# Cheirogaleid diversity and evolution: big questions about small primates

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# Abstract

The family Cheirogaleidae is arguably the most interesting group of primates alive today. Within this single clade, hypothesized to have originated approximately 25 - 30 Mya, we find the world's smallest living primate (genus *Microcebus*), one species that went "missing" for more than three decades (genus *Allocebus*), the only known obligate hibernator within the primates (genus *Cheirogaleus*), the only primate species that preys upon other members of its phylogenetic family (genus *Mirza*), and also, a taxonomic system that has exploded within the past two decades. This taxonomic explosion has been decidedly lopsided, however. Whereas the genus *Allocebus* has remained monotypic, containing the single species A. trichotis since its original description in 1875 (Günther 1875), the genus *Microcebus* (mouse lemurs) has gone from a two species system as recently as 1993 to one that that now contains more than 20 recognized species. This apparent skew in species-level diversity cries out for further exploration. Is it an artifact of organismal and geographic sampling bias, with certain species and ecosystems preferentially sampled, or is it based in biology, with some branches of the cheirogaleid tree (namely, the mouse lemurs) intrinsically more prone to evolutionary divergence? An exploration of these themes and questions is our goal in this chapter.

#### Introduction

The first genus level phylogeny of the cheirogaleid lemurs was published by Rumpler et al. (1994) and has remained virtually unchanged in the subsequent decades. Using karyotype data and restriction fragment analysis, the authors found strong support for the phylogeny illustrated in Figure 1. Notably, Rumpler and Albignac (1972) had long before discovered that the karyotype of *Phaner* (2n = 46) is quite distinct from that of the other four genera (2n = 66), leading those authors to propose a two-subfamily taxonomy of the Cheirogaleidae, the monotypic Phanerinae (including only the genus *Phaner*) and the Cheirogaleinae (comprising the four remaining genera). More recent molecular phylogenetic analyses have sampled more densely at the species level and have yielded fresh insights into inter-specific relationships within the various genera, while leaving the "skeleton" of the phylogeny unchanged. The stability of the cheirogaleid clade has made divergence time estimations feasible. Divergence time analysis has consistently shown the basal radiation of mouse lemurs to be on the order of 10 - 9 Mya (Thiele et al. 2013; Yang and Yoder 2003). Interestingly, the Thiele et al. (2013) study found the dwarf lemur radiation to be of approximately the same age, with a basal divergence date of 9.6 Mya (depending upon the loci examined). These authors concluded that the genus *Cheirogaleus* contains deeply divergent lineages "which are considerably older than several species of mouse lemur" (p. 602). Similar conclusions were reached by Springer et al. (2012), though with slightly younger age estimates with ~ 7 Mya for mouse lemurs and ~9 Mya for dwarf lemurs. Unfortunately, none of the divergence time studies to date has included the basal lineage, genus *Phaner*, and thus all age estimates of the ancestral cheirogaleid radiation will be underestimates. That said, all studies agree in finding diversification within the Cheirogaleidae to have originated by the late Oligocene, at least.

Though it is true that several molecular phylogenetic studies have shown a weak relationship between *Phaner* and *Lepilemur* (e.g., Masters et al. 2013; Roos et al. 2004; Springer et al. 2012), this result is likely to be an artifact of the rapid rate of mitochondrial evolution perhaps exacerbating the effects of long-branch attraction (Felsenstein 1978; Hillis 1996; Huelsenbeck 1997; Wiens and Hollingsworth 2000). Rather, a synthetic view

of recent molecular phylogenetic studies indicates that it is the entire cheirogaleid clade that is the sister to the genus *Lepilemur* (e.g., see Masters et al. 2013; Yoder 2013 for recent reviews). Looking more closely at the cheirogaleid clade, the dwarf lemurs (Groeneveld et al. 2010; Groeneveld et al. 2009; Thiele et al. 2013) and the mouse lemurs (Heckman et al. 2007; Heckman et al. 2006; Weisrock et al. 2010; Yoder et al. 2000) have shown complicated taxonomic expansions and rearrangements (Tables 1 & 2). In the majority of studies that have examined both mitochondrial (mtDNA) and nuclear (nDNA) DNA, it is typical to find poorly supported internal nodes and a high level of gene tree discordance across the loci under investigation (Heckman et al. 2007; Weisrock et al. 2010). Such results are typical of species radiations that are both recent and explosive (Knowles and Carstens 2007; Moore 1995; Shaffer and Thomson 2007). Within the mouse lemur clade, several studies have shown strong support for three deep lineages, one that contains M. murinus plus M. griseorufus, another deeply-diverged lineage represented by M. ravelobensis, M. danfossi, and M. bongolavensis, and a third lineage that is comprised of all other mouse lemur species including strong support for distal subclade comprised of M. berthae, M. rufus, and M. myoxinus (Figure 2) (Heckman et al. 2007; Heckman et al. 2006; Weisrock et al. 2010; Weisrock et al. 2012). This latter subclade is especially intriguing given that *M. rufus* (an eastern, rainforest adapted animal) is markedly divergent both ecologically and geographically from *M. berthae* and *M. myoxinus*, both of which occur in the dry deciduous forests of western Madagascar.

