

Post-introduction dynamics and genetic variability in an isolated Japanese sika deer (*Cervus nippon*) population



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1. Introduction

For natural populations it is difficult to assess the long-term impact of genetic drift since populations are rarely completely isolated from each other and gene flow antagonizes drift's effects. In order to get an unbiased estimate of effective population size (N_e), a population under study should be isolated from other populations.



Nakanoshima Island

- 520 ha
- located in Lake Toya, Hokkaido, Japan
- Sika deer population grown from three deer (one male and two females) introduced during 1957-1966
- has a well-described post-introduction population history
- three population declines in 1984, 2001 and 2004

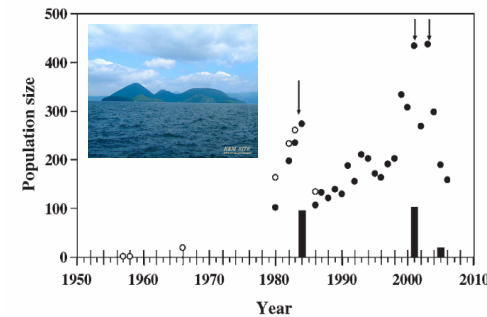


Fig. 1 Population changes of sika deer on Nakanoshima Island, 1957-2006. Black bars show the removals, open circles show estimated population size, black circles show minimum population ground counts, and arrows show population declines (Kaji et al. 2009).

2. Questions

Is there a reduction of genetic diversity over time caused by genetic drift in this isolated population?

- study temporal changes in genetic diversity
- estimate the effective population size (N_e) over time

3. Materials and Methods

- Genotyping 505 individuals using seven microsatellite loci for years 1984, 1997, 1998, 1999, 2001, 2002, 2003, and 2004
- Changes in allelic richness (AR), F_{is} , H_o , and H_e for each year as genetic diversity changes (FSTAT)
- Genotypic differentiation among years (GENEPOP)
- Degree of genetic differentiation among years (AMOVA, ARLEQUIN)
- F_{st} over years for genetic distance (Mantel test, ARLEQUIN)
- N_e and N_e/N_c for each year (OneSamp)

4. Results

- No trends toward a decrease of genetic diversity indices (Table 1, Fig. 2)
- There was genotypic differentiation between 1984 and 2001 ($p = 0.02$), 1984 and 2004 ($p = 0.05$)
- N_e and N_e/N_c ranged from 21.4 to 33.0 and 0.05 to 0.12 (Fig. 3)
- A significant reduction (35%) in N_e between 1984 and 1997 (Fig. 3)

Table 1. Estimators of genetic indices for studied years

Year	N_c	N studied	A	AR	F_{is}	H_o	H_e
1984	273	65	3.43	3.03	0.132	0.35	0.41
1997	191	25	3.00	2.99	-0.064	0.41	0.39
1998	203	28	3.00	2.95	-0.011	0.39	0.39
1999	333	62	3.14	3.09	0.048	0.39	0.41
2001	401	125	3.57	3.12	0.025	0.40	0.41
2002	269	55	3.57	3.16	-0.030	0.42	0.41
2003	437	57	3.29	3.05	0.021	0.39	0.40
2004	297	88	3.43	3.15	-0.047	0.45	0.43
Average	300.5	63.1	4.29	3.13	0.009	0.40	0.41

N_c : census size

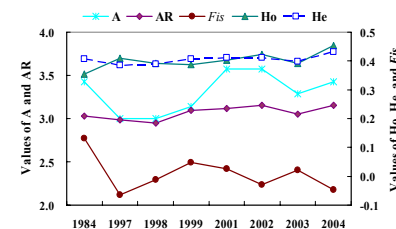


Fig. 2. Temporal changes of main genetic diversity indices for Nakanoshima sika deer population from 1984 to 2004.

- No significant genetic differences among years (AMOVA)
- Genetic distance (F_{st}) was positively correlated with time (Mantel test, $r = 0.39$, $P = 0.02$) (Fig. 4)

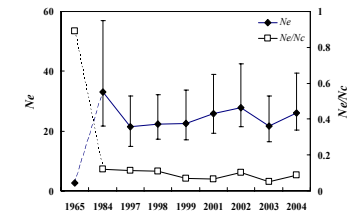


Fig. 3. N_e and N_e/N_c of Nakanoshima Island. Dots indicate point estimates and vertical lines indicate 95% confidence intervals.

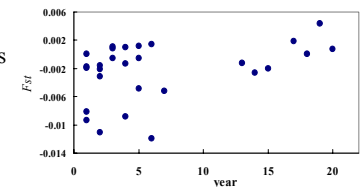


Fig. 4. Correlation between F_{st} and year. Mantel test, $r = 0.39$, $P = 0.02$.

5. Conclusion

- No clear reduction of genetic diversity over time caused by genetic drift on the isolated population which experienced three population declines
- Slight genetic changes occurred during the population declines in 1984, 2001, and 2004
- The first population decline in 1984 may have led to changes in N_e in the islands' entire population

6. Future directions

- Apply SNPs for analyses of non-coding (neutral) and coding (genes under selection) regions
- Determine if the degree of genetic diversity is strongly linked to the life history traits
- Extend the study to investigate adaptive evolution resulting from antagonistic interaction between deer and plants (diet for the sika deer)