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Systematic Studies of Korean Rodents. V. Morphometric and Chromosomal Analyses on Island Populations of Striped Field Mice (*Apodemus agrarius coreae*) in Southwestern Coasts of the Korean Peninsula

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한국산 설치류의 계통분류학적 연구 . 5. 한반도 남서해안의 섬들에 살고있는 등줄쥐들의 형태적 형질 및 염색체의 분석

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적 요

한국 남서연안및 섬등의 8개지역에서 등줄쥐((*Apodemus agrarius*)의 표본들을 채집하였다. 한반도의 여타지역및 제주도의 표본들과 같이 두골및 외부측정치를 포함하는 형태적형질의 분석과 염색체 핵형의 비교분석을 실시하였다.

염색체 분석에 있어서 한국내의 표본들간에 핵형상의 차이는 없었다. 형태적 형질의 분석에 있어서 완도및 보길도에서 채집된 표본들은 제주도의 표본들과 함께 large-size group(큰 형)을 형성했다(*Apodemus agrarius chejuensis*). 반면에 진도및 하조도의 표본들은 남서연안을 포함하는 한반도지역에서 채집된 표본들과 함께 small-size group(작은 형)을 이루었다(*A. agrarius coreae*).

완도및 보길도에 큰 형의 등줄쥐들이 현재 서식하고 있는 이유는 전에 살았던 작은 형의 등줄쥐들이 전멸되고, 제주도로 부터 인간에 의해서 이주된 큰 형의 등줄쥐들로 대체되었기 때문이라고 추정하였다.

Key words: Morphometry, Chromosome, *Apodemus agrarius*, Korea

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INTRODUCTION

The genus *Apodemus* of about 12 species is confined to the Palaearctic and northern part of the Oriental region: *A. agrarius* Pallas (striped field mice), inhabiting from West Germany to Korea, is a distinct species regarded as the sole member of the subgenus *Apodemus* (Corbet, 1978).

Thomas (1906) described striped field mice from the Korean peninsula and Jeju island as a single subspecies, *Apodemus agrarius coreae*. Jones and Johnson(1965) reported that four subspecies of *A. agrarius* were recognized in Korea: *A. agrarius manchuria* in the extreme northern part, *A. agrarius pallescens* in the coastal lowlands of southern and southwestern Korea, *A. agrarius coreae* throughout the major portion of the peninsula, and *A. agrarius chejuensis* in Jeju island.

Corbet (1978) noted that most of subspecies of *Apodemus agrarius* were designated on the basis of slight differences in pelage colour and/or mean body size. Moreover, age variation, secondary sexual variation, and geographic variation of morphomertic characters should be analyzed before subspecific status is considered (Mayr, 1969): chromosomal and electrophoretic analyses are also necessary to perform (Koh, 1981).

Kral (1970) reported that the karyotype of *A. agrarius* from various localities of Eurasia is consisted of 40 acrocentric and eight metacentric chromosomes with diploid number of 48. In chromosomal analyses with samples of striped field mice from ten localities in Korea (*A. agrarius coreae* and *A. agrarius chejuensis*) the diploid number is constant 48 with the complement of 40 acrocentric and 8 metacentrics (Koh, 1982; Koh, 1987).

Based on uni-and multivariate analyses with 31 morphometric characters of *A. agrarius coreae* from Chongju, evident age variation and no significant secondary sexual variation were revealed (Koh, 1983). In morphometric analyses with samples of three subspecies of *A. agrarius* from 12 localities of Korea it was reported that *A. agrarius pallescens* is a synonym of *A. agrarius coreae* and that *A. agrarius chejuensis* is a large-size group and *A. agrarius coreae* is a small-size group (Koh, 1985; Koh, 1986; Koh, 1987).