The chapter by Groves (this volume) gives a comprehensive summary of the finest details of cheirogaleid taxonomy, leaving little need for us to cover the same ground. Rather, we here examine the evidence that has driven the dazzling proliferation of species designations in one genus (*Microcebus*) while leaving others essentially unchanged since their original descriptions (i.e., *Allocebus, Mirza and Phaner*). Not terribly surprisingly, the proliferation of mouse lemur species coincides closely with the advent of readily available DNA sequences via the polymerase chain reaction (PCR) and with the development of user-friendly software for phylogenetic analysis of these sequences (e.g., Swofford 1990). An empirical investigation of the mouse lemur radiation has verified the theoretical predictions of recent and rapid species diversification (Weisrock et al. 2012). These

authors, in an effort to apply a multi-locus approach to reconstructing a species-level phylogeny for the mouse lemurs, found that the lingering effects of incomplete lineage sorting within the mouse lemur radiation severely compromise our ability to conduct standard phylogenetic analysis. That study, despite its inability to resolve the mouse lemur species tree, nonetheless came to a fundamental conclusion: depending upon which alleles were selected for concatenation in the multi-locus analysis, phylogenetic resolutions could differ, often dramatically, and with convincing statistical support. Thus, mouse lemurs show the classic hallmarks of a rapid species radiation wherein phylogenetic relationships will be difficult to reconstruct.

### **Lumping and Splitting**

Prior to the ready acquisition of DNA sequences for phylogenetic analysis, primatologists had favored a two-species taxonomy of mouse lemurs that included M. murinus, a longeared gray animal from the southern and western regions of Madagascar, and M. rufus, a short-eared reddish animal from the east. Martin (1972), in particular, made note of the differing habitats and ecological constraints defining the two species, with *M. murinus* inhabiting dry deciduous and xerophytic forest and specializing on insectivory, and M. rufus inhabiting humid rain forest and showing dietary tendencies toward omnivory. This taxonomic stability first quavered with the description of a third, measurably smaller, species from the dry deciduous forests of western Madagascar (Schmid and Kappeler 1994). Initially, this third species was referred to as *M. myoxinus*, though this designation was to be shortly overturned by Rasoloarison et al. (2000). In the interim, a fourth and much larger species was identified in northwestern Madagascar and designated as *M*. ravelobensis (Zimmermann et al. 1998). Thus, even though new mouse lemur species were being recognized and described at an increasing rate throughout the 1990s, the pace was rather moderate when species designations relied upon combined assessments of ecology and morphology.

The pace accelerated abruptly with the introduction of genetic data into the species discovery process. With the combined efforts of a morphological team lead by

Rasoloarison et al. (2000) and a genetics team led by Yoder et al. (2000), the rate of taxonomic revision accelerated rapidly with the description of five new species. Along with the revised taxonomy of *M. myoxinus*, now recognized as *M. berthae*, so began the era of seemingly outlandish taxonomic proliferation. In two decades, *Microcebus* expanded from a genus containing two species to one containing at least 20 species (Andriantompohavana et al. 2006; Kappeler et al. 2005; Louis et al. 2006; Louis et al. 2008; Olivieri et al. 2007; Radespiel et al. 2008; Radespiel et al. 2012; Rasoloarison et al. 2013), and with many of these based primarily if not entirely on small DNA datasets.

