

F-3.2.1 Specifications for a Management System of the Genetic Diversity Information of Rare Species of Wild Animals

Contact Person Makoto M. Watanabe
Section Director, Environmental Biology Division
National Institute for Environmental Studies
Environment Agency
Onogawa 16-2, Tsukuba, Ibaraki 305 Japan
Tel: +81-298-50-2555, Fax:+81-298-51-4732
E-mail: mmw@nies.go.jp

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Abstract The purpose of this study is to make a basic design for acquiring and storing a genetic information of endemic, rare, vulnerable or endangered species of wild animals. Basic information collected from the *ex-situ* population and natural population is separated into three categories; 1) taxonomic information including 5 and 6 items in natural and *ex-situ* populations, respectively, 2) breeding information including 12 and 14 items in natural and *ex-situ* populations, respectively, 3) environmental information including 10 and 25 items in natural and *ex-situ* populations, respectively. In addition to these basic informations, organ, tissue, cell and genetic characteristics were encoded. Breeding data of the inbred lines of Japanese quail (K-H and K-L) was processed at all 47 generations according to the format of breeding information. The egg-laying and hatching rates of K-H line tended to decrease from generation to generation, showing inbreeding depression.

Key Words breeding information, environmental information, *ex-situ* population, genetic information, inbreeding depression, Japanese quail, taxonomic information

1. Introduction

One of the important products of the United nations Conference on Environment and Development (UNCED) in June, 1992 in Rio de Janeiro points directly to the need for adopting measures for the *ex-situ* conservation of components of biodiversity¹⁾. In this case, data, information, knowledge, and wisdom are essential tools for facilitating the action program of comprehensive *ex-situ* conservation. In USA, information of threatened wild animals is systematically upgraded using modern computer technique. For example, in ISIS (International Species Inventory System), various information and data regarding wild animals including number of the breeding animals, birth place, age, sex, progeny, death rate, etc. have been encoded and processed in computer.

There are 72 kinds of endangered species and 65 kinds of vulnerable species in vertebrates in Japan. Especially, of 536 species of birds living in Japan, 119 species are listed as threatened species including 27 endangered, 27 vulnerable, and 65 rare species. So far 13 species of birds have been extinct. Nevertheless, no technology applicable for in-situ conservation has been developed and even database system of threatened animal species has not yet been established. So it is a matter of high priority to adopt measures for the *ex-situ* conservation of threatened animal species and to collect and process a genetic information of them. In the present study, as a first step to develop technique and system for *ex-situ* conservation of threatened animal species, a basic design for acquiring and storing a genetic information of threatened animal was made using birds as model animal.

2. Research Objective

The purpose of this study is to make a basic design for acquiring and storing a genetic information of endemic, rare, vulnerable or endangered species of wild animals.

Table 1. Items of breeding information of birds

Natural population	<i>Ex-situ</i> population
1) number of population	1) male and female number (0-9999)
2) male and female number	2) number of pairings (0-9999)
3) number of pairings	3) coefficient of blood kin (0-1)
4) hatching number	4) coefficient of inbreeding (0-1)
5) rearing number	5) adaptive index (0-100%)
6) relationship	6) egg-laying rate (0-100%)
7) symmetry	7) fertilization rate (0-100%)
8) nesting type	8) hatching rate (0-100%)
9) egg-laying time	9) rearing rate (0-100%)
10) egg-laying days	10) weight of eggs (0-10,000g)
11) number of eggs	11) weight (0-100kg)
12) others	12) discontinuance of development (0-100% at early stage of development, 0-100% at late stage, 0-100% death)
	13) mutation (plumage color:0-100%, deformation:0-100%)
	14) others

Table 2. Items of environmental information in birds

Natural population	<i>Ex-situ</i> population
1) habitat	1. Environmental Control
2) breeding region	1) air conditioning: temperature (0-60°C), humidity (0-100%), ventilation (0- 100/hr)
3) overwintering region	2) illumination condition: dark period (0- 24hr), light period (0-24hr), light intensity (0-5,000 lx)
4) flight route	3) feeding condition: foods (1-5), times (1- 9999), volume (0-10,000g)
5) number of coming flying	4) water condition: water quality (1-3), times (1-9999), volume (0-10L)
6) foods	5) rearing form: cage (1-5), density (1- 1000/m ³), form (1-10)
7) courtship behavior	6) others
8) rearing action	2. Microbial Control
9) environmental fluctuation	1) pathogenic inspection: grade (1-5), result (0-1)
10) others	2) microflora inspection: flora (1-5), result (0-1)
	3) food inspection: grade (1-5), result (0-1)
	4) inspection of water quality: water quality (1-3), result (0-1)
	5) others

3. Results

3-1. Specification for a management system of genetic diversity information

(1) Categories of fundamental information for *ex-situ* conservation of threatened animal species.

