

**Systematic Studies on Korean Rodents: VIII. Analyses of Morphometric Characters, Chromosomal Karyotype, and Mitochondrial DNA Restriction Fragments in Siberian Chipmunks from Korea (*Tamias sibiricus barberi* Johnson and Jones), with the Comparison of Morphometric Characters of Siberian Chipmunks from Manchuria (*Tamias sibiricus orientalis* Bonhote)**

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**ABSTRACT**

Samples of Siberian chipmunks (*Tamias sibiricus barberi*) from Korea were analyzed by multivariate, air-drying, and blot-hybridization methods in order to determine the degree of variations of morphological characters, chromosomal karyotype, and mtDNA restriction fragment patterns, respectively. Moreover, morphometric characters of samples of Siberian chipmunks from Manchuria (*T. sibiricus orientalis*) were also analyzed in order to clarify the taxonomic status of the subspecies *barberi*.

Siberian chipmunks from six localities in Korea were in morphometric characters more or less similar with one another and Siberian chipmunks from Manchuria were not so distinct enough to form a subgroup. Siberian chipmunks from four localities in Korea were identical in their karyotypes ( $2n = 38$ ): samples from three localities in Korea were more or less similar in their mtDNA fragment patterns.

Siberian chipmunks from Korea appeared to be a homogeneous population and as noted by Corbet (1978) subspecies *barberi* is the synonym of subspecies *orientalis*. The scientific name of Siberian chipmunks from Korea and Manchuria is *T. sibiricus orientalis*, although systematic studies with the samples from North Korea, Manchuria and China will be necessary for their taxonomic reconsideration.

Key words: Systematics. Morphometry. Karyotype. mtDNA. Rodent. *Tamias sibiricus*. Korea

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## INTRODUCTION

Developments in the areas of molecular, cyto- and numerical taxonomy are enormous and there have been a conflict between molecular biologists and morphologists about the merits of their data (Maxon & Wilson, 1975; Fergusson, 1980). However, modern molecular techniques have not yet pushed comparative morphology into the shadows (Patterson, 1987) 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 (Mayr & Ashlock, 1991).

Genus *Tamias* (= *Eutamias*) is composed of 17 species of chipmunks and one of them, Siberian chipmunk, *T. sibiricus* Laxmann, inhabits in the eastern Palaearctic from Siberia to Hokkaido (Corbet & Hill, 1991), although Ellis & Maxon (1979) recognized two genera of *Tamias* and *Eutamias*. In Korea, Jones & Johnson (1965) recognized two subspecies of Siberian chipmunks (*T. sibiricus orientalis* from extreme northern part and *T. sibiricus barberi* from central to southern parts), although Won (1967) classified Siberian chipmunks in Korea as *T. sibiricus asiaticus*. Corbet (1978) summarized 13 nominal subspecies of *T. sibiricus* into four subspecies (*sibiricus*, *albogularis*, *barberi*, *lineatus*), but he was doubtful about the validity of the subspecific status of *barberi*, indicating that the subspecies *barberi* might be the synonym of the subspecies *orientalis* (= *sibiricus*).

Taxonomic works on Siberian chipmunks in Korea were based on the description of pelage colour and a few morphological characters, and the subspecific classification of them are still in doubt. Therefore, in this study, morphological characters, chromosomal karyotype, and mtDNA restriction fragment patterns in Siberian chipmunks from Korea (*T. sibiricus barberi*) were analyzed to determine the degree of their variations. Moreover, morphometric characters of samples from Manchuria (*T. sibiricus orientalis*) were analyzed together to clarify taxonomic status of the subspecies *barberi*.

## MATERIALS AND METHODS

### Materials

Sixty six samples of Siberian chipmunks, *Tamias sibiricus*, from seven localities in Korea and Manchuria (58 of *T. sibiricus barberi* from six localities in Korea; 8 of *T. sibiricus orientalis* from one locality in Manchuria) were used for morphometric analyses as shown in Table 1. Skins and skulls of 58 samples from Korea are stored in the collection of the author, Dept. of Biology, Chungbuk University. Eight samples from Manchuria were in the collection of U. S. National Museum of Natural History, Washington, U.S.A.