Not surprisingly, there has been resistence from the primatological community, with assertions made of "a remarkable lack of introspection" (Tattersall 2007) as well as concerns that "species are based solely on evidence of genetic distance and diagnostic characters of mitochondrial DNA sequences sampled from a few individuals per location" (Markolf et al. 2011). We take these concerns seriously, and indeed, this is the impetuous for our contribution to this very special volume on "Evolutionary Biology and Ecology of the Cheirogaleidae". Here, we wish to address the issue of species recognition both specifically --- asking how many species of mouse lemurs are there? And are they "real"? --and more generally, examining the criteria and analytical framework for recognizing species. Though it is something of a tautology to say that species are the product of speciation, it is useful to remind ourselves that "speciation is a multi-level process unfolding through time and space" (Abbott et al. 2013; p.231). In this vein, de Queiroz (2007) has elegantly made the point that by attempting to pin a name to an organismal unit that is the product of an ongoing process we are setting ourselves up for disagreement and controversy. Here, we couch our discussion in the light of Simpson's Evolutionary Species Concept as expressed in Weisrock et al. (2010). That is, a "lineage (an ancestraldescendent sequence of populations) evolving separately from others and with its own unitary evolutionary role and tendencies" (Simpson 1961). As for how to identify these lineages as species, de Queiroz (2007; p. 879) again describes matters succinctly by pointing out that "all of the properties formerly treated as secondary species criteria are relevant to species delimitation to the extent that they provide evidence of lineage

separation ... and thus more lines of evidence are associated with a higher degree of corroboration."

In other words, an integrative approach that combines genetic distance, morphometric distinction, behavioral variation and biogeographic separation establishes the lines of evidence supporting species recognition hypotheses (Markolf et al. 2013). Moreover, the careful assessment of this evidence can justify the recognition of species identities, even when there is clear-cut indication of limited gene flow among and between hypothesized species (Yoder, 2014), a phenomenon that is clearly of significance for the mouse lemur radiation (Hapke et al. 2011; Rakotondranary et al. 2011a).

#### What is it about mouse lemurs?

Why is it that mouse lemurs show such clear patterns of genetic divergence and evolutionary isolation even though they are morphologically and ecologically so similar? One putative explanation relates to their nocturnal habits. Primatologists have sporadically discussed the possible relationship between nocturnality and cryptic speciation for several decades, though it is an essay on bats that offers the most detailed analysis. In a perceptive essay on the issue, Jones (1997) describes the biological complexities of cryptic species, particularly as they relate to nocturnality. In Jones's view, the lack of visual information concomitant with a noctunal lifestyle will be compensated by other means of inter-individual signaling and communication such as acoustic and olfactory cues. Moreover, Jones predicted that biologists are significantly underestimating evolutionary diversity when we rely solely on visual information (i.e., morphological characters) as our guide for species identification, asserting that untold amounts of genetic biodiversity will be underappreciated using such methods. Jones anticipated that "advances in molecular biology may allow insights into speciation in cryptic species" (p. 345), a scenario that has been unfolding over the past two decades as we have investigated the mouse lemur radiation. Despite the appeal of Jones's cryptic speciation hypothesis, we must note that all cheirogaleid primates are nocturnal, so the apparent imbalance in species diversity within the clade cannot be reduced to this single explanation. Moreover,

and even more complicated, biologists have found it difficult to explain how primate species that occupy the same ecological niche --- as mouse lemurs appear to do --- and are difficult if not impossible to distinguish morphologically, can co-exist sympatrically (Dammhahn and Kappeler 2008b; Radespiel et al. 2006; Rakotondranary and Ganzhorn 2011; Rakotondranary et al. 2011a; Rakotondranary et al. 2011b; Thoren et al. 2011b). As we have gained increased knowledge of the precise details of mouse lemur behavioral ecology, however, these mysteries are resolving.

### Mouse Lemurs as a Model System

Rather than view these conundrums as obstacles to biodiversity discovery, we believe that mouse lemurs can more usefully be presented as a model system for investigating the often subtle and overlooked biological forces that can drive species radiations and maintain species boundaries (though these forces may act differentially, with some as "drivers" and others as "maintainers"). Beyond the intriguing idea of looking towards alternative signaling mechanisms of olfactory and acoustic communication for driving and maintaining species boundaries (e.g., Braune et al. 2005; Braune et al. 2008; Hohenbrink et al. 2012; Leliveld et al. 2011; Scheumann et al. 2007; Yoder et al. 2014), it is becoming increasingly clear that painstaking investigations of behavior and ecology are necessary for disentangling the relevant parameters (e.g., see Radespiel, this volume).

