxonomic status of these three species.

The inter-relationships amongst *Galagoidea orinus*, *Galagoidea rondoensis*, and the species belonging to the Zanzibar complex were not fully resolved. More data – and possibly more samples from multiple populations – are needed to better elucidate the phylogeny of the Eastern clade. However, the deep divergence dates within this clade (approximately 10–11 Mya for the split between *G. orinus, G. rondoensis*, and the Zanzibar complex) suggest that the diversity within dwarf galagos may be higher than currently recognized. *Galagoidea rondoensis* is the most physically distinctive and smallest (c. 60 g) *Galagoidea* in East Africa supporting this deep divergence date, whereas *orinus* although small (c. 100 g) is phenotypically more similar to the Zanzibar complex (Butynski et al., 2013). As members of *Galagoidea* are almost exclusively forest-dependent species, their radiation was most likely driven by the expansion and later contraction and isolation processes of the equatorial forests of Africa that has occurred over the last 30 Mya.

Over the last two decades, similar primate radiations, such as those of *Lepilemur* and *Microcebus*, have undergone dramatic taxonomic revisions, mainly based on new molecular data. Although some authors argued that the consequent increase in recognized lemur species might be a result of ‘taxonomic inflation’ (Isaac, Mallet & Mace, 2004; Tattersall, 2007, 2013; Markolf, Brammeier & Kappeler, 2011), the actual diversity within nocturnal lemurs is probably much higher than previously thought based on morphological data only (Weisrock et al., 2010; Thiele et al., 2013; Zimmermann & Radespiel, 2014). In contrast to Malagasy lemurs, very little research has been conducted on galagos and very limited genetic data are available for most species. For instance, in this study we presented the first genetic data for the Rondo galago (*Galagoides rondoensis*), one of the most threatened species of primates (Mittermeier et al., 2014). Age estimates indicate a deep split between the southern (Ruawa Forest Reserve) and northern (Pande Forest Reserve) populations (∼2.5 Mya). These two populations are separated by the Rufiji river, which has been proposed as a biogeographical barrier for several species of mammals (Kingdon, 1971; Weber, 2001; Butynski et al., 2006). Unfortunately the data set available today for this taxon is still very limited and more samples are required to elucidate the biogeography and taxonomy of this species.

The greater galagos (genus *Otolemur*) were inferred as the sister group to the squirrel galagos (genus *Sciurocheirus*) with high support. This result is in agreement with previous studies on galagid phylogeny (DelPero et al., 2000; Roos et al., 2004; Masters et al., 2007; Chatterjee et al., 2009; Fabre et al., 2009; Springer et al., 2012). However, all these studies – including this one – were based on mitochondrial DNA and no nuclear data are available yet for members of the genus *Sciurocheirus*. Further research should aim to include multiple loci to confirm the sister-group relationship between these two genera.

Interestingly, both *Galagoides demidoff* and *Galago senegalensis* were inferred as paraphyletic in our phylogenetic reconstructions. However, this result is probably a consequence of taxonomic misallocation of members of the two species. Inaccurate classification of specimens in museum collections is very common within galagids (Pożzi et al., 2014a), and in particular members of the species *Galagoides thomasi* / *demidoff* and *Galago moholi* / *senegalensis* are commonly misclassified. As a consequence, their taxonomy and biogeography is still poorly known and further studies should be conducted to investigate the genetic variation of these widely distributed species.

In contrast to the strong support for the monophyly of the family Galaginae, the monophyly status of the family Lorisidae was not confirmed. As in previous studies, the interrelationships amongst Galaginae (galagos), Perodicticinae (African lorisids), and Lorisinae (Asian lorisids) were not fully resolved. To date the only strong and unambiguous molecular evidence for the monophyletic status of the family Lorisidae is provided by the presence of three mobile elements, short interspersed elements (Roos et al., 2004). Most molecular studies based on sequence data – either mitochondrial or nuclear – have failed to provide strong support for the monophyly of this family, and many studies have proposed alternative topologies, with the galagids more closely related to either the Asian (Goodman et al., 1998; Yoder et al., 2001; Roos et al., 2004; Masters et al., 2007; Chatterjee et al., 2009; Matsui et al., 2009; Pożzi et al., 2014a, b) or the African lorisids (Dene et al., 1976; Finstermeier et al., 2013; this study). Multiple reasons might explain this pattern, including the presence of incomplete lineage sorting or ancient horizontal gene flow. Although further studies including longer (and possibly more informative) sequences might clarify the phylogenetic relationships of these three lineages at the molecular level, it remains likely that the three subfamilies emerged very rapidly after the origins of the Lorisiformes (Pożzi et al., 2014a). This has critical implications in understanding the evolution of this primate group. Given the high level of morphological and behavioural traits shared between Asian and African lorisids, these lineages were either characterized by a relatively rapid evolution of those adaptations or – even more surprisingly – they represent one of the most spectacular examples of parallel evolution amongst primates (Goodman et al., 1998; Yoder et al., 2001). The deep divergence for both the Perodicticinae (23 Mya) and the Lorisinae (29 Mya) suggests that the two subfamilies should be elevated to the family level. Within primates, most families have in fact similar or even younger ages. Future research should better investigate morphological, behavioural, and ecological differences across these two groups, with special attention to the poorly studied pottos and angwantibos, in order to provide support for this revision of lorisiform taxonomy.