Nineteen samples from four localities (3 from Mt. Seolak, 5 from Mt. Weolak, 9 from Goesan, and 2 from Cheongju) were also used for chromosomal karyotype analyses and fifteen specimens from three localities (1 from Mt. Seolak, 2 from Mt. Weolak, and 12 from Goesan) were utilized for restriction fragment analyses of mtDNA.

### Morphometric analyses

Analyses were based on four external and 27 cranial characters (for details see Koh, 1983) and samples from each locality were grouped as Operational Taxonomic Units, OTUs (see Table 1). Each specimen was assigned to one of four age classes, subadult, young adult, middle-aged adult, and old adult based on the eruption of upper third molar, degree of tooth-wear, and pelage colour (for details see Koh, 1983). Sixty six samples were classified into 15 subadults, 27 young adults, and 24 middle-aged adults (see Table 1); young and middle-aged adults were used for further analyses.

For the analyses of geographic variation, discriminant and cluster methods were used by subprograms DISCRIM and CLUSTER of SPSS/pc+, respectively. Principal component analysis by subprograms EIGEN and PROJ and minimum spanning tree by MST of NTSYS/pc were also carried out.

### Chromosomal analyses

The bone-marrow *in vivo* method of Ford and Hamerton (1956) was used for the preparation of chromosome slides (for details see Koh, 1982).

### Restriction fragment length polymorphisms, RFLPs, of mtDNA

Mitochondrial DNA was visualized from southern blots (Southern, 1975) of total cellular DNA. DNA isolation from liver, electrophoresis, Southern transfer, and hybridization were described by Davis (1986): eight restriction enzymes were *Pst* I, *EcoR* V, *Bam*H I, *Hind* III, *Dra* I, *Pvu* II, *Stu* I, and *EcoR* I. Sequence divergences in base substitutions per nucleotide (p) in per cent were estimated by the method of Upholt (1977) and phenogram was constructed by single linkage method and Unweighted Pair Group Method with Arithmetic means, UPGMA (Sneath & Sokal, 1973).

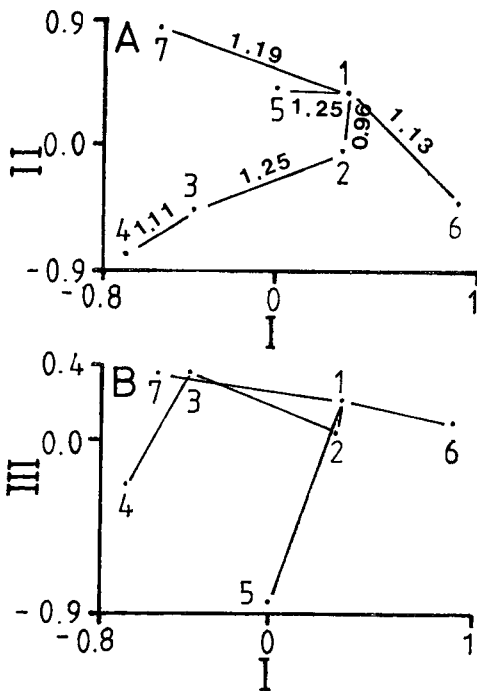
**Table 1.** Subspecies name, locality, and number of samples of Siberian chipmunks from Korea (*Tamias sibiricus barberi*) and Manchuria (*T. sibiricus orientalis*) used for morphometric analyses. The age classes are subadult (SA), young adult (YA), and middle-aged adult (MA).

Subspecies	Locality	OTU	No. of samples			Total
			SA	YA	MA	
<i>barberi</i>	Mt. Seolak, Korea	1		4	4	8
	Mt. Weolak, Korea	2	2	4	10	16
	Goesan, Chungbuk, Korea	3	3	5	6	14
	Cheongju, Chungbuk, Korea	4	9	4	2	15
	Mt. Chiri, Korea	5		1		1
	Mt. Palgong, Korea	6		4		4
<i>orientalis</i>	Kirin, Manchuria	7	1	5	2	8
		Total	15	27	24	66