Among mouse lemurs, *Microcebus murinus* is unique in having a relatively vast geographic distribution. Whereas all other *Microcebus* species have geographically limited ranges --- with some restricted to isolated forest fragments --- *M. murinus* is distributed along most of the western half and along the south of the island. It is presently not known what are the genotypic and phenotypic traits possessed by *M. murinus* that apparently confer an adaptive flexibility that has promoted its spread across vast areas of Madagascar (but see chapter by Radespiel, this volume). Like other species within the genus, *M. murinus* is known to exhibit episodic bouts of torpor, presumably in the face of resource limitations. Unlike other species, however, there appears to be a sex bias to this behavior that is distinctive. For example, *M. murinus* populations have been shown to exhibit different torporing

patterns both by age and by sex (Schmid 1999; Schmid and Kappeler 1998; Terrien et al. 2010a; Terrien et al. 2010b), with one study finding that whereas 73% of females undergo prolonged torpor bouts, only 19% of males show the same behavior (Schmid 1999). Over the extensive range of *M. murinus*, the species has been confirmed or hypothesized to overlap with multiple congeners including *M. griseorufus* (its sister species), *M. berthae*, *M. myoxinus*, *M. bongolavensis*, and *M. ravelobensis*. And though it remains to be confirmed, there is the potential for overlap with *M. tavaratra*, *M. sambarinensis*, and *M. danfossi* given the latitudinal distribution of these species. Irrespective of their sympatric status, all species in the genus compared to *M. murinus* show much smaller species ranges, with some showing alarming patterns of geographic restriction and microendemism.

Here, we review the literature on the behavioral ecology of *Microcebus*, focusing on three regions of sympatric overlap between *M. murinus* and *M. griseorufus*, *M. berthae*, and *M. ravelobensis*, respectively. Notably, all of these investigations of ecological and behavioral distinction in sympatry involve *M. murinus*, by far the most geographically widespread of the recognized species of mouse lemur. Potentially, this introduces an unwanted bias to the generalities and conclusions that can be drawn from a synthetic view of these studies, but at present, they are the best available. Moreover, despite their relatively limited taxonomic scope, these studies provide insight into the subtlety and power of environmental forces that can create almost invisible niche heterogeneity wherein each species can occupy a unique ecological domain.

# Mouse lemur niche heterogeneity: from southern to northern Madagascar

# Lessons from Microcebus griseorufus

One example of this pattern of sympatry couples *M. murinus* with *M. griseorufus*, with multiple lines of evidence for distribution overlap and potential hybridization between the two species in southern Madagascar. Within their respective ranges, *M. murinus* and *M. griseorufus* exhibit marked differences in abundance. *M. murinus* is typically common throughout its range and has been studied extensively since its description (Kappeler and Rasoloarison 2003). Conversely, *M. griseorufus* has been recorded from relatively few

locations within a narrow range in the southwest of the island in the recent past and remains poorly studied (Bohr et al. 2011; Genin 2008; Kobbe et al. 2011). A recent study (Blair et al. 2014) used a multilocus coalescent framework to test the hypothesis that the relatively limited range of *M. griseorufus* relative to *M. murinus* is the consequence of peripatric speciation wherein *M. griseorufus* was initially formed via the isolation of a relatively small ancestral population that was on the geographic limits of a more widely distributed ancestral *M. murinus* population. The study rejected this hypothesis soundly, finding instead that historical demographic data much better fit a model of allopatric divergence from a range-restricted common ancestor in southwestern Madagascar, with subsequent range expansions for *M. murinus*. Whether due to ecological constraint (Bohr et al. 2011) or interspecific competition, *M. griseorufus* is presently restricted to the arid spiny forest in the south, whereas *M. murinus* has successfully expanded northward throughout much of western Madagascar and to limited areas in the southeast.

*Microcebus griseorufus* is special within the mouse lemur radiation for apparently thriving in one of the most challenging environments inhabited by any primate: the dry spiny forests of the southwest. Rainfall and accordingly resources are unpredictable both in amount and distribution, and this species has developed a number of physiological and behavioral strategies for coping with this uncertainty. A four-year study of one population showed that individuals used daily torpor and expressed opportunistic seasonal fattening when food availability was high, reverting to dependence on plant exudates when experiencing periods of regional drought (Génin 2008). Another long-term study showed that *griseorufus* shows high levels of seasonal as well as individual flexibility in thermoregulation (Kobbe et al. 2011). Whereas all individuals remained normothermic during the rainy season when resources are abundant, heterothermy ranging from irregular short torpor bouts, to regular daily torpor, to prolonged torpor of a few days, and even hibernation over several weeks were observed during the dry season. When compared with *M. murinus*, *M. griseorufus* shows an interesting combination of habitat fidelity, strongly preferring spiny forest to gallery or transitional forest types, as well as greater flexibility in thermoregulation.

