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KARYOTYPES OF THE LONG-TAILED VOLE (*MICROTUS LONGICAUDUS*) IN ISOLATED MOUNTAIN RANGES OF THE AMERICAN SOUTHWEST

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ABSTRACT.—The long-tailed vole (*Microtus longicaudus*) exhibits karyotypic variation in western North America. In the American Southwest, the species has a disjunct, relict distribution. However, karyotypes obtained from 20 specimens in 5 isolated mountain ranges (White Mountains, Arizona; Mount Taylor and the Sangre de Cristo, Jemez, and Mogollon mountains, New Mexico) exhibited no variation. These and previously reported karyotypes from the region had a diploid number (2n) of 56 and fundamental number (FN) of 84, which is the most commonly reported karyotype for the species.

Key words: long-tailed vole, *Microtus longicaudus*, chromosome, karyotype, American Southwest.

The long-tailed vole (*Microtus longicaudus*) is broadly distributed throughout western North America from Alaska south to southern California, Arizona, and New Mexico (Hall 1981, Smolen and Keller 1987). Whereas most species of voles (*Microtus*) from the North American mainland have a unique but invariant karyotype, considerable variation in chromosomal complement has been found in populations of *Microtus longicaudus* from the western United States. (Judd and Cross 1980; Table 1). The most widespread and commonly reported karyotype consists of 10 pairs of large- to medium-sized metacentric or submetacentric chromosomes, 12 pairs of large to small acrocentrics or subtelocentrics, and 5 pairs of small metacentric chromosomes (diploid number [2n] = 56; fundamental number [FN] = 84). This form has been found in southeastern Washington, northwestern Oregon, Colorado, New Mexico, and Arizona (Matthey 1955, Hsu and Benirschke 1969, Judd and Cross 1980). Deviations from the 2n = 56 form have been found in the Cascade Range in southern Oregon and northern California (2n = 57, 58, 59, 62, 66, and 70; Judd and Cross 1980), and also in northern Utah (2n = 64; Modi 1985). These chromosome morphologies were similar to the 2n = 56 form except for the presence of 1–14 minute metacentric B chromosomes. Judd and

Cross (1980) also reported a pericentric inversion resulting in the absence of one pair of small acrocentric chromosomes and the presence of an extra pair of small metacentric chromosomes in populations from the Cascade Range (Table 1).

Microtus longicaudus reaches its southeastern range limits in the American Southwest (Hall 1981). There it is discontinuously distributed on isolated mountaintops, where it inhabits mesic coniferous forests (Smolen and Keller 1987). This distribution pattern was a product of post-Pleistocene vicariant fragmentation of formerly widespread coniferous forest habitats as a result of climatic warming (Frey et al. 2007). As a result of this isolation, disjunct populations exhibit considerable morphological variation, and 5 subspecies have been named (Findley and Jones 1962, Hoffmeister 1986). However, little is known about karyotypic variation within these highly isolated populations. Judd and Cross (1980) examined karyotypes from 3 populations, including the Jemez and Sacramento mountains in New Mexico and the White Mountains in Arizona. Each had the typical 2n = 56 form, although sample sizes for the Jemez (n = 3) and White (n = 1) mountains were small (Table 1). Consequently, the purpose of this study was to describe additional karyotypes from isolated

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TABLE 1. Summary of known chromosome data for *Microtus longicaudus*, including diploid number (2n), number of pairs of small metacentric chromosomes (M), number of metacentric B chromosomes (B), and sample size (n).

Location	2n	M	B	n	Reference
Palouse / Northern Rocky Mountains					
Washington, Whitman Co.	56	5	0	1	Matthey (1955)
Columbia River					
Oregon, Columbia Co.	56	5	0	2	Hsu and Benirschke (1969)
Cascade Range					
Oregon, Jackson Co.	58	6	2	1	Judd and Cross (1980)
	62	6	6	3	
Oregon, Klamath Co.	57	6	1	2	Judd and Cross (1980)
	59	6	3	1	
Oregon, Lake Co.	66	6	10	3	Judd and Cross (1980)
California, Siskiyou Co.	66	6	10	1	Judd and Cross (1980)
	70	6	14	1	
Central Rocky Mountains					
Utah, Weber Co.	64	5	8	1	Modi (1985)
Utah, Salt Lake Co.	64	5	8	1	Modi (1985)
Southern Rocky Mountains					
Colorado, Larimer Co.	56	5	0	1	Judd and Cross (1980)
New Mexico, Santa Fe Co. (Sangre de Cristo Mountains)	56	5	0	5	this study
New Mexico, Sandoval Co. (Jemez Mountains)	56	5	0	3	Judd and Cross (1980)
	56	5	0	9	this study
New Mexico, Cibola Co. (Mount Taylor)	56	5	0	3	this study
New Mexico, Lincoln Co. (Sacramento Mountains)	56	5	0	10	Judd and Cross (1980)
New Mexico, Catron Co. (Mogollon Mountains)	56	5	0	1	this study
Arizona, Apache Co. (White Mountains)	56	5	0	1	Judd and Cross (1980)
	56	5	0	2	this study

