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Short communication

The Bolivian bamboo rat, *Dactylomys boliviensis* (Rodentia: Echimyidae), a new record for chromosome number in a mammal

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The family Echimyidae, a highly diverse group of rodents, occurs throughout most of Central and South America. There are 16 recent genera and about 70 living species (Woods 1993), however, new taxa continue to be described (e. g., Da Silva 1998; Patton et al. 2000). To date no comprehensive phylogenetic analysis is available for the group although great advances have been forthcoming (e. g., Lara et al. 1996; Patton et al. 2000). The group is highly diversified ecologically and has had a long evolutionary history in South America (Patterson and Pascual 1972; Woods 1982). Karyologically, less than half of the species have been analyzed but it is known that there is considerable variation in diploid (from 2n = 14 to 2n = 96) and fundamental numbers (from FNa = 18 to FNa = 144) (Tab. 1). One of the most specialized groups within the Echimyidae is the subfamily of bamboo rats (Dactylomyinae). Woods (1993) placed three genera in the subfamily Dactylomyinae; *Dactyloms*, *Kannabateomys*, and *Olallamys*. The biology and evolutionary relationships of the Dactylomyinae are poorly known, likely due to their rarity to collectors and subsequent scarcity in museum collections. What is known is well summarized in Patton et al. (2000). Until recently (Aniskin 1993) no information on the chromosomal complement of any member of this group was available.

As part of a long-term survey of the mammals of Bolivia, many new and important records for the country were collected (Anderson 1997). In July of 1992 and May of 1996, we took a total of five specimens of *Dactylomys boliviensis* (Bolivian bamboo rat) from a locality in the Yungas of La Paz (Salazar et al. 1994). Here we report the karyotype of this species, the highest chromosomal number known in a mammal.

The individuals were located and collected at night in a dense stand of bamboo and secondary growth within the village of La Reserva (Departamento La Paz, Nor Yungas, La Reserva, elev. 840 m, 15° 44′ S, 67° 31′ W) by following their distinctive calls and eye shine. The village of La Reserva lies along Rio La Reserva, a small tributary of the Caranavi River. The village is at the bottom of a valley in the subtropical montane forest that covers most of the eastern Andean slopes between 15° and 17° S latitude in the Cordillera Oriental of Bolivia. The foothills at this elevation are cov-

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Fig. 1. Standard karyotype of *Dactylomys boliviensis*.

ered with semi-deciduous vegetation intermingled with columnar cacti and bromeliads. The forest is drier and sparser than at higher elevations. Compared to forests at higher and lower elevations, the trees are smaller, more highly branched, and most grow in open sun. The east facing slope above the river is steep, with much vegetation, some secondary growth, and banana and tangerine cultivation. Palms and tree ferns are absent (Salazar et al. 1994).

Chromosomal preparations were obtained using the technique described in Anderson et al. (1987). Metaphase cells were photographed and scored to determine the diploid (2n) and fundamental numbers (FNa). One of us (JLD) scored 5 slides per animal and over 20 spreads per slide to determine chromosome numbers. The analysis of the morphology of the chromosomes was based on 10 metaphase plates from three individuals. Nomenclature for chromosome morphology and fundamental number follows Patton (1967).

Chromosome slides, tissue samples, and cell suspensions are deposited in the Division of Biological Materials, Museum of Southwestern Biology (MSB). Voucher specimens are deposited at MSB (MSB 68547, MSB 85627, NK 40537), the American Museum of Natural History (AMNH 264887, 264884), and the Colección Boliviana de Fauna (CBF 2608), in La Paz, Bolivia.

The standard karyotype of *Dactylomys boliviensis* is highly asymmetrical, composed of 26 pairs of metacentric or sub-metacentric autosomes and 32 pairs of acrocentric autosomes. The X chromosome is a large sub-metacentric and the Y chromosome is a medium sub-metacentric. The resulting karyotype has a diploid count of 2n = 118 and FNa of 168 (Fig. 1). Chromo-

Table 1. Diploid (2n) and fundamental number (FN) for members of the family Echimyidae.

