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## **Short communication**

# Karyotypes of some members of the genus *Cavia* (Rodentia: Caviidae) from Bolivia

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The genus *Cavia* Pallas, 1766 is distributed across South America inhabiting an array of diverse habitats. Six species are currently recognized (Kilpatrick and Woods 2005), however, as with many South American taxa, a thorough understanding of the genus is lacking. Within Bolivia, *Cavia* occupies mesic lowlands, Andean forests, and arid highlands, accordingly, the various forms exhibit a high degree of morphological and phenotypic variation. The paucity of specimens and work on this genus within Bolivia has left the taxonomy and systematics of these forms in an uncertain state.

Cavia nana Thomas, 1917 was described from Yungas forest on the eastern versant of the Bolivian Andes (Dpto. La Paz, Chulumani) based on morphological and phenotypic characters (Thomas 1917) and represents the only named form with its type locality within Bolivia. However, Hückinghaus (1961) synonymized C. nana and C. tschudii sodalis Thomas, 1926 under C. aperea sodalis, stating insufficient differences in cranial morphology. Cabrera (1961), recognized both species for Bolivia, C. t. sodalis in the extreme south and C. nana from the Yungas. Woods (1993) included C. nana in the synonymy of C. aperea but did not include Bolivia in the distributional range. In the most comprehensive treatment of Bolivian

mammals, Anderson (1997) included all Bolivian specimens under the name Cavia tschudii nana. However, he suggested that, "...the species and subspecies assignments for Bolivia must be regarded as quite tentative." Salazar-Bravo et al. (2003) followed suit by also employing the name C. tschudi (sic) nana for the wild forms but included in remarks that "...there appear to be at least two species of wild cavies in Bolivia. However, it is unclear what the appropriate species names may be, or even if any available names would apply..." Most recently, Woods and Kilpatrick (2005) listed C. tschudii as the only Cavia species occurring in Bolivia and included C. nana in the tschudii synonymy but did not recognize it as a valid subspecies. Thus, due to both a lack of understanding of the level of morphological and phenotypic variation within the Bolivian forms, unknown species limits due to unsampled geographic areas, and disagreement of previous authors, there has been a general lack of both systematic and taxonomic resolution.

The aim of this study is to provide further resolution to the understanding of the *Cavia* forms within Bolivia through the addition of karyological data. To date, the little chromosomal information known for the genus comes from Argentinean, Brazilian, and

domestic forms (Tab. 1). Herein, we present the first karyotypes for Bolivian forms, including those for a highland specimen assigned to *C. tschudii*, a specimen from the type locality of *C. nana* from the eastern versant of the Andes and specimens recently assigned to *C. aperea* from the Bolivian lowlands (Spotorno et al. 2004).

Specimens were collected and karyotyped from three Bolivian localities in the departments of Santa Cruz and La Paz, in the summer of 1991 and spring of 2003. These localities incorporated the three major biomes in Bolivia (Altiplano, lowland grasslands, and Andean Yungas forest) where *Cavia* occurs. Voucher specimens are deposited in the Museum of Southwestern Biology, University of New Mexico (MSB and NK), the American Museum of Natural History (AMNH), and the Colección Boliviana de Fauna (CBF). Karyotypes, tissues, and other ancillary data are deposited in the MSB.

The catalog numbers, specific localities and the habitats they represent are as follows: AMNH 264468, Santa Cruz, 3 km N by road of Torrecillas, 17°51′S, 64°38′ W, 2625 m. (Altiplano); MSB 67330, Santa Cruz, Noel Kempff Mercado National Park, 6 km S of camp Los Fierros, 14°34′30″S, 60°52′ 45″W, ca. 450 m (Lowland grasslands); and NK 116565, La Paz, Sud Yungas, Apa Apa, 16°22′31″S, 67°30′53″W, 1605 m (Andean Yungas forest).

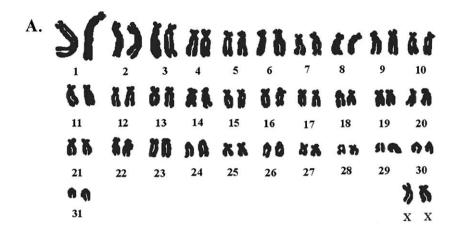
Chromosome preparations were obtained from bone marrow following procedures outlined in Anderson et al. (1987) for the Altiplano and lowland specimens and according to Patton (1967) for the Yungas specimen. Conventionally stained karyotypes were obtained for all specimens. Diploid number was calculated on a minimum of 20 equal numbered metaphase spreads per animal. Chromosome morphology and fundamental number (FN) designation followed Patton (1967). Autosomal FN for the lowland and Yungas specimens were based on examination of a minimum of 10 photographed metaphase spreads, while only three spreads were of sufficient quality in the C. tschudii specimen.

