

**F-1 Analysis and Conservation of Biodiversity on a Geographical Scale (Abstract of the Final Report)**

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### 1. Introduction

Rapid decrease of biodiversity in recent years on the worldwide scale urges to investigate the surviving mechanism of wild species and build a proper plan to conserve those species. Local populations of wild species usually have individual organisms emigrate to each other. This type of connection through the movement of individuals, which is forming a metapopulation, is disrupted if their habitat areas are lost or fragmented through urbanization and land development. As the disruption of connection between populations could multiply the extinction rate of the wild species, the understanding of population networks is crucial to biodiversity conservation.

It is, however, not easy to address to how a particular species respond to the habitat fragmentation. A variety of geographical components may be involved in habitat utilization of wild species, so that objective evaluation is hindered by a mixture of topography, climate, geology, and human activity. Furthermore, the species-specific ecology and behaviors complicate the response, masking the relationship between organisms and their habitat. GIS (geographical information system)-based databases and GIS computer applications may improve these problems in order to enable the statistically-oriented analysis of the relationship.

On the other hand, certain types of genetic traits are strongly affected by the movement of individuals between local populations, thus reflecting the degree in which the connection between populations persists. Genetic analysis with proper genetic markers may describe how strong and in which way local populations are connected. Integration of the GIS techniques and the genetic marker procedure would offer a strong tool to the analysis and conservation of biodiversity on the geographical scale.

### 2. Research Objective

One of the major factors causing the decline of biodiversity is habitat loss and fragmentation by human activities. We aimed to investigate how populations of wild species utilize habitat environment and how habitat arrangement affects the survival of populations, especially in the case of fragmentation. In order to do this study, we planned to compile GIS-based databases of distributions of target species and their habitat environment. From the databases, the relationship between wild species and habitat could be formulated to enable mapping of species distribution according to changes in habitat conditions. If mathematical modeling of the relationship is accomplished, that will help to

extend our reaching points to a much broader geographical scale. We also aimed to analyze the connection between populations by adopting the genetic markers. If we succeed to select or develop proper genetic markers in the analysis of the uniqueness and relatedness of populations and species, that will help to evaluate the value of local biodiversity as well as to assess the integrity of populations as a metapopulation.

### 3. Methods

We compiled available data of distributions of wild species and their habitat into GIS-based database in the ArcView (ESRI) data format. The data sources were the surveys of fauna and flora performed by the Japanese Government, municipal offices and ourselves. On those databases, we analyzed the relationship between the species and the environmental components by using the regression analysis or other models such as the individual-based model. Genetic analysis was performed using genetic markers selected from mitochondrial DNA, nuclear microsatellite DNA and allozymes. Relatedness between populations and related species were estimated with the genealogical computer programs such as Phylip 3.5c.

### 4. Results

#### F-1.1.1 Association between Habitat and Wildlife in a Geographical Scale

The watersheds of Naka River and lower Tone River in Ibaraki and Tochigi Prefectures were chosen as case study areas of regional conservation planning. Geographical features, vegetations and patterns of land use in 1960s and 1990s and data sets of the fauna from the National Survey on the Natural Environment made by the Ministry of the Environment were integrated into GIS-based databases. In the about 30- year period, extensive areas of paddy and crop fields were transformed into housing and industrial area and coniferous forest plantations were transformed into deciduous secondary forest. Extensive reed beds along riverside and lakeshores got shrank and fragmented in that period, but the total area of reed beds was almost consistent because many small isolated reed beds were formed on abandoned paddy fields. The habitat suitability analysis models which provide the distribution of potential habitat useful for conservation planning were developed for the damselfly and the great reed warbler. Habitat suitability for the damselfly was explained by vegetation cover on the stream, warmth index, and altitude with the accuracy of 80%. The occurrence probability of the warbler in a reed bed was explained by the altitude of the reed bed and the distance from the nearest large reed bed. Habitat suitability for the great reed warbler was influenced by the arrangement of reed beds as well as their quality. The level of irreplaceability<sup>1)</sup> identifies the priority area for conservation planning. New calculation algorithms for irreplaceability were developed, which drastically reduced calculation time. Calculated irreplaceability in Kanto area revealed that the priority area was present in the urbanized area as well as in natural and suburban areas.

#### F-1.1.2 Situation, Movement and Factorial Analysis of Shrinkage and Fragmentation of Habitat on a Geographical Scale

In the alluvial fan, pumping-up of groundwater for agricultural use lowers levels of groundwater and spring water. In turn, water flows of rivers on the alluvial fan is reduced and, even interrupted in some sections temporally. This type of physical fragmentation of river flow may influence biodiversity in a bad way. We investigated the present condition of fragmentation of rivers and the influence of fragmentation on fishes in the Nasunogahara fan.

In the Nasunogahara fan, the land cover was greatly transformed from forest to paddy

fields during the period of 1940s -1960s. The increase of paddy fields brought about fall of the groundwater level, and the reduction of forest spoiled the ability of recharging groundwater. Then, the groundwater level was lowered further. In early spring the pumping-up of irrigation water was in a great volume and the groundwater level fell more than 10 m. It was the major factor of drying up or reducing spring water, which was abundant at the center of the fan before.

The Dou River, a tributary of Naka River, flows through the area where land use was greatly altered and many weirs for agricultural irrigation were created. The physical fragmentation of rivers occurred owing to lowered groundwater level and pump-up of irrigation water. We revealed that the level of physical fragmentation was strong enough to inhibit fish movements along the river course, being a major factor of reducing fish diversity.

