

F-1.4.1 Population viability analysis at the metapopulation level

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Abstract Environmental threats, such as habitat size reduction or environmental pollution, may not cause immediate extinction of a population but shorten the expected time to extinction. We develop a method to estimate the mean time to extinction for a density-dependent population with environmental fluctuation, and discuss the relative magnitude of impact caused by the reduction in the habitat area and the reduction of survivorship due to environmental pollution. Second, we studied two population systems; *Aster kantoensis* natural populations and *Callosobruchus chinensis* experimental systems. Based on field survey of *A. kantoensis*, a lattice model was constructed to calculate an extinction rate of the metapopulation. In experimental systems, a black mutant strain was used for estimating projection matrix. Based on the projection matrix of each genotype, extinction rate of a metapopulation is calculated using an individual-based model. Third, the simulation study indicated that the number of accumulated deleterious mutation significantly change due to changing the shape of the habitat. The extinction risk increased when the habitats were long and narrow and when the habitats were subdivided. The present simulation models will be useful to determine conserved area of endangered species.

Key Words Extinction risk, Metapopulation, Mutation meltdown, population viability analysis, computer simulation

1. Introduction

An increasing number of wildlife populations are being threatened by human impacts and secondary effects of environmental fluctuations and global environmental changes. Population viability analysis has been developed to assess extinction risk and to compare alternative management options. In this part, we took three different approaches to assess extinction risk of threatened species. The final goal of the research project is to assess the extinction risk of declining populations, to evaluate the effects of potential management strategies, and finally to prevent endangered species from extinction.

2. Extinction risk analysis of populations: mathematical study for risk management in conservation biology

Environmental threats, such as habitat size reduction or environmental pollution, may not cause immediate extinction of a population but shorten the expected time to extinction. We develop a method to estimate the mean time to extinction for a density-dependent population with environmental fluctuation.

2.1 Estimation of extinction risk using a formula based on a very simple model

We study a method to evaluate the extinction risk of a density-dependent population ¹⁾. We choose a mathematically tractable case as a "canonical model" which incorporates logistic population growth combined with environmental and demographic stochasticities as a stochastic differential equation. We first derive formulas of mean extinction time, expressed in terms of a multiple integral and in regression formulas. We discuss the relative impact of the decrease in habitat size and the decrease in survivorship presumably in terms of a common currency of mean extinction time.

2.2 How can we estimate the extinction risk based on time series data?

We then study an approximate maximum likelihood (AML) estimate of three parameters (intrinsic growth rate r , carrying capacity K , and environmental stochasticity) from a time series of population size. The AML estimate of r has a significant bias, but by adopting Monte Carlo method, we can remove the bias very effectively (bias corrected estimate). We can also determine the confidence interval of the estimate based on Monte Carlo method. If the length of the time series is mildly long (with 40 to 50 data points), parameter estimation with Monte Carlo sampling bias correction has a relatively small variance. However, if the time series is short (less or equal to 10 data points), the estimate has a large variance and is not reliable. If we know intrinsic growth rate r , the estimate of K and σ the mean extinction time T are reliable even if only a short time series is available. We illustrate the method by a freshwater fish, Japanese crucian carp (*Carassius auratus* subsp.) in Lake Biwa, in which the growth rate and environmental noise of crucian carp are estimated using fishery records.

2.3 Comparison of risk between different populations or different species.

We often face a choice between alternative conservation policies that cause extinction risk of two or more populations (or species) in different ways. Such a choice can be performed by combining extinction risk of multiple populations, given the knowledge of expected time to extinction of populations under different policies. We first show that different ways to combine the risk of multiple populations recommend very different policies as the optimal. We then propose a unified criterion that becomes different criteria in different settings. The optimal criterion depends critically on (1) "time scale" -- whether we are to maximize the survivorship of populations in ten years or in several hundred years from now; (2) "cost of policy change" -- whether the policy can be freely altered once the extinction of some species are observed, or the policy once chosen cannot be changed without paying a large cost; and (3) "redundancy" -- whether the stable survival of a single population is good as the survival of many population, or each population has its own value and the performance of a policy is proportional to the number of surviving populations.