Jeju island was formed by series of volcanic activities at the end of Tertiary period in Cenozoic era (Park, 1985) and in recent it was 20,000 years since this island had been isolated from the Korean peninsula by the rise of sea level (Seyfert and Sirkin, 1984). Geographically isolated populations may be either species or subspecies (Wiley, 1982). When there is no intermediate between two parapatric groups they are different species (Ross, 1974). Many islands such as Wan, Jin, and Chuja islands connect Jeju island to the Korean peninsula. These islands can be land-bridge islands already had a fauna and flora when they became separated from the mainland (Gorman, 1979). These islands might be sweepstake route of dispersal, as stated by Simpson (1940) and founders (Mayr, 1982) of two size groups of *A. agrarius* might inhabit there.

Objective of this paper is to analyze morphometric characters and karyotypes of samples of striped field mice, *Apodemus agrarius,* from insular populations of southwestern coasts of the Korean peninsula in order to determine the range of variation compared with those in samples of the mainland and Jeju island.

MATERIALS AND METHODS

Materials

Nineteen samples from four localities in southwestern coasts and 24 samples from four localities in southwestern islands were trapped and prepared for phenetic analysis: 246 samples from seven localities in the mainland and 31 samples from two localities in Jeju island were also utilized (for subspecies name, locality, and number of specimens see Table 1). For chromosomal analyses one or two samples from each of eight localities in southwestern coasts and islands were used.

Samples were collected with live traps and specimens for chromosomal analysis were kept alive for a few days before chromosomal analyses were conducted. Skins and skulls of all samples are in the collection of the author, Department of Biology, Chungbuk University, Chongju, Korea.

Chromosomal analyses

Analyses were performed according to procedures detailed in Koh (1987). The metaphase chromosome of one sample (K-290) from Wan island is shown here because same results were obtained in the other specimens.

Table 1. Specimens examined. SA, YA, MA, and OA indicate subadult, young adult, middle-aged adult, and old adult, respectively.

Species	Locality	Age classes				Total	OTU
		SA	YA	MA	OA		
Apodemus agrarius coreae	Mokpo		1	2	1	4	1
	Gohung		2	2		4	2
	Youngkwang		6	2		8	3
	Haenam		3			3	4
	Jin island	1	12	6		19	5
	Hajo island		1			1	6
	Wan island		1	2		3	7
	Bogil island		1			1	8
	Chongju	37	43	42	9	131	9
	Mungyong	1	7	12	2	22	10
	Mt. Weolak	9	8	15	3	35	11
	Mt. Seolak		3	2		5	13
	Mt. Palgong	3	4	9	4	20	14
	Kunsan		1	6	1	8	15
Apodemus agrarius chejuensis	Mosulpo		3	9	1	13	16
	Sanchondan		7	10	1	18	17
	Total	55	112	128	25	320	

Phenetic analyses

Analyses were based on four external and 27 cranial characters, as listed in Koh (1983). Three hundred and twenty samples were classified according to the criteria noted in Koh (1983) into 55 subadults, 112 young adults, 128 middle-aged adults, and 25 old adults (see Table 1). The specimens of young adults and middle-aged adults were used for further analyses.

Sample statistics such as mean and standard deviation were calculated by ELEMSTAT program of Interactive Statistical Programs, ISP (HP-3000/58 computer, Chungbuk University). For ordination methods principal component analysis, PCA, was performed from individual measurements of 31 characters using subprogram PCAS of ISP. However, the data were singular. Therefore, 13 characters (1, 3, 4, 6, 9, 13, 16, 19, 20, 22, 25, 28 and 30), showing significant difference among means of the four OTU's in *A. agrarius coreae* (see Koh, 1985), were selected and used for PCA (the means of 13 selected characters were also used and the measurements from the OTU's with one sample were considered as the mean of each OTU).

For cluster asnalyses SPSS-PC+ programs were used. Raw data were first standardized. Squared Euclidean distance matrix was calculated and OTU's were grouped by Unweighted Pair Group Method using Arithmatic Averages, UPGMA (program Cluster).

Table 2. Summary of chromosomes counted in 14 samples of *Apodemus agrarius coreae* from eight localities in southwestern coasts and islands. M and T indicate number of metacentric and acrocentric chromosomes, respectively.