Taxon	2n	FN	Reference
Dactylomys boliviensis	118	168	this report
Dactylomys dactylinus	94	144	Aniskin (1993)
Echimys blainvillei	50	94	Reig (1989)
Echimys dasythrix	96	102	Lima et al. (1998)
Echimys semivillosus	94	134	Aguilera et al. (1998)
Echimys sp.	90	108	Lima et al. (1998)
Echimys sp.	90	110	Aniskin (1993)
Echimys sp.	90	112	Reig (1989)
Isothrix bistriata	60	116	Patton et al. (2000)
Isothrix bistriata	60	120	Lima et al. (1998)
Isothrix pagurus	22	38	Patton and Emmons (1985)
Isothrix sinnamariensis	28	42	Vie et al. (1996)
Makalata armata	70	120	Lima et al. (1998)
Makalata didelphoides	66	106	Lima et al. (1998)
Clyomys laticeps	34	60	Reig (1989)
Euryzygomatomys guiara	46	82	Aniskin (1993)
Euryzygomatomys spinosus	46	92	Reig (1989)
Hoplomys gymnurus	46		Aniskin (1993)
Lonchothrix emiliae	60	116	Aniskin (1993)
Mesomys hispidus	60	120	Lima et al. (1998)
Mesomys hispidus	60	116	Patton et al. (2000)
Mesomys occultus	42	54	Patton et al. (2000)
Proechimys albispinus	60	116	Leal-Mesquita et al. (1992)
Proechimys amphicoricus	26	44	Reig (1989)
Proechimys brevicauda	28–30	48–50	Gardner and Emmons (1984)
Proechimys canicollis	24	44	Gardner and Emmons (1984)
Proechimys cuvieri	28	46	Maia and Langguth (1993)
Proechimys decumanus	30	54	Gardner and Emmons (1984)
Proechimys echinothrix	32	69	Patton et al. (2000)
Proechimys gardneri	40	56	Patton et al. (2000)
Proechimys goeldii	24	44	Patton et al. (2000)
Proechimys guiarae	44–50	72–76	Gardner and Emmons (1984)
Proechimys gularis	30	48	Gardner and Emmons (1984)
Proechimys guyannensis	40	54–56	Gardner and Emmons (1984)
Proechimys iheringi	62–65	117–124	Reig (1989)
Proechimys kulinae	34	52	Patton et al. (2000)
Proechimys mincae	48	68	Gardner and Emmons (1984)
Proechimys oconnelli	32	52	Gardner and Emmons (1984)
Proechimys oris	30	52–56	Gardner and Emmons (1984)
Proechimys pattoni	40	56	Patton et al. (2000)
Proechimys poliopus	42	76	Gardner and Emmons (1984)
Proechimys quadruplicatus	28	44	Gardner and Emmons (1984)
Proechimys semispinosus	30	50–54	Gardner and Emmons (1984)
Proechimys simonsi	32	58	Gardner and Emmons (1984)
Proechimys steerei	24	42	Gardner and Emmons (1984)
Proechimys trinitatus	62	80	Gardner and Emmons (1984)
Proechimys urichi	62	88	Gardner and Emmons (1984)
Proechimys yonenagae	54	104	Leal-Mesquita et al. (1992), Rocha (1995)
Proechimys sp.	34	56	Aniskin (1993)
Proechimys sp.	14–16	18	Reig (1989)
Proechimys sp. (Balta)	40	56	Reig (1989)
Proechimys sp. (Barinas)	62	74	Gardner and Emmons (1984)
Thricomys aperoides	26	48	Leal-Mesquita et al. (1993)
Thricomys aperoides	30	54	Reig (1989)
Thricomys aperoides	30	50	Aniskin (1993)

