Title	Studies on spatial genetic structure in an expanding sika deer (Cervus nippon) population of Hokkaido : the implication for management [an abstract of dissertation and a summary of dissertation review]
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学位論文内容の要旨

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学位論文題名

Studies on spatial genetic structure in an expanding sika deer (*Cervus nippon*) population of Hokkaido: the implication for management
（個体数が増加し，分布が拡大しているエゾシカ個体群における遺伝的な空間構造に関する研究：個体群管理と関連させて）

Since the 1980s, the sika deer (*Cervus nippon*) population of Hokkaido, Japan, has grown, resulting in range expansion and overabundance, which led to the damage of agricultural land, forests, and natural vegetation, in addition to increased number of traffic collisions. The management and control of the deer population are critical for ecosystem management. Studies on spatial genetic structure of the deer population provide valuable information about conservation and management policies.

To assess the effects of this range expansion on the spatial genetic structure of the population, I compared subpopulation structures during two different periods (1991-1996, and 2008-2010), using mitochondrial DNA (D-loop) and microsatellite (9 loci). The number of gene-based subpopulations decreased across the 15-year period; specifically from four to three subpopulations based on mtDNA, and from two to one subpopulation based on microsatellite DNA. The fusion of the two northern subpopulations caused the change to the mtDNA-based structure, which might be explained by the dispersal of females from higher to lower density subpopulation. In comparison, the reason for the change in the microsatellite DNA-based structure was unclear, because no significant genetic differentiation was observed between the two study periods. A stable mtDNA-based structure was maintained in the north and central area separated by a west-to-east boundary, while a north-to-south boundary in eastern Hokkaido maintained stability in the eastern subpopulation versus all other subpopulation.

To answer whether genetic differentiation occurs associated with migratory partitioning (migratory and philopatry), I analyzed mtDNA and microsatellite DNA genetic features of female sika deer that were radio-tracked by Igota et al. (2004). The two clusters (cluster mt1 and mt2) that were detected based on mtDNA analyses showed highly significant genetic differentiation. However, these clusters did not perfectly match migratory habits (migrants and non-migrants). Cluster mt1 consisted of migrants and non-migrants, while only migrants were found in cluster mt2. Similarly, individuals belonging to the two clusters (cluster ms1 and ms2) that were detected based on microsatellite DNA analyses did not perfectly match migratory habits. Cluster ms1 consisted of migrants and non-migrants, while only migrants were found in cluster ms2. Individuals belonging to both of cluster mt1 and ms1 were seven, while individuals belonging to both of cluster mt2 and ms2 were 13. The seven were migrants that moved toward the north from their wintering site in summer, while 10 of the 13 were non-migrants that did not leave their wintering site in summer. The seven and 10 individuals were distinctive about both mtDNA and microsatellite DNA features, and they showed the same migratory habit. These results indicate that there were genetically distinctive group associated with migratory habits in a sika deer population in Hokkaido.

In Hokkaido, the Conservation and Management Plan for Sika deer (CMPS) has been encouraging hunters to target female sika deer in areas of high population density, because the removal of adult females with high reproductive value represents the most efficient strategy of controlling abundant populations. The management units (MUs) of CMPS are defined as western and eastern subpopulations, differing from the subpopulation structure identified in this study. These MUs may not demographically work well, because female-biased hunting effort in mtDNA-based subpopulation 2000mtE would not impact the neighboring subpopulation 2000mtN. Since the dispersal of females between 2000mtE and 2000mtN was limited, the 2000mtN population size would continue to increase, despite the successful control of the 2000mtE. Therefore, the management units should be revised based on an mtDNA-based structure identified in this study.