Erratum

Replacement of legend for Figure 1 appeared in The Journal of Poultry Science 52 (3): 167–175, 2015:

Fig. 1. Avian species designated as “nationally endangered species of wild fauna and flora” under the conservation and propagation programs. (A) Short-tailed albatross (*Diomedea albatrus*), (B) Japanese Crested Ibis (*Nipponia nippon*), (C) Japanese crane (*Grus japonensis*), (D) Blakiston’s fish owl (*Ketupa blakistoni blakistoni*), (E) Golden eagle (*Aquila chrysaetos japonica*), (F) Okinawa woodpecker (*Sapheopipo noguchii*), (G) White’s thrush (*Zoothera dauma major*), (H) Amami Woodcock (*Scolopax mira*), (I) Common Murre, Guillemot (*Uria aalge inornata*), (J) Tufted Puffin (*Lunda cirrhata*), (K) Okinawa Rail (*Gallirallus okinawae*), (L) White-tailed eagle (*Haliaeetus albicilla albicilla*), (M) Steller’s sea eagle (*Haliaeetus pelagicus*), (N) Japanese wood pigeon (*Columba janthina nitens*), (O) Ptarmigan (*Lagopus mutus japonicas*)
As of 2014, 89 species have been legally designated as “nationally endangered species of wild fauna and flora,” including 37 avian species in Japan. To facilitate the breeding of endangered species and the maintenance of protected habitats, a program for the rehabilitation of natural habitats and maintenance of viable populations is being established by the Ministry of the Environment and other related ministries for 49 of the species on the above list. The programs have already been established for 15 such avian species, and are currently managed by zoos or local authorities. Maintaining genetic diversity is necessary to ensure the stable procreation of endangered species. A decline in breeding potential due to inbreeding can be prevented by careful maintenance of genetic diversity. In addition to the prevention of inbreeding depression, the maintenance of genetic diversity safeguards species’ resistance to pathogens, as well as their capacity to cope with environmental change. This manuscript reports on the status of currently available genetic information for nationally endangered avian species in Japan, with a particular focus on the 15 species included in the conservation and propagation program. In the NCBI “Nucleotide” database, 315 entries were related to sequence information from the 15 endangered species. Mitochondrial DNA-related sequences constituted 238 (75.6%) of these entries. In the NCBI “Genome” database, genome sequence entries for three species were found. As is the case with mitochondrial DNA, microsatellite loci are very useful for endangered species conservation to evaluate genetic diversity. However, information about the endangered avian species’ microsatellite makers is limited. This situation could have a considerable negative impact on captive breeding projects in particular. Hence, the development of microsatellite markers for these species is a priority.

Key words: microsatellite, mitochondrial DNA, nationally endangered species

What are “Nationally Endangered Species of Wild Fauna and Flora”?

With the aim of preserving biodiversity and the natural environment, thus enabling human habitants to maintain a healthy lifestyle, the Act for the Conservation of Endangered Species of Wild Fauna and Flora was established in 1992 (last revised in 2014). The details of this law were made publicly available by the Ministry of Environment, Japan (MOE), on a dedicated website: http://www.env.go.jp/nature/yasei/hozonho/index.html.

According to Article 4 of the act, species that are faced
porting stable populations. Maintenance of genetic diversity is also necessary to ensure stable procreation. A decline in breeding potential due to inbreeding can be prevented by maintaining genetic diversity. In addition to the prevention of inbreeding depression, the maintenance of genetic diversity also promotes a continuing ability to resist pathogens, as well as a capacity for adapting to changes in habitat environment. In this paper, the status of genetic information on the avian species included on the list of nationally endangered species in Japan was presented, and in particular, the 15 avian species for which the conservation and propagation programs were established.

Status of Genetic Data Available for Avian Species Included in the Conservation and Propagation Program

The availability of genetic information for the 15 avian species, as of December 2014, was investigated using the National Center for Biotechnology Information (NCBI) “Nucleotide” and “Genome” databases. The scientific names

