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TITLE: COMPUTER SYMBIOSIS-EMERGENCE OF SYMBIOTIC BEHAVIOR THROUGH EVOLUTION-

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Computer Symbiosis —Emergence of Symbiotic Behavior through Evolution—

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Abstract

Symbiosis is altruistic cooperation between distinct species. It is one of the most effective evolutionary processes, but its dynamics are not well understood as yet. A simple model of symbiosis is introduced, where we consider interactions between hosts and parasites and also mutations of hosts and parasites. It is found that a symbiotic state emerges for a suitable range of mutation rates. The symbiotic state is not static, but dynamically oscillates. Harmful parasites violating symbiosis appear periodically, but are rapidly extinguished by hosts and other parasites, and the symbiotic state is recovered. The emergence of "Tit for Tat" strategy to maintain symbiosis is discussed.

Keywords: Symbiosis, Loose symbiosis, Tit for Tat, Mutation, Host, Parasite

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1)on leave from Research Institute of Fundamental Physics, Kyoto University, Kyoto 606, Japan

2)on leave from Institute of Physics, College of Arts and Sciences, Univ. of Tokyo, Tokyo 153, Japan attractor of the symbiotic state is not a fixed point but a limit cycle.

2 Model

We assume that each species of host and parasite is represented by a simple binary sequence of length L. Thus hosts and parasites can have 2^L different genotypes. The population of individuals of each genotype j is chosen to take a contiuuous value, and is denoted by h_j and p_j corresponding to a host type j and a parasite type j, respectively. The dynamics are as follows:

(1) Mutation of hosts and parasites: Hosts as well as parasites can mutate to other genotypes by only 1 bit. Hosts cannot become parasites or *vice versa*, that is, they mutate only among themselves. Since we restrict the gene space in a bit string of length L, each genotype has L neighbors reached by a 1-bit mutation. Such mutation allows hosts to escape from harmful parasites, whereas parasites follow the host by mutation.

(2) Interaction of hosts and parasites: For most parasites, hosts are uni-directionally exploited by parasites. The more advantage a parasite bears through the interaction with a host, the less advantage (or the more damage) the host bears by the interaction. If both a parasite and a host happen to take advantage of each other, such a pair of parasites and hosts is said to be in a symbiotic relation.

(3) Interaction among parasites: A competition is included among parasites but not among hosts. We assume that different types suppress each other, but the suppression by the same genotype is not included. No mutual or self suppression is assumed for the host system. The host can only increase or decrease its number by interacting with parasites.

From the assumptions (1)-(3), we can write down the following set of equations on the population of i-th species of hosts $h_i(t)$ and that of parasites $p_i(t)$:

$$\frac{dp_j}{dt} = \sum_{k=1}^{2^L} a_{kj}^P p_j h_k - \sum_{i \neq j} p_i p_j + \mu_P \sum_{j'} (p_{j'} - p_j), \tag{1}$$

$$\frac{dh_j}{dt} = \sum_{k=1}^{2^L} a_{kj}^H h_j p_k + \mu_H \sum_{j'} (h_{j'} - h_j), \tag{2}$$

where the summation over j' runs over all 1-bit neighbors of the binary sequence j.

By setting a bit length L equal to 7, we represent each genotype as $0 = 0000000, 1 = 0000001, 2 = 0000010, 3 = 0000011, \cdots, 127 = 1111111$. In the system of equations above, the bit information is embedded in the terms of interaction and mutation. With respect to the constraint (2), the interaction terms a_{kj}^P and a_{kj}^H must have the following properties.

(i) We call the pair of indices k, j a *symbiotic pair* if both a_{kj}^P and a_{kj}^H are positive. The interactions are always feeded initially with at least symbiotic pair.

(ii) If a host and a parasite do not form a symbiotic pair, then the parasite gets an additional positive gain by the interaction whereas the host is subjected to the same but negative additional interaction. This difference of the sign in the additional interaction term sets apart a parasite from a host.

We adopt the simplest form with these constraints as follows:

hosts and parasites increase, till the state becomes unstable and dissolves. Through the spread in gene space, parasites reach the most harmful species to the host type 85. Thus the parasite with the genotype 42(= 127-85) appears. (Note that 85=1010101 and 42=0101010). Since the parasite can exploit the host most strongly, its number increases. In order to recover the original symbiotic state, this harmful parasite must be eliminated. In the present case this elimination occurs through the decrease of host type 85 by mutation and the suppression of parasite type 42 from other parasite types. A symbiotic pair of host and parasite drives down the parasite type 42, and a symbiotic state of type 86 has again been established.