Locality	Specimen number	Chromosome frequency 46	47	48	49	50	2n	M	T
Mokpo	K-486	1		88	1		48	8	10
	K-488		1	11	1		48	8	10
Gohung	K-373			4			48	8	10
	K-374			8	1	1	48	8	10
Youngkwang	K-526		1	12			48	8	10
	K-527			10	1		48	8	10
Haenam	K-669		1	9			48	8	10
	K-670	1		13	1		48	8	10
Jin island	K-362	1		14			48	8	10
	K-365		1	9	1		48	8	10
Hajo island	K-372		1	6			48	8	10
Wan island	K-290	1	2	21			48	8	10
	K-377		1	13			48	8	10
Bogil island	K-378		1	7			48	8	10

RESULTS

Chromosomal analyses

Diploid chromosome number, chromosome complement, and chromosome frequency of 14 samples of striped field mice, from eight localities in southwestern coasts and islands are shown in Table 2. The

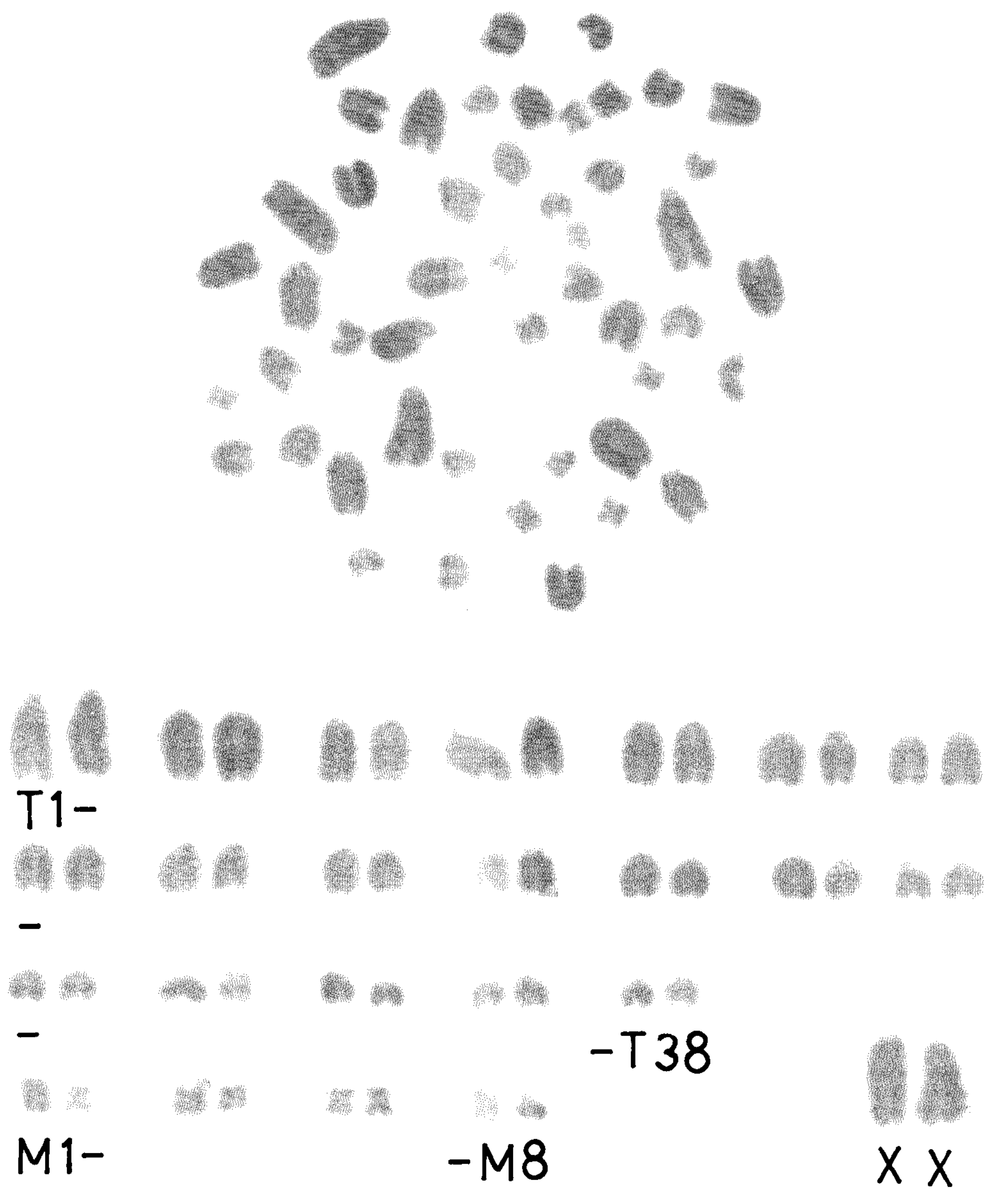

Fig. 1. Metaphase chromosome and idiogram of a striped field mouse (K-290), *Apodemus agrarius*, from Wan island. M and T indicate metacentric and acrocentric chromosomes, respectively.

idiogram of one sample (K-290) of striped field mouse from Wan island is shown in Fig. 1. The karyotype in all samples is consisted of 40 acrocentric and eight metacentric chromosomes with the diploid number of 48.

