First Records of the Southern Red-backed Vole, *Myodes gapperi*, in the Yukon

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Twenty Southern Red-backed Voles, *Myodes gapperi*, were collected in July 2004 in the LaBiche River valley of southeastern Yukon. Specimens were identified using morphological characteristics and analysis of cytochrome *b* gene sequences. These are the first records of this species in the Yukon. No Northern Red-backed Voles, *M. rutilus*, were collected and it is not known whether the two species are sympatric or parapatric in the Yukon. Further survey work is needed in southeastern Yukon to better delineate the extent of the northwestern range of this species and the extent, if any, of introgression with *M. rutilus*.

Key Words: Southern Red-backed Vole, *Myodes gapperi*, distribution, Yukon.

The Southern Red-backed Vole (*Myodes* [formerly *Clethrionomys* see Musser et al. 2005] *gapperi*) is broadly distributed across the boreal, montane, Pacific coastal, and other conifer-dominated forests of North America (Banfield 1974; Merritt 1981; Batzli 1999). Youngman (1975) did not report *M. gapperi* from the Yukon, in part, because he was of the opinion that *M. gapperi* and the Northern Red-backed Vole (*M. rutilus*) were conspecific. Cook et al. (2004), however, provided molecular data that reinforced the separate status of *M. gapperi* and *M. rutilus*. North American species of *Myodes*, including *M. gapperi* and *M. rutilus*, are cryptic and field identification is highly problematic where congeners come into contact (Merritt 1981; McPhee 1984; Runck 2001, Nagorsen 2002, 2005; Cook et al. 2004). Therefore, we considered that *M. gapperi* may have been overlooked in the Yukon due to the difficulty in distinguishing specimens from *M. rutilus* in the field, and a general paucity of mammalian diversity surveys in most of the Yukon. Based on the distribution of *M. gapperi* in adjacent northeastern British Columbia and southwestern Northwest Territories (Banfield 1974; Nagorsen 2005) we suspected the greatest likelihood of finding the species in the Yukon was in the Liard River Watershed. In summer 2004, we undertook a brief field survey of mammalian diversity in the boreal forest of southeastern Yukon, partially with an aim to procuring specimens of *M. gapperi*. Here, we provide the first records of the Southern Red-backed Vole in the Yukon.

Methods

On 28 July – 2 August 2004, we used pitfall and snap traps to collect shrews and rodents in the LaBiche River Valley (60.126°N, 124.064°W) of southeastern Yukon. Seven habitats were sampled: wet meadows and shrub thickets adjacent to Beaver (*Castor canadensis*) ponds; xeric grassy meadows; riparian old-growth White Spruce (*Picea glauca*) forest; lowland Black Spruce (*Picea mariana*) forest; subalpine old-growth Spruce-fir (*Abies lasiocarpa*) forest; second-growth mixedwood forest; and regenerating clearcut forest. All habitats were sampled with snap traps. We established 14 variable length traplines (ca. 100 m – 250 m) in each of the seven habitat types. Trap stations were set 10 m apart on the traplines. One Museum Special snap trap and one Victor snap trap (Woodstream, Lititz, Pennsylvannia) were set at each trapping station. Traps were baited with oats and peanut butter, run for 2-3 days and checked each morning. In addition to the snap traps, we established three traplines of metal conical pitfall traps in the wet meadow habitats, primarly to capture soricids. Pitfall traps were 25 cm in height and 15 cm in diameter at the top. Pitfall traps were also arranged in traplines with one trapline in each of the wet meadows sampled. Traps were spaced about 10 m apart, with 15 or 20 traps per trapline, and installed flush with the ground surface. Pitfall traps were not baited and they were left open for 3-5 days. Each morning we checked the traps and processed the captures.

