

F-1 Studies on the extinction processes of wildlife populations

Contact person Yoshitaka Tsubaki, Deputy Director
Environmental Biology Division
National Institute for Environmental Studies
Environment Agency
Onogawa 16-2, Tsukuba, Ibaraki 305, Japan
Tel: +81-298-50-2482 Fax: +81-298-50-2577
E-mail: tsubaki@nies.go.jp

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Due to habitat destruction and fragmentation caused by human activity, many animals and plants have reduced their population size. Such small populations are suggested to be more vulnerable to extinction than before because of reduced genetic variability, greater effects of demographic and environmental variability, and higher susceptibility to disease infection.

Wild populations of plants and animals were studied on genetic variability together with morphological, ecological and bio-geographical traits. A general hypothesis predicts that genetic variability decreases as the population decreases. This hypothesis was supported in some of the studied populations, but was not in others. Further investigations are necessary to clarify factors and process that generate genetic variability in each population. Fluctuating asymmetry (FA) was found to be an indicator of qualities of individuals and populations or genetic variability, however, there were also several cases where FA was not a useful indicator. We need more information about the general usefulness of FA before we use it in biological conservation.

Ecological and genetic interactions between *Eupatorium makinoi* and geminiviruses were examined. Virus infection decreased growth rate and survivorship under controlled condition and was a major mortality factor in the field. While geminiviruses were genetically highly variable in the host-range gene, suggesting high ability of adaptive changes against host's resistance, *E. makinoi* had genetically variable resistance genes. We investigated prevalence of canine distemper virus (CDV) infection in Japanese dogs genetically, seroepidemiologically and histopathologically. Japanese raccoon dogs were naturally infected with recent type of CDV which are prevalent in dogs.

Organisms in a coevolutionarily-developed species interaction is prone to go extinct in case partner organisms are damaged or lost due to habitat change or invader organisms. Such an interaction was studied for entomophilous flowers and pollinator bees in patchy habitats such as islands or river deltas. It has been revealed that invading bees are one of the greatest threats to survival of both the flowers and pollinators. Ant communities were also investigated in relation to vegetation types on several islands. Allozyme variation of European and Japanese bumblebees was investigated in order to develop a reliable genetic marker for monitoring the hybridization between them in the field.

A method to estimate the mean time to extinction was developed for a density-dependent population with an environmental fluctuation. We also developed a method to estimate parameters (r , K and environmental stochasticity) from a relatively short time series of population size. The simulation study indicated that the number of accumulated deleterious mutation significantly change due to changing the shape of the habitat.