Phenetic analyses

Two dimensional configurations from individual measurements of 13 selected characters of 112 young adults are shown in Fig. 2 (numerals indicate OTU numbers). The correlations between characters and principal components are given in Table 3 (factors I, II, and III represented 50, 8, and 7 per cent of the variance, respectively). The means were also used and the results are also shown in Fig. 3 (factors I, II, and III represented 56, 11, and 10 per cent of the variance, respectively).

Two dimensional configurations from PCA with individual measurements of 13 selected characters of

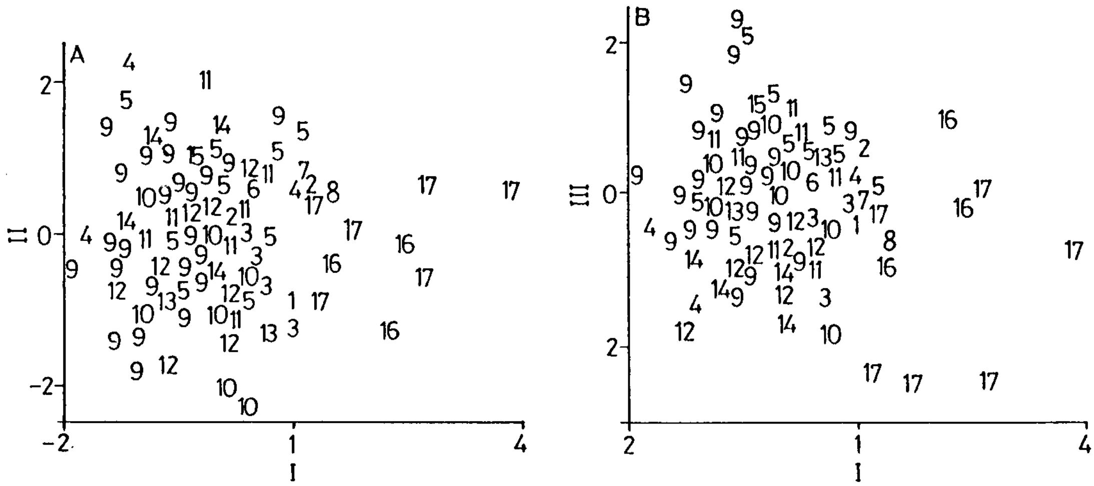

Fig. 2. Projections of 112 young adults of *Apodemus agrarius* based on principal component analysis in three dimensions. Numerals indicate OTU number. For locality of each OTU see Table 1. A, Samples ordinated with factor I vs. factor II; B, Samples ordinated with factor I vs. factor III.