In our present model, we have not found a fixed symbiotic state. After the system returns to a symbiotic state, the state lasts for a while but it again is destroyed. The present symbiotic state thus appears as a temporally periodic state. Two era repeat periodically; long symbiotic era (180 time steps in Fig.1) where the population increases slowly, and a shorter era (10 time steps in Fig.1) in which harmful parasite suddenly increases, and then is eliminated accompanied by the decrease of populations of hosts. It should be noted that the duration of the latter era is much shorter (less than 1/10) than that of the symbiotic era.

Neither quasiperiodic nor chaotic, but only a periodic temporal change has been observed.

The appearance of symbiosis is dependent on the initial distribution of hosts and parasites in gene space. We have studied some typical initial distributions as follows:

a) One type of parasite versus a random or homogeneous distribution of host types.

b) One type of a host versus a random or homogeneous distribution of parasite types.

c) Both types are randomly distributed.

d) One type of parasite versus one type of host.

Out of above conditions, we have not found a stable symbiotic state for the conditions b) and c). Since various types of parasites already exist, hosts cannot escape from them, and are extinguished.

For suitable sets of parameters, a periodic symbiotic state is observed under the conditions a) and d). Hosts mutate so that they can form a symbiotic pair with the initially given type of parasite. Symbiosis lasts for a long time (say 200 time steps) and disintegrates, but it recovers through the punishment of harmful parasites, as has been discussed in the above. Even if the initial Hamming distance between hosts and parasites is large (say the types 85 and 42), the symbiotic pair is developed if the mutation rate of hosts is moderately large.

Next, let us discuss the condition of emergence of the symbiotic behavior in our model. By varying parameters in our model, we have found that the above dynamical symbiotic state exists only in a small parameter regime. The following conditions are found to be necessary for successful symbiosis:

1) A mutation rate of hosts (μ_H) should be larger than that of parasites (μ_P). Too large mutation rate of hosts, however, brings the extinction again.

misses an essential quality of evolution. To study the evolutionary process, we need a model with a landscape which changes temporarily, depending upon the population of all species. The present model gives a simple example of this class of dynamics.

2) Our symbiosis appears only as a dynamical state. This class of symbiosis is predicted by L. Margulis [1] as "loose symbiosis". Symbiosis can be formed but it may dissolve again. It is a function of time. There are several reasons for the dissolution of a symbiotic relationship, as Margulis has pointed out. She also argues that the growth rates of partners should be approximately equal in order to keep a symbiotic relationship [1].

In the present model, the approximately same positive values for $\overline{a^P}$ and $\overline{a^H}$ lead to an approximately equal growth rates for hosts and parasites. A dissolution of the symbiotic state of the present model is caused by the unbalance of these order parameters.

3) The importance of host-parasite interaction for the development of polymorphism has often been stressed (see e.g., [7]). Let us consider a collection of ensembles of hosts and put parasites on each ensemble. Hosts in each ensemble may evolve to different genotypes (e.g. a different symbiotic pair). Thus polymorphism of hosts is induced by the interaction with parasites. If there exists a competition among different hosts types, this picture may not be justifiable.

4) Other choices of interactions: Modification of parasite-parasite interaction or the inclusion of host-host interaction may be important. We have also studied a model in which parasites suppress themselves. It seems that the inclusion of this self-suppression term destroys the symbiotic state. Other choices of host-parasite interaction terms may be worth considering.

5) In our model we have assumed that all parasites and all hosts interact with each other. This assumption may be artificial. It may be better to use a model with the interaction only among restricted sets of hosts and parasites. A simple example is a model on a lattice (see also [5]). It is expected that this kind of restricted interaction enhances the stability of symbiotic state, since the host which promotes a symbiotic relation with some parasite is no more exploited from other harmful parasites. In our long ranged coupling model, however, such symbiotic hosts may be exploited by other parasites.

6) Use of sex [8]: As stressed by Hamilton and others, recombination can be more effective than mere mutation. One of the reason for this is that mere mutation cannot memorise the effective genetic sequences against the past parasites, but recombination does. Recombination is thought to be especially useful to protect from the attack of parasites, since it makes a large uncorrelated jump.

