Articles

Species Status of the Colombian Spider Monkey, *Ateles belzebuth hybridus*

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The species status among various groups of spider monkeys (*Ateles*) was recently determined by comparison of mitochondrial and nuclear DNA variation (Collins and Dubach, in prep. a, c). The traditional pelage-based taxonomy of *Ateles,* as proposed by Kellogg and Goldman (1944), and used by most researchers since that time, was demonstrated to have little or no correlation to the actual genetic relationships among the various species and subspecies of spider monkeys (Collins and Dubach, in prep. a). Overall, the conclusions of Collins and Dubach (in prep. a, b, c), which supported four species of spider monkeys (*A. paniscus, A. belzebuth, A. hybridus* and *A. geoffroyi*), were very similar to those reached by Froehlich *et al.* (1991), with one important exception. (See Figure 1 for distribution and constitution of *Ateles* species.)

This brief communication focuses on that exception, which composed one of the four primary clades discovered by Collins and Dubach (in prep. a) on examination of mitochondrial DNA variation. This clade contained genetic haplotypes referred to previously as *A. belzebuth hybridus* (Kellogg and Goldman, 1944; Konstant *et al.*, 1985; Groves, 1989). *A. b. hybridus* occurs primarily along the Río Magdalena valley of Colombia, with isolated populations in northeastern Colombia and the mountainous regions of northwestern Venezuela around Lake Maracaibo (Kellogg and Goldman, 1944; Hernández-Camacho and Cooper, 1976; Norconk *et al.*, 1996) (Fig. 1).

Investigation of the genetic variation among all *Ateles* haplotypes found no support to group haplotypes described as *A. b. hybridus* with other haplotypes previously classified as *A. belzebuth* based on pelage (Collins and Dubach, in prep. a, c). Genetic investigations (Collins and Dubach, in prep. a, c) also differed from the taxonomy supported by Froehlich *et al.* (1991) by removing *A. b. hybridus* from a clade also containing *A. geoffroyi* and *A. fusciceps.* Froehlich *et al.* (1991) support uniting all trans-Andean forms in one species with various subspecies. Collins and Dubach (in prep. a, c) propose that *A. b. hybridus* is a separate species, *A. hybridus*. Thus, *A. hybridus*, represents the former subspecies *A. b. hybridus* of Kellogg and Goldman (1944), Konstant *et al.* (1985) and Groves (1989) and *A. g. hybridus* of Froehlich *et al.* (1991).

The suggestion that *A. hybridus* is a separate species may have important implications for the conservation of this primate. *A. hybridus* is listed as endangered by Mittermeier *et al.* (1989) and Rylands *et al.* (1997). The IUCN identifies endangered species/subspecies as those with a 20% chance of extinction in the wild in 20 years or five of its generations. *A. hybridus* is threatened by both hunting pressure and habitat fragmentation throughout its present distribution. *Ateles* are found primarily in the top canopy layers of low, humid, primary, evergreen, never-flooded, rainforest at elevations below 800 meters (Hernández-Camacho and Cooper, 1976; Van Roosmalen, 1980; Madden and Albuja, 1987). They are large frugivores with large home range requirements (Milton, 1981). Thus, small isolated forest fragments can rarely support populations of this primate. The combination of habitat destruction, hunting pressure, and a long inter-birth interval can result in small fragmented populations. This seems to represent the present status of *A. hybridus* in Colombia (Hernández-Camacho and Cooper, 1976; Hernández-Camacho and Defler, 1989; Rylands *et al.*, 1997). Uncorrected, the probability that this particular primate will survive in small isolated forest fragments is believed to be very low (Collins and Dubach, in prep. b).

Genetic and Biogeographical Evidence of Species Status

At present the Eastern Cordillera of the northern range of the Andes in Colombia (Haffer, 1987) combined with the Llanos Savannas of Colombia and Venezuela effectively prevent genetic exchange between *A. hybridus* and *A. b. belzebuth* (van der Hammen, 1982; Froehlich *et al.*, 1991; Norconk *et al.*, 1996). The western cordillera of the Andes and the Río Cauca are possible barriers to present day gene flow between *A. geoffroyi (fusciceps)* and *A. hybridus*.