Table 3. Principal components I, II, and III expressed as correlations between characters and individual components from an analysis with 13 selected characters of 112 young adults of *Apodemus agrarius* in Korea.

Character	Factor I	Factor II	Factor III	Character	Factor I	Factor II	Factor III
1	0.94	-0.16	-0.09	3	0.77	0.21	0.34
4	0.81	0.07	0.07	6	0.61	0.08	-0.43
9	0.45	0.54	-0.42	13	0.50	0.41	-0.18
16	0.45	-0.68	-0.45	19	0.87	-0.19	0.12
20	0.75	0.47	0.15	22	0.90	-0.09	0.04
25	0.79	-0.01	-0.14	28	0.47	0.10	0.17
30	0.64	-0.14	0.46				
% of trace	50	8	7				

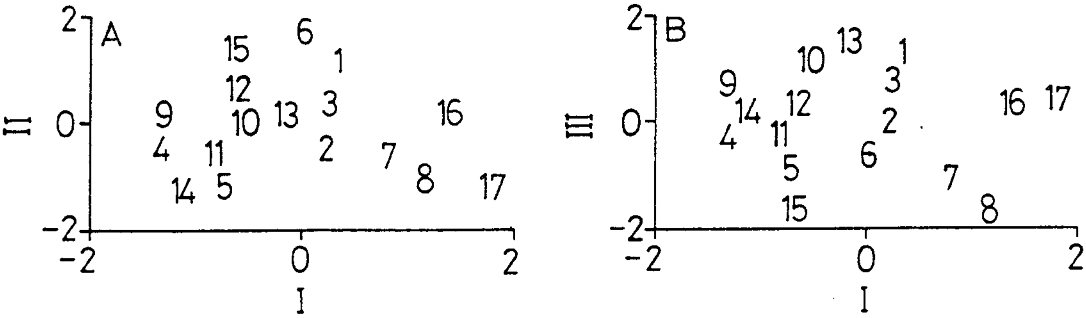

Fig. 3. Projections of young adults of *Apodemus agrarius* (17 OTU's) based on principal component analysis. A, OTU's ordinated with factor I vs. factor II; B, OTU's ordinated with factor I vs. factor III.

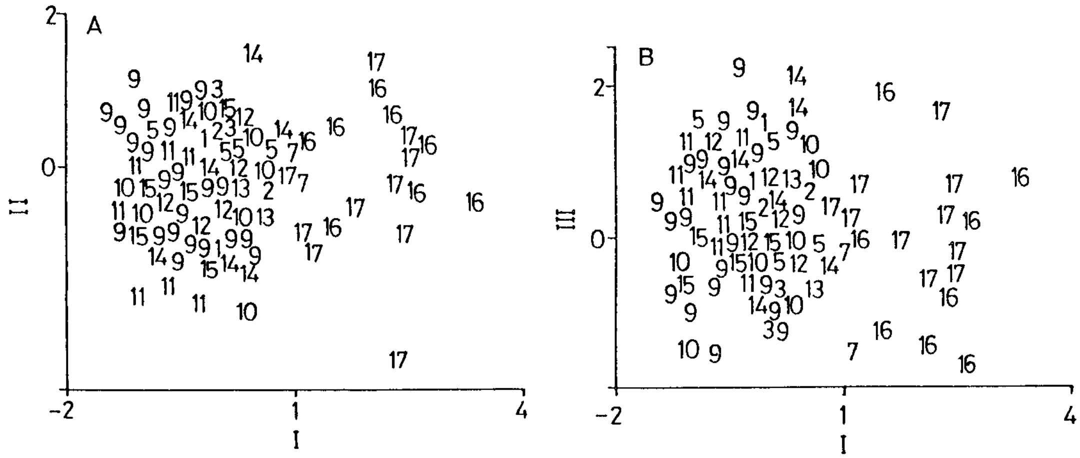

Fig. 4. Projections of 128 middle-aged adults of *Apodemus agrarius* based on principal component analysis in three dimensions. Numerals indicate OTU number. For locality of each OTU see Table 1. A, Samples ordinated with factor I vs. factor II; B, Samples ordinated with factor I vs. factor III.