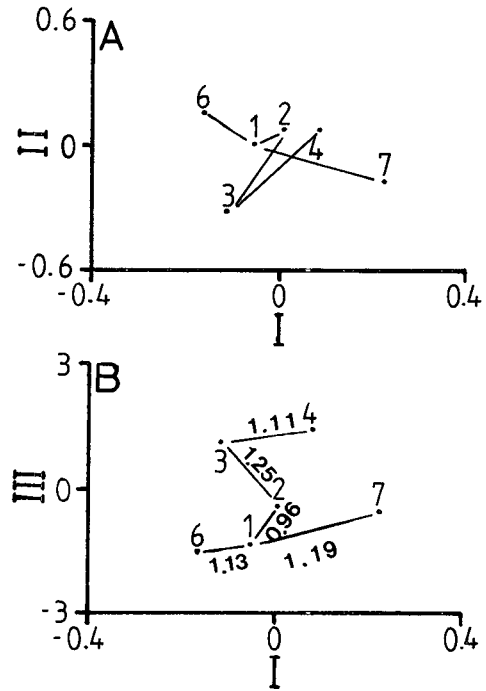
## RESULTS

### Morphometric analyses

Two dimensional plottings of seven OTUs of young Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 6) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by principal component analysis with the means of 31 morphometric characters are shown in Fig. 1: minimum spanning tree is superimposed on the plots with minimum distance shown and factors I, II, and III represented 33, 27, and 20 per cent of the variance, respectively. Two dimensional configurations of six OTUs of young Siberian chipmunks from Korea (*T. sibiricus barberi*, OTUs 1 to 4 and 6) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by discriminant analysis with the individual measurements are also shown in Fig. 2: functions I, II, and III represented 76, 22, and 2 per cent of the variance and minimum spanning tree with minimum distances is superimposed on the centroids of six OTUs. For locality of each OTU see Table 1.



**Fig. 1.** Plottings of seven OTUs of young Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 6) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by principal component analysis with the means of 31 morphometric characters. Minimum spanning tree is superimposed on the plots with minimum distances shown. For locality of each OTU see Table 1.

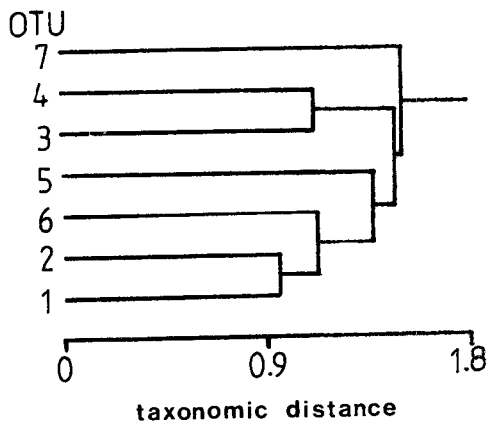


**Fig. 2.** Projections of six OTUs of young Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1, 2, 3, 4, and 6) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by discriminant analysis with individual measurements of 31 morphometric characters. Minimum spanning tree with minimum distances is superimposed on the group centroids of six OTUs. For locality of each OTU see Table 1.

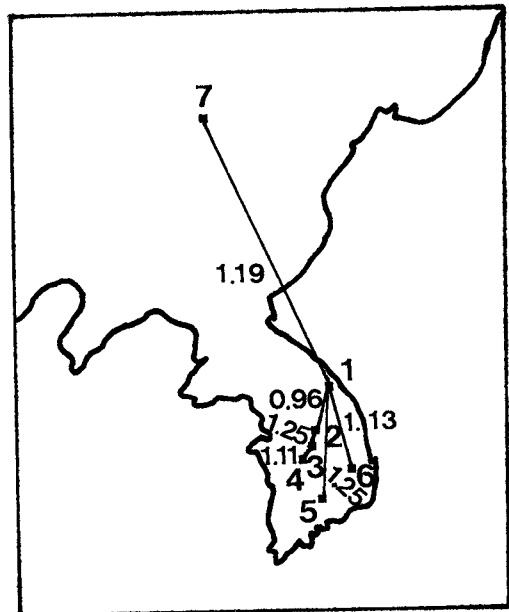
of six OTUs. Seven OTUs of young Siberian chipmunks from Korea and Manchuria were grouped by UPGMA with taxonomic distances calculated from the means of 31 morphometric characters, as shown in Fig. 3. Minimum spanning tree with minimum distance is also superimposed on the map showing the localities of seven OTUs of Siberian chipmunks (Fig. 4).

