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A note on karyotypes of *Sorex caecutiens* (Mammalia, Insectivora) from Cheju Island, Korea

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Abstract — Karyotypes of *Sorex caecutiens* from Cheju Island of Korea were examined with conventional staining and G-banding by trypsin treatment stained with Giemsa (GTG). The diploid and fundamental autosomal arm numbers were 42 and 66, respectively. The autosomal complement in the karyotype comprised six pairs of metacentrics, seven pairs of submetacentrics or subtelocentrics, and seven pairs of acrocentrics. The X was a largest acrocentric chromosome, and the Y was a small subtelocentric chromosome. Chromosomal constitutions and G-banding pattern of *S. caecutiens* from Cheju Island were essentially identical to those reported for *S. shinto* from Honshu Island, Japan. This similarity may indicate the ancestral character of the monophyletic *S. caecutiens/shinto* group.

Key words: Cheju Island, G-banding, karyotype, *Sorex caecutiens*, *Sorex shinto*,

INTRODUCTION

Molecular phylogenetic analyses reveal that *Sorex caecutiens* Laxmann, 1788 and *S. shinto* Thomas, 1905 are a monophyletic *Sorex caecutiens/shinto* group (Ohdachi *et al.* 1997; 2001). According to analyses based on mitochondrial DNA sequences (Ohdachi *et al.* 1997; 2001) and restriction fragment length polymorphism of the nuclear ribosomal DNA spacer region (Naitoh 2003), *Sorex caecutiens* occurs throughout the northern parts of the Eurasian Continent and neighboring islands, while *Sorex shinto* is confined only to Honshu, Sado, and Shikoku Islands of Japan. The conventional karyotype of *S. caecutiens* from the Eurasian Continent (Fredga 1968; Skaren and Halkka 1966) is quite similar to that of *S. shinto* from Honshu Island of Japan (Tada and Obara 1988; Tsuchiya 1984), however, the karyotype of *S. caecutiens* from Hokkaido Island of Japan differs from the others of the *S. caecutens/shinto* group in the arm ratio of one bi-armed autosomal pair. This difference is probably the result of pericentric inversion (Tada and Obara 1988; Takagi and Fujimaki 1966; Tsuchiya 1984). Moreover, based on the comparison of G-banded karyotypes, Biltueva *et al.* (2000) reported the occurrence of pericentric inversion between the karyotype of *S. caecutiens* from Novosibirsk of Russia and those of *S. caecutiens* from Hokkaido Island and *S. shinto* from Honshu Island, suggesting that *S. caecutiens* of Novosibirsk has a unique autosomal pair as an autapomorphic character.

Indeed, various cases of intraspecific chromosomal polymorphisms are known in shrews (Bystrakova *et al.* 2003; Fredga 2003; King 1993; Zima *et al.* 1998). Therefore, different chromosome races are likely in the *S. caecutiens/shinto* group. On the basis of mitochondrial cytochrome *b* gene sequences, Ohdachi *et al.* (2003) reported that *S. caecutiens* from Cheju Island, Korea diverged from the continental or Korean Peninsula populations. It can be expected that the chromosomal constitution of the Cheju Island population, isolated from the Eurasian Continent, differs from others of the *S. caecutens/shinto* group due to the effect of genetic drift in small populations.

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To confirm this conjecture, we examined the conventional and G-banded karyotypes of *S. caecutiens* from Cheju Island and compared them to those of the *S. caecutiens/sinto* group described previously (TADA and OBARA 1988; TAKAGI and FUJIMAKI 1966; TSUCHIYA 1984).

MATERIALS AND METHODS

Two males and one female *Sorex caecutiens* were collected on 13-19 October 1999 in Cheju Island, Korea (Fig. 1). Chromosomal preparations were made from skin fibroblasts according to our routine air-drying method (ROTHFELS and SIMINOVITCH 1958). After these preparations, conventional Giemsa staining was carried out. To identify each autosomal pair and both sex chromosomes, G-banding by trypsin treatment stained with Giemsa (GTG) was performed with the routine cytogenetical technique (SEABRIGHT 1971).