A.R

1. population (1/95)
2. male and female number (1 male)
3. number of pairings (0)
4. number of hatching (0)
5. rearing number (0)
6. egg-laying time (4 and 5 M)
7. number of eggs (0)

A.E.

1. distribution (Sado)
2. breeding region (Sado)
3. overwintering region (Sado)
4. flight route (0)
5. number of coming flying (0)
6. foods (X)
7. courship behavior (5)
8. rearing action (1)
9. environmental fluctuation (1)

Fig.1. Display of breeding (R) and environmental (E) information in natural population (A) of Japanese Crested Ibis, *Nipponia nippon*

Fundamental information collected from *ex-situ* population and natural population from which the former was originated is separated into three categories; i) taxonomic information, ii) breeding information and iii) environmental information.

i) Taxonomic information: This includes taxonomy (Phyla, Class, Order, Family, Genus, Species, Subspecies), individual name, sex, weight and morphological characteristics in the *ex-situ* and natural populations. In addition to these items, information on genetic background is included in the *ex-situ* population.

ii) Breeding information (Table 1): This includes 12 items in natural population and 14 items in the *ex-situ* population. The input of all items of breeding information of *ex-situ* population can be carried out with three processing patterns.

iii) Environmental information (Table 2): This includes 10 items in natural population. In the *ex-situ* population, this is separated into the environmental and microbial controls according to the concept of experimental zoology for artificial breeding and includes 25 items totally. The input of all items can be carried out with about ten processing patterns.

(2) Encoding organ, tissue, and cell of birds.

Satoh²⁾ encoded each of organ, tissue and cell according to anatomical classification in reference to "Veterinary Histological Terms" published by Gakuso-sha, Tokyo (1993). The organs of bird are classified to 14 categories including blood, cuticle system, locomotion system, digestive system, urinary system, male genital system, female genital system, respiratory system, circulatory system, nervous system, sensory system, hematopoietic system, endocrine system and others. A number of tissues and cells were encoded under the 14 categories. Our coding system is fundamentally similar to the Satoh's system but newly includes primordial germ cells.

(3) Encoding genes of birds

Chromosome numbers of birds are larger than those of mammals. For instance, the chromosome number of quail is $2n=78$ composed of large chromosome of six pairs and small one of 23 pairs. However, compared with mammals, little is known of genetic characteristics of birds. Here, genetic information of birds is separated into the three categories, 1) mutation loci including plumage color and isozyme, 2) immune response loci including MHC and T-cells, and 3) mitochondria DNA.

B.R.

- 1) male and female number (male 100, female 100)
- 2) number of pairings (21 /generation)
- 3) coefficient of blood kin (0.68)
- 4) coefficient of inbreeding (0.65)
- 5) adaptive index (41%)
- 6) egg-laying rate (82%)
- 7) fertilization rate (94%)
- 8) hatching rate (46%)
- 9) rearing rate (70%)
- 10) weight of eggs (7.8g)
- 11) weight (male 90g, female 110g)
- 12) discontinuance of development
(30% at early stage of development, 20% at late stage, 4% death)
- 13) mutation (plumage color:0%, deformation:0%)
- 14) others

B.E.

1. Environmental Control

- 1) air conditioning: temperature (23C), humidity (55%), ventilation (50/hr)
- 2) illumination condition: dark period (10hr), light period (14hr), light intensity (1,200 lx)
- 3) feeding condition: foods (1), times (9999), volume (15g/day)
- 4) water condition: water quality (2), times (9999), volume (0.01L/day)
- 5) rearing form: cage (1), density (100/m³), form (1)
- 6) others

2. Microbial Control

- 1) pathogenic inspection: grade (1), result (0)
- 2) microflora inspection: flora (1), result (0)
- 3) food inspection: grade (5), result (0)
- 4) inspection of water quality: water quality (3), result (0)
- 5) others

Fig. 2. Display of breeding (R) and environmental (E) information of *ex-situ* population (B) of 40th generation of Japanese Quail, *Coturnix japonica*

3-2. Output of data and information

All the data contained in our management system are displayed according to the format shown in Figs. 1 and 2.