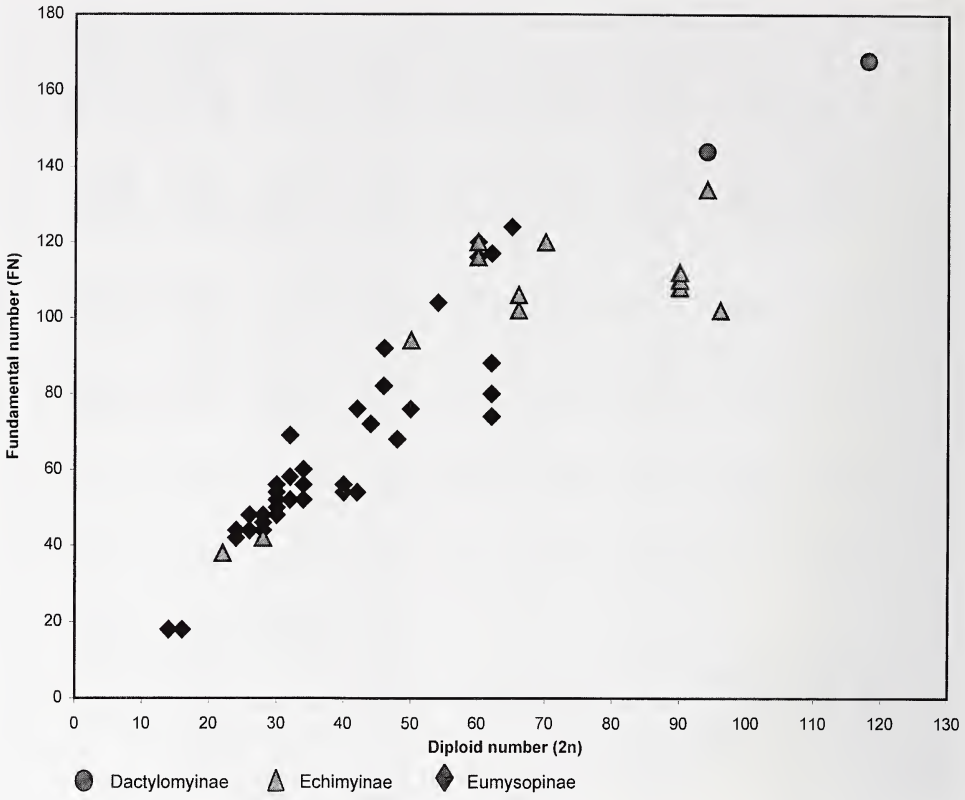

Fig. 2. Karyogram of known echimyid karyotypes.

some pair nine exhibits the characteristic satellite chromosome found in other echimyid rodents.

No chromosomal information is available for *Kannabateomys*, *Olallamys*, or *D. peruanus*. Aniskin (1993) described the karyotype of *D. dactylinus* (2n = 94, Fn = 144) from the Loreto Department in Peru. The karyotype of *D. boliviensis* differs from that of *D. dactylinus* by the presence of one additional set of meta or sub-metacentric pairs, and 10 pairs of acrocentric chromosomes although comparisons are difficult due to the fact that Aniskin (1993) did not identify sex chromosomes. At least 14 Robertsonian rearrangements would be necessary to transform the karyotype of one species into the other.

We compiled a list of all species of echimyid rodents for which data were available (Tab. 1) and created a karyograph (Iami and Crozier 1980) based on chromosomal and fundamental numbers (Fig. 2). A definite pattern of subfamily grouping is clear where two species of *Dactylomys* assume the highest positions on the plot and the echimyine rodents (*Echimys*, *Makalata*, *Isothrix*) are positioned at an intermediate level (with the exception of *I. pagurus* and *I. sinnamariensis*). The most speciose and karyologically studied group is the Eumysopinae (represented in this sample by *Proechimys*, *Clyomys*, *Euryzygomatomys*, *Hoplomys*, *Lonchothrix*, *Mesomys*, and *Trichomys*). For the most part these fall at the lower end of (Fig. 2). To date, no eumysopids have been found with a $2n > 65$.

Lima et al. (1998) proposed that Robertsonian rearrangements were more important in the evolution of the karyotype of arbo-

real echimyids than other chromosomal rearrangements because karyotypes of this group appeared to show higher levels of variation in diploid numbers than in fundamental numbers. Our data do not support Lima et al. (1998). We found statistically significant differences in the levels of variation between diploid and fundamental number for the arboreal echimyids (Kruskal-Wallis; $P < 0.004$), terrestrial echimyids (One-way ANOVA; $\alpha = 0.05$; $P < 0.004$), and for the entire echimyid radiation (Kruskal-Wallis; $P < 0.001$). However, in all cases the fundamental number varied more than the diploid number, suggesting that pericentric inversions may be more common. None the less it is quite likely that several processes may have influenced the evolution of the karyotype in this group.

Prior to our results, the highest chromosome number reported for a mammal was $2n = 102$ in *Tympanoctomys barrerae* (Contreras et al 1990). These authors also suggested that the family Octodontidae presented the greatest chromosomal diversity. While this remains true for Fundamental number, the Echimyidae now represent the family with the greatest diversity in diploid number ($2n = 14$ to $2n = 118$).

Although *Tympanoctomys* and *Dactylomys* represent terminal branches in two different families of South American hystricognath rodents with a long history on this continent, they also share another characteristic: both occupy restricted ecological niches and posses highly specialized life history traits. We concur with Contreras et al. (1990) in suggesting that the high chromosomal count appears to be a derived character.

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