Table 4. Principal components I, II, and III expressed as correlations between characters and individual components from an analysis with 13 selected characters of 128 middle-aged adults of *Apodemus agrarius* in Korea.

Character	Factor I	Factor II	Factor III	Character	Factor I	Factor II	Factor III
1	0.95	-0.01	-0.07	3	0.38	0.76	0.36
4	0.81	0.04	-0.01	6	0.74	-0.31	-0.07
9	0.56	-0.33	0.40	13	0.50	-0.06	0.55
16	0.68	-0.41	-0.06	19	0.87	0.01	-0.11
20	0.80	0.17	-0.00	22	0.92	0.06	-0.01
25	0.84	-0.05	0.08	28	0.55	0.20	-0.09
30	0.66	0.22	-0.31				
% of trace	54	8	7				

128 middle-aged adults are shown in Fig. 4 (numerals indicate OTU numbers). The correlation between characters and the principal component are given in Table 4 (factors I, II, and III represented 54, 8, and 7 per cent of the variance, respectively). The means were also used and the configurations are shown in Fig. 5 (factors I, II, and III represented 65, 12, and 7 per cent of the variance, respectively).

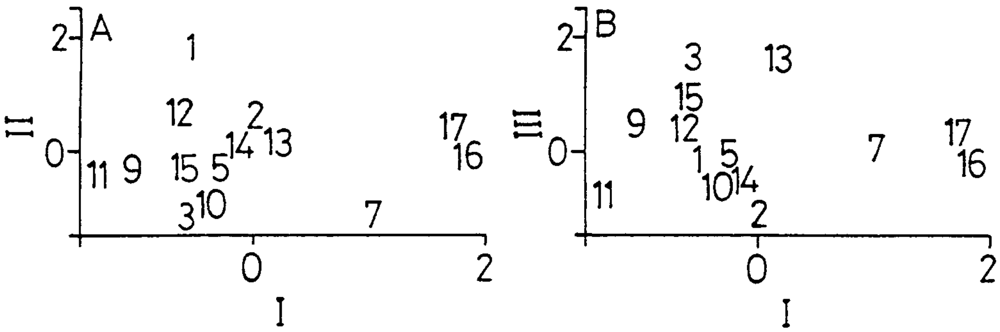

Fig. 5. Projections of middle-aged adults of *Apodemus agrarius* (14 OTU's) based on principal component analysis. A, OTU's ordinated with factor I vs. factor II.; B, OTU's ordinated with factor I vs. factor III.

