VARIATION IN FITNESS AND MOLECULAR EVOLUTION

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1. Introduction

Molecular studies, especially of proteins and nucleic acids have added important new insights into evolutionary processes by providing new ways of investigating and measuring evolutionary rates over long periods of time. In particular, the estimation of the mean time necessary for an amino acid substitution (Zuckerkandl and Pauling [30]) has rightly generated much interest and has given considerable stimulus to further investigation into the mechanisms of evolution.

There seems, at the present time, to be substantial disagreement as to the meaning of the quantities observed and their interpretation in evolutionary terms (see, for example, Kimura and Ohta [16] who give citations to the relevant literature). Specifically, the analysis of data on molecular evolution has led to a revival of the old controversy concerning the relative roles in evolution of random genetic drift and selection.

In this paper, we shall extend some considerations that were made in a book that appeared recently. We shall also review some experiments on computer simulation of molecular evolution that were done some two years ago, and also review the molecular evidence from a variety of sources and organisms concerning the roles of random genetic drift and selection in evolution. The model of molecular evolution which we have used for computer simulation was designed to evaluate mean evolutionary time, both for neutral mutations and also for mutations which have an effect on fitness. It also provides an estimate of the extent of polymorphism for a given locus at any given time.

2. The computer model

Since the number of possible changes in a protein molecule is very large, we have used, as have others, a model in which every allele of a gene that can be

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