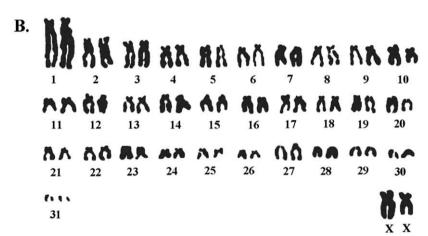
The three specimens above, as well as four additional lowland specimens (AMNH 264466, 264467, MSB 67331, CBF 2188) which were examined only for diploid number, exhibited a 2N complement of 64 (Fig. 1) as is common for the genus (Tab. 1), but see Cherem et al. (1999) for the lone exception. Variation in chromosome morphology resulting in two distinct FN values was found. The lowland C. aperea and Yungas karyotypes displayed an equal FN of 114 and were composed of 26 submetacentric or subtelocentric pairs and five acrocentric pairs. The Altiplano C. tschudii karvotype differed in chromosome morphology of between three and five chromosome pairs. That is, the

Table 1. Reported	karvotynes	of charies	of the	applie Co	wia
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Species	2 <i>N</i>	FN*	Locality	Source
C. a. aperea	64	116	Brazil: Pernambuco	Maia (1984)
C. a. pamparum	64	124	Argentina: Entre Rios	George et al. (1972)
C. a. pamparum	64	124	Brazil: Parana and Rio de Janeiro	Referenced in Gava et al. (1998), Maia (1984)
C. fulgida	64	124	Brazil: Parana and Rio de Janeiro	Referenced in Gava et al. (1998), Maia (1984)
C. magna	64	124	Brazil: Rio Grande do Sol	Referenced in Gava et al. (1998), Maia (1984)
C. intermedia	62	108	Brazil: Santa Catarina; Molegues do Sul Islands	Cherem et al. (1999), Gava et al. (1998)
Domestic quinea pig	64	90	Laboratory bred	Cohen and Pinsky (1966)
Domestic guinea pig	64	94	Laboratory bred	Awa et al. (1959)

<sup>\*</sup>FN values given are for autosomal chromosomes, Gava et al. (1998) assigned a FN=112 for C intermedia by including the female sex chromosomes.





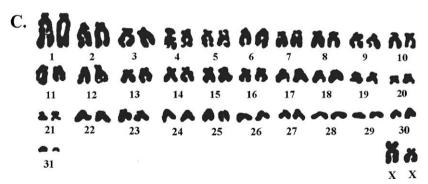


Fig. 1. Standard karyotypes of *Cavia* from 3 localities in Bolivia. (A) *Cavia nana* topotype (NK 116565) 2N=64, FN=114. (B) *Cavia aperea* (MSB 67330) 2N=64, FN=114. (C) *Cavia tschudii* (AMNH 264468) 2N=64, FN=104-108.

highland karyotype contained 21–23 submetacentric or subtelocentric pairs and eight to 10 acrocentric pairs. Two pairs could not be classified as either subtelocentric or acrocentric, resulting in a FN ranging from 104 to 108. All three forms had medium submetacentric X chromosomes. The Y chromosome of the *C. tschudii* specimen was a small submetacentric, no males from the lowlands or Yungas were karyotyped.

Two karyotypic forms have been reported previously for *C. aperea* subspecies. These include a FN=116 (27 biarmed, 4 acrocentric), described by Maia (1984) in specimens from Pernambuco, Brazil and assigned to the nominate subspecies *C. a. aperea* Erxleben, 1777, and those with a fully biarmed complement and FN=124 from Entre Ríos, Argentina for *C. a. pamparum* Thomas, 1901 (George et al. 1972). The Bolivian lowland and Yungas karyotypes appear most similar to that of the nominate subspecies from Brazil, differing only in gross morphology of a single chromosome pair.

While no other karyotypes of highland forms are available for comparison, the Bolivian C. tschudii karyotype is clearly distinct from not only the other Bolivian forms but also from all other published Cavia karyotypes (Tab. 1), exhibiting the lowest FN among investigated non-domestic Cavia forms. Only C. intermedia Cherem, Olimpio, and Ximenez, 1999, with a lower diploid number (2n=62), and the domesticated guinea pig (Awa et al. 1957; Cohen and Pinsky 1966) have equal or lower FN values. While addressing the domestication issue is not the aim of this study, when deriving the karyotype of the domestic guinea pig from that of a wild form,

the *C. tschudii* karyotype represents the path of fewest changes, a relationship with strong support based on molecular data as well (Spotorno et al. 2004) but see Trillmich et al. (2004) for an alternate hypothesis.

These results provide support for the presence of both *C. tschudii* and *C. aperea* within Bolivia and suggest that the Yungas form may be more closely allied with the lowland *C. aperea* group than with *C. tschudii* of the highlands. While the addition of these new karyotypic data serve to fill some important gaps in our chromosomal knowledge, a more robust phylogeny of the genus and additional chromosomal information on highland forms is needed before we can assess the utility of karyotypic information in helping to define species limits or propose hypotheses regarding chromosomal evolution within this group.

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