Early genetic work found that M. griseorufus and M. murinus show species-specific mtDNA haplotypes, which at the time was regarded as evidence for reproductive isolation in sympatry (Yoder et al. 2002). More recent and sophisticated genetic analyses that examined both mitochondrial and nuclear autosomal loci have revealed a much more complicated picture of genetic exchange between the two species (Gligor et al. 2009; Hapke et al. 2011). In the 2009 study, the authors found that whereas mitochondrial haplotypes displayed a sharply delimited boundary at the eastern edge of spiny forest, nuclear loci yielded evidence for a mixed ancestry of mouse lemurs in the ecotone between the spiny forest habitat of *M. griseorufus* and the littoral forest habitat of *M. murinus*. In this case, the authors concluded that asymmetric nuclear introgression was due to male-biased dispersal, divergent environmental selection, and an expansion of dry spiny forest in the course of aridification (Gligor et al. 2009). In the 2011 study, in another field setting, the authors found that whereas *M. griseorufus* is restricted to the spiny forest habitat, *M. murinus* occurs in the gallery forest but locally invades the dryer habitat of *M. griseorufus*. In this setting, the authors found evidence for bidirectional introgressive hybridization, in contrast to the asymmetric patterns previously observed. In comparing the two settings and the coincident patterns of introgressive gene flow, the authors found that hybridization could enhance the adaptability of mouse lemurs without necessarily leading to a loss of distinctiveness (Hapke et al. 2011), a finding very much in keeping with emerging views of the genomics of speciation (Seehausen et al. 2014; Yoder 2014). Finally, and in keeping with the "sine qua non" of speciation theory, a recent study by Sommer et al. (2014) has found that hybrids formed by *M. murinus* and *M. griseorufus* show reduced fitness as measured by higher parasite loads.

To summarize, it appears that interactions between *M. murinus* and *M. griseorufus* can differ depending upon ecological and environmental context. This has been confirmed empirically: when the two species exist in allopatry, both behave as ecological generalists, yet, when they occur in sympatry, both species show distinct microhabitat preferences, allowing them to partition the environment (Rakotondranary and Ganzhorn 2011). Moreover, stable isotope analysis revealed that their dietary niches diverge most markedly in the dry "lean" season (Rakotondranary et al. 2011b). The results pertaining to *M*.

griseorufus and M. murinus have been extended to a three-species comparison in southeastern Madagascar where they co-occur with M. rufus. This study further confirmed the preference for gallery forest in M. murinus and spiny forest for M. griseorufus, adding the observation that M. rufus shows a strong fidelity to evergreen humid forest (Rakotondranary et al. 2011a).

Finally, with regard to heterothermy, *M. griseorufus* was found to exhibt even greater flexibility than *M. murinus*, with individuals exhibiting variability in energy-saving strategies ranging from irregular short torpor bouts, regular daily torpor, prolonged torpor of a few days, and hibernation over several weeks as a function of individual variation in fat reserves (Kobbe et al. 2011). Moreover, *M. griseorufus* also exhibits similar dietary flexibility between habitats and seasons (Crowley et al. 2014) that the relative ecological success of *M. murinus* is even more enigmatic. Taken together, these patterns of range expansion, ecological flexibility, and potential competitive advantage make this pair of species a particularly interesting system for future studies within the mouse lemur radiation.

### Lessons from *Microcebus berthae*

As M. griseorufus overlaps with M. murinus in the south, so does M. berthae in the west, though with a considerably smaller area of geographic overlap (Schäffler and Kappeler 2014). Detailed field studies are emerging to illustrate that just as with M. griseorufus, M. berthae and M. murinus partition their environment in subtle though biologically meaningful ways. Both species are omnivorous and experience similar seasonal fluctuations in food supply (Schwab & Ganzhorn 2004); nonetheless, they exhibit fine-grained differences in annidation. Feeding niche overlap is high in terms of food categories, but stable isotope analyses revealed niche differentiation in fruit and animal matter ( $\delta^{15}N$ ), but not in basal resources ( $\delta^{13}C$ ) (Dammhahn and Kappeler 2010; Dammhahn and Kappeler 2014). M. berthae is more insectivorous and has a narrower feeding niche than M. murinus, which includes more fruits and gum in its diet (Dammhahn and Kappeler 2008a), resulting in different intra-specific competitive regimes and spatial requirements (Dammhahn and Kappeler 2010). In addition, M. berthae does not hibernate and is less able

