

# THE NUMBER OF MUTANT FORMS MAINTAINED IN A POPULATION

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## 1. Introduction

Experimental and empirical studies appear to indicate the existence of large numbers of polymorphisms in wild populations. It is desirable to formulate a model which qualitatively explains the relative importance of the pressures of selection, mutation and random drift in maintaining these polymorphisms. An equivalent problem investigated by Fisher [3] concerned the rate of mutation necessary in order to maintain a sufficient number of heterozygous loci which thus contribute toward genetic variance.

In recent years there has been much interest in the related problem of determining the number of alleles (alternative gene types) that can be maintained by mutation. It is this problem that the subsequent analysis is primarily aimed at; however, it directly adds insight into the question of clarifying the reasons for the large numbers of polymorphisms observed. Kimura and Crow [11] and Ewens [2] have investigated quantitatively the situation when each mutant form that arises is different from previous forms. Either due to selective disadvantages, mutation or migration pressures, or random sampling effects due to finite population size, the resulting subpopulation generated by each mutant form ultimately becomes extinct. The reasons for studying these models are set forth in Kimura and Crow at length and are not repeated here. For further bibliographic references on this subject we refer to Wright [14].

The model not formulated precisely but probably implicit in Kimura and Crow [11] and explicit in Ewens [2] is of the following structure. The population consists of  $2N$  genes each capable of mutating in any generation with probability  $\nu$  and thereby creating new allelic types. The fluctuations of the population size of a particular allelic line is assumed to be governed by the classical Fisher-Wright process. That is, if the number of representatives of the particular allele is  $i$ , then the probability that the number of the allele in question changes to  $j$  in the next generation is given by

$$(1.1) \quad P_{ij} = \binom{2N}{j} \left[ \frac{i(1-\nu)}{2N} \right]^j \left[ 1 - \frac{i(1-\nu)}{2N} \right]^{2N-j}, \quad j = 0, 1, \dots, 2N,$$

where  $-i\nu$  is the expected decrease in  $i$  due to mutation to new alleles.

We expect on the average  $2N\nu$  new allelic types to arise per generation. At

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