2.4 Future problems

There are several directions to which the analysis should be extended: model aggregation, evaluating community effects, and risk/benefit analyses in conservation.

2.4.1 Model aggregation:

Realistic computer simulation models include various population structures, including age and size structures with possible dormant stages, spatial structure with multiple subpopulations connected by migration, competitors, parasites and other species closely interacting with the population. These can be analyzed only through computer simulation. However the method developed here gives a possibility of alternative approaches based on model aggregation, or a method of predicting realistic and complex model using a simplified model as a surrogate. We may generate a time series data from such a realistic computer

simulation model, and then obtain three "effective" parameters by fitting to the canonical model. Then using the mathematical formula, we can estimate the mean extinction time. By comparing predictions based on a simplified model and those from the detailed simulation model, we can know the magnitude of error, and the situation in which such a method can be applicable. Note that the parameter r estimated by this method may not be the same as the real biological intrinsic growth rate r , but it is an "effective" r , useful in predicting the extinction risk of the populations.

2.4.2 Evaluating community effects:

The method we adopted here is based on a population model with a single species. Extinction of a species may propagate through chains of interaction and result in extinction of a large number of species. This effect varies between species, and between habitats and is very difficult to generalize, which is why we choose a single-population model as a basis of evaluating extinction risk. But we should attempt to evaluate the community effects in a few very well studied system.

2.4.3 Risk/benefit analyses in conservation

In environmental risk management of dealing with human health risk, cost-effectiveness analysis (or risk-benefit analysis) has been adopted as a method of encouraging rational decision making. It may be quite useful to develop cost-effectiveness analysis in the field of conservation biology as well. To do this, we need to have a reliable method to estimate population extinction risk. Since it is often the case that we do not have sufficient amount of data to estimate many parameters included in realistic computer simulation models, we here discussed an estimate of extinction risk based on a limited amount of data.

3. Metapopulation dynamics and extinction risk

3.1. Persistence of *Aster kantoensis* populations under environmental disturbance

An endangered composite herb, *Aster kantoensis*, is biennial and a representative inhabitant of gravelly flood plains. Until 1970s, *A. kantoensis* formed many dense stands throughout the middle reaches of the River Tama in Tokyo. However, the species has declined rapidly in recent years and is now listed in the national red data book. Seedlings and rosettes of *A. kantoensis* are tolerant on soils with low humidity and oligotrophic conditions. They need open flood plains with gravels to establish and develop in the riverside habitat, because the height is 5 to 10 cm and they are likely to be shaded by other perennial plants. The local government has controlled water levels of the River Tama, which inhibits floods and decreases the gravelly flood plains. Long-term monitoring suggests that reduction in colonization success should be one of major causes for the rapid decline of a metapopulation in the River Tama.

A population dynamics model should be indispensable to assess the extinction risk of *A. kantoensis* in near future, so that it can incorporate not only spatial structures of the *A. kantoensis* metapopulation but also information transfer from microscopic processes to macroscopic patterns: from the survivorship of seedlings and rosettes and the reproductive success of flowerings in local patches to metapopulation dynamics in a whole middle reaches of the River Tama. Each local patch has in general ten- or fifteen-year "longevity" from an open plain emergence by a flood, through seedling establishment and generation cycles, to elimination due to invasion and covering-up by other competitively dominant perennials. A district population has several to twenty local patches with different "ages", and the metapopulation is an ensemble of district populations with different "histories".