to use spontaneous torpor than *M. murinus* (Ortmann et al. 1997; Schmid et al. 2000). These studies lend further support to the notion of a strong propensity for *M. berthae* and *M. murinus* to partition the environment spatially by microhabitat, with the two species showing a non-overlapping "checkerboard" pattern of spatial segregation in sympatry (Schwab and Ganzhorn 2004), and with *M. berthae* occupying home ranges nearly twice as large as those of *M. murinus* (Dammhahn and Kappeler 2005). More recent analyses indicate that the distribution and abundance of the two mouse lemur species may also depend on that of other cheirogaleid members of their local community, with *Cheirogaleus medius* locally displacing *M. murinus* and *Mirza coquereli* acting as an opportunistic predator of *M. murinus* (Schäffler et al. ms.). Thus, coexistence of mouse lemurs here and elsewhere may also be stabilized by additional factors and species.

#### Lessons from *Microcebus ravelobensis*

Perhaps the most intensively studied of the areas of species overlap is that in the far northwest of Madagascar where *M. murinus* and *M. ravelobensis* occur sympatrically. A range of behavioral differences diagnoses the two species. Spatially, densities of *M. murinus* have been shown to increase with altitude while those of *M. ravelobensis* decrease (Rakotondravony and Radespiel 2009). And, as with the other two species comparisons, detailed ecological studies have shown distinct differences in microhabitat choice and species-specific patterns of spatial distribution (Rendigs et al. 2003), including choice of nest site type and composition of nesting groups. Whereas *M. murinus* tends towards female-only sleeping groups, *M. ravelobensis* is more likely to show mixed sex sleeping groups (Radespiel et al. 2003). Dietary distinctions are also detectable, though they are subtle (Radespiel et al. 2006; Sehen et al. 2010; Thoren et al. 2011b). In direct interactions, *M. murinus* is dominant when paired with *M. ravelobensis*, despite a lack of a significant size difference (Thoren et al. 2011a).

Surprisingly, *M. ravelobensis* also appears to violate at least two of the "rules" that govern mouse lemur behavior. Whereas studies of other species (primarily, of *M. murinus*) consistently show patterns of a strong bias towards male dispersal and female philopatry (Schliehe-Diecks et al. 2012), male dispersal in *M. ravelobensis* is significantly delayed

(Radespiel et al. 2009). The greatest surprise, however, relates to female dominance. Whereas behavioral studies of all other mouse lemur species show strong patterns of female dominance, *M. ravelobensis* does not (Eichmueller et al. 2013). Whether and how these behavioral differences contribute to species coexistence remains to be explored in more detail.

#### Now what?

The section above will, we hope, convince the reader that the remarkable taxonomic proliferation of mouse lemur species has biological merit. It appears that these animals are using an array of behavioral, dietary, physiological, and signaling mechanisms to divide up their world and maintain their separate evolutionary trajectories, thus destined for unique evolutionary endpoints. But many challenges remain towards fully comprehending this fascinating species radiation. Their diminutive size, nocturnal habits, and remote geographic distribution require determined and sometimes extraordinary effort on the part of field biologists who wish to study these petit primates. We predict that the coming years will continue to provide rich insight into the unique ecological and behavioral traits of these animals that in turn will further inform our understanding of the mechanisms that have driven and continue to maintain species boundaries.

But what can be done immediately, and over the coming few years, to deepen our understanding of species diversity, not just of mouse lemurs, but of the entire cheirogaleid clade? As was predicted by Jones (1997), genetic data have opened up a previously obscured world of biodiversity in the cryptic mouse and dwarf lemur radiations. Presently, these studies provide a very lopsided view of rampant speciation on one branch in the clade (i.e., the mouse lemurs) and virtual evolutionary stasis in others (e.g., *Allocebus*). This begs for further exploration. Is it a function of intrinsic biology? Do mouse lemurs have some innate genomic or phenotypic properties that predispose them to divergent speciation? Or is it rather a function of sampling bias and experimental approach?

