

EFFECTS OF SELFING ON SELECTION FOR RECOMBINATION

D. CHARLESWORTH, B. CHARLESWORTH AND C. STROBECK*

*School of Biological Sciences, University of Sussex,
Brighton, BN1 9QG England*

Manuscript received May 5, 1976

Revised copy received December 7, 1976

ABSTRACT

This paper describes the results of computer simulations of selection on a locus which affects the rate of recombination between a pair of loci under selection. Four different models of selection for increased recombination were examined. In our first two models, which involve hitchhiking effects, increased levels of selfing can lead to increased selection for recombination, but need not always do so. With two models of selection for recombination caused by fluctuations in the environment, increased selfing always led to increased selection for recombination. Constant-environment models with nonadditive fitnesses at the two selected loci were also studied. Selfing increased selection for modifiers decreasing recombination, compared with random-mating populations in which indeed there might be no selection for decreased recombination. At high levels of selfing, the intensity of selection against recombination was sometimes found to weaken again.

CYTOLOGICAL observations on several groups of flowering plants have shown that self-pollinating species often tend to have higher chiasma frequencies than closely related outcrossing species (STEBBINS 1950, pp. 180–181, 1958; GRANT 1958; LEWIS and JOHN 1963, p. 281; ZARCHI *et al.* 1972). These observations have generally been interpreted in terms of MATHER's antithesis between the needs of immediate fitness and long-term adaptability (MATHER 1943). For example, STEBBINS (1950) states that:

“ . . . in the predominantly self-fertilized species the ability of the rare heterozygous interracial hybrids to produce many new gene recombinations is of particularly high selective value as a means of adapting the species to new conditions. In these species, therefore, fitness and constancy are secured entirely through self-pollination and homozygosity, while the mechanism for flexibility and adaptation to new situations consists of short periods of great heterozygosity, following interracial hybridization. During these periods, natural selection is acting with great intensity, and a high recombination index is of great value.”

It is not entirely clear whether the advantage of recombination envisaged here is to the group or to the individual. STEBBINS, in an earlier passage (p. 155), states that:

“ . . . in discussing the selective value of genetic systems we must consider primarily the advantage a particular system gives to the progeny of those who have it and the evolutionary

* Present address: Department of Genetics, University of Alberta, Edmonton, Alberta, Canada.

possibilities which it holds out to the race. The immediate advantages or disadvantages of the system are of secondary importance."

One may reasonably question whether the evolutionary advantage of increased release of variability in occasional outcrosses in selfing species would be capable of generating the rather fine-scaled differences in recombination rates between selfing and outcrossing species reported by the authors referred to above. For example, in the studies of GARBER (1956, 1958) reviewed by LEWIS and JOHN (1963), the chiasma frequencies per bivalent varied from 1.9 to 1.7 in the inbreeding species of *Collinsia*, and from 1.7 to 1.1 in the outbreeding species. It therefore seems of interest to study models of individual selection for increased recombination (*e.g.*, STURTEVANT and MATHER 1938; WILLIAMS 1975; FELSENSTEIN and YOKOYAMA 1976; MAYNARD SMITH 1976; STROBECK, MAYNARD SMITH and CHARLESWORTH 1976; CHARLESWORTH 1976) in self-fertilizing populations. In view of the observations reviewed above, one would be unhappy with any model that does not give increased selection for recombination when the rate of selfing is increased. This paper therefore describes investigations of the effects of different rates of self-fertilization on a number of mechanisms that promote the evolution of increased recombination by individual selection.

We will also investigate the effect of selfing in a two-locus system with constant fitnesses and with modifiers decreasing the recombination fraction. If selection for modifiers reducing recombination is weaker in selfing than in random-mating populations, this could provide another explanation for the increased degree of recombination that is observed in selfing species, compared with their outbreeding relatives. The results of FELDMAN and BALKAU (1972) suggest that this is probably not the correct explanation for these findings. These authors showed that there can be selection against recombination in a completely selfing population, even without linkage disequilibrium between the genes. It seems likely that a similar effect would occur with intermediate rates of selfing. We have therefore done computer simulations of modifiers that decrease recombination rates, with several types of fitness matrices. As discussed in more detail below, our results agree with those of FELDMAN and BALKAU and show that selfing may lead to selection for decreased recombination, even when the fitness interactions are such that there is no such selection in a random-mating population.