RESULTS AND DISCUSSION

The number of metaphase plates of *Sorex caecutiens* examined is shown in Table 1. All three specimens carried the diploid number (2n) of 42 and fundamental autosomal arm number (FN) of 66. The autosomal complement in the karyotype comprised six pairs of metacentrics, seven pairs of submetacentrics or subtelocentrics, and seven pairs of acrocentrics. The X was a largest acrocentric chromosome, and the Y was a small subtelocentric chromosome (Fig. 2a). These chromosomal characteristics were essentially identical to those of *S. caecutiens* from the Eurasian Continent (FREDGA 1968; SKAREN and HALKKA 1966) and *S.*

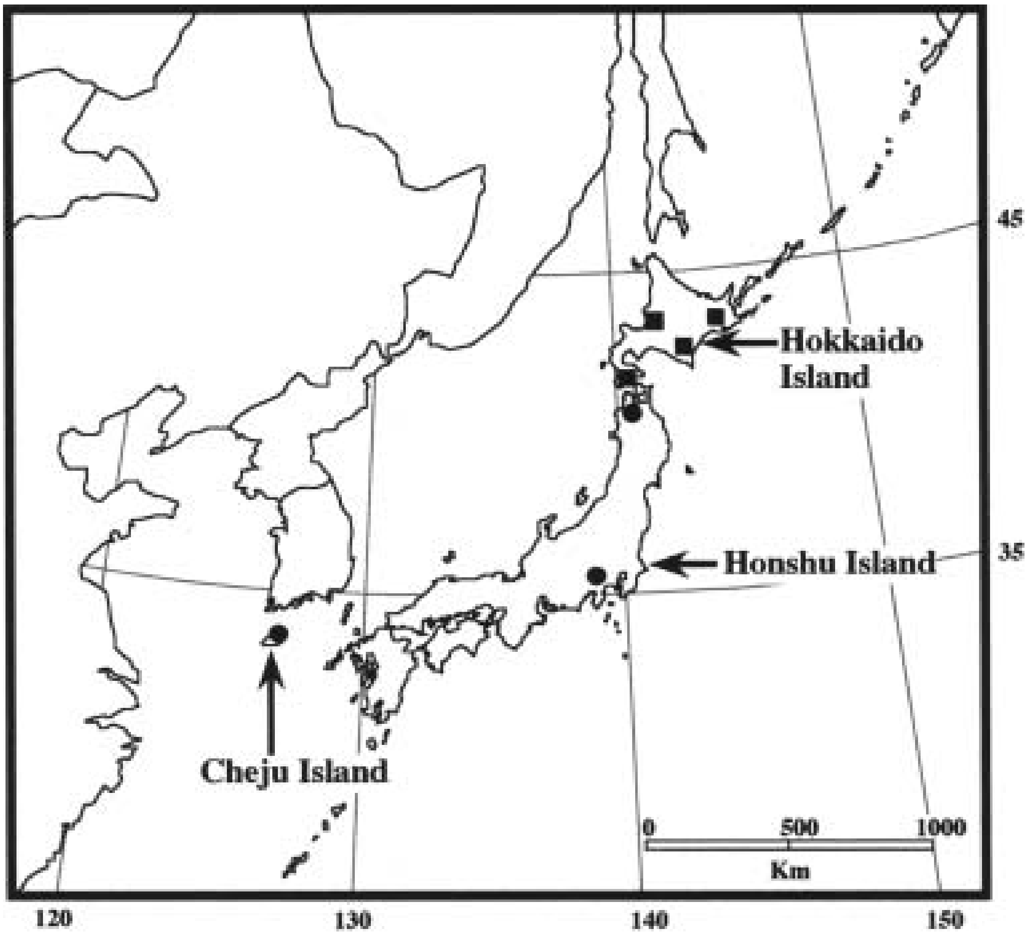

Fig. 1 — Distribution of chromosome races of the *S. caecutiens/shinto* group in East Asia, based on the present (Cheju Island) and previous studies (TADA and OBARA 1988; TAKAGI and FUJIMAKI 1966; TSUCHIYA 1984). The sampling localities of Cheju and Honshu Island karyotype (solid circle) and Hokkaido Island karyotype (solid square) are indicated.

Table 1 — Number of metaphase plates of *Sorex caecutiens* from Cheju Island, Korea. Number of karyotyped plates out of observed plates shown in parentheses.

Identity number	Sex	conventional staining	GTG staining
991019-3	♂	13 (6)	4 (4)
991013-2	♂	14 (6)	27 (6)
991016-3	♀	12 (6)	9 (2)

shinto from Honshu Island, Japan (Tada and Obara 1988; Tsuchiya 1984). Moreover, the G-banded karyotype of *Sorex caecutiens* from Cheju Island (Fig. 2b) seemed to be identical to that of *S. shinto* as reported by Tada and Obara (1988) and Tsuchiya (1984). Therefore, we did not find a distinct new chromosome race of the *S. caecutiens/shinto* group in the Cheju Island population.