Phylogenetic analysis of mitochondrial (Collins and Dubach, in prep. a) and nuclear DNA (Collins and Dubach, in prep. c) suggests *A. hybridus* forms a monophyletic group without clear ties to any other spider monkey clades (Collins and Dubach, in prep. a). *A. b. hybridus* haplotypes always group together, with high bootstrap support ranging from 92% -100% in parsimony and distance based analyses of mitochondrial regions (Collins and Dubach, in prep. a). The combined phylogenetic analyses for the mitochondrial DNA regions investigated reflect a variety of different, inconsistent relationships between the *A. hybridus* clade and the other primary clades among the various phylogenies. Genetic distances between *A. hybridus* and all other spider monkey populations are the highest observed in the mitochondrial DNA analysis (Collins and Dubach, in prep. a). Thus, no clear relationship of *A. hybridus* populations to any other *Ateles* populations are evident.

Limited nuclear DNA evidence produces a phylogeny which unites haplotypes of *A. hybridus* with 62%-66% bootstrap support (Collins and Dubach, in prep. c). Twenty-one percent of the total variation in the nuclear data set occurs between these haplotypes and those of *A. g. robustus*. Thus, limited evidence exists for the union of these two species as suggested by Froehlich *et al.* (1991), instead supporting *A. hybridus* as a distinct species (Collins and Dubach, in prep.). Based on the current findings, *A. hybridus* appears to constitute a separate species of *Ateles*.

Gene flow between parapatric populations of *A. g. robustus* and *A. hybridus* along the northern reaches of the Río Cauca

Cover photograph by Russell A. Mittermeier: The white-fronted capuchin, *Cebus albifrons* from Colombia.