A program for simulating the genetics of three loci was used. The population could either be random-mating, or could be assumed to be partially selfing. The three loci will be called *A*, *B* and *C*. Loci *A* and *B* are assumed to have effects on fitness, and to be linked. Locus *C* is a modifier of the rate of recombination between *A* and *B*, and is assumed to have no fitness effect of its own; it is assumed to be either linked to *A* and *B*, but to the right of *B*, or else unlinked to them. The recombination fraction *B-C* will be written R_{BC} . The *C* gene could be assumed to be either dominant or recessive. It is assumed to have no effect on recombination between *B* and *C*, but to alter the frequency of crossing over between *A* and *B*.

The computer runs which we describe in this paper are designed to investigate

three different modes of selection for recombination. The main differences between these three models were in the fitness matrices describing the effects of loci A and B , and in the order in which variation at the loci was introduced into the population. These details will be described below.

MODELS OF SELECTION FOR INCREASED RECOMBINATION

First model: This model has been the subject of a recent paper (STROBECK, MAYNARD SMITH and CHARLESWORTH 1976). Locus A is assumed to be heterotic. An advantageous mutation then occurs at locus B . The modifier gene (locus C) is assumed to be segregating in the population, and we then ask the question: how does the gene frequency of the modifier change after the advantageous mutation? In order to simulate this situation, the initial genotype frequencies were calculated, taking into account the amount of selfing, by formulae derived by STROBECK (in preparation) for a heterotic gene (A) and a linked neutral locus (C). These frequencies were modified so as to simulate the introduction of a small frequency of a gamete carrying the mutation at the B locus. The population was then simulated through a series of generations, usually about 200, until the modifier frequency stopped changing.

In order to get a true picture of the selection for recombination in this model, it is not sufficient to do just one run, introducing the advantageous mutation into a single gamete type. For example, it is obvious that if the advantageous mutation arises in coupling with the modifier gene, there might be a bigger increase in the modifier frequency than in the repulsion case. With the random-mating situation, it is therefore necessary to do runs of both the coupling and repulsion cases (STROBECK, MAYNARD SMITH and CHARLESWORTH 1976) and thus obtain the expected change in the modifier frequency. With selfing, the situation is more complex still, since we cannot assume that each gamete is present in random-mating proportions with the other gametes in the population. It is nevertheless possible to obtain a value for the expected change in the modifier frequency by doing a set of four runs for the repulsion case, and four for the case of coupling; in each run of a set, the advantageous mutation is introduced into the same gamete type, but into a different genotype in each case. For example, suppose that we want to investigate the change in frequency of the modifier allele C_2 , compared with C_1 , when an advantageous mutant B_2 arises in a population containing only B_1 ; the A locus is assumed to be polymorphic for alleles A_1 and A_2 . Then a mutation in coupling with the modifier would be

either $A_1 B_1 C_2 \longrightarrow A_1 B_2 C_2$

or $A_2 B_1 C_2 \longrightarrow A_2 B_2 C_2$

If we confine our attention to gametes containing A_2 , there are four genotypes in which the mutation may occur:

$A_2 B_1 C_2$ / $A_2 B_1 C_2$

$A_2 B_1 C_2$ / $A_2 B_1 C_1$

$A_2 B_1 C_2$ / $A_1 B_1 C_2$

$A_2 B_1 C_2$ / $A_1 B_1 C_1$

These four constitute a set of coupling runs. A similar set of four, with $A_2 B_1 C_1$ on the left, were used for the repulsion runs. Each run gives a value for the change in C_2 frequency. The average change, weighting the respective changes by the frequencies of occurrence of the genotypes in the initial population, can then be calculated. The situation is simplified if we assume symmetry at the A locus, *i.e.*, the two selection coefficients are equal, so that the frequencies of A_1 and A_2 are equal. In this situation, the 8 runs described above are sufficient, and one does not have to run the further sets with the gametes containing A_1 .