The Cheju Island population of *S. caecutiens* has been geographically isolated from the others of the *S. caecutiens/shinto* group. Unlike the Hokkaido Island and Novosibirsk populations, its G-banded karyotype was quite similar to that of *S. shinto* from Honshu Island, Japan (Tada and Obara 1988; Tsuchiya 1984). Therefore, at least three chromosome races of *S. caecutiens* (Hokkaido Island, Novosibirsk, and Cheju Island races) have arisen from autosomal inversions. The distribution of chromosome races in East Asia is shown in Fig. 1. Based on molecular phylogenetic analyses, Ohdachi *et al.* (2001) reported that *S. shinto* is clearly separated from *S. caecutiens*, although both species form a monophyletic group. In addition, Ohdachi *et al.* (2003) used molecular data to place the Cheju Island population in the group consisting of *caecutiens* specimens from the Eurasian Continent. These findings are also sup-

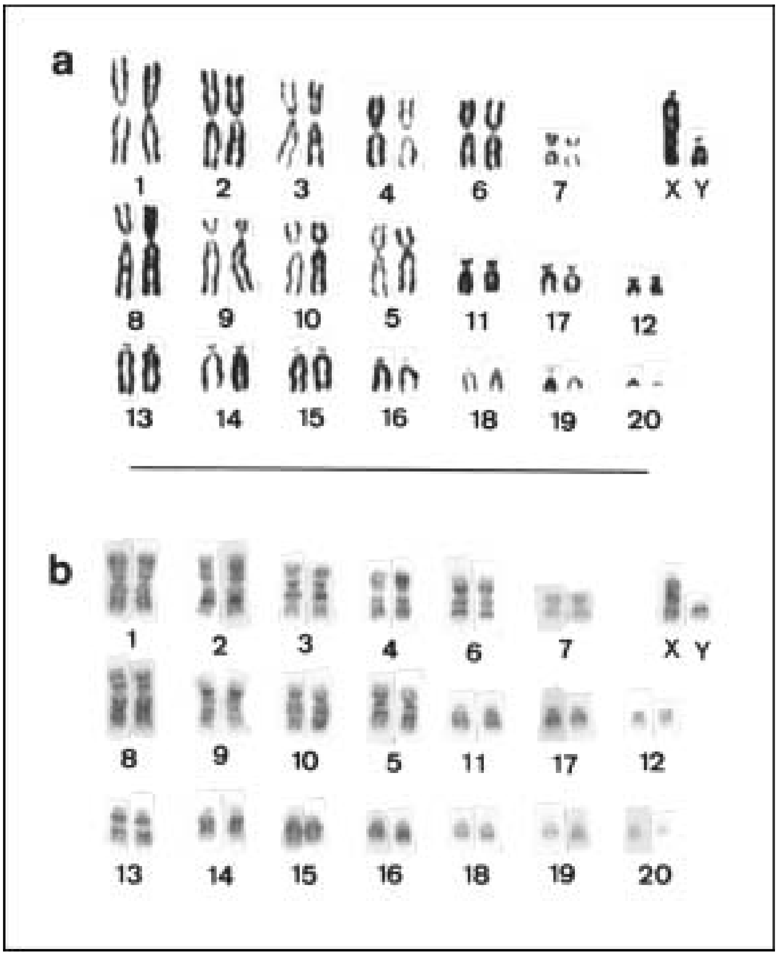

Fig. 2 — Conventional (a) and G-banded (b) karyotypes of a male *Sorex caecutiens* from Cheju Island of Korea. Metacentric, submetacentric or subtelocentric, and acrocentric autosomes are shown in the upper, middle, and lower lines, respectively. Both sex chromosomes are also shown in the upper right corner. Numbers correspond to those of *Sorex shinto* as reported by Tada and Obara (1988).

ported with analysis on the basis of restriction fragment length polymorphism of the nuclear ribosomal DNA spacer region (Naitoh 2003). The karyological relationships of the *S. caecutiens/shinto* group, however, do not correspond to these molecular phylogenetic relationships. The Cheju Island population is karyologically closer to *S. shinto* than to *S. caecutiens* of Hokkaido Island and Novosibirsk. Therefore, the karyotype shared by *S. shinto* and *S. caecutiens* of Cheju Island may be an ancestral character of the *S. caecutiens/shinto* group. The karyotypes of the Hokkaido Island and Novosibirsk populations would have derived from this ancestral karyotype by pericentric inversions. To test this supposition, further cytogenetical study of the *S. caecutiens/shinto* group by comparative chromosomal analysis of many specimens from different localities should be conducted with differential staining techniques.

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