Two dimensional plottings of five OTUs of middle-aged Siberian chipmunks from Korea (*T. sibiricus barberi*, OTUs 1 to 4) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by principal component analysis with the means of 31 morphometric characters are shown in Fig. 5: minimum spanning tree is superimposed on the plots with minimum distance and factors I, II, and III represented 49, 22, and 16 per cent of the variance, respectively. Five OTUs of middle-aged Siberian chipmunks were also grouped by UPGMA with taxonomic distances, as shown in Fig. 6. Two dimensional configurations of five OTUs of middle-aged Siberian chipmunks by discriminant analyses with the individual measurements are shown in Fig. 7: functions I, II, and III represented 81, 12, and 5 per cent of the variance and the group centroids were plotted with minimum spanning tree superimposed on the plots (minimum distances are also given).

In these morphometric analyses as shown in Figs. 1 to 7, Siberian chipmunks from Korea (*T. sibiricus barberi*, OTUs 1 to 6) are found to be more or less similar in morphometric characters with one another. Moreover, Siberian chipmunks from Manchuria (*T. sibiricus orientalis*, OTU 7) are not so different enough to form a distinct subgroup, indicating that *T. sibiricus barberi* is not different



**Fig. 3.** Grouping of seven OTUs of young Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 6) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by UPGMA with the means of 31 morphometric characters. For locality of each OTU see Table 1.



**Fig. 4.** Minimum spanning tree superimposed on the map showing the seven OTUs of Siberian chipmunks from Korea and Manchuria. Minimum distances were calculated from the means of 31 morphometric characters of young adults and numerals indicate OTUs. For locality and subspecies name of each OTU see Table 1.

from *T. sibiricus orientalis* in morphometric characters.

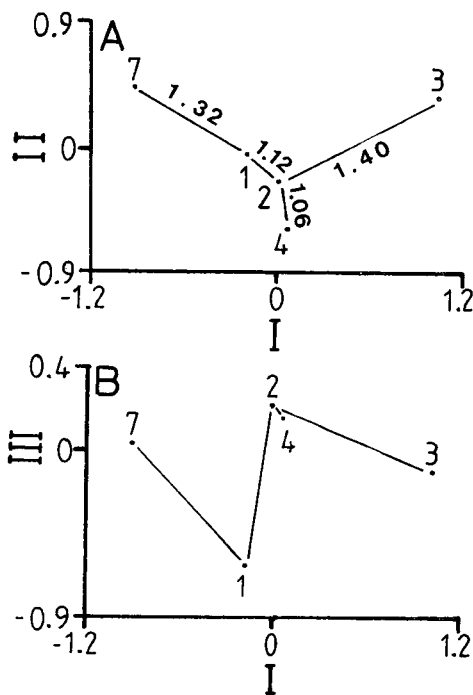
**Chromosomal analyses**

The chromosomal karyotype of 19 Siberian chipmunks from four localities in Korea were identical, and representative karyotype of one Siberian chipmunk (no. 754, , from Cheongju) is shown in Fig. 8: diploid chromosome number is 38 with the complements of three large metacentric pairs(group I, 1 to 3), four large submetacentric pairs (group II, 4 to 7), six large acrocentric pairs (group III; 8 to 13), one small metacentric pair (group IV, 14), and four small metacentric to acrocentric pairs (group V, 15 to 18), large metacentric X, and small metacentric Y.

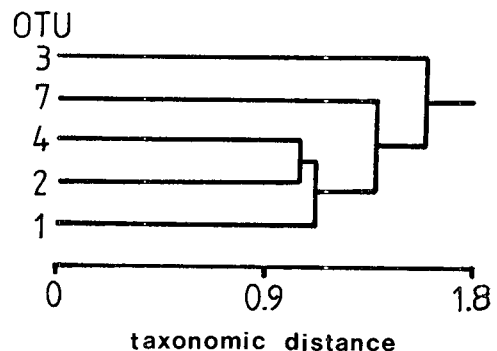
**Mitochondrial DNA analyses**

A total of 26 restriction fragments were recognized and five clones were revealed (see Table 2). In mtDNA genotypes of five clones, fragment patterns by five of eight restriction enzymes, *Pst* I, *Hind* III, *Dra* I, *Pvu* II, and *Eco*R I, were identical. Moreover, four of 15 samples from three localities (no. 437 from Mt. Seolak; no. 459 from Mt. Weolak; nos. 746 and 747 from Goesan) were found to have the same mtDNA genotype, clone 1.