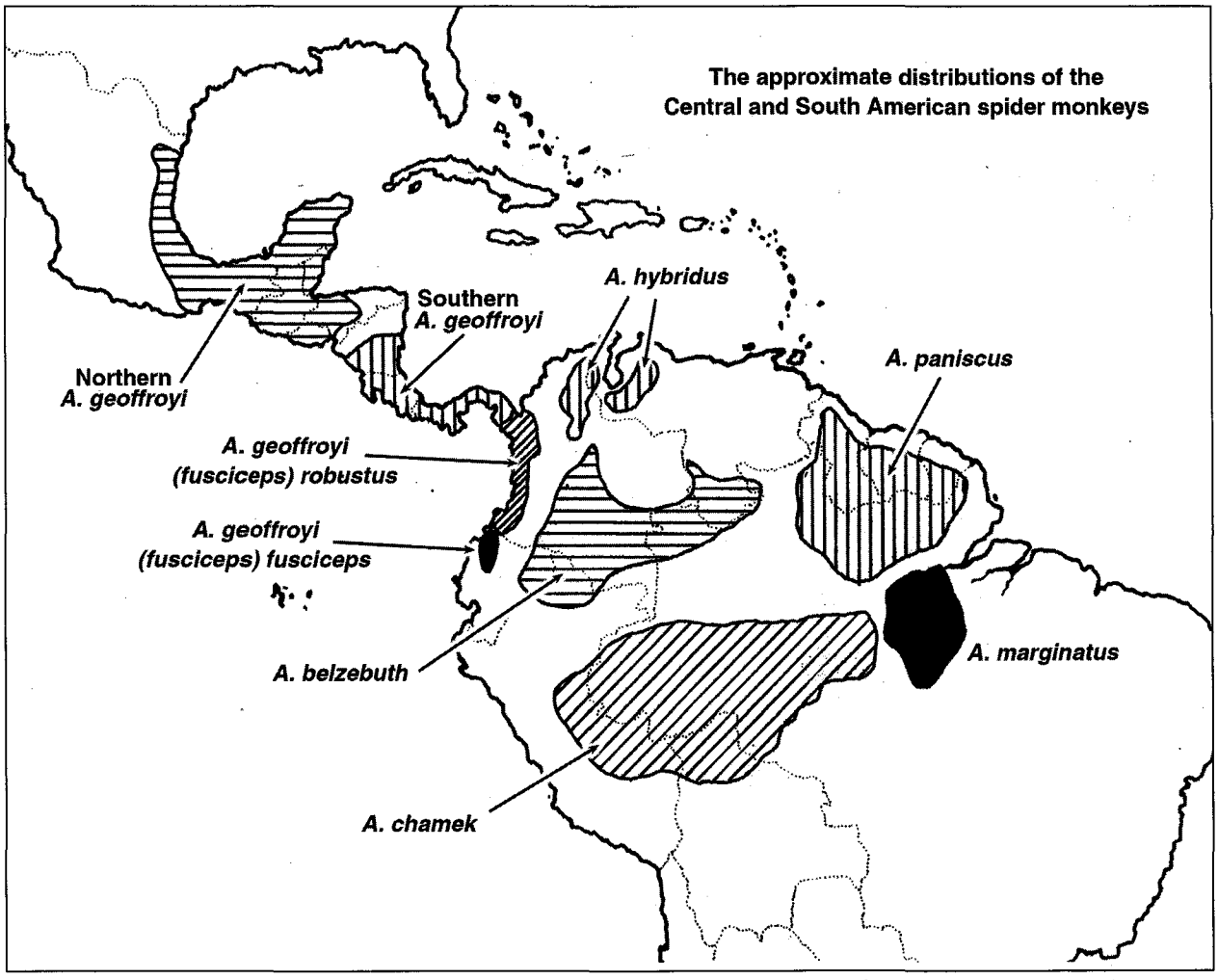

Figure 1. The approximate distributions of the Central and South American spider monkeys, *Ateles*. Map by Stephen D. Nash.

does not seem to occur, even though no obvious geological barriers exist in this region at the present time. A comparison with the taxonomic boundaries of two other primates, *Alouatta seniculus* and *A. palliata*, delineated from one another in this same area (Rowe, 1996) supports the distinction between *A. hybridus* and *A. g. robustus*, as well.

A discussion of biogeographic processes which may have created this species, and which have exerted pressure on all spider monkey populations, are provided in detail by Collins and Dubach (in prep. b). It would appear that the ancestors to *A. hybridus* and *A. geoffroyi* crossed the eastern cordillera of the Andes prior to the complete end of uplift of the chain during the late Pliocene, approximately 3 mya (van der Hammen, 1982; Haffer, 1987; Collins and Dubach, in prep. b). Local molecular clock calculations for all trans-Andean *Ateles* species' last common ancestor of 3.1 mya corroborates this hypothesis (Collins and Dubach in prep. b). Since that time *A. hybridus* has been isolated from *A. belzebuth* through uplift of the eastern cordillera of the Andes and by the Llanos Savannas of Colombia and Venezuela (van der Hammen, 1982; Haffer, 1987).

Spider monkeys apparently migrated into the Isthmus of Panama, and *A. hybridus* has been secondarily isolated from Central American and Choco populations by continued uplift of the western cordillera of the Andes and ecological fluctuations in habitat during the Pleistocene (Collins and Dubach, in prep. b). All *A. hybridus* haplotypes share a last common ancestor 1.4 mya, during the early Pleistocene. It appears there were marked periods of very dry and very wet climates in the middle and upper Magdalena valley during the Pleistocene (van der Hammen, 1982; Haffer, 1987). The lower valley appears to have fluctuated between forest savanna types during drier phases and inundated "floating meadows" during the interstitial periods (van der Hammen, 1982). It is, thus, possible that spider monkeys, with a preference for unflooded, primary forest, may have been pushed back and forth, up and down the valley in response to changing Pleistocene biomes, which effectively kept them isolated from genetic exchange with other spider monkeys (Collins and Dubach, in prep. b).

Conclusions

With a limited geographic distribution, habitat fragmentation, and hunting pressure all acting against this group of spider monkeys, the suggestion that they represent a separate species presents a new challenge to their conservation. Rylands *et al.* (1997) identify eight possible protected areas where *A. hybridus* is thought to occur, but its existence has been confirmed in only three (Rylands *et*

al., 1997). Many of these protected areas are found outside of the traditionally recognized range of *A. hybridus*. Additionally, large areas of available habitat and many spider monkeys will likely be lost with completion of the Urra II dam on the Río San Jorge in Colombia (Rylands *et al.*, 1997). The conclusions from the phylogenetic and biogeographic investigations of *Ateles* (Collins and Dubach, in prep. a, b, c) should be used in conjunction with the proposed new species status of this population of spider monkeys (Collins and Dubach, in prep. a, c) to direct increased attention to conservation efforts aimed at protecting this Neotropical primate.

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New Observations on *Cebus kaapori* Queiroz, 1992, in Eastern Brazilian Amazonia

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Cebus kaapori is a new species of untufted capuchin monkey recently described by Queiroz (1992). It is similar to *Cebus olivaceus*, and data from molecular studies indicate that this new form is differentiated from *C. olivaceus* at no