3-3. Application of the management system

The inbred lines of Japanese quail (K-H and K-L) have been maintained over 47 generations in the National Institute for Environmental Studies. Breeding data was processed at every generation according to the format of breeding information as shown in Table 1. The changes of breeding ability including fertilization rate, egg-laying rate, hatching rate and death rate can be displayed over 47 generations as shown in Fig. 3. From this figure, it is clear that egg-laying and hatching rates tend to decrease from generation to generation, showing inbreeding depression. Further analysis on these data will allow us to predict the generation time when the inbred line K-H will be extinct and to analyze the embryological or genetic factors responsible for inbreeding depression.

We are now trying to visualize the huge data by converting them into an appropriate graphic expression so that we can easily find the interesting phenomena .

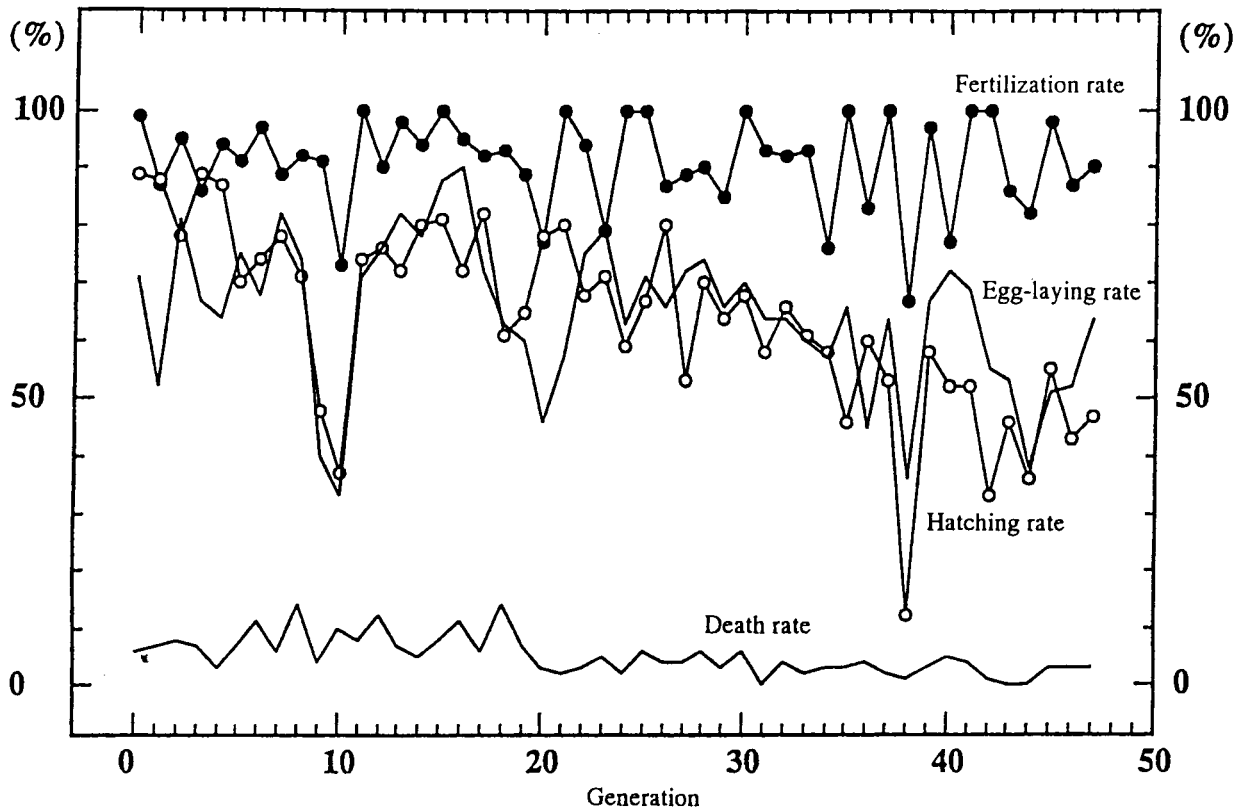


Fig. 3. Changes of breeding ability of inbred line (K-H) of Japanese quail

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