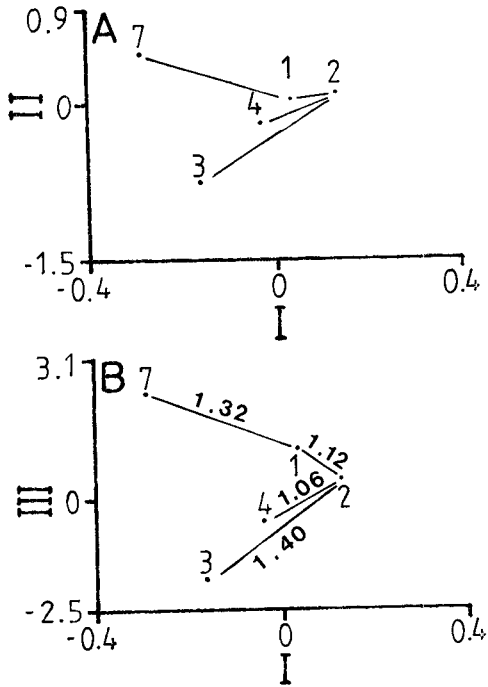
Fig. 9 shows the groupings of five mtDNA clones by single linkage method (A) and UPGMA (B) with nucleotide-sequence divergences (p in percent) given in Table 3. Nucleotide-sequence divergences are varied from 0.41% to 1.49%. Clones 3 and 5 (eight samples from Goesan) appeared to be somewhat diverged from clones 1, 2, and 4 of seven samples from three localities



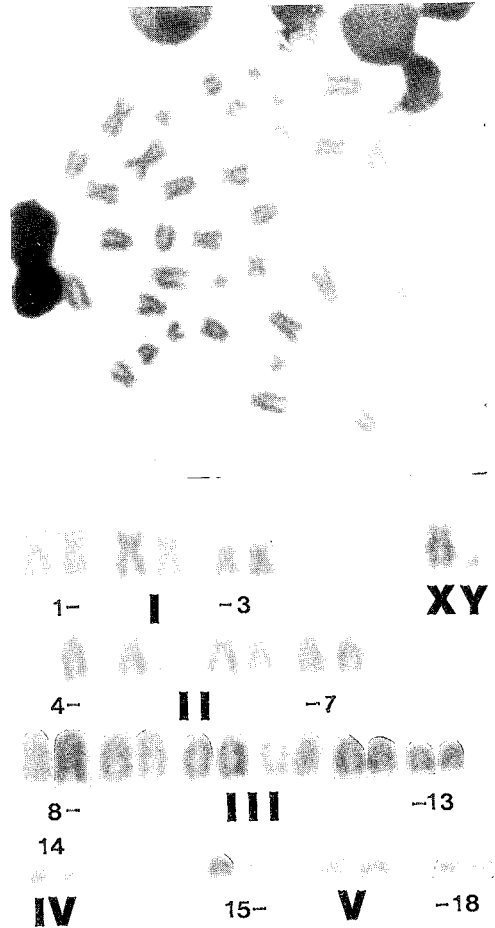
**Fig. 5.** Plottings of five OTUs of middle-aged Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 4) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by principal component analysis with the means of 31 morphometric characters. Minimum spanning tree is superimposed on the plots with minimum distances shown. For locality of each OTU see Table 1.



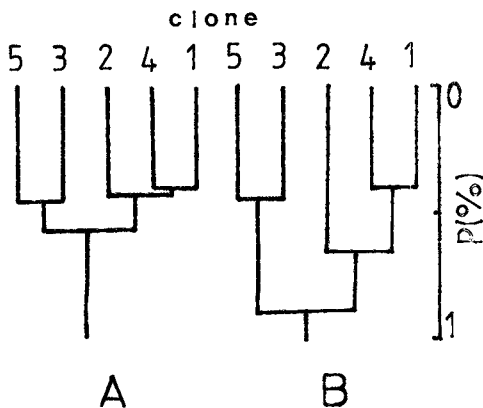
**Fig. 6.** Grouping of five OTUs of middle-aged Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 4) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by UPGMA with the means of 31 morphometric characters. For locality of each OTU see Table 1.



