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seals/km² in March and April, respectively) than those reported in eastern Sakhalin. A large number of pups suggest that the study area is an important breeding center.

A baseline for cranial features was obtained by examining the 23 measurements and 2 nonmetrical attributes of 152 seals collected at the Nemuro Strait, Hokkaido. The development of morphometrical characteristics of skulls ceased at 7.9 years and 11.9 years for males and females, respectively. The sutures were half ankylosed till approximately 10 years of age in both sexes. The sagittal crest appeared from about 5 years in

males. Large individual variations in the skull were noted in the feeding, breathing, and facial-expression apparatus.

In addition, genetic features of spotted seals in Hokkaido were investigated using mitochondrial DNA (mtDNA) sequencing. From 66 spotted seals, 57 haplotypes were identified. Phylogenetic trees did not indicate clear geographic differences between the Sea of Okhotsk and Japan coasts. It showed a high level of diversity in spotted seal mtDNA, and it is reasonable for the ecological features of this species to have a high mobile ability and be distributed over a wide range.

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Studies on Genetic and Morphological Characteristics and Conservation of Red Deer (*Cervus elaphus*) in Xinjiang, China

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Studies of genetic and morphological characteristics of red deer (*Cervus elaphus*), with implications for their conservation in Xinjiang, China.

This study was carried out based on the following four objectives :

1. To analyze the phylogenetic relationships among Chinese, European, and North American red deer.
2. To sample and analyze geographic variations of skull morphology in red deer of Xinjiang, China.
3. To assess genetic diversity of the Tarim red deer subspecies based on studies of mi-

cro-satellite DNA.

4. To suggest conservation measures to protect red deer populations, based on data of the present study.

The main parts of this dissertation are as follows :

1. Molecular Phylogeography of the Red Deer (*Cervus elaphus*) Populations in Xinjiang of China : Comparison with Other Asian, European, and North American Populations

To determine the phylogeography of red deer (*Cervus elaphus*) populations of Xinjiang,

we identified control region sequences, and then compared geographic variations and phylogenetic relationships among Xinjiang populations and other populations from Asia, Europe, and North America. The red deer mtDNA control region included different copies of tandem repeat sequence of 38 to 43-bp motifs. This allowed us to clearly distinguish the Western lineage from the Eastern lineage of this species in Eurasia. The western lineage was evident among the Tarim populations from southern Xinjiang and the European populations, all of which had four copies of the motifs. By contrast, the Eastern lineage consisted of populations from northern Xinjiang (Tianshan and Altai Mountains), other Asian areas (Alashan, Gansu, Tibet, Mongolia, and northeastern China), and North America, all of which shared six copies of the motifs. MtDNA phylogenetic trees showed that there are two major clusters of haplotypes associated with the Western and Eastern lineages, and that sub-groupings of haplotypes in each cluster were congruent with their geographic distributions. The present study revealed that a geographic boundary separating the Western lineage from the Eastern lineage exists between the Tarim Basin and the Tianshan Mountains in Xinjiang. The phylogenetic proximity of North American populations with those of northern Xinjiang, northeastern China, and Mongolia, supports the view that red deer migrated from northeastern Eurasia to North America along the land-bridge (Beringia) formed between the two continents during late Pleistocene glaciation.

2. Geographic Variations of Skull Morphology in the Red Deer (*Cervus elaphus*) of Xinjiang, China

Variations of 14 cranial morphological characteristics of Xinjiang red deer (*Cervus*

elaphus) were investigated using multivariate principle component analysis of samples from three distinct populations (Tarim, Tianshan, and Altai populations). Deer from the Altai population had greater PRIN 1 values and smaller PRIN 2 values than those from the Tarim population. PRIN 1 and PRIN 2 values for deer from the Tianshan population were intermediate to values for the other two populations, but were closer to values for the Altai deer. Habitats of Altai and Tianshan populations are characterized by coniferous forests and a cold climate, whereas those of the Tarim population are riparian poplar forests in desert regions with hot summers. Morphological similarity of deer from the Altai and Tianshan populations may reflect the similarity of habitat, while the unique morphological characteristics of Tarim deer may reflect adaptations to a desert climate.

3. A Preliminary Study of the Genetic Diversity of the Xinjiang Tarim Red Deer (*Cervus elaphus yarkandensis*) Based on Microsatellite DNA Analysis

To evaluate the genetic diversity of the Xinjiang Tarim red deer (*Cervus elaphus yarkandensis*) population, we analyzed the frequencies of microsatellite alleles. Samples were collected from three isolated populations in Xaya, Lopnur and Qarqan of Xinjiang. Although 10 microsatellite loci were examined, alleles of 133 to 190 base-pairs were detected for only three loci: BM5004, BM4208 and BM 888. The average observed multilocus heterozygosity was 0.08 ± 0.04 for the Xaya, 0 for the Lopnur, and 0.17 ± 0.08 for the Qarqan population. The average heterozygosity of all populations was 0.08 ± 0.02 . The observed heterozygosities were significantly lower than the expected values. The present results suggest that the bottleneck effect has occurred in

the populations of the Xinjiang Tarim red deer.

4. Conservation Status of the Endangered Tarim Red Deer, *Cervus elaphus yarkandensis*

Morphological and genetic analyses showed that the Tarim red deer belongs to the

western (European) red deer lineage and likely experienced an historic population bottleneck. These results suggest that the Tarim red deer is a unique subspecies which warrants higher level protection than its current status in China. Conservation programs should be implemented to stop the fragmentation and deterioration of habitat conditions.

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The physiology and life-history parameters of reproduction in Steller sea lions, spotted seals and ribbon seals from the coastal waters of Hokkaido

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Reproduction is the most important process in wildlife because it directly influences the viability of a population. This study was designed to better understand the physiology and life-history parameters of reproduction in Steller sea lions (*Eumetopias jubatus*), spotted seals (*Phoca largha*) and ribbon seals (*Phoca fasciata*) that migrate from Russian waters to the coastal waters of Hokkaido in winter.

The ovaries, uterus and placenta were collected from harvested female sea lions and seals that have been in the coastal waters of the Nemuro Strait, northeast Hokkaido, Japan, between late January and early April, 1995-1999. Thin sections were made for immunohistochemistry and histology analyses.

Firstly, I analyzed the localization of steroidogenic enzymes (P450 scc, 3 β HSD and P450 arom) in the corpus luteum and placenta of Steller sea lions, spotted seals and ribbon seals. P450 scc and 3 β HSD were present in all luteal cells of each corpus luteum, and

most luteal cells was immunostained for P450 arom. P450 scc and 3 β HSD immunostained negatively in placentae, however, P450 arom was present in the syncytiotrophoblasts. These findings suggest that (1) corpora lutea of these species synthesize pregnenolone, progesterone and estrogen during the late gestational period, and (2) placentae of these species are not capable of synthesizing progesterone, although they are capable of synthesizing estrogen. These characteristics are similar to those of some terrestrial carnivores in the suborder Caniformia.

Secondly, I analyzed the localization of prolactin receptors in the pregnant corpora lutea from the three pinniped species. Prolactin receptors were present in all luteal cells of each corpus luteum. This suggests that pinnipeds require prolactin to maintain corpora lutea during late pregnancy, as for other terrestrial carnivores.

The average age of sexual maturity in female Steller sea lions, based on the presence of corpora lutea or retrograde corpora lutea,