With no selfing, STROBECK, MAYNARD SMITH and CHARLESWORTH (1976) concluded that recombination is strongly favored in this model situation only when the original recombination frequency between A and B is extremely small, and when the modifier gene C_2 is recessive, and is closely linked to the AB region. Table 1 shows a selection of our results. It is evident that the same conclusion holds when there is selfing at a rate of 0.8. Considering first the case when the modifier is tightly linked to B ($R_{BC} = 0.01$), Table 1 shows that selfing may either increase or decrease the expected change in the modifier frequency. The only case which gives an increased expected change is that at the top of Table 1. Turning to the case when the modifier is unlinked ($R_{BC} = 0.5$), the modifier is only weakly selected when there is no selfing, but selfing increases the expected change considerably. This is true for both dominant and recessive modifiers. Without selfing, the selection for a modifier of recombination is weaker, the higher the value of the unmodified recombination fraction for the $A-B$ interval. Table 1 shows some examples of this. With selfing, there can be non-negligible selection for increased recombination, even when A and B are quite loosely linked. For example, with 80% selfing, Table 1 shows instances of expected changes of 1–3% in the modifier frequency, even when the unmodified recombination fraction between A and B is 0.1, whereas there is no change without selfing.

Second model: This model is based on an idea presented by FELSENSTEIN and YOKOYAMA (1976). Advantageous mutations are assumed to occur at two different loci. The population contains a modifier of the recombination frequency between them. When the second advantageous mutation occurs, it is clear that there may be selection for the modifier, since individuals with the modified recombination rate will have an improved probability of leaving offspring which have both advantageous genes. As in the previous model, we are therefore interested in the expected change in the modifier, taking into account the frequencies of the various genotypes in which the second advantageous mutation could occur.

The initial populations were set up with the modifier gene segregating at the desired frequency, and with the genotype frequencies calculated by the usual formula for a neutral gene in a selfing population (CROW and KIMURA 1970). In addition, these frequencies were modified so as to simulate a mutation at locus A (first advantageous mutation). After several generations, a second advantageous mutation, at locus B , was simulated, and the run continued until the modifier frequency stopped changing. It is obvious that the selection for recom-

bination in this situation will depend on the time between the two mutations. If the first advantageous gene has risen to a high frequency before the second mutation happens, there will not be strong selection for recombination between them. This expectation is borne out by the results of these runs. We will describe the results when the first advantageous mutation (A_2) had an initial frequency of 0.0005, and will confine ourselves to the case when the second mutation occurred 25 generations after the first. With these assumptions, the A_2 allele is still rare when the second mutation ($B_1 \rightarrow B_2$) occurs, and the predominant genotype at the A locus is $A_1 A_1$. We can therefore assess the degree of selection for the modifier by considering the result of introducing B_2 into A_1 gametes only, both in coupling and repulsion with the modifier gene, as explained for our first model.

Some results are shown in Table 2. The conclusions are similar to those from the simulations of the first model. Strong selection for increased recombination was obtained only when the modifier was tightly linked to the selected loci, and when the original value of the recombination frequency between A and B was zero. Unlike the previous model, this system sometimes generates selection against a modifier that increases recombination; this selection is only slightly increased with selfing. In this model, indeed, there is selection against recombination, rather than for it, unless the selected loci are initially almost completely linked. Complete linkage was assumed by FELSENSTEIN and YOKOYAMA (1976).

TABLE 1

Summary of results of simulations of our first model

| Recombination frequency between A and B | | Modifier action | R_{BC} | Expected change in modifier frequency | |
|--|-------------------|--------------------|----------|--|----------------|
| Original value | Modified value | | | No selfing | 80% selfing |
| 0 | 0.01 | Recessive | 0.01 | 0.2631 | 0.3163 |
| 0.001 | 0.01 | Recessive | 0.01 | 0.0199 | 0.0174 |
| 0 | 0.01 | Recessive | 0.5 | 0.0002 | 0.0223 |
| 0.001 | 0.01 | Recessive | 0.5 | 0.0002 | 0.0140 |
| 0.1 | 0.5 | Recessive | 0.5 | 0.000001 | 0.0142 |
| 0 | 0.01 | Dominant | 0.01 | 0.0309 | 0.0228 |
| 0.001 | 0.01 | Dominant | 0.01 | 0.0214 | 0.0156 |
| 0 | 0.01 | Dominant | 0.5 | 0.0004 | 0.0209 |
| 0.001 | 0.01 | Dominant | 0.5 | 0.0003 | 0.0163 |
| 0.1 | 0.5 | Dominant | 0.5 | 0 | 0.0244 |

Fitness parameters

| | | |
|-----------|-----------|-----|
| Locus A | $A_1 A_1$ | 0.5 |
| | $A_1 A_2$ | 1 |
| | $A_2 A_2$ | 0.5 |
| Locus B | $B_1 B_1$ | 0.8 |
| | $B_1 B_2$ | 1 |
| | $B_2 B_2$ | 1.2 |

Multiplicative fitnesses assumed.

