

Phylogeography of Elegant Scops Owl (*Otus elegans*)

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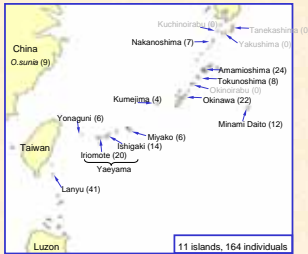
Introduction

- Elegant Scops Owl (*Otus elegans*) is distributed on some western Pacific islands.
- Some of these islands was connected in the past as the fall of sea level in the glacier period, but some are not.
- The contemporary population structure should be shaped by both isolation and dispersal.

Study aims

Using molecular markers to reveal the genetic diversity, population structure, gene flow and demographic history of Elegant Scops Owls on Ryuku and Lanyu islands

Study material



Genetic marker

I. Mitochondrial DNA: 1,665 bp complete Cytochrome *b* (1,142 bp) and NADH dehydrogenase subunit 6 (ND6) gene (522 bp)

II. Microsatellite: 13 loci

Result I. Genetic diversity

Island	N	No. of Haplotype	Hd	π
Nakanoshima	7	2	0.286	0.00017
Amamioshima	24	12	0.924	0.00355
Tokunoshima	8	2	0.429	0.00026
Okinawa	22	5	0.671	0.00712
Daito	12	1	0	0
Kumejima	4	3	0.833	0.0007
Miyako	6	2	0.333	0.0002
Yaeyama	34	4	0.405	0.00029
Ishigaki	14	4	0.648	0.00051
Iriomote	20	3	0.195	0.00012
Yonaguni	6	1	0	0
Lanyu	41	1	0	0
Total	164	18	0.705	0.01073

Hd: haplotype diversity. π : nucleotide diversity

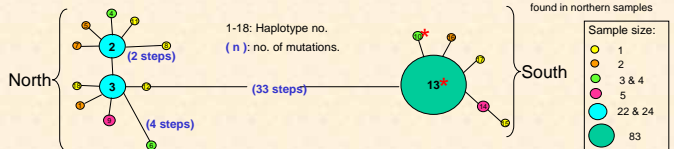
Microsatellite	N	Mean no. of allele / locus	Allelic richness	Ho	He
Amamioshima	24	8.00	6.77	0.81	0.81
Okinawa	21	4.62	6.85	0.83	0.83
Daito	12	7.77	4.62	0.78	0.71
Yaeyama	34	7.54	6.23	0.82	0.80
Lanyu	41	6.69	5.46	0.74	0.73
Total	132	10.5	6.57		

Ho: observed heterozygosity; He: expected heterozygosity

- Genetic diversities are higher in northern island populations.
- No mtDNA variation was found in Lanyu and Daito populations.
- Microsatellite diversities are lower in Lanyu and Daito populations than other island populations.

II. Phylogenetics and population differentiation

A. Minimum Spanning Network (mtDNA)

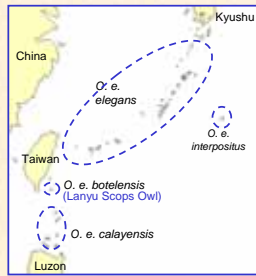


- Deep divergence exists between northern and southern island populations.
- Long-term isolation.
- Some southern haplotypes can be found in northern populations.
- potential gene flow.

B. F_{st}	microsatellite				
	Amamioshima	Okinawa	Daito	Yaeyama	Lanyu
Amamioshima	-----	0.009	0.051 **	0.013 **	0.053 **
Okinawa	0.040	-----	0.073 **	0.014 **	0.046 **
Daito	0.066	0.110	-----	0.053 **	0.113 **
Yaeyama	0.922 **	0.828 **	0.990 **	-----	0.027 **
Lanyu	0.937 **	0.853 **	1.000 **	0.100 *	-----

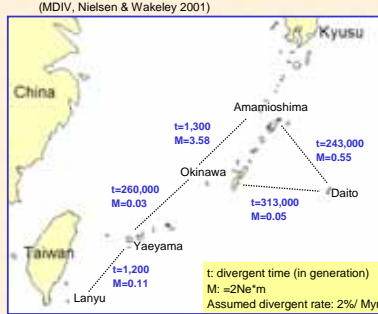
- Significant population differentiation are present among most island populations.

Current taxonomic status of *Otus elegans*



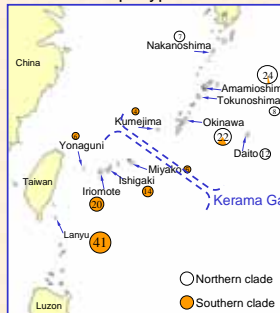
III. Gene flow

A. Bayesian estimation of divergence vs. migration over historical time



- Different divergent history and migration rate among islands.
- Amamioshima and Okinawa populations were separated relatively recently, with frequent gene flow after separation.
- Long-term divergence with little migration between Okinawa and Yaeyama.
- Lanyu population was diverged from Yaeyama recently, but few gene flow after separation.
- Daito population might originated from Amamioshima, instead of Okinawa.

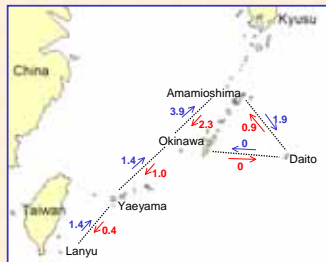
B. mtDNA haplotype distribution



- The two haplotype groups were roughly separated by Kerama Gap.
- Four southern haplotypes were found in Okinawa and one found in Amamioshima.
- Kumejima owls was from southern population.

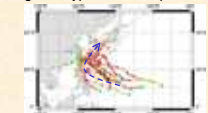
----- asymmetric migration?

C. Maximum likelihood estimation of migration rates (MIGRATE 1.6.8 Beerli 2002)



- Asymmetric migration between populations
- More northward than southward migration
- The direction of asymmetric migration coincide with the direction of typhoon.

Eg. The typhoons of Japan in 2004



(http://agora.ex.nii.ac.jp/digital-typhoon/news/index.html.en)

IV. Demographic history

Maximum likelihood estimation of population growth rates based on the coalescent (Fluctuate 1.4, Kuhner *et al.* 1998)

	g ± SD	Relative N 15,000 years ago**	Population trend
Amamioshima	-99.51 ± 63.34	1.003	Slightly declining
Amamioshima-1*	1,208.79 ± 503.83	0.964	Slightly increasing
Okinawa	-287.66 ± 80.53	1.009	Slightly declining
Okinawa-4 *	1,774 ± 1,171.164	0.948	Slightly increasing
Yaeyama	10,000 ± 4,500.73	0.741	Increasing

*: removing samples which carried southern haplotype
 **: time of Last Glacier Maximum
 g: exponential growth rate in 1/ μ generation
 μ : mutation rate (assume 2% per Myr)
 generation time= 5 years
 $N_{t(0)} = e^{-g \cdot t}$

- No significant population decline was detected since last glacier period.

Summary

- The population of *O. elegans* had experienced a long period of north-south isolation.
- Different degrees of genetic differentiation exist among some populations.
- Cross-ocean dispersal exists.
- The direction of gene flow is asymmetric, more individuals move northwards than southwards.
- The reduction of land mass due the rise of sea level after glacier period did not result in significant population decline.

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