A SELECTION MODEL FOR SEX GENES AND THE SEX RATIO
DYNAMICS IN HAPLOID DIOECIOUS POPULATIONS

Kuniyoshi OHTA

Tokyo Keizai University, Kokubunji, Tokyo

SUMMARY

A simple model is proposed of natural selection for sex genes in haploid dioecious populations. It is shown that evolution by means of mutation and gene selection will ultimately lead to the globally stable population sex ratio of $1/2$.

1. Introduction

Ever since Fisher's(1930) famous but cryptic suggestion, sex ratio theory has been studied by a number of authors from the viewpoint of natural selection. Most of them, including Fisher(1930), have concerned with the case where the sex ratio of offspring in diploid organisms is controlled by their parental gene(s).

This paper deals with a more simple case where the sex of a haploid dioecious organism is controlled by a certain gene locus carried in the organism itself(Ohta, 1980).

2. Modelling and Analysis

Suppose a sufficiently large population of haploid dioecious organisms with nonoverlapping generations, and consider a gene locus affecting the sex expression of the organisms. Assume that there are two alleles, A_1 and A_2 , at this locus and that the organism carrying the allele A_1 or A_2 becomes female with probability ρ_1 or ρ_2 , respectively. Denote by q_1 the frequency of the sex (controlling) gene A_1 in the total population including both sexes. Then the "sex ratio", or the proportion of females in the population, u , is given by

$$u = (\rho_1 - \rho_2)q_1 + \rho_2. \quad (1)$$

If we assume random mating, normal segregation, and no other selection, the transformation from the gene frequency q_1 in one generation to the corresponding frequency q_1' in the next generation will be given by

$$q_1' = \frac{1}{2} \left[\frac{\rho_1 q_1}{(\rho_1 - \rho_2)q_1 + \rho_2} + \frac{(1 - \rho_1)q_1}{(\rho_2 - \rho_1)q_1 + 1 - \rho_2} \right], \quad (2)$$

so that the evolutionary dynamics of the sex ratio could also be found from this recurrence equation.

The local stability analysis of the fixed

points of (2) is summarized in Fig.1, which shows the stability domain in the parameter space (ρ_1, ρ_2) for each fixed point of q_1 , together with the corresponding value of u obtained from (1).

Note that if $\rho_1 = \rho_2$ any value of q_1 and hence of u is a fixed point and neutrally stable. If $\rho_1 \neq \rho_2$ there is only one locally stable fixed point of q_1 or u for each fixed parameter set (ρ_1, ρ_2) , as shown in Fig.1, so we note also that the local stability actually implies the global stability.

Fig.1. Stability domain in the parameter space of each fixed point of q_1 or u .

3. Discussion

The interior fixed point $q_1 = (1 - 2\rho_2) / 2(\rho_1 - \rho_2)$ manifests the genetic polymorphism for the variation of probability of sex expression. As we see in Fig.1, it is remarkable that this polymorphic state yields the population sex ratio of 1/2 and is globally stable as far as $(\rho_1 - 1/2)(\rho_2 - 1/2) < 0$.

In addition, even if $(\rho_1 - 1/2)(\rho_2 - 1/2) \geq 0$ Fig.1 shows that the allele producing the "sex probability" with a smaller deviation from 1/2 should be selected for, so that if one considers our problem in the evolutionary time scale of great length, it might be expected that a number of repetitions of mutation and selection would ultimately lead to the globally stable population sex ratio of 1/2.

Finally, as a numerical example, we shall take $(\rho_1, \rho_2) = (1, 0)$. Then the globally stable gene frequency and the globally stable population sex ratio both become 1/2. Evidently this is the case in which the sex factor A_1 produces always female organisms, while the other factor A_2 male organisms.

References

- Fisher, R. A. (1930). "The Genetical Theory of Natural Selection". Oxford Univ. Press, Oxford.
- Ohta, K. (1980). Abstracts of the Second Int. Congr. Syst. Evol. Biol..