In our problem, recombination is useful for hosts for the same reason, to escape from the attack of parasites. Recombination, however, may in fact hinder the symbiotic relationship, since recombination may instantly create non-symbiotic hosts and parasites. If the distribution of genotypes is almost completely concentrated on the symbiotic pair, recombination almost always creates the symbiotic pair, since recombination just mixes existing genotypes. Thus the above drawback may be removed. It is

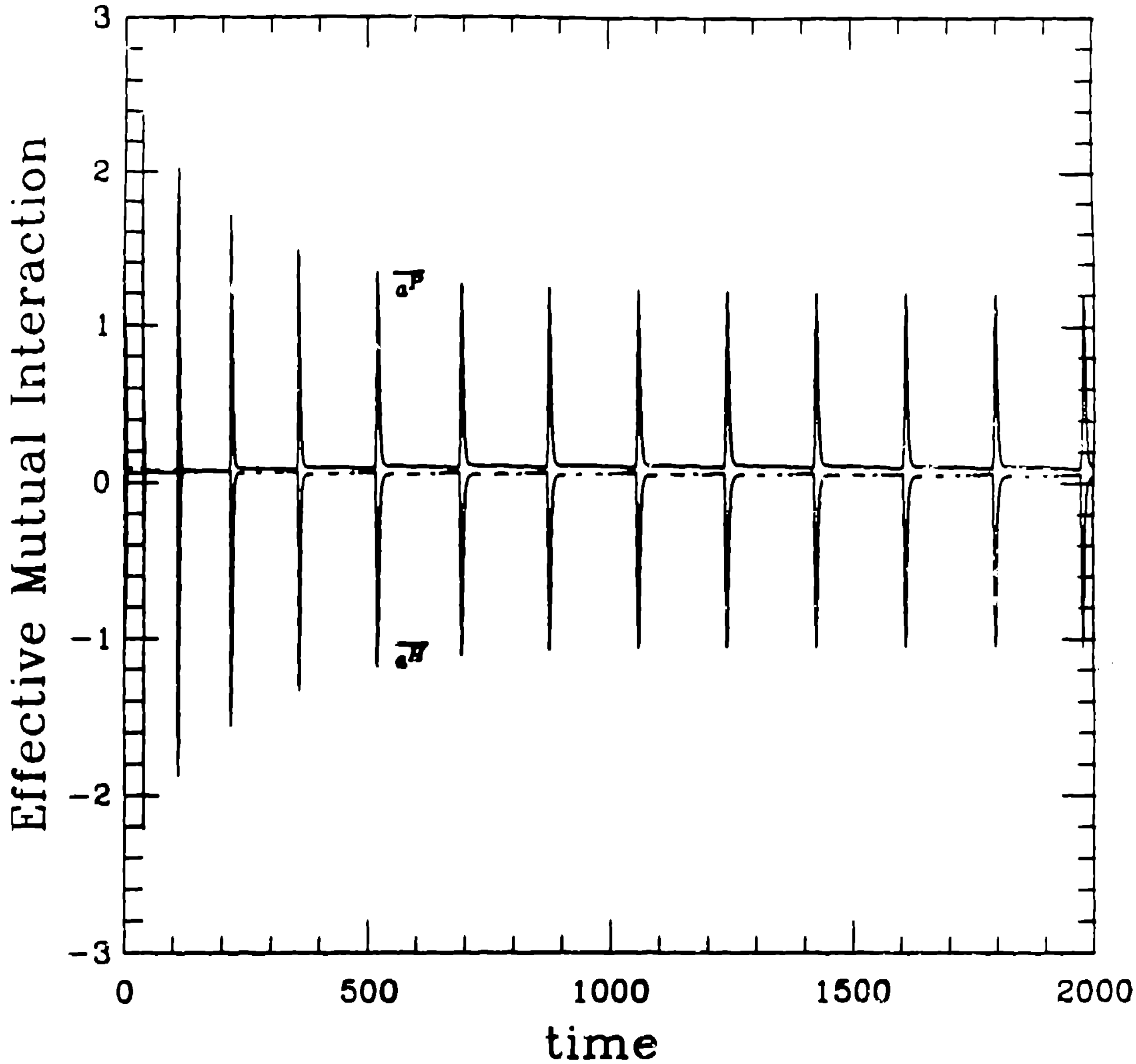
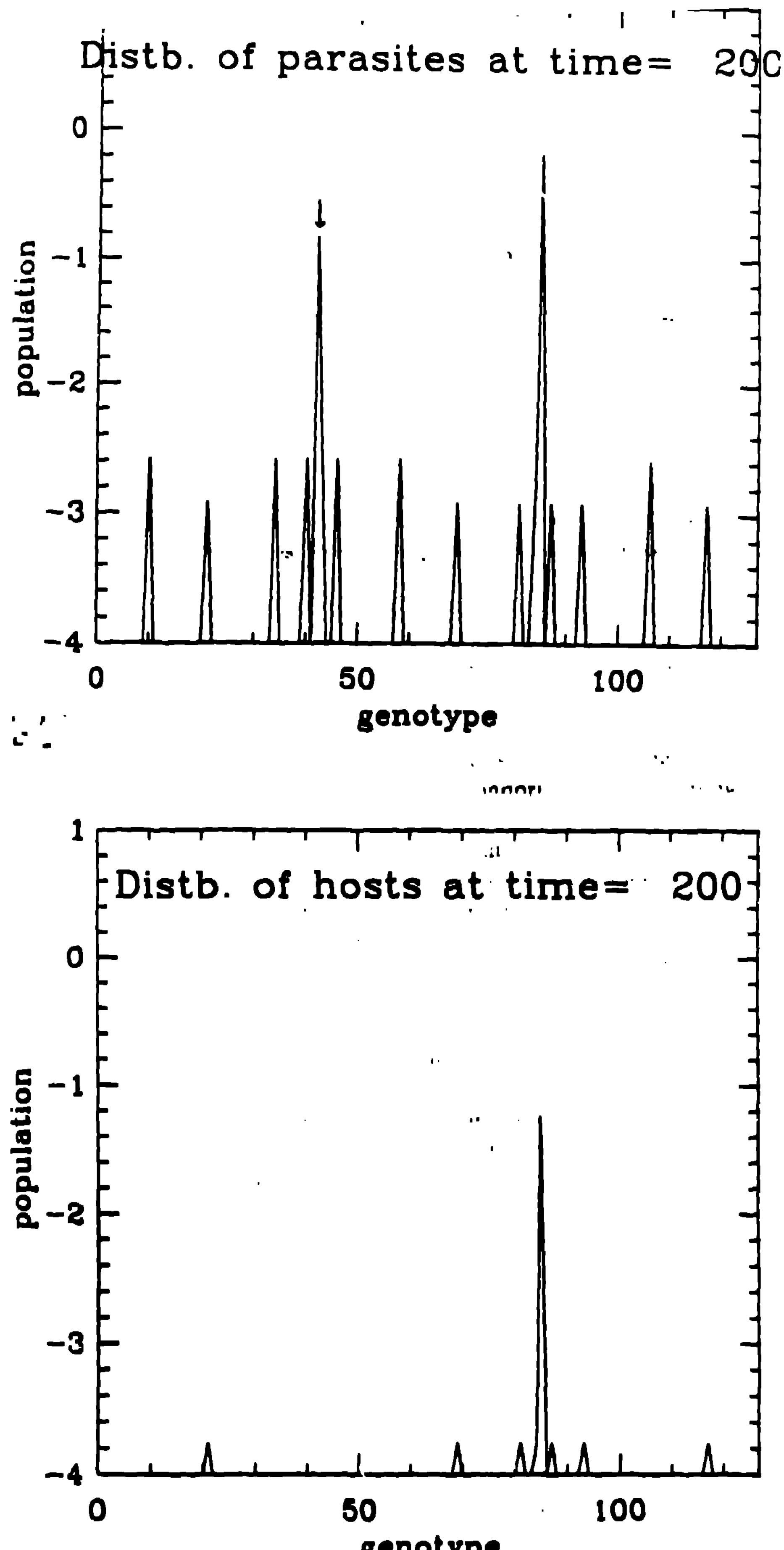


