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How many genera and species of woolly monkeys (Atelidae, Platyrrhine, Primates) are there? The first molecular analysis of *Lagothrix flavicauda*, an endemic Peruvian primate species



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ABSTRACT

We sequenced COI and COII mitochondrial genes of 141 Neotropical woolly monkeys to provide new insights concerning their phylogeography and phylogenetic relationships. For the first time, eight individuals of the endemic and extremely rare Peruvian yellow-tailed woolly monkey (flavicauda) were sequenced at these genes and compared with other Lagothrix taxa (poeppigii, lagotricha, lugens and cana). There were four main results. (1) L. flavicauda showed a gene diversity of zero, whereas poeppigii and lugens showed high levels of gene diversity and lagotricha and cana showed more modest levels of gene diversity. The absence of gene diversity found for L. flavicauda strongly supports that it is one of the 25 more endangered primates on earth; (2) Our genetic distance and phylogenetic analyses, which included many cases of genetic introgression and recent hybridization, suggest that all woolly monkeys could be included in one unique genus, Lagotrix, divided into two species: L. flavicauda and L. lagotricha. The last species is divided into at least four subspecies. Our molecular results agree with Fooden's (1963) classification, but do not support the classification proposed by Groves (2001). (3) Poeppigii was the first taxon within L. lagotricha to experience a mitochondrial haplotype diversification, while cana and lagotricha experienced more recent mitochondrial haplotype diversification; (4) Poeppigii and lagotricha were the taxa which showed the greatest evidence of population expansions in different Pleistocene periods, whereas lugens experienced a population declination in the last 25,000 YA.

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1. Introduction

Lagothrix (E. Geoffroy, 1812) is one of four Neotropical Primate genera of the Atelidae family—containing the largest living primates in Latin America. These primates have distinct thick woolly fur (woolly monkeys), strong prehensile tails and occupy a critically important niche linked to the successful dispersal and recruitment of trees (Levi and Peres, 2013). Thus, their conservation is of prime concern, not just for sake of the woolly monkeys themselves, but also for the preservation of Amazonian forests. Rightly so, conservation biology depends on the identification and description of species and agreed upon taxonomic categories. However, unfortunately, there is general disagreement among primatologists over the taxonomy of Lagothrix. It is our intention to resolve this debate by the presentation of new molecular findings.

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Here, we begin with a brief review of the literature regarding taxonomic characters of *Lagothrix*. A more detailed review along with references are provided in Table 1. Fooden (1963) determined that this genus was integrated by two species: *L. flavicauda* (yellow-tailed woolly monkey), an endemic species in Peru, and *L. lagotricha* (Humboldt's woolly monkey), distributed in Colombia, Venezuela, Ecuador, Peru, Brazil and recently discovered in Bolivia (Wallace and Painter, 1999).

Ever since Alexander von Humboldt provided the first description of the yellow-tailed woolly monkey in 1812, there have been consistent changes in its taxonomy. During this time it has been redefined, placed together with *Ateles*, separated from *L. lagotricha*, and even considered as a full genus (Table 1). These variations in taxonomy may be due to the lack of molecular data needed to help determine the relationship of *flavicauda* with other *Lagothrix* and *Atelidae* taxa.

Taxonomic questions of this species are further complicated because of the difficulty in finding samples. It has a very limited

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Table 1Chronology of taxonomy regarding the yellow-tailed woolly monkey.

Date	Author(s)	Summary
1812	von Humboldt	Analyzed skins and determined yellow-tailed woolly monkey to be Simia flavicauda
1927(a,b)	Thomas	Redefined the yellow-tailed woolly monkeys as Oreonax hendeei
1963	Fooden	Combined Simia flavicauda and Oreanax hendeii into a single species called Lagothrix flavicauda
2001	Groves	Based on an examination of skulls from museums, Lagothrix flavicauda is grouped with Ateles and considered separate from Lagothrix lagotricha. Flavicauda was considered a full genus called Oreonax flavicauda
2008(a,b)	Rosenberger	Oreonax is not different from Lagothrax. The yellow-tailed woolly monkey is renamed as Lagothrix flavicauda

geographic distribution in the Peruvian premontane, montane and cloud forests between 1500 and 3000 m above sea level (masl). Many of these areas are inaccessible and the species has an extremely small population size. The species probably has a distribution in the Peruvian Departments of Amazonas, San Martin, Huánuco, Loreto and La Libertad as predicted by an ecological model (Pacheco et al., 2007). However, the species presence has only been verified in two Peruvian Departments, Amazonas and San Martin (DeLuycker, 2007; Shanee et al., 2008). Leo Luna (1989) did report nine locations where this species was present in the 1980s; however, its presence could not be demonstrated in other areas where this species was previously reported during the 1970s and 1980s (Pedro Ruiz Gallo; Yambrasbamba, Gira-Sisa Reserve, Shimbayacu). More recently, DeLuycker (2007) and Shanee et al. (2008) showed a detailed study where this taxon is distributed (Table 2).