<table>
<thead>
<tr>
<th>Species</th>
<th>Endemic in Japan</th>
<th>Population in Japan</th>
<th>Program planner</th>
<th>Authorities to conduct the program</th>
</tr>
</thead>
<tbody>
<tr>
<td>White’s thrush (Zoothera dauma major) (subspecies) (Singing birds)</td>
<td></td>
<td>***83</td>
<td>Environment Agency, MAFF (1999)</td>
<td></td>
</tr>
<tr>
<td>Common Murre, Guillemot (Uria aalge inornata)</td>
<td></td>
<td>***20</td>
<td>Environment Agency (2001)</td>
<td></td>
</tr>
<tr>
<td>Tufted Puffin (Lunda cirrhata)</td>
<td></td>
<td>***10 pairs</td>
<td>Environment Agency (2001)</td>
<td></td>
</tr>
<tr>
<td>Steller’s sea eagle (Haliaeetus pelagicus) (wintering number)</td>
<td></td>
<td>***1,400–1,700</td>
<td>Environment Agency, MAFF, MLIT, MOE (2005)</td>
<td></td>
</tr>
<tr>
<td>Ptarmigan (Lagopus mutus japonicas)</td>
<td></td>
<td>***3000</td>
<td>Environment Agency, MAFF, MOE (2012)</td>
<td></td>
</tr>
</tbody>
</table>

of each species were used as search keywords. From the search results, the data from genetic analyses of populations endemic to Japan were selected. When the number of hits was very high, “Scientific name + JAPAN” was used as a keyword to filter the results.

In the “Nucleotide” database, the total number of entries relating to sequence information from the 15 endangered bird species was 315 (Table 2.). Sequences relating to mitochondrial DNA constituted 238 (75.6%) of the 315. The 238 sequence entries included four full-length mitochondrial genome sequences (Japanese Crested Ibis (Nipponia nippon): 2, Okinawa rail (Gallirallus blakistoni blakistoni): 2), 101 D-loop sequences, 74 COI sequences, 46 control region sequences, five 12S rRNA sequences, three Cytb sequences, and five other sequences. In the “Genome” database, genome sequence entries for three species were found, including Japanese Crested Ibis (1,201.48 Mb, Accession No. JMFH 00000000), Golden Eagle (Aquila chrysaetos) (923.79 Mb JJRL00000000.1), and White-tailed Eagle (Haliaeetus albicilla) (923.79 Mb JJRL00000000.1).

General Information and Status of Genetic Data Registration for Each Avian Species Included in the Conservation and Propagation Program

(Species information in this section was obtained from the Japan Integrated Biodiversity Information System (J-IBIS; http://www.biodic.go.jp/J-IBIS.html)

IUCN 2014 (The IUCN Red List of Threatened Species. Version 2014.3.; http://www.iucnredlist.org) unless otherwise noted.

The abbreviated form of ministries’ names appeared in this
section are as follows:
The Ministry of Education, Culture, Sports, Science and Technology: MEXT
The Ministry of Agriculture, Forestry, and Fisheries: MAFF
The Ministry of the Environment: MOE (The ministry was established in 2001 reforming from the Environmental Agency.)
The Ministry of Land, Infrastructure, Transport and Tourism: MLIT

Short-tailed Albatross (Diomedea albatrus) (Fig. 1 (A))

The conservation and propagation program of the Short-tailed Albatross was compiled by the Environment Agency in 1993. The program was subsequently revised by MEXT, MAFF, and MOE in 2006. The Tokyo Metropolitan government and the Yamashina Institute for Ornithology were officially accredited as the authorities driving this program.

This species was considered extinct in 1949 due to over-exploitation by the feather trade, but around 10 individuals were discovered on Torishima Island in 1951. Another population was found on Minamikojima Island (Senkaku Islands) in 1971. Currently, this species is widely distributed in the Northern Pacific Ocean, and continues to breed on Torishima Island and Minamikojima Island. In addition, in 2010, a single chick hatched on Midway Atoll. The estimated global population was 2,364 individuals (1,922 birds in the Northern Pacific Ocean, and continues to breed on Torishima Island and Minamikojima Island. In addition, in 2010, a single chick hatched on Midway Atoll. The estimated global population was 2,364 individuals (1,922 birds on Torishima Island and 442 birds on Minamikojima Island) during the breeding season of 2006–2007.