Initial frequency of modifier = 0.2.

If the selected loci are able to recombine in the initial population, the two advantageous genes are able to get into coupling, and further increases in the recombination fraction are selectively disadvantageous, because the favored combination is broken up.

In most of the cases we tested, where conditions were such as to favor increasing the recombination rate, an increase in the amount of selfing gave rise to a bigger (often substantially bigger) expected change in the modifier frequency.

When the initial frequency of the modifier was given the value 0.2, instead of 0.0005, the expected changes in the modifier frequency were affected. Using parameter values that gave small expected changes in Table 2, the effect of starting the run with the modifier already present at quite high frequency was that the expected change became negative. When the expected change in Table 2 was large, however, we sometimes found an even larger change when the modifier was already at a frequency of 0.2. For instance, with the parameters of the top two lines of Table 2, the expected changes, when the initial modifier frequency was 0.2, were 0.4488 with no selfing, and 0.7000, with 80% selfing.

Third model: In this section we will present results of simulation of selection for recombination in populations subjected to fluctuations in the environment (STURTEVANT and MATHER 1938; CHARLESWORTH 1976). This type of system was simulated as follows. First, a population was set up with both loci *A* and *B* segregating, and this was run for several generations, during which time the fitness matrix was changed at regular intervals from one set of values to another. Then a mutation at the modifier locus was simulated, and the run continued, with the same alternation of the fitnesses. The progress of the modifier gene frequency was followed. Generally it changed slowly so that we could only see whether it was increasing or decreasing in frequency; in some of the runs, where

TABLE 2

Results of some simulations of our second model

| Recombination frequency between <i>A</i> and <i>B</i> | | Modifier action | R_{BC} | Expected change in modifier frequency | |
|--|-------------------|--------------------|----------|--|----------------|
| Original value | Modified value | | | No selfing | 80% selfing |
| 0 | 0.01 | Recessive | 0.01 | 0.3291 | 0.8496 |
| 0.001 | 0.01 | Recessive | 0.01 | -0.004 | -0.005 |
| 0 | 0.01 | Recessive | 0.5 | -0 | 0.0209 |
| 0.01 | 0.5 | Recessive | 0.01 | -0.004 | -0.005 |
| 0 | 0.01 | Dominant | 0.01 | 0.1127 | 0.1580 |
| 0.001 | 0.01 | Dominant | 0.01 | -0.00002 | -0.0004 |
| 0 | 0.01 | Dominant | 0.5 | 0.00001 | 0.0184 |
| 0.01 | 0.5 | Dominant | 0.01 | -0.002 | -0.002 |

Fitness parameters

| | | |
|-------------------------------|-----------|-----|
| (Locus <i>A</i> or <i>B</i>) | $A_1 A_1$ | 0.8 |
| | $A_1 A_2$ | 1.0 |
| | $A_2 A_2$ | 1.2 |

Multiplicative fitnesses assumed.

Initial frequency of modifier was 0.0005.

quicker changes occurred, we could continue the run until the modifier frequency stopped changing.

The first model which we will consider is the one described by CHARLESWORTH (1976). Loci A and B are both assumed to be heterotic, and the environment is assumed to change from time to time in such a way that the gamete types $A_1 B_2$ and $A_2 B_1$ are favored at some periods, whereas $A_1 B_1$ and $A_2 B_2$ are favored at other times. This system maintains variability at both loci, and can provide a selection pressure in favor of recombination.

Some results of these runs are shown in Figures 1 and 2, which show the mean recombination fraction between loci A and B in the population as a whole. Figure 1 shows the results for an unlinked modifier, with the fitness matrices of Table 3. The period of oscillation between the two fitness matrices was 10 generations. Such a situation is of course unlikely to occur in nature, but is