Recent work focused on the dwarf lemurs (genus *Cheirogaleus*) appears to suggest the latter, at least to some appreciable extent. Thiele et al. (2013) forcefully make the case that taxonomic partitioning can strongly influence interpretations of species range limits and genetic diversity among any number of other important measures of biodiversity. By directly comparing homologous data within the same analytical framework for mouse and dwarf lemurs (e.g., see their Figure 4), these authors are able to make a strong case for claiming either that mouse lemur diversity is overestimated, or dwarf lemur diversity is underestimated. We suspect that the most likely explanation is "a bit of both". Accordingly, the conclusion must be drawn that much work lies ahead before we can claim that the full diversity of the cheirogaleid clade is known.

So how do we proceed? From the earliest phases of "mouse lemur mania" there have been repeated calls for an integrative approach to species discovery, one that takes into account morphology, behavior, ecology, sensory signaling, geography, and autosomal as well as sexlinked genetic loci (e.g., Heckman et al. 2006; Markolf et al. 2011; Weisrock et al. 2010; Yoder et al. 2005; Yoder et al. 2000; Zimmermann and Radespiel 2014). The collection of behavioral and ecological data is arduous and time-consuming, however, with results slow to emerge. We therefore make the urgent call that the community of scientists interested in species discovery within this fascinating clade of primates adopt a uniform genetic "toolkit" such that each individual, population, and putative species can be examined within a general and universal framework, much as has been recently illustrated in the Thiele et al. (2013) study. Moreover, when depositing genetic data, investigators should be assiduous in also depositing their aligned matrices. It is well understood that the process of sequence alignment is rife with assumptions. When investigators are required to download individual gene sequences, concatenate and align them, assumptions made (either computationally or by eye) can impact downstream results, especially with regard to the estimation of branch lengths in phylogenetic analysis --- the very evidence upon which so many species hypotheses have been founded (e.g., Thiele et al. 2013; Weisrock et al. 2010; Yoder et al. 2000). If such standards can be developed and implemented, we can enter a new era of analysis wherein investigators work as a community, united in the goals

of biodiversity discovery and conservation of the Cheirogaleidae as a whole. This approach will be both collegial and scientifically rigorous.

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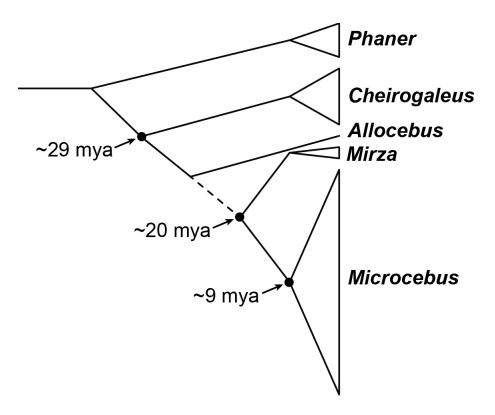
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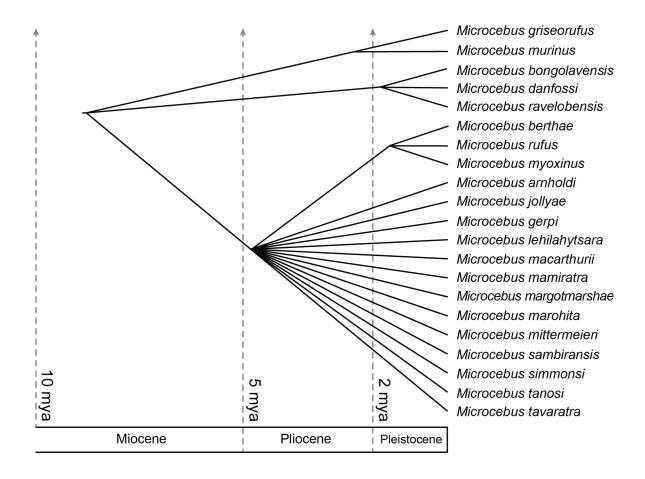
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**Figure 1.** A generalized phylogeny for the Cheirogaleidae. Relationships among genera represent a consensus across multiple phylogenetic studies. Branches within multi-species genera are collapsed for simplicity, with clade size proportional to taxonomic diversity. Branch lengths are not proportional to time due to a lack of divergence time estimates for nodes involving *Allocebus* and *Phaner*. Mean estimated divergence times are presented for some nodes (Yang and Yoder, 2003; Yoder and Yang, 2004; Thiele et al., 2013). The dashed line highlights the fact that, in the multilocus study of Weisrock et al. (2012), the number of gene trees that support the *Mirza-Microcebus* clade is roughly similar to the number of gene trees supporting an alternative placement of *Allocebus* and *Microcebus* in a clade. In contrast, all remaining branches received support from the majority of sampled loci.