Captures were tentatively identified to species, measured, aged, weighed, sexed, and examined for reproductive condition. Whole carcasses were frozen on site. Species were tentatively identified in the field using morphological, pelage, and dental characteristics, following Nagorsen (2002) and van Zyll de Jong (1983). Because of the difficulty in distinguishing *M. rutilus* from *M. gapperi* in the field, we undertook subsequent laboratory investigations at Idaho State University (Pocatello, Idaho) to confirm our field identifications. All skulls were examined for fusion of the post-palatal bridge (Merritt 1981; Nagorsen 2002) and the first 600 base pairs (bp) of mitochondrial cytochrome *b* gene were examined to confirm species identification. Restriction enzyme screening and sequencing of cytochrome *b* followed established protocols for *Myodes* (Runck and Cook 2005). All individuals underwent restriction enzyme digestion using the restriction enzyme ALU I to determine the presence of the restriction site AGCT which is found in the 600 bp fragment of the cytochrome *b* gene in *M. rutilus* but not *M. gapperi* (Runck 2001). Five random individuals were sequenced for the first 600 bp of the cytochrome *b* gene and were used in a phylogenetic reconstruction using published sequences of *Myodes* (Cook et al. 2004; Runck and Cook 2005), representing *M. gapperi* ($n = 10$), *M. rutilus* ($n = 2$), *M. californicus* ($n = 1$), *M. glareolus* ($n = 1$), and *M. rufocanus* ($n = 1$). Sequences for specimens not collected in LaBiche (Figure 1) were taken from GenBank. Phylogeographic reconstruction was conducted using neighbor-joining framework in PAUP b10 (Swofford 2002) using the Tamura and Nei (1993) model of sequence evolution as determined through Modeltest (Posada and Crandall 2000).

Results and Discussion

We captured 20 *Myodes* during sampling. Field identification, based on morphological (tail and pelage) characteristics, suggested that all captures were of *M. gapperi*. Further, 15 of the 20 specimens had complete post-palatal bridges, which is a primary diagnostic characteristic of *M. gapperi* (Merritt 1981; Nagorsen 2002). Two specimens had incomplete post-palatal bridges and the bridges of a further three were broken by the traps and not usable as a diagnostic character. Genetic analyses using restriction enzyme screening and sequencing of cytochrome *b* gene confirmed that all 20 specimens of *Myodes* collected in the LaBiche River Valley were *M. gapperi* (Figure 1).

The Southern Red-backed Vole is now added to the list of mammals in the Yukon. This is the first additional rodent found in the Yukon since Youngman (1975). These 20 specimens were deposited at the Museum of Southwestern Biology at the University of New Mexico (Albuquerque, New Mexico).

Capture rates were 0.28 per 100 trap nights (TN) and 1.32 per 100 TN in pitfall and snap traps, respectively. Captures of *M. gapperi* represented the range of sex and age classes (5 adult females, 7 adult males, 5 juvenile females, and 3 juvenile males), confirming that a breeding population was present. *M. gapperi* were taken in all of the habitats sampled. Species caught in association with *M. gapperi* in the LaBiche River Valley included: Meadow Voles (*Microtus pennsylvanicus*, $n = 14$), Deer Mice (*Peromyscus maniculatus*, $n = 13$), Meadow Jumping Mice (*Zapus hudsonius*, $n = 10$), Eastern Heather Vole (*Phenacomys ungava*, $n = 1$), Masked Shrew (*Sorex cinereus*, $n = 1$), Pygmy Shrew (*Sorex hoyi*, $n = 1$), and Dusky Shrews (*Sorex monticolus*, $n = 2$).

We do not know the extent of the range of the Southern Red-backed Vole in the Yukon. They have been collected, however, near Fort Liard, Northwest Territories (S. Carrière, unpublished data; Runck and Cook 2005). Specimens from near Watson Lake, Yukon (ca. 270 km W of the present study; $n = 43$), were also analyzed in the lab using skull and genetic characters and they were determined to be *M. rutilus* (T. S. Jung and A. M. Runck, unpublished data), suggesting that *M. gapperi* may not be widely distributed in southern Yukon. Perhaps *M. gapperi* is restricted in the Yukon to the extension of the Boreal Plain ecoregion in the extreme southeast. Further surveys from nearby river valleys, and subsequent DNA analysis, are needed to better document the ranges and contact zone of *M. gapperi* and *M. rutilus* in southeastern Yukon and adjacent British Columbia and Northwest Territories. Our discovery of *M. gapperi* in extreme southeastern Yukon, along with that of the Yukon's only records of Northern Long-eared Bats (*Myotis septentrionalis*; Jung et al. 2005) and other taxa (e.g., some species of neotropical migrant passerines: Eckert et al. 1997), suggests that this ecoregion may be a zoogeographically unique part of the Yukon.