Eighty-three entries of sequence information are registered in the NCBI “Nucleotide” database. There are 82 mitochondrial DNA sequences: 46 control region sequences (Eda et al., 2010; Kuro-o et al., 2010), 29 D-loop sequences (Eda et al., 2011, 2012), three mitochondrial Cytochrome Oxidase Subunit I (COI) sequences (Saitoh et al., 2015) and four mitochondrial DNA sequences including Cytb-1, ND6-1, ND6-2 genes for Cytb, NADH dehydrogenase subunit 6, complete cds; Cytb-2 pseudogene for Cytb; tRNA-Thr-1, tRNA-Thr-2, tRNA-Pro-1, tRNA-Pro-2, tRNA-Glu-1, tRNA-Glu-2, complete sequence; control region 1 complete sequence and control region 2 partial sequence (Eda et al., 2010). In addition, one DRD4 gene sequence (Abe et al., 2011) is registered. There is no whole-genome sequence data for this species in the Genome database.

Japanese Crested Ibis (Nipponia nippon) (Fig. 1 (B))

The conservation and propagation program of the Japanese Crested Ibis was compiled by the Environment Agency in 1993. The program was subsequently revised by MAFF, MLIT, and MOE in 2004. Sado city, Ishikawa prefecture (Ishikawa zoo), Izumo city, Nagaoka city, and Niigata University were officially accredited as the authorities responsible for the program.

Historically, the habitat of the Japanese Crested Ibis included the Russian Far East, Japan, and People’s Republic of China (PRC), the Korean peninsula, and Taiwan. The Japanese population of the species went extinct in 2003. The only remaining wild population is distributed only in PRC (about 500 individuals in 2006). Captive breeding was successful in Japan using individuals presented by PRC. The captive population reached 221 as of August 1, 2014 (MOE, http://www.env.go.jp/nature/toki/sect_re/07mat01.pdf). A reintroduction program in Japan was started in 2008 and 159 individuals were released as of September 8, 2014 (MOE, http://www.env.go.jp/nature/toki/sect_re/07mat02.pdf).

Twenty-three entries of sequence information are registered in the NCBI “Nucleotide” database. These include 12 registered sequences originating from mitochondrial DNA: two complete sequences (Accession No. NC_008132, AB104902), five D-loop sequences, four COI sequences (Saitoh et al., 2015), and one Cytb sequence (Accession No. AB044287). In addition, the genes for three MHC class II molecules (Accession No. 872444, AB872442, AB872443), two Dopamine receptors D4 (Accession No. AB856529, AB856530), one BRD2 gene (AB890383), one PGH α gene (AB089503), one FSH β gene (AB089502), one TSH β gene (AB089501), one non-W CHD gene (AB049444), and one W-linked CHD gene (AB049443) are registered. The whole-genome sequence is registered in the “Genome” database (1,201.48 Mb, Accession No. JMFH00000000).

Japanese Crane (Grus japonensis) (Fig. 1 (C))

The conservation and propagation program of the Japanese Crane was compiled by the Environment Agency, MAFF, and the Ministry of Construction in 1993. This species occurs in East Asia. The main breeding ground of this species is along the Amur River and its tributary. In addition, there is a wild population located in eastern Hokkaido. The main wintering grounds of the mainland population are the Yellow River delta and the coast of the Jiangsu province, PRC, and the Demilitarized Zone between North Korea and South Korea. The Hokkaido population is not migratory. The population size across the entire range of the species is presumed to be 2,750 individuals, of which approximately 1,200 individuals are distributed in eastern Hokkaido.

Twenty-three entries of sequence information are registered in the NCBI “Nucleotide” database. The sequence information derived from mitochondrial DNA consists of 16 sequences: 12 D-loop sequences (Hasegawa et al., 1999; Miura et al., 2013; AB669093; AB669094; AB669095), three COI sequences (Saitoh et al., 2015), and one 12S rRNA to ND6 (Hasegawa et al., 1999). In addition, seven micro-satellite regions (gt, ca, and tc repeat region) (Hasegawa et al., 2000) are registered. No whole-genome sequence data for this species is registered in the “Genome” database.

Blakiston’s Fish Owl (Ketupa blakistoni blakistoni) (Fig. 1 (D))