**Figure 2.** A phylogeny depicting our current best understanding of phylogenetic relationships within *Microcebus*. As the figure indicated, considerable uncertainty remains regarding the interrelationships among mouse lemur species. Branches are scaled to be proportional to time.

Table 1 Evidence for and history of taxonomic revisions to the genus  $\it Microcebus$  (mouse lemurs)

Latin binomial	Common	Original	Synonyms/Revisions	Publication
	name	evidence		
M. murinus	Gray mouse lemur	morphology		Miller (1777)
M. rufus	Brown mouse lemur	morphology	M. smithii (Gray, 1842)	Geoffroy (1834)
M. myoxinus	Pygmy mouse lemur	morphology	(Peters, 1852)	Schmid & Kappeler (1994)
M. ravelobensis	Golden-brown mouse lemur	morphology		Zimmerman et al. (1998)
M. tavaratra	Northern rufous mouse lemur	morphology		Rasoloarison et al. (2000)
M. sambariensis	Sambirano mouse lemur	morphology		Rasoloarison et al. (2000)
M. griseorufus	Reddish-grey mouse lemur	morphology	Kollman (1910)	Rasoloarison et al. (2000)
M. berthae	Madame Berthe's mouse lemur	morphology	M. myoxinus (Schmid & Kappeler, 1994))	Rasoloarison et al. (2000)
M. griseorus		morphology		Rasoloarison et al. (2000)
M. lehilahytsara	Goodman's mouse lemur	morphology; mtDNA		Roos & Kappeler (2005)
M. mittermeieri	Mittermeier's mouse lemur	morphology; mtDNA		Louis et al. (2006)
M. jollyae	Jolly's mouse lemur	morphology; mtDNA		Louis et al. (2006)
M. simmonsi	Simmons' mouse lemur	morphology; mtDNA		Louis et al. (2006)
M. mamiratra	Claire's mouse lemur	morphology; mtDNA	M. lokobensis (Olivieri et al., 2007)	Andriantompohavana et al. (2006)
M. margotmarshae	Margot Marsh's mouse lemur	morphology; mtDNA		Andriantompohavana et al. (2006)
M. bongolavensis	Bongolava mouse lemur	morphology; mtDNA		Olivieri et al. (2007)
M. danfossi	Danfoss' mouse lemur	morphology; mtDNA		Olivieri et al. (2007)
M. lokobensis	Lokobe mouse lemur	morphology; mtDNA	M. mamiratra (Andriantompohavana et al., 2006)	Olivieri et al. (2007)
M. arnholdi	Arnhold's mouse lemur	morphology; mtDNA		Louis et al. (2008)

M. spp.		morphology; mtDNA	Radespiel et al. (2008)
M. macarthurii	MacArthur's mouse lemur	morphology; mtDNA	Radespiel et al. (2008)
M. gerpi	GERP's mouse lemur	morphology; mtDNA	Radespiel et al. (2012)
M. marohitra	Marohitra mouse lemur	morphology; mtDNA; nDNA	Rasoloarison et al. (2013)
M. tanosi	Anosy mouse lemur	morphology; mtDNA; nDNA	Rasoloarison et al. (2013)

**Note**: All species descriptions take geographic distributions into account as evidence for species designation.

Table 2 Evidence for and history of taxonomic revisions to the genus *Cheirogaleus* (dwarf lemurs)

Latin binomial	Common name	Original evidence	Publication	
C. medius	fat-tailed dwarf lemur	morphology	Saint-Hilaire (1812)	
C. adipicaudatus	southern at-tailed	morphology	Grandidier (1868)	
	dwarf lemur			
C. major	greater dwarf lemur	morphology	Saint-Hilaire (1812)	
C. crossleyi	furry-eared dwarf	morphology	Grandidier (1870)	
	lemur			
C. sibreei	Sibree's dwarf lemur	morphology	Forsyth Major (1896)	
C. ravus	greater iron gray	morphology	Groves (2000)	
	dwarf lemur			
C. minusculus	lesser iron gray dwarf	morphology	Groves (2000)	
	lemur			
C. lavasoensis	Lavasoa dwarf lemur	morphology; mtDNA;	Thiele et al. (2013)	
		nDNA		

**Note**: All species descriptions take geographic distributions into account as evidence for species designation.