Lack of Mitochondrial DNA Sequence Divergence between Two Subspecies of the Siberian Weasel from Korea: *Mustela sibirica coreanus* from the Korean Peninsula and *M. s. quelpartis* from Jeju Island

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**ABSTRACT**

The objective of this study was to determine the degree of mitochondrial DNA (mtDNA) divergence between two subspecies of *Mustela sibirica* from Korea (*M. s. coreanus* on the Korean Peninsula and *M. s. quelpartis* on Jeju Island) and to examine the taxonomic status of *M. s. quelpartis*. Thus, we obtained complete sequences of mtDNA cytochrome *b* gene (1,140 bp) from the two subspecies, and these sequences were compared to a corresponding haplotype of *M. s. coreanus*, downloaded from GenBank. From this analysis, it was observed that the sequences from monogenic *M. s. quelpartis* on Jeju Island were identical to the sequences of four *M. s. coreanus* from four locations across the Korean Peninsula, and that the two subspecies formed a single clade; the average nucleotide distance between the two subspecies was 0.26% (range, 0.00 to 0.53%). We found that the subspecies *quelpartis* is not genetically distinct from the subspecies *coreanus*, and that this cytochrome *b* sequencing result does not support the current classification, distinguishing these two subspecies by pelage color. Further systematic analyses using morphometric characters and other DNA markers are necessary to confirm the taxonomic status of *M. s. quelpartis*.

**Keywords:** DNA systematics, cytochrome *b* gene, *Mustela sibirica*, Korean Peninsula, Jeju Island
haplotypes were obtained from 25 specimens of two subspecies at eight Korean locations. The PCR thermal cycle sites, model selection, calculation of nucleotide distances, and tree constructions with 1,000 bootstrapped replications were conducted using MEGA5 (Tamura et al., 2011). The Jukes-Cantor model, showing the lowest Bayesian Information Criterion scores, was selected, and neighbor-joining and maximum-likelihood trees were constructed. Martes americana (accession no: AY121344) was used as out group.

RESULTS

Fourteen haplotypes were identified from 25 cytochrome b sequences (1,140 bp) of two Mustela sibirica subspecies in Korea (Table 1). One haplotype (JsJj01) was revealed from nine specimens of M. s. quelpartis at two locations on Jeju Island (four specimens at Seoguipo and five specimens at Jeju), and 13 haplotypes were identified from 16 specimens of M. s. coreanus at six locations on the Korean Peninsula (haplotype Jr01 from Mt. Jiri; CejSrWaSa01 from four locations of Cheongju, Mt. Songri, Mt. Weolak, and Mt. Seolak; Cej02-Cej04 from Cheongju; Sr02 from Mt. Songri; Cuj01-Cuj03 from Chungju; Wa02-Wa04 from Mt. Weolak; and Sa02 from Mt. Seolak). Fourteen cytochrome b haplotypes of two M. sibirica subspecies are deposited in GenBank under accession nos. JQ739185-JQ739198.

Within 15 cytochrome b haplotypes (14 haplotypes from this study and one haplotype from GenBank), 20 sites (1.75%) were variable, and nine sites (0.79%) were parsimonious informative. The average Jukes-Cantor nucleotide distance among the 14 haplotypes of M. s. coreanus was 0.46% (range, 0.00 to 0.79%), and, among them, one haplotype (Wa03) from Mt. Weolak was identical to another haplotype (GenBank accession no: AB564135) from Mt. Jiri.

Additionally, one haplotype (JsJj01) of M. s. quelpartis from nine specimens at two locations on Jeju Island was identical to one haplotype (CejSrWaSr01) of M. s. coreanus, from four specimens at four locations on the Korean Peninsula, and the average distance between M. s. quelpartis and M. s. coreanus was 0.26% (range, 0.00 to 0.53%). Neighbor-joining and maximum-parsimony trees with 15 haplotypes from two subspecies of M. sibirica are shown in Fig. 1. All 15 haplotypes formed a single clade, indicating that the subspec-
ies quelpartis is not genetically distinct from the subspecies coreanus.

DISCUSSION

Bradley and Baker (2001) noted that a genetic distance of <2% based on the cytochrome b gene was typical of population and infraspecific variation. In this study, M. s. quelpartis from Jeju Island was monogenic, and the average distance among 14 haplotypes of M. s. coreanus was 0.46% (range, 0.00 to 0.79%), indicating that genetic divergence within each of the two M. sibirica subspecies, based on the cytochrome b gene, was low (<1%). Further studies with additional specimens are needed to confirm this conclusion.

Johnson et al. (2000) noted that island populations should diverge over time (genetically and morphologically) from respective mainland species populations. In this study of cytochrome b sequences (see Fig. 1) two subspecies of M. sibirica formed a single clade and haplotype JsJj01 from nine M. s. quelpartis at two locations on Jeju Island was identical to haplotype CjSrWaSr01 from four M. s. coreanus at four locations across the Korean Peninsula. Average nucleotide distance between the two subspecies was 0.26% (range, 0.00 to 0.53%), indicating that M. s. quelpartis from Jeju Island was not genetically divergent from M. s. coreanus on the Korean Peninsula.

In addition, Lomolino et al. (2010) noted that isolated animals and plants dispersed across formerly submerged land bridges, during the last glacial maxima. Thus, we considered that the lack of divergence between the two M. sibirica subspecies (see Fig. 1) may have resulted from the free dispersal of the Siberian weasels (M. sibirica) from the Korean Peninsula to Jeju Island through land bridges formed during the last glacial maxima.

However, M. s. quelpartis from Jeju Island is distinct in pelage color from M. s. coreanus on the Korean Peninsula (Thomas, 1906). We found that the results from this cytochrome b sequencing study (see Fig. 1) do not support the current M. sibirica subspecies classification.

A subspecies is an aggregate of phenetically similar populations of a species differing taxonomically from other populations of that species (Mayr and Ashlock, 1991), and it was advocated that a classification should be the product of all available characters distributed as widely and evenly as possible over the organisms studied (Huelsenbeck et al., 1996). Thus, we conclude that M. s. quelpartis from Jeju Island is a subspecies with only morphological differences.

The shortcomings of using mtDNA sequences for the systematics of hares (genus Lepus) were pointed out, and it has been recommended to include nuclear gene pool evidence (Slimen et al., 2008). Morphometric and genetic analyses with nuclear and other mtDNA markers from the two M. sibirica subspecies have not been performed yet, and we propose further systematic analyses with morphometric characters and other DNA markers to confirm the taxonomic status of M. s. quelpartis.
REFERENCES


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