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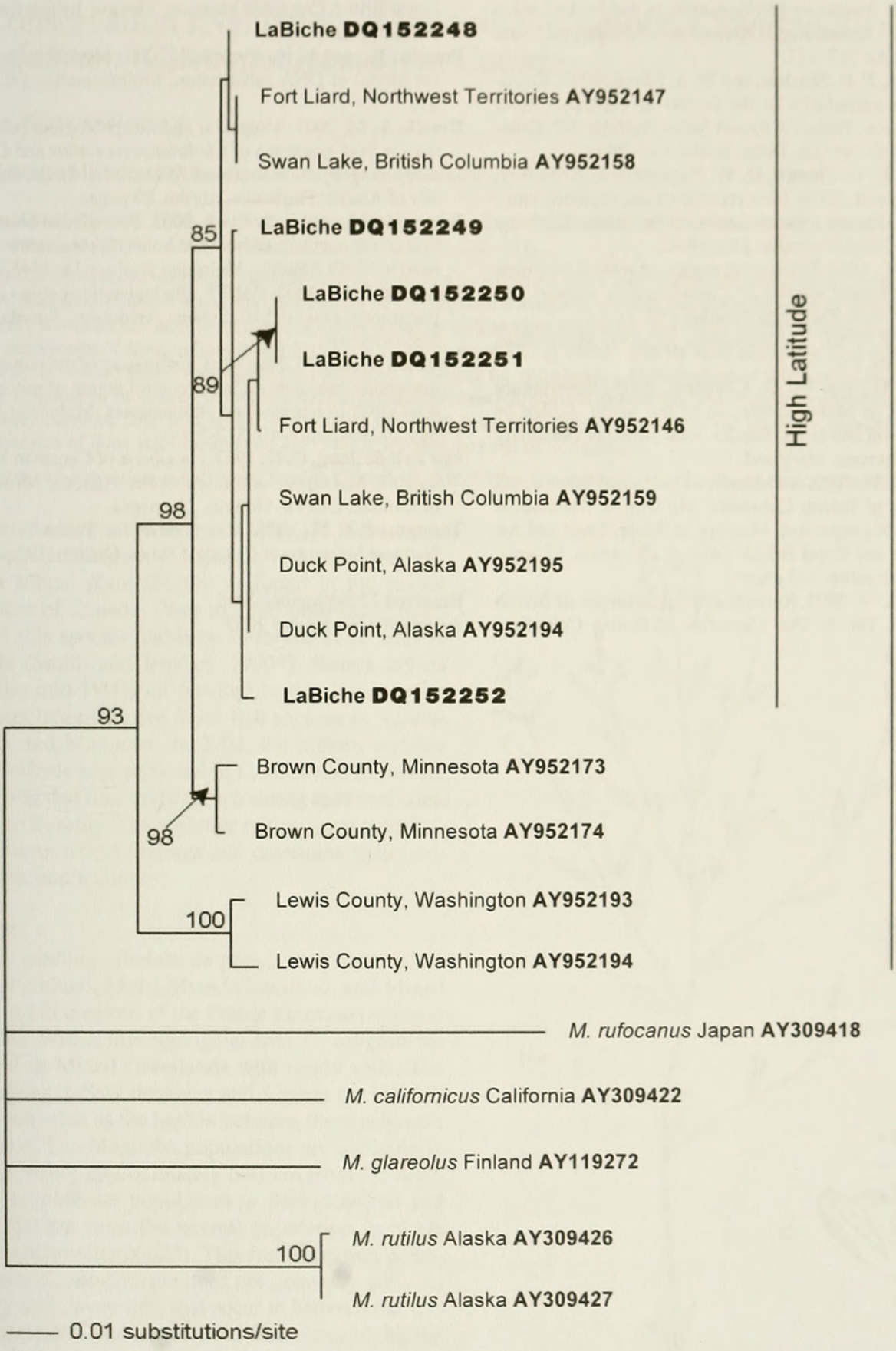

FIGURE 1. Placement of five specimens of *Myodes gapperi* (LaBiche DQ152248-DQ152252) captured in the LaBiche River Valley, Yukon, based a neighbor-joining analysis of cytochrome *b* gene sequences (600 bp) of these specimens and compared to sequences of other *Myodes*. GenBank accession numbers for sequences used are included for each specimen. Numbers above the branches represent bootstrap support values for those nodes.

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