**Fig. 7.** Projections of five OTUs of middle-aged Siberian chipmunks from Korea (*Tamias sibiricus barberi*, OTUs 1 to 4) and from Manchuria (*T. sibiricus orientalis*, OTU 7) by discriminant analysis with individual measurements of 31 morphometric characters. Minimum spanning tree with minimum distances is superimposed on the group centroids of six-OTUs. For locality of each OTU see Table 1.



**Fig. 8.** Representative chromosomal karyotype in a Siberian chipmunk (no. 437 from Cheongju, Korea), *Tamias sibiricus barberi*. Roman numerals from I to V indicate the chromosome groups by Nadler *et al.*(1969).



**Fig. 9.** Groupings of five mtDNA clones in Siberian chipmunks from Korea (*Tamias sibiricus barberi*). The nucleotide-sequence divergences (p) in per cent were used for single linkage method, A, and UPGMA, B. For locality of each clone see Table 2.

**Table 2.** Mitochondrial DNA genotypes, and clones in 15 samples of Siberian chipmunks from three localities in Korea (*Tamias sibiricus barberi*). Mitochondrial genotypes were based on the fragment patterns, resulted from the digestion with eight restriction enzymes, *Pst* I, *EcoR* V, *Bam*H I, *Hind* III, *Dra* I, *Pvu* II, *Stu* I, and *EcoR* I.

Locality (OTU)	Specimen no.	mt DNA genotype	Clone
Mt. Seolak (1)	437	1 1 1 1 1 1 1 1	1
Mt. Weolak (2)	459	1 1 1 1 1 1 1 1	1
Mt. Weolak (2)	429	1 2 1 1 1 1 1 1	2
Goesan (3)	746, 747	1 1 1 1 1 1 1 1	1
Goesan (3)	749	1 1 2 1 1 1 1 1	3
Goesan (3)	750, 752	1 1 3 1 1 1 1 1	4
Goesan (3)	741, 742, 743, 744, 745, 748, 751	1 1 2 1 1 1 2 1	5

(one from Mt. Seolak, two from Mt. Weolak, and four from Goesan), but they are not so distinct to form a subgroup. In summary, 15 samples of Siberian chipmunks from three localities in Korea (*T. sibiricus barberi*) were more or less similar in their mtDNA fragment patterns.

In the present results based on the analyses of morphometric characters, chromosomal karyotype, and mtDNA RFLPs (see Figs. 1 to 9 and Tables 1 to 3), it is concluded that samples of Siberian chipmunks from Korea (*T. sibiricus barberi*) are more or less similar in their morphometric characters, karyotype, and mtDNA restriction patterns. Moreover, it is apparent that *T. sibiricus barberi* is not different from *T. sibiricus orientalis* in morphometric characters.

## DISCUSSION

Boyce (1969) noted that average linkage, or UPGMA represents a distance matrix of random points better than either complete or single linkage. The relationships between close neighbors are frequently distorted in an ordination, especially one based on principal component analysis, PCA (Rohlf, 1970), and it is useful to superimpose minimum spanning tree on the plots by ordination methods (Kruskal, 1956). Sneath & Sokal (1973) stated that there are no satisfactory methods for telling whether clustering or ordination is most appropriate. Furthermore, Clifford & Stephenson (1975) noted that discriminant analysis ordinated two or more a priori defined groups as that there is minimum overlap and maximum separation among them, whereas PCA makes no assumption about the existence of grouping among the OTUs. In this morphometric analyses, cluster analyses by UPGMA and minimum spanning tree, principal component analysis, and discriminant analysis were used with the same data and similar results were obtained, as shown in Figs. 1 to 7.