In contrast to the ambiguous status of the Lorisidae, our study confirmed the monophyletic status of both subfamilies and all the four lorisid genera with high support values. This result corroborates previous molecular studies based on mitochondrial and nuclear data (Chatterjee et al., 2009; Fabre et al., 2009; Perelman et al., 2011; Springer et al., 2012). Interestingly, whereas *Perodicticus* and *Nycticebus* have early origins in the Miocene, the genus *Loris* originated only quite recently, in the Pleistocene. In our study we included only one species of angwantibo (*Arctocebus calabarenosis*) so no conclusions can be drawn regarding the origin of this genus. Within *Perodicticus*, current taxonomy recognizes three different species: *Perodicticus potto* (Western potto), *Perodicticus iberanus* (Eastern potto),
and Perodicticus edwardsi (Milne-Edwards’ potto) (Butynski et al., 2013; Nekaris, 2013b). The divergence dates obtained in our study (> 5 Mya) support species status for these three forms of pottos, but to date no obvious ecological and/or behavioural differences have been reported amongst the three putative species (E. R. Pimley, pers. comm.). Long-term studies including radio tracking are needed to discover whether behavioural data elucidate the genetic differences.

With an origin in the Middle Miocene (~11 Mya), Nycticebus is the oldest and most diverse genus within the lorisids. The lineage leading to the pygmy slow loris (Nycticebus pygmaeus) is the first to emerge in this group. Date estimates show a wide gap (roughly 6 million years) between the divergence of N. pygmaeus and the radiation of the remaining Nycticebus species. This relatively deep divergence between N. pygmaeus and other species of slow lorises might explain other stark ecological differences, which may lend support to the distinction of these species at the generic level. Such differences include but are not limited to several unique traits of N. pygmaeus, which is the only slow loris known to live sympatrically with other Nycticebus spp., to exhibit hairless ears, to show seasonal changes in coat colour, to regularly give birth to twins, and to exhibit a multi-male multi-female rather than a unimale, uni-female social system (Nekaris & Bearder, 2011).

CONCLUSIONS

In this study we present the largest dated phylogeny for the Lorisiformes. Our results support the general conclusions of previous studies based on nuclear data. Moreover they elucidate phylogenetic relationships for many species never included before in a molecular phylogeny. Overall our results imply that the diversity of the lorisiforms remains substantially underestimated and that previously unnoticed cryptic diversity might be present within many lineages, particularly in Africa. The process of determining true species diversity within the lorisiforms is more than academic. Currently 60% of primates are threatened with extinction (Mittermeier et al., 2013, 2014). Lorisiform primates suffer from extreme deforestation, bushmeat hunting, and use in traditional medicine and the pet trade (Starr et al., 2010; Nijman et al., 2011; Nijman, Nekaris & Bickford, 2012). Identification of further taxa, either those geographically isolated such as the dwarf galagos of East Africa, or of more diversity within currently widespread ‘species’ such as Nycticebus bengalensis, would dramatically alter the vulnerability of the lorisiform primates to extinction, making an understanding of their taxonomy an area of urgent conservation action.

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REFERENCES


**SUPPORTING INFORMATION**

Additional Supporting Information may be found in the online version of this article at the publisher’s web-site:

**Table S1.** List of the specimens used in the present study including specimen source, provider, and GenBank accession numbers.

**Table S2.** Results from alternative tree topology (Kishino–Hasegawa and Shimodaira–Hasegawa) tests for the relationships amongst Galagidae, Perodicticinae, and Lorisinae. The likelihoods and differences from the most probable topology are shown.

**Table S3.** Support values and date estimates with 95% highest probability densities (HPDs) for both unconstrained and constrained topologies (see text for details). Analyses were run using BEAST 1.7.5.