populations of *M. longicaudus* in the American Southwest. This study includes examination of other specimens from the White and Jemez mountains as well as specimens from 3 additional mountain ranges in New Mexico, from which karyotypes have not previously been reported (i.e., Mount Taylor, Mogollon, and Sangre de Cristo mountains).

We prepared standard metaphase karyotypes from bone marrow cells of 20 wild-caught *M. longicaudus* following the procedure of Lee and Elder (1980; see Appendix for locations) and used a hypotonic solution of potassium chloride to facilitate the spreading of chromosomes. After completing the staining process, we scanned the slides under a microscope and selected chromosome spreads that yielded nonoverlap of chromosomes and the greatest detail of centromere position. We used a video monitor connected to the microscope to enlarge the image. We examined 5–10 chromosomal spreads for each specimen in order to establish a diploid number and chromosome structure.

All specimens examined had a 2n of 56 and an FN of 84 and were similar in structure to other 2n = 56 karyotypes previously reported for this species (Matthey 1955, Hsu and Benirschke 1969, Judd and Cross 1980). None

of the specimens possessed supernumerary chromosomes or exhibited evidence of pericentric inversions.

In a phylogenetic analysis of the mitochondrial cytochrome *b* gene (*cyt-b*), Conroy and Cook (2000) found that *M. longicaudus* was represented by at least 5 primary clades. The most divergent *cyt-b* clade, which exhibited levels of differentiation equivalent to species-level differences in the genus, was found in the southern Rocky Mountains (i.e., including specimens from southeastern Wyoming, Colorado, New Mexico, and eastern Arizona) and corresponded to most of the distribution of the 2n = 56 karyotype described in this study (Table 1). However, other 2n = 56 specimens from the Palouse and Columbia rivers were from geographic regions contained in separate *cyt-b* clades. Lessa et al. (2003) found that the phylogenetic signal of *cyt-b* within *M. longicaudus* in the American Southwest was consistent with historical demographic expansion rather than geographic subdivision. In contrast, no evidence for historical demographic expansion was observed for populations of *M. longicaudus* throughout much of the remainder of the continental U.S. Thus, the *cyt-b* results appear to be generally consistent with the

geographic patterns of karyotypic variation in *M. longicaudus*. Populations from the American Southwest are invariant, perhaps as a result of more recent colonization, while populations in much of the western U.S. are highly variable, perhaps as a result of longer periods of isolation. However, we caution that all reported karyotypes from southwestern *M. longicaudus* are from the same subspecies (*M. l. longicaudus*) and that examination of other, more-geographically isolated subspecies in Arizona may reveal additional variation. Finally, we recommend further analyses of the patterns of geographical concordance between karyotypic and molecular variation in this species.

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APPENDIX. Specimens examined and their geographic localities; NK numbers correspond to samples in the Museum of Southwestern Biology, University of New Mexico.

ARIZONA: *Apache Co.*—15.9 mi. S, 10.1 mi. E Springerville, Terry Flat, Escudilla Mountain, T6N, R31E, sec. 19 (NK 20115, NK 20116).

NEW MEXICO: *Catron Co.*—12.1 mi. E Mogollon, Willow Creek, T10S, R17W, NW 1/4 sec. 34 (NK 20131). *Cibola Co.*—6 mi. N, 14 mi. E Grants, Mount Taylor, T12N, R7E (NK 9766, NK 9767, NK 9777). *Santa Fe Co.*—5 mi. N, 8 mi. E Santa Fe (NK 1010, NK 1011, NK 1013, NK 1014, NK 1015). *Sandoval Co.*—3 mi. N, 9.5 mi. E Jemez Springs (NK 1703, NK 1706, NK 1708, NK 1710, NK 1712, NK 1714, NK 1715, NK 1716, NK 1718).