The present model has a multi-layer structure of different scales which corresponds to

local patches, district populations, and a whole metapopulation of *A. kantoensis*. I applied a projection matrix model with survival and reproductive elements to population processes in a local patch, whose values were estimated by plot-based surveys as well as data stocks of past environmental assessments. A district population consists of a cellular environment and is formulated as a lattice model with dispersal of seeds between cells, or local patches. A whole metapopulation has an upper-level, unidimensional lattice which corresponds to a series of district populations along the river. Control parameters are the frequency of floods and the eutrophication level of the river, the latter of which relates to the soil fertilization and determines the time to invasion of the perennial plants. Based on the model prediction, I try an extinction risk assessment of *A. kantoensis* in the River Tama.

3.2. Deleterious mutant effect on *Callosobruchus chinensis* experimental systems

A black mutant strain (sCbl) of *Callosobruchus chinensis* was used for estimating projection matrix, which was compared with that of wild-type strain (jC). Based on the projection matrix of each genotype, extinction rate of a metapopulation is calculated using an individual-based model. The black mutant was found in 1972 as a recessive and deleterious mutant. All F1 show wild-type phenotype and F2 is separated at wild:black=3:1, so the genetics follows usual 1-ocus_two-allele system. Age-specific survivorship and age-specific reproductive ability were experimentally estimated for sCbl, jC, and F1.

sCbl has significantly lower fecundity and hatchability than jC. sCbl females ended oviposition and died earlier than jC. When F1 was produced, the number of F1 adults produced by P females depends on whether the mother was sCbl or jC. If the mother was sCbl, the number of offspring produced became lower. The cross F1xF1 shows 3 (wild): 1 (black) ratio. Though it followed Mendelian segregation of 1-ocus_two-allele system, production of F2 by F1 depended on whether the mother is sCbl. The cytoplasmic factor affected the productive ability of F1 generation.

Based on the projection matrix of each genotype, an individual-based model was constructed to examine an extinction rate of a metapopulation. An individual has age, a genotype and a mother's type. Mating occurs randomly within a local population of small size, n , and the metapopulation consists of N local populations. In each mating, a projection matrix is referred and an element was chosen depending on its age. Individuals migrate between local populations at a small frequency, m . The project is now on-going and some tentative results are; the extinction rate depends on m , n , and N .

4. The effect of habitat shapes on the accumulation of deleterious mutation.

4.1 Introduction

Demographic events and genetic load are important factors affecting the probability of the extinctions of small populations. Although there have been some controversy as to whether or not the accumulations of deleterious alleles significantly lead small populations to extinctions^{2,3,4)}, there are some evidence of the effect of genetic factors on extinctions from mathematical models³⁾ and empirical studies⁴⁾.

4.2 Results

I conducted individual-based simulation model to examine the effects of the shape of habitat on the probability of extinction due to both genetic load and stochastic demography. The simulation models assumed that (1) individuals are continuously distributed in a habitat, (2) Females mates with males within a neighboring area (mating area), (3) Offspring disperse from their birth site. The dispersal distance were short relative to the area of the

habitat. (4) The reproductive rates of females are determined by the densities within neighboring area, the number of accumulated deleterious mutations, and stochastic factors, (5) The genome size of individuals are 10000. The mutation rates (u) and the variability effects of deleterious alleles (s) were set at 0.2 per genome per generation and 0.025, respectively, The u and s are usually unknown except a very few organisms such as *Drosophila*. Thus, the purpose of the study is not to estimate the mean time to extinctions, but to assess which the changes of factors increase significantly the probability of extinctions.

4.3 Discussion

The simulation study indicated that the effects of demographic stochasticity did not significantly vary responding to the shape of continuously distributed habitat, but the number of accumulated deleterious mutation significantly change due to changing the shape of the habitat. The extinction risk increased when the habitat were long and narrow. In addition, when habitats were subdivided, and migration among subpopulations were moderately low (>5 individuals per generation), the extinction risk significantly increased. The number of accumulated homozygous deleterious loci increase responding both decreasing genetic neighborhood size and total population size. The effect of the total population size would be affected by the shape and the fragmentation of the habitats. The present simulation models will be useful to determine conserved area of endangered species.

Reference

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