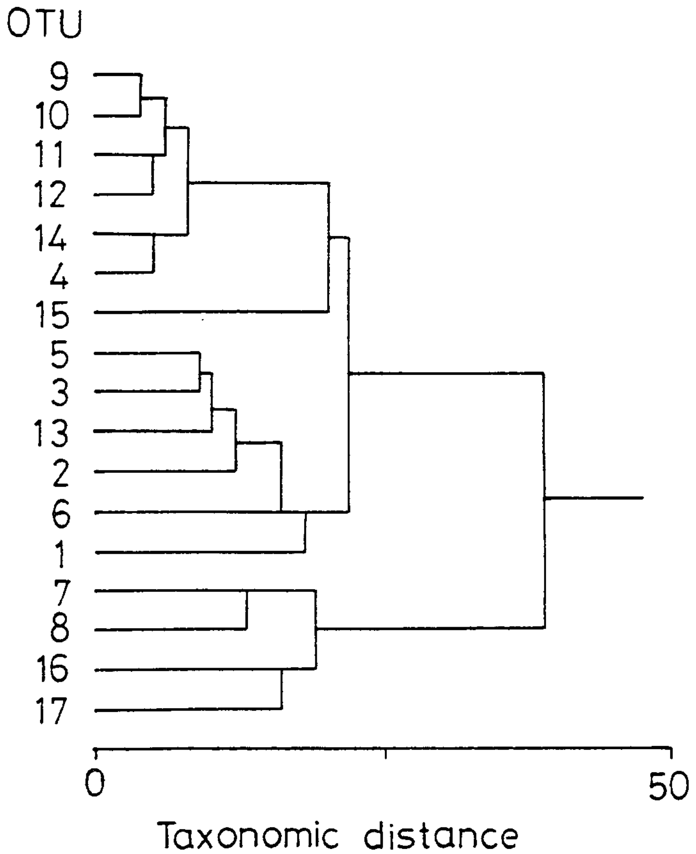

Fig. 6. Groupings of 17 OTU's of *Apodemus agrarius* based on UPGMA analysis using Eucl dean taxonomic distance from standardized means of young adults. For locality of each OTU see Table 1.

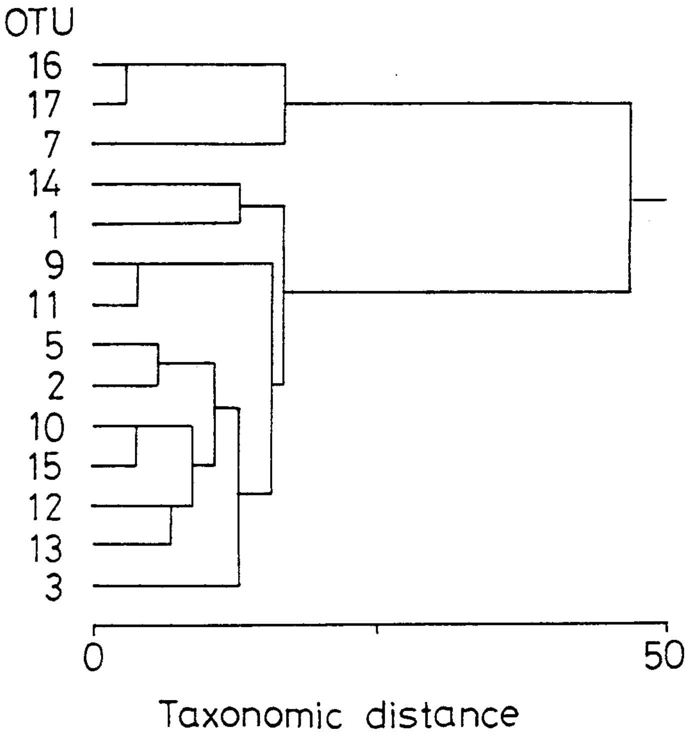

Fig. 7. Groupings of 14 OTU's of *Apodemus agrarius* based on UPGMA analysis using Euclidean taxonomic distance from standardized means of middle-aged adults. For locality of each OTU see Table 1.

The young adults and middle-aged adults were also grouped by UPGMA cluster analyses in Figs. 6 and 7, respectively.

Two size groups (a small-size group of OTU's 1-6 and 9-15; a large-size group of OTU's 7, 8, 16, and 17) were found to be evident (see Figs. 2 to 7).

In summary, samples from southwestern coasts (OTU's 1-4), two of four southwestern islands (OTU's 5 and 6) and the mainland (OTU's 9-15) are smaller than samples from the other two southwestern islands (OTU's 7 and 8) and Jeju island (OTU's 16 and 17) in morphometric analyses, whereas no variation was revealed among 14 samples from southwestern coasts and islands (OTU's 1 to 8) in chromosomal analyses.

DISCUSSION

Kral (1970) and Koh (1982 and 1987) reported karyotypes of striped field mice, *Apodemus agrarius*, in Eurasia except Korea and those in the Korean peninsula and Jeju island, respectively. In this present study chromosomal analyses were conducted with samples from eight localities in southwestern coasts and islands (see Table 2 and Fig. 1) and it is confirmed that striped field mice in Eurasia including Korea were similar in karyotypes.