Based on a few external characters, Jones and Johnson (1965) stated that Siberian chipmunks from most of the Korean peninsula is different from Siberian chipmunks in the northernmost region of Korea (*Tamias sibiricus orientalis*) and they classified the former into *T. sibiricus barberi*. But Corbet (1978) doubted the classification of the subspecies *barberi*, indicating that Siberian chipmunks from Korea is *orientalis* (= *sibiricus*). The methods of numerical taxonomy based on equal weighting and overall similarity seemed inapplicable in defining higher categories above the species level (Farris,



1966). On the other hand, Flake and Turner (1968) stated that the numerical approach offers potential for the resolution of taxonomic problems for populations at infraspecific level.

By morphometric analyses as shown in Figs. 1 to 7, Siberian chipmunks from Korea (*T. sibiricus barberi*, OTUs 1 to 6) are more or less similar in morphometric characters with one another, but Siberian chipmunks from Manchuria (*T. sibiricus orientalis*, OTU 7) are not so different enough to form a distinct subgroup. It is concluded that the designation of the subspecies *barberi* is not valid, as noted by Corbet (1978), although further analyses with more samples from North Korea, Manchuria, and China are necessary to confirm this conclusion and to clarify the taxonomic status of the subspecies *orientalis*, in order.

The role of chromosomal rearrangements in speciation and intraspecific polymorphism has been intensively studied and discussed (Bush *et al.*, 1977; King, 1993). Nadler & Block (1962) stated that all chipmunks (*Tamias* and/or *Eutamias*) have the same diploid number ( $2n = 38$ ), but different fundamental number due to pericentric inversion ( $FN = 58-60$ ). Nadler *et al.* (1969) noted that Siberian chipmunks from China (*Tamias sibiricus*) have the diploid number of 38 with the chromosomal complements of three pairs of large meta (group I), four pairs of large submeta (group II), six pairs of large acro (group III), one pair of small meta (group IV), four pairs of small submeta to acrocentric autosomes (group V): X is large metacentric and Y is small metacentric chromosome. Kang and Kim (1963) stated that diploid number of Siberian chipmunks from unknown locality in Korea is 38 with the complements of 4 pairs of meta to submeta, 13 pairs of acro, and one pair of telocentric autosomes: X is large acrocentric and Y is small telocentric chromosome.

In the present study, chromosomal karyotype of 19 Siberian chipmunks from four localities in Korea were identical, and the representative karyotype (Fig. 8) appeared to be the same as that of samples from China by Nadler *et al.* (1969). Moreover, the present karyotype appeared to be comparable with the idiogram shown by Kang and Kim (1963), i.e., four pairs of metacentric chromosomes (= groups I and IV), 14 pairs of acro to telocentric chromosomes (= groups II, III, and V), large acrocentric X (= large metacentric X), and small telocentric Y (= small metacentric?, but it is not shown in the idiogram). It is concluded that Siberian chipmunks (*Tamias sibiricus*) from China to Korea are identical in their chromosomal karyotype.

Mitochondrial DNA studies are important to infer maternal lineages among closely related species and infraspecific populations (Avice, 1986; Moritz *et al.*, 1987). The analysis of RFLPs, is simple and it is possible to analyze more loci per individual by them than by sequencing (Hillis & Moritz, 1990). The greatest infraspecific sequence divergence among mtDNA clones of *Apodemus sylvaticus* was 1.4%, and *A. flavicollis*, 1.0% (Tegelstrom & Jaarola, 1989). The maximum sequence divergence in *Rattus norvegicus* is 0.8% (Brown & Simpson, 1981). The nucleotide-divergence values among seven mtDNA clones of *Apodemus agrarius coreae* from Korea ranged from 0.22% to 2.31% (Koh *et al.*, 1993), and those between two mtDNA clones of *Cryptomys hottentotus natalensis* was 1.7% (Honeycutt *et al.*, 1987). On the other hand, sequence divergence between *Peromyscus maniculatus* mtDNA clones from continental North America was as high as 7% and seven assemblages were revealed (Lansmann *et al.*, 1983).

In this study with mtDNA of 15 samples of *Tamias sibiricus barberi* from three localities in Korea (see Tables 2 and 3 and Fig. 9), four samples from three localities were found to have a identical genotype. Furthermore, no distinct subgroup was formed among five mtDNA clones, although the

**Table 3.** Nucleotide-sequence divergences (p in per cent) among five mtDNA clones in Siberian chipmunks from Korea (*Tamias sibiricus barberi*). The locality and numbers of specimens in each clone are given in Table 2.