The conservation and propagation program of the Blakiston’s Fish Owl was compiled by the Environment Agency and MAFF in 1993. Kushiro city (Kushiro city zoo) and Nemuro city were officially accredited as the authorities responsible for the program. This species is distributed in the Russian Far East, PRC, and Japan. A subspecies, Ketupa blakistoni blakistoni, occurs in Hokkaido. The number of
Fig. 1. Avian species designated as “nationally endangered species of wild fauna and flora” under the conservation and propagation programs. (A) Short-tailed albatross (Diomedea albatrus), (B) Japanese Crested Ibis (Nipponia nippon), (C) Japanese crane (Grus japonensis), (D) Blakiston’s fish owl (Ketupa blakistoni blakistoni), (E) Golden eagle (Aquila chrysaetos japonica), (F) Okinawa woodpecker (Sapheopipo noguchii), (G) White’s thrush (Zoothera dauma major), (H) Amami Woodcock (Scolopax mira), (I) Common Murre, Guillemot (Uria aalge inornata), (J) Tufted Puffin (Lunda cirrhata), (K) Okinawa Rail (Gallirallus okinawae), (L) White-tailed eagle (Haliaeetus albicilla albicilla), (M) Steller’s sea eagle (Haliaeetus pelagicus), (N) Japanese wood pigeon (Columba janthina nitens), (O) Ptarmigan (Lagopus mutus japonicas)
individuals occurring across the entire range of the species is estimated to be 1,500–4,000. The Hokkaido population is composed of about only 120 individuals. Sixty-four entries of sequence information are registered in the NCBI “Nucleotide” database. There are 13 sequences derived from mitochondrial DNA: seven D-loop sequences (Omote et al., 2013), five COI sequences (Saitoh et al., 2015), and one Cytb sequence (Omote et al., 2013). In addition, 49 centromere repeat region sequences (Yamada et al., 2004) and two W-chromosome sex markers (AB536728; AB536729) are registered. No whole-genome sequences have been entered in the “Genome” database.

**Golden Eagle (Aquila chrysaetos japonica) (Fig. 1 (E))**

The conservation and propagation program of the Golden Eagle was compiled by the Environment Agency and MAFF in 1996. This species is widely distributed across the northern hemisphere. Aquila chrysaetos japonica, one of its subspecies, occurs in the mountainous area from Hokkaido to Kyushu in Japan. The number of individuals populating the entire range of the species’ distribution is presumed to be 170,000 individuals. It is estimated that less than 500 individuals inhabit Japan. Eleven entries of sequence information are registered in the NCBI “Nucleotide” database. Five D-loop sequences (Masuda et al., 1998), one COI sequence (Saitoh et al., 2015), and one 12SrRNA sequence (Nobata et al., 2007) were derived from mitochondrial DNA. Additionally, two CHD1Z (Ito et al., 2003) and two CHDW (Ito et al., 2003) sequences are registered. Moreover, the Golden Eagle’s whole-genome sequence data is registered in the “Genome” database (1,192.73 Mb, Accession No. JRUM00000000.1).

**Okinawa Woodpecker (Sapheopipo noguchii) (Fig. 1 (F))**

The conservation and propagation program of the Okinawa Woodpecker was compiled by the Environment Agency and MAFF in 1998. The species is endemic to Japan, with multiple subspecies distributed in an evergreen broadleaf forest of northern Okinawajima Island. The population is estimated to comprise approximately 150–584 individuals. There are four sequences originating from mitochondrial DNA registered in the NCBI “Nucleotide” database: two COI sequences (Saitoh et al., 2015), one Cytb sequence (Winkler et al., 2005), and one 12SrRNA sequence (Winkler et al., 2014). Whole-genome sequence analysis data for this species is not registered in the “Genome” database.

**White’s Thrush (Zoothera dauma major) (Fig. 1 (G))**

The conservation and propagation program of the White’s Thrush was compiled by the Environment Agency and MAFF in 1999. The species is endemic to Japan, with the subspecies distributed only on Amami Oshima Island. The number of individuals was estimated to be 83 in 2002. Twenty mitochondrial DNA COI sequences (Saitoh et al., 2015) and one AVT2R sequence (Abe et al., 2012) are registered in the NCBI “Nucleotide” database. No whole-genome sequence analysis data is registered in the “Genome” database.

**Amami Woodcock (Scolopax mira) (Fig. 1 (H))**

The conservation and propagation program of the Amami Woodcock was compiled by the Environment Agency and MAFF in 1999. The species is endemic to Japan, distributed on Amami Oshima Island, Kakeromajima Island, Tokunoshima Island, Okinawajima Island, and Tokashikijima Island. The population is estimated to be comprised 3,500–15,000 individuals. There are six mitochondrial DNA COI sequences (Saitoh et al., 2015) registered in the NCBI “Nucleotide” database. No genome analysis sequence data is registered in the “Genome” database.