In morphometric analyses with striped field mice from Korea, however, two size groups (a small-size group and a large-size group) were revealed (see Figs. 2 to 7), as reported by Koh (1987). Wilson *et al.*

(1975) noted that in mammalian phylogenetics the rates of anatomical and chromosomal evolution are rather close. Bykova *et al.* (1978) also found that Asian mountain vole, *Altico leminus,* from Yukitia and Chukot are appreciably different in karyotypes and morphology. Dobzhansky (1972), however, noted that genetic divergence and speciation may occur without a rearrangement of the genetic materials in the chromosomes, although more often the two processes go hand in hand.

Population levels of striped field mice on Wan, Bogil, and Hajo islands appeared to be very low during this study as judged by very low trap success compared to that on the mainland and Jin island. The collection of samples from Bigum, Docho, Nohwa, Sangjo, Oenaro, Naenaro, and Chuja islands were conducted in vein, indicating that striped field mice on these small islands are near extinct. The expected life of a population will be related to its size, i.e., populations numbered in tens and hundreds will become extinct fairly rapidly, while those counted in thousands will persist indefinitely (Gorman *et al.,* 1979). The species composition of any local community is subject to change with time as local populations of species die out and are reestablished by immigration and that this dynamic studies had received particular attention for island conditions (Diamond and May, 1977).

A cline is directional change of characters or gene frequency within a species over geographic distance (Johnson, 1976). Fewer examples involve large frequency change over short units of distance, the so-called step cline: the absence of gene flow results in a step cline (Endler, 1977). Some general categories of extrinsic isolating factors for the isolation of infraspecific populations through which dispersal is limited without causing reproductive isolation are geographical, temporal, and ecological barriers (Edwards, 1954). Koh (1986) reported that a step cline was revealed in morphometric characters between *Apodemus agrarius chejuensis* from Jeju island and *A. agrarius coreae* from the Korean peninsula. In this morphometric analyses samples from Wan and Bogil islands formed a large-size group (*A. agrarius chejuensis*) with samples from Jeju island, whereas samples from Jin and Hajo islands formed a small-size group (*A. agrarius coreae*) with samples from the Korean peninsula including southwestern coasts (see Figs. 2 to 7).

Traditionally islands have been described as either oceanic or continental (= land bridge): continental islands lie on a continental shelf and are separated from the mainland by rather shallow water (about 150m or less): they are connected to the mainland during the Pleistocene and became isolated 10,00 years ago, although isolation time have been variable: continental islands have faunas very similar to those on the mainland (Wilcox, 1978; Jameson, 1981). Moreover, the equilibrium theory of island biogeography (MacArthur and Wilson, 1967) proposes that species composition in some biotas may be explained by an equilibrium resulting from a balance of immigration by extinction.

Southwestern islands in Korea such as Wan, Bogil, Jin, Hajo, and Jeju islands are continental islands and seem to have been isolated from the mainland at different times. Therefore, it is supposed that small-size population of striped field mice in Wan and Bogil islands were extinct and replaced by large-size population of striped field mice immigrated from Jeju island by humans.

In future it will be necessary to perform morphometric and electrophoretic analyses with specimens from the area connecting Haenam and Wan island in order to clarify subspecific status of *Apodemus agrarius chejuensis.*

ABSTRACT

Samples of striped field mice, *Apodemus agrarius* Pallas, from eight localities in southwestern islands and coasts in Korea were collected and analyzed together with samples from the mainland and Jeju island.

In chromosomal analyses no variation was revealed in karyotypes among samples from Korea. In morphometric analyses samples from Wan and Bogil islands formed a large-size group (*A. agrarius chejuensis*) with those from Jeju island, whereas samples from Jin and Hajo islands formed a small-size group (*A. agrarius coreae*) with those from the mainland including southwestern coasts.

It is supposed that small-size population of striped field mice in Wan and Bogil islands were extinct and replaced by large-szie population of striped field mice immigrated from Jeju island by humans.

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