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Correction for the misidentification of a shrew in Sakhalin by Abe et al. (1997), by analysis of the full nucleotide sequence of the mitochondrial cytochrome b gene

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Abstract One shrew specimen which is identified as *Sorex unguiculatus* in Abe et al. (1997) was reexamined. According to morphological characters and nucleotide sequences of the mitochondrial cytochrome b gene, it is re-identified as *Sorex isodon*.

METHODS AND RESULTS

Abe et al. (1997) published a list of small mammals inhabiting southern Sakhalin in *Wildlife Conservation Japan*, vol. 2, no. 1., where they listed a long-clawed shrew from Trudovoe Village (location 9) as *Sorex unguiculatus* Dobson. Later, I, one of the authors of the former report, reexamined the specimen (specimen code, 94sak10) and found that it had gradually reducing tooth height from the first to fifth unicuspids, much shorter forefoot claws, and a greater value of "unicuspid row length/upper tooth row length" (3.02 mm/8.75 mm) than ordinary *S. unguiculatus*. According to Dolgov (1985), such characteristics are those for *Sorex sinalis* Thomas, and it is now widely accepted that *S. sinalis* in Sakhalin as described by Dolgov (1985) is known as dusky shrew, *Sorex isodon* Turov (Hutterer, 1993).

Moreover, to confirm the identification of 94sak10 as *S. isodon*, I compared the mitochondrial cytochrome b gene (1140 bases) full nucleotide sequence of unambiguous *S. unguiculatus* specimens. First, the region which covers the whole cytochrome b region was amplified by PCR, using a forward primer 5'-AAAAACCATCGTTGTTATTCAACT-3' (L14734) and a reverse primer 5'-TAGAATGTCAGCTTTGG GTGCT-3' (H15985). Primer codes in parentheses indicate the 3' end position of the equivalent human mitochondrial DNA (L, light strande and H, heavy strand). Next, the region was sequenced by an autosequencer (ABI Prism 377) using the dye-terminator method. Sequencing was conducted for 94sak10 and 30 *S. unguiculatus* from Hokkaido, Sakhalin, and Primorski territory. The sequence of 94sak10 was easily distinguished from those of *S. unguiculatus* by dendrograms drawn by the neighbor joining and maximum parsimony methods (figures not shown). For example, the bootstrap value of the monophyly of the 30 *S. unguiculatus* analyzed was 100% (1000 replications), indicating that the identified *S. isodon* is clustered out of *S. unguiculatus*, in the neighbor joining method with multiple substitution correction (Thompson et al., 1994) when a pig (Randi et al., 1996) is an outgroup. Sequences of 94sak10 and two *S. unguiculatus* specimens from Hokkaido and Sakhalin are shown in Fig. 1.

Based on the morphological and molecular characteristics mentioned above, 94sak10 in Trudovoe Village in Abe et al. (1996) identified as *S. unguiculatus* must be changed to *S. isodon*. *Sorex isodon* has been previously recorded in southern Sakhalin (e.g., Voronov, 1974; Dolgov, 1985), but was not recorded by Abe et al. (1997) due to misidentification.

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Fig. 1. Full nucleotide sequences (1140 bases) of the mitochondrial cytochrome b gene of 94sak10 (*S. isodon*) and *S. unguiculatus*. Dots denote consensus bases. *S. ung.* (Sak), *S. unguiculatus* in Sakhalin (code, 94sak-1); *S. ung.* (Hok), *S. unguiculatus* in Hokkaido (95/9/7-11).

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