**Common Murre, Guillemot (Uria aalge inornata) (Fig. 1 (I))**

The conservation and propagation program of the Guillemot was compiled by MOE in 2001. The species is distributed across the low-arctic and boreal waters of the north Atlantic and north Pacific. The estimated number of individuals occurring across the entire distribution regions is about 18 million. Uria aalge inornata is one of the subspecies found in Japan. Teuritou Island in Hokkaido is one of its breeding grounds. The estimated number of individuals of this species on Teuritou Island is only approximately 20.

One COI mitochondrial DNA sequence (Saitoh et al., 2015) originating from Japanese data is registered in the NCBI “Nucleotide” database. No known genome analysis has been conducted.

**Tufted Puffin (Lunda cirrhata) (Fig. 1 (J))**

The conservation and propagation program for the preservation of the Tufted Puffin was compiled by MOE in 2001. The species is widely distributed across the subarctic zone of the North Pacific. One of its Japanese breeding areas is in eastern Hokkaido. The population of this particular species is declining, with the present population estimated at only 10 pairs. Yururitou Island and Moyururitou Island are currently the primary breeding ground for this species. Seven COI sequences of mitochondrial DNA (Saitoh et al., 2015), one CHDZ sequence (AB597010), and one CHDW sequence (AB597009) originating from Japanese data are registered in the NCBI “Nucleotide” database. No genome analysis results have been registered in the “Genome” database.

**Okinawa Rail (Gallirallus okinawae) (Fig. 1 (K))**

The conservation and propagation program of the Okinawa Rail was compiled by MEXT, MAFF, MLIT, and MOE in 2004. The species is endemic to Japan and found only on the northern part of Okinawajima Island. The estimated population in 1985 was 1,500–2,100 individuals. Subsequently, the population decreased and by 2004 numbered only 717 individuals. Major threats to its habitat
include logging, dam construction, agricultural development, and golf course construction. In addition, threats persist due to road and predation by the introduced Javan Mongoose (*Herpestes javanicus*), feral dogs, and feral cats.

Two complete sequences of mitochondrial DNA (Ozaki *et al.*, 2010) are registered in the NCBI “Nucleotide” database, along with eight COI sequences (Saitoh *et al.*, 2015). Whole-genome sequencing is currently underway at the National Institute for Environmental Studies, Japan.

**White-tailed Eagle (Haliaeetus albicilla albicilla) (Fig. 1 (L))**

The conservation and propagation program of the White-tailed Eagle was compiled by MEXT, MAFF, MLIT, and MOE in 2005. This species is widely distributed across Eurasia and has been reintroduced in Scotland. In Japan, one of the subspecies, *Haliaeetus albicilla albicilla*, breeds in Hokkaido. The individuals that breed in the Russian Far East winter in Hokkaido and the on the northern part of Honshu. The estimated number of individuals occurring across its entire range is 20,300–39,600. The breeding population in Hokkaido is considered to have increased slightly since the 1990s. The number of migratory individuals flying from the Russian Far East to winter is 550–850. The winter population is found mainly in Hokkaido and northern Honshu.

Six sequences originating from mitochondrial DNA are available: five COI sequences (Saitoh *et al.*, 2015) and one 12SrRNA sequence (Nobata *et al.*, 2007) in the NCBI “Nucleotide” database registered as information originating from Japan. One whole-genome sequence is registered in the “Genome” database (923.79 Mb JJRL.00000000.1).

**Steller’s Sea eagle (Haliaeetus pelagicus) (Fig. 1 (M))**

The conservation and propagation program of Steller’s Sea Eagle was compiled by MEXT, MAFF, MLIT, and MOE in 2005. This species breeds in the Russian Far East, and most of the winter population remains on the southern Kuril Islands and Hokkaido, Japan. The estimated total population over its entire range is 4,600–5,100 individuals, of which 1,400–1,700 individuals winter in Japan (mainly in the eastern part of Hokkaido).

One 12SrRNA sequence (Nobata *et al.*, 2007) from mitochondrial DNA is registered in the NCBI “Nucleotide” database as originating from Japan. There is no whole-genome sequence data for this species entered into the NCBI “Genome” database.

**Japanese Wood Pigeon (Columba janthina nitens) (Fig. 1 (N))**

The conservation and propagation program of the Japanese wood pigeon was compiled by MEXT, MAFF, and MOE in 2006. The Tokyo Metropolitan government (Ueno Zoo and Tama Zoo) is officially accredited as the authority responsible for the program. There are three subspecies of *Columba janthina*, including *Columba janthina nitens* that is distributed only on the Bonin Islands and the Volcano Islands. The population is estimated to be about 30–40 individuals on the Bonin Islands.