#### F-1.2 Studies on the Effects of Interactions between Biotopes on the Grassland Biodiversity

Grasslands not only conserve diversified organisms specific to the grasslands, but also threaten the local biodiversity by establishment of alien plants and invasion of those plants from the grasslands. This study evaluated the positive and negative contributions of grasslands to the grassland insect diversity and local plant diversity by landscape-scale biological surveys and analyses using GIS .

Dung beetles and horseflies were surveyed in 18 pastures in the basin of Naka River, Tochigi, over three years. Diversity and community structures of those insects in the pastures were clarified. Geographical and biological factors that influence on the distribution and community structure of the insects were also elucidated by multivariate statistical analyses. The model estimating the dung beetle diversity was obtained using fractal dimensions of landscape elements around the pastures. The mapping of dung beetle diversity in Tochigi was performed using the model.

Distribution maps of exotic weeds, which invaded into Japan via imported grains, were established in the Basin of Naka River. The habitat of these weeds was different from each other. The target species were classified into two groups namely, species existing only in farm area and species existing also out of farm area. As the result of logistic regression analysis, statistically significant formulas were obtained in all species analyzed. The formulas fitting well are considered to be applicable to the nationwide estimation of the weeds, after verification in the other areas.

##### F-1.3.1 Metapopulation Analysis of Threats to Local Populations

The genetic and ecological investigations of local populations of three species, the threespine stickleback (*Gasterosteus aculeatus*), the Japanese clouded Apollo butterfly (*Parnassius glacialis*), and the bumblebees (*Bombus* spp.), were conducted to delineate how these populations have been diversified and how they can be conserved. Genetic markers such as microsatellite genes, mitochondrial genes, and allozymes worked well in this investigation in clarifying genealogical relationships among the local populations. Therefore, it is crucial in conserving local populations to find proper genetic markers. Local populations had unique features of genetic compositions and ecological habits marked by the units of the topography of terrain and water body. These units often coincided with the river basin or sub-basin. Conservation planning of local populations should take into account river basins as the basis of conserved area. Ecological habits especially concerning about breeding habits were revealed to keep the uniqueness of local populations as behavioral barriers.

Indiscriminate transplanting and accidental introduction of individuals from other populations would damage the uniqueness of the target population, or even delay the recovery of threatened populations.

#### F-1.3.2 Spatial and Temporal Dynamics of Bird Colonies

Colonial birds can be a good indicator to monitor environmental changes in a regional scale because they use several habitat types within a large home range. The primary purpose of this study is to develop a new technique to monitor colonies of birds and their habitat efficiently.

We selected colonial egrets (family Ardeidae) as the model birds because they share breeding colonies, but differ in habitat selection for foraging. Breeding colonies were searched by aerial survey in Ibaraki and Shiga Prefectures. Aerial survey was very efficient to find breeding colonies; we took only a few days to find about 20 colonies in the Ibaraki area of 6,000km<sup>2</sup>. Population sizes were estimated by the combination of counting egrets on aerial photographs and counting egrets departing from colonies. The density of egrets was not different between the two regions, but piscivorous species were more common in Shiga region, where the density of foraging egrets in rivers was much higher than in Ibaraki.

#### F-1.4 Analysis of Metapopulation Structure and Genetic Diversity of Wildlife

We studied the structure of metapopulation and genetic diversity of wildlife mammals and birds to establish the conservation for wildlife biodiversity. Distribution of the Japanese squirrel *Sciurus lis* in the western Tokyo City were affected by forest fragmentation. Squirrels living in better habitat tended to have smaller home ranges and live longer than those in worse habitat. Genetic variation decreased in populations of isolated forest, especially in females. The genetic status of Asian black bears *Ursus thibetanus* was examined using two molecular markers, microsatellite genes and mitochondrial genes in the western part of Honshu, Japan. Judging from the data obtained with both markers, the level of gene flow was very low among remaining populations. A numerical model of the Oshima Peninsula brown bear population was constructed by means of IBM (individual-based model), and the bears' tendency of dependence on human activity for food was examined. The results indicated that high ratio of human-dependent bears could lead both to severe bear hazard to human and to bear extinction. We developed four pairs of primers for amplification of mitochondrial 12S rRNA fragments in the black woodpecker and three other sympatric woodpeckers. Since each primer pair gave a PCR product in only one of the examined species, these primer sets will be useful in identifying the species of woodpeckers. We determined mitochondrial 12S rRNA and cytochrome *b* gene sequences of three species of Japanese leporids. The species were shown to be distinct from one another. The three regions of the Japanese archipelago have their own leporid taxon, each with a different extent of genetic endemism. Estimation of extinction risk based on ecological and genetic technique was useful to understand the structure of metapopulation and actual status of wildlife.

#### Discussion

Wild species with different habitat preferences and distributions on various geographical scales were investigated in this study. The GIS-based habitat suitability analysis proved to work well in describing the relationship between wild organisms and their habitat environment. The constructed mathematical models succeeded to explain the relationship

within our research areas. The models will work in a broader area, given that they are improved by parameter adjustment and incorporation of additional parameters, and help to proceed the conservation planning.

Genetic analysis with aid of appropriate genetic markers revealed the uniqueness and relatedness of populations and species ranging on a broad geographical scale. As genetic uniqueness is often related with ecological habitat preference, we should focus on the uniqueness in performing the habitat suitability analysis. Although this association was not integrated into our analysis of habitat-organism relationships, it will be helpful to take into account the genealogical grouping of local populations for habitat suitability analysis.

Establishing a reliable way to estimate the habitat of wild species on a geographical scale is very much helpful to performing conservation planning effectively. Applying indices such as irreplaceability make the process open and easy to review. Genetic information, of course, adds the uniqueness measure of local diversity to the process.

### **Reference**

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