Fig.1: Temporal evolution of order parameters $\overline{a^H}$ and $\overline{a^P}$. A symbiotic state occurs when both parameters have positive values. If the order parameter for hosts takes a negative value, it is out of the symbiotic state. A symbiotic state disintegrates periodically when values of $\overline{a^H}$ and $\overline{a^P}$ close together. The simulation is excuted with parameter values f_P=0.05, f_H=0.1, μ_P=0.001 and μ_H=0.002.


Distb. of parasites at time= 200
population
genotype
0
-1
-2
-3
-4
0
50
100
Distb. of hosts at time= 200
population
genotype
1
0
-1
-2
-3
-4
0
50
100

(b2)

Fig. 2

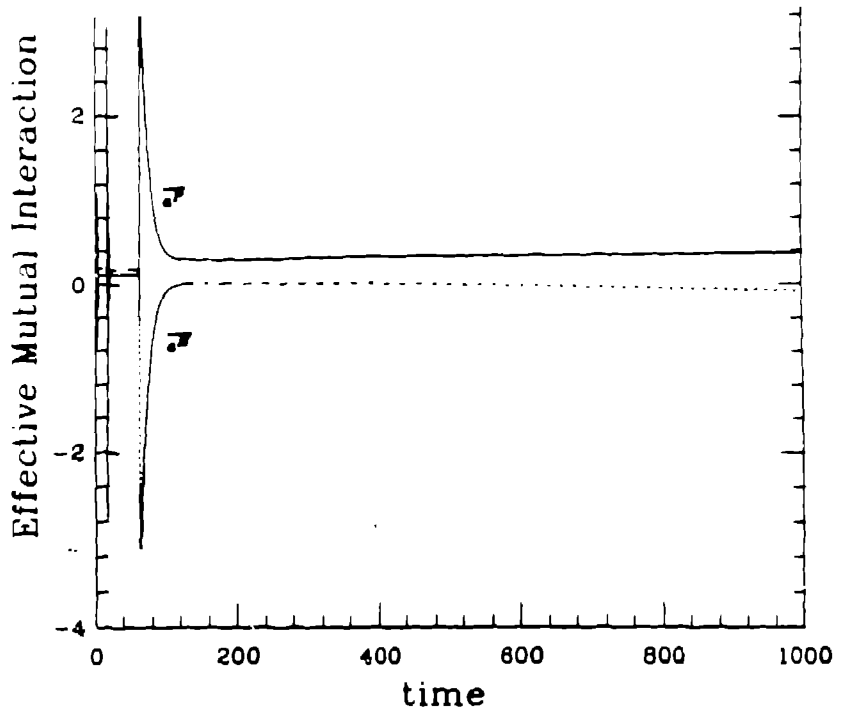


Fig.3: A disintegration of a symbiotic state at time=300 can be seen in the temporal evolution of order parameters. The simulation is excuted with parameter values f_P=0.1, f_H=0.2, μ_P=0.001 and μ_H=0.002.

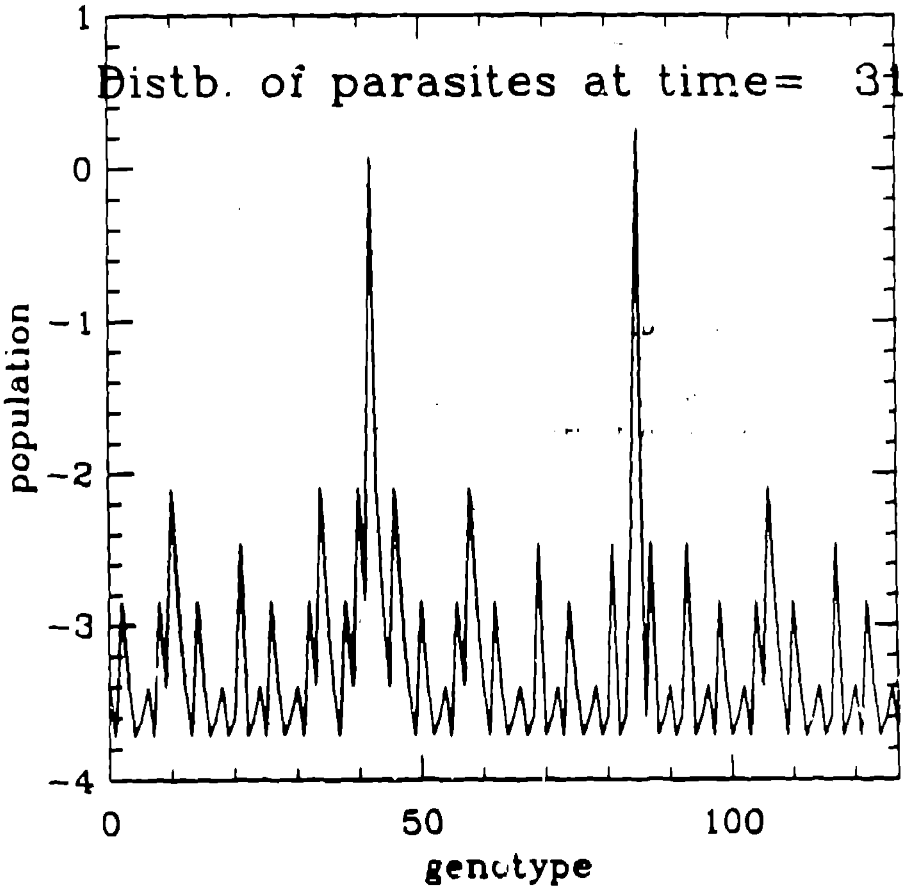


Fig.4: If the host cannot beat the most harmful parasite, parasites spread out in gene space. After this event, all hosts are extinguished by parasites. This unsuccessful case imulated with the same parameter values as Fig. 3.