Clone	1	2	3	4
2	0.43			
3	0.43	1.49		
4	0.41	0.87	0.57	
5	0.92	0.92	0.45	1.06

nucleotide divergences among the mtDNA clones ranged from 0.41% to 1.49%. Moreover, in these morphometric and chromosomal analyses, as shown in Figs. 1 to 8, Siberian chipmunks from Korea are more or less similar in morphometric characters and they are identical in their karyotype. Therefore, it is concluded that Siberian chipmunks from Korea are a homogeneous subgroup in their mtDNA restriction patterns, chromosomal karyotype, and morphometric characters.

Restriction fragment length polymorphisms have been invaluable for the analyses of matrilineal relationships between distinct forms in the pocket gopher, *Geomys* (Davis, 1986). In this mtDNA RFLP analyses (see Table 2), localities of four samples with identical mtDNA genotype were Mt. Seolak, Mt. Weolak, and Goesan, which are geographically adjacent regions (see Fig. 4). In this morphometric analysis (see Figs. 1 and 7), minimum spanning tree connects samples from Mt. Seolak (OTU 1) to Goesan (OTU 3) through Mt. Weolak (OTU 2), and samples of OTUs 1, 2, and 3 have the same karyotype, as mentioned above, indicating that samples from these three localities are closely related in their mtDNA genotype, chromosomal karyotype, and morphological characters. Moreover, in the minimum spanning tree with morphometric characters (see Fig. 4) samples from Mt. Seolak (OTU 1) seems to be the center of all samples from Korea (OTUs 2 to 6) and samples from Manchuria (OTU 7) as well, indicating that Siberian chipmunks from Korea might be dispersed from Manchuria through Mt. Seolak.

The evolutionary rate of mtDNA was estimated to be about 2% in one million years (Avice, 1986). In the present study based on mtDNA restriction fragments of Siberian chipmunks from Korea, maximum nucleotide-divergence was 1.49%, indicating that they are present in Korea at least 0.75 million years ago. Siberian chipmunks are first known from the Pliocene of Poland and China (Black, 1972), and it is certain that they dispersed to Korea after the beginning of the Pliocene, 5.5 million years ago.

In future, it is necessary to analyze samples of Siberian chipmunks from North Korea to China through Manchuria in order to determine their lineage by morphometric and mtDNA analyses and to clarify their taxonomic status.

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한국산 설치류의 계통분류학적 연구: 8. 다람쥐(*Tamias sibiricus barberi* Johnson and Jones)의 형태적 형질, 염색체 핵형 및 미토콘드리아 DNA 절단 단편의 분석과 만주다람쥐(*Tamias sibiricus orientalis* Bonhote)와의 형태적 형질의 비교

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요 약

한국에 살고 있는 다람쥐(*Tamias sibiricus barberi*)의 형태적 형질, 염색체 핵형 및 미토콘드리아 DNA 절단단편의 변이의 정도를 파악하기 위하여, 다변량분석, 골수세포 및 blot-hybridization법으로 표본들을 분석하였다. 아종 *barberi*의 분류학적 재검토를 위하여, 만주에 살고 있는 다람쥐(*Tamias sibiricus orientalis*)의 표본들의 형태적 형질들도 함께 분석하였다.

한국의 6개 지역의 다람쥐는 서로 형태적으로 유사했으며, 만주산 다람쥐는 한국의 다람쥐와 다른 군을 형성할 정도로 뚜렷한 형태적 차이를 보이지는 않았다. 한국의 4개 지역의 다람쥐는 동일한 핵형( $2n = 38$ )을 가졌고, 5개 미토콘드리아 DNA clone이 나타난 한국의 3개 지역의 다람쥐의 미토콘드리아 절단단편의 양상도 서로 유사하였다.

한국산 다람쥐는 단일한 집단이며, Corbet(1978)가 지적했던대로 아종 *barberi*는 아종 *orientalis*의 synonym임이었다. 한국과 만주산 다람쥐의 학명은 *T. sibiricus orientalis*이지만, 분류학적 재검토를 위하여 북한, 만주 및 중국의 표본들을 사용한 계통분류학적 연구가 필요하다고 본다.