No thorough censes have been carried out of this taxon, but Nowak (1999) estimated that there were less than 250 individuals (although this number could be somewhat greater) in the wild.

Also, there are no individuals of this species found in any of the world's public zoos. This species is listed as Critically Endangered by IUCN in 2014 and it is classified as one of the 25 most endangered primate taxa (Mittermeier et al., 2007).

Humboldt's Woolly monkey (*Lagothrix lagotricha*) has also undergone taxonomic changes since its first description by Humbodt in 1812. Its taxonomy is based on Fooden's analysis of 312 specimens (Fooden, 1963). He identified four different subspecies within *Lagothrix lagotricha*: *L. l. lugens*, *L. l. lagotricha*, *L. l. poeppigii*, and *L. l. cana*. Their distributions and phenotypes are described in Table 3. Groves (2001), however, elevated these *L. lagotricha* taxa to the status of different species. Thus, this author considered the existence of two woolly monkey genera, *Oreonax*, with a unique species, *O. flavicauda*, and *Lagothrix* with four species: *L. lugens*, *L. lagotricha*, *L. poeppigii* and *L. cana*.

Only two molecular studies have been published to help resolve the systematics questions regarding the wooly monkeys (Botero et al., 2010; Ruiz-García and Pinedo 2010).

Botero et al. (2010) analyzed 16 samples collected from Colombian zoos. Unfortunately, as often occurs with these kind of samples, the authors could not determine the exact geographical origins of their exemplars. Additionally, only phenotype individuals belonging to lugens and lagothricha were enclosed in their study. The authors sequenced two mitochondrial genes (mtCOII and the mt D-loop), analyzed the karyotypes, and provided three main and important conclusions. They determined that there were no significant differences in the variation of karyotype frequency at chromosomes 4, 7 and 24 between lugens and lagotricha. This finding supported a subspecies status rather than a species status for these Lagothrix taxa. They obtained a similar conclusion when they constructed and analyzed a Bayesian tree with lugens and lagothricha haplotypes intermixed. The authors also detected a very recent split between lugens and lagothricha at the beginning of the Holocene.

Ruiz-García and Pinedo (2010), analyzed the mitochondrial *COII* gene (*mtCOII*) of 97 *Lagothrix lagotricha* specimens, belonging to the

 Table 2

 Geographic distribution of yellow-tailed woolly monkey in Peru.

Distribution	References
 Nine locations within two Peruvian Departments 1. Between Pongo de Rentema and Bagua 2. Two points in the Ulcubamba River 3. Two points between the Chiriago and Mayo Rivers 4. One point west of Chachapoyas 5. One point between Rioja and Mendoza 6. Two points in the Southwestern area of the San Martin 7. Department Frontier with La Libertad near Achiras and Paulina 	Leo Luna (1989)
 Wide areas Three or four regions within two Peruvian Departments (Amazon and San Martin Departments) 1. Colan Cordillera (641 km²) 2. Upper Mayo River (1820 km²) 3. Abiseo River National Park (2740 km²) 4. Maybe, Laguna de los Cóndores 	DeLuycker (2007)
Precise areas • Five locations within the Amazon Department 1. Santa Rosa 2. Shipasbamba 3. Abra Patricia 4. Gocta 5. La Perla de Limasa	Shanee et al. (2008)
 Three locations within the Martin Department 1. Paitoja 2. Colca 3. Nuevo Mendoza 	Shanee et al. (2008)

lugens, lagotricha, poeppigii and cana taxa. This study produced several important findings. Poeppigii and lugens showed the highest levels of gene diversity, whereas lagotricha and cana showed the lowest. The authors also suggested that an ancestor of poeppigii was a possible candidate for the beginning of the diversification of L. lagotricha. They also detected different mitochondrial lineages within poeppigii and lugens and even hybrid individuals between lagothricha and lugens, between lagothricha and poeppigii and between lugens and poeppigii. Also, all of their samples came from the wild and hybridization was considered to be natural among these taxa. Such an interpretation suggests that these taxa are subspecies and not full species as claimed by Groves (2001). The beginning of the mitochondrial haplotype diversification in L. lagotricha began around 2.5 MYA—coinciding with the beginning of the Pleistocene. Lastly, the authors' data supports haplotype diversification within poeppigii and lugens during the first and second Pleistocene glacial periods and the diversification of lagothricha and cana during the third and fourth Pleistocene glaciations. Their results agree quite well with the results reported in the previous mentioned work of Botero et al. (2010). That is, both taxa are subspecies and not full species such as suggested by Groves (2001).

In this study, we sequenced two mitochondrial genes, the cytochrome c oxidase subunits I and II (mt COI and COII). The

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