Fifty entries of sequence data derived from mitochondrial DNA are registered in NCBI “Nucleotide” database: 43 D-loop (Seki, 2006; Seki *et al.*, 2007; Unpublished AB615362, AB615361, AB615360, AB615359, AB615358, AB615357, AB615356 and AB698856), and seven COI sequences (Saitoh *et al.*, 2015). There are no entries of whole-genome sequence data in the “Genome” database.

**Ptarmigan (Lagopus mutus japonicas) (Fig. 1 (O))**

The conservation and propagation program of the Rock Ptarmigan was compiled by MEXT, MAFF, and MOE in 2012. *Lagopus mutus* is widely distributed across the northern hemisphere. One of the subspecies, *Lagopus muta japonica*, is distributed across the alpine zone of central Honshu, Japan. The global population is estimated to be 8,000,000 individuals. The population of *Lagopus muta japonica* is estimated to be 3,000 individuals.

There are three sequences of mitochondrial DNA in the NCBI “Nucleotide” database: two COI sequences (Saitoh *et al.*, 2015) and one tRNA-Glu-srRNA sequence (Unpublished AB006673). There are no entries of whole-genome sequence data in the “Genome” database.

**Future Directions**

As discussed in the present review, the available sequence information from the avian species included in the established conservation and propagation program is almost entirely from mitochondrial sequences. In particular, D-loop, COI and control region sequences have been submitted. Phylogeographical study using D-loop and control region sequences are important for endangered species conservation to know existence of distinct genetic groups such as evolutionarily significant units (Ryder, 1986) and management units (Moritz, 1994). Phylogeographical study should be conducted using not only the present samples but also the past samples such as museum samples, ancient samples to reconstruct the past genetic structure. This kind of approach has already been applied for some endangered species (e.g. Eda *et al.*, 2012) and should be applied for the species for which reintroduction and/or translocation might be implemented (e.g. the Okinawa rail). The information of the past genetic structure can be used to identify the releasing points for individuals with specific genetic backgrounds.

In addition to mitochondrial DNA, microsatellite loci are highly useful in the estimation of genetic diversity. Of the endangered bird species, genetic diversity has been estimated using microsatellite markers in the Japanese Crested Ibis (Uran et al., 2013; Tsubono *et al.*, 2014), Japanese Crane (Hasegawa *et al.*, 2000; Zou *et al.*, 2010), Blakiston’s Fish Owl (Omote *et al.*, 2012), Golden Eagle (Dawny *et al.*, 2009), Common Murre (Ibaruchi *et al.*, 2000; Morris-Pocock *et al.*, 2008), White-tailed Eagle (Moritiz, 1994). White-tailed eagle (Molecular Ecology Resources Primer Development Consortium, 2012), Japanese wood pigeon (Ando *et al.*, 2011), and the Ptarmigan (Bech *et al.*, 2013). However, among these, research focusing on Japanese populations was conducted for only...
four species: Japanese Crested Ibis, Japanese Crane, Blakiston’s Fish Owl, and the Japanese Wood Pigeon. This implies that 11 endangered species have no reported genetic information with regard to microsatellite markers. This lack of information could have a considerable negative impact on captive breeding projects for endangered species. Captive breeding usually involves a small founder population, and hence declines in genetic diversity must necessarily be minimized. Conservation and propagation programs for 13 of the endangered species include captive breeding projects. For five of these species, the Okinawa Woodpecker, Tufted Puffin, Okinawa Rail, and White’s thrush, Amami Woodcock, Okinawa Rail, there are no available information on microsatellite markers. Hence, if captive breeding is to be effectively implemented for these five species, it is essential to pursue the information required to conduct microsatellite-based estimations of their genetic diversity.

Furthermore, whole-genome analysis has been performed for only 3 species: the Japanese Crested Ibis, Golden Eagle, and White-tailed Eagle. Genome analysis of the endangered species will promote conservation genetic research for these endangered species. In addition, the analysis could reveal genetic factor of extinction risks. Thus we should start whole genome sequences for other 12 species, especially endemic endangered species such as Okinawa woodpecker, White’s thrush, Amami Woodcock, Oinawa Rail, and Japanese wood pigeon.

References


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