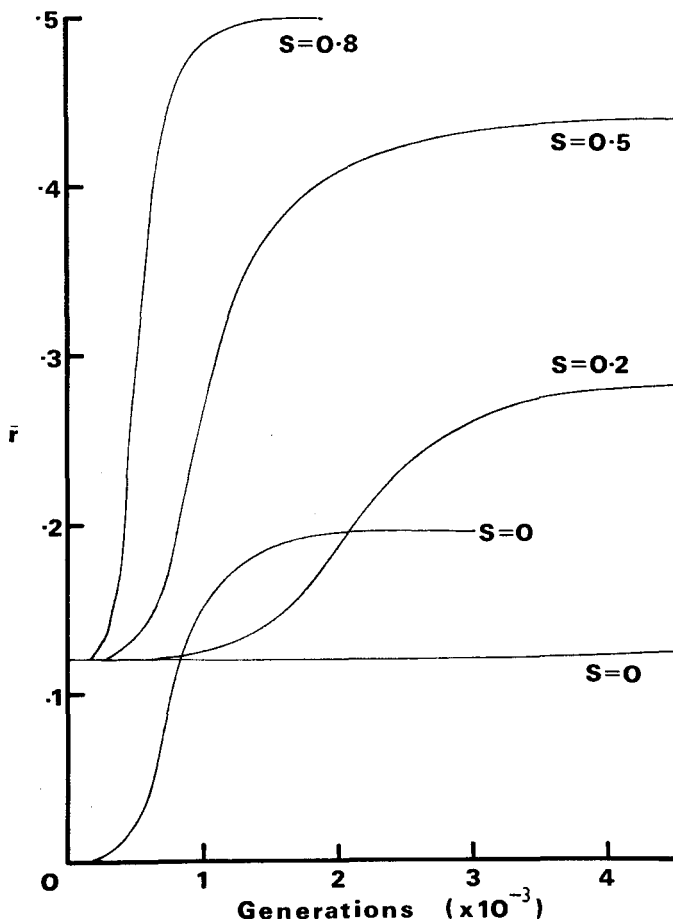


FIGURE 1.—Effect of selfing rate (S) on the mean recombination fraction (\bar{r}) in a fluctuating environment. The two fitness matrices of Table 3 were alternated at 10 generation intervals. The modifier gene is assumed to be unlinked to the selected loci.

simply used to demonstrate that selection for increased recombination can occur, and to study the effect of selfing on this process. The case of a stochastically varying environment was studied by CHARLESWORTH (1976), for a random-mating population; no qualitatively new effects were found, compared with the cyclical case. A modifier with intermediate dominance was assumed, giving a value of 0.25 in the heterozygotes and 0.5 in the homozygotes. Starting with an unmodified recombination fraction of 0.12 and with no selfing, the modifier gene was very weakly selected for. (When the unmodified recombination fraction was zero, however, much quicker changes occurred. This case, which was not studied by CHARLESWORTH (1976), is also shown in Figure 1). With selfing, selection was much stronger, and an equilibrium level of the population recombination fraction was reached in about 1,000 to 4,000 generations; the equilibrium level depended strongly on the amount of selfing. For example, with 95% selfing, the equilibrium level of the population recombination fraction was 0.5, and this level was reached in 1,000 generations. With 80% selfing, the same final result was reached more slowly, in about 1,400 generations. With 50% selfing, the recombination fraction rose to above 0.4 in 2,000 generations, and then changed more slowly and was still rising a little when the run ended, at 4,400 generations. It seems likely that the equilibrium level for this case lies below 0.5, because a run with the same parameter values except that the unmodified recombination fraction was 0.5, and the modified values 0.25 and 0.12, gave the result that such a modifier was selected for, *i.e.*, the recombination fraction was reduced to a value below 0.5. By similar reasoning, we confirm the result suggested by Figure 1, that with 20% selfing the modifier was selected for until the mean recombination rate in the population reached its equilibrium level of about 0.29.

Figure 2 illustrates the effect of changing the recombination fraction between the modifier locus and the *B* locus. As already reported by CHARLESWORTH (1976), a linked modifier is selected for more strongly than an unlinked one. Figure 2 shows that this is also true when there is selfing, and that in this type of situation selfing still strongly affects the rate of selection for a modifier of recombination, and also the equilibrium that the population reaches.

Qualitatively similar results have been obtained with other fitness values, and with different periods of oscillation between the alternative fitness matrices. With weak selection, the recombination modifier changed much more slowly in frequency than with the fitness matrices of Table 3. Nevertheless, equilibrium at a recombination fraction of 0.5 was possible, and the equilibrium recombination fraction was higher with selfing than in random mating populations.

We have also carried out simulations of the model proposed by STURTEVANT and MATHER (1938), in which three environments alternate. This model has not previously been studied quantitatively, even for the case of random-mating populations. In the first environment (C), one of the alleles at each locus is selected for (say *A* and *B*). In the second environment (D), the alternative alleles (*a* and *b*) are selected for, at each of the two loci. In each of these environments, fitnesses are multiplicative. Regular alternation of these two states can maintain variability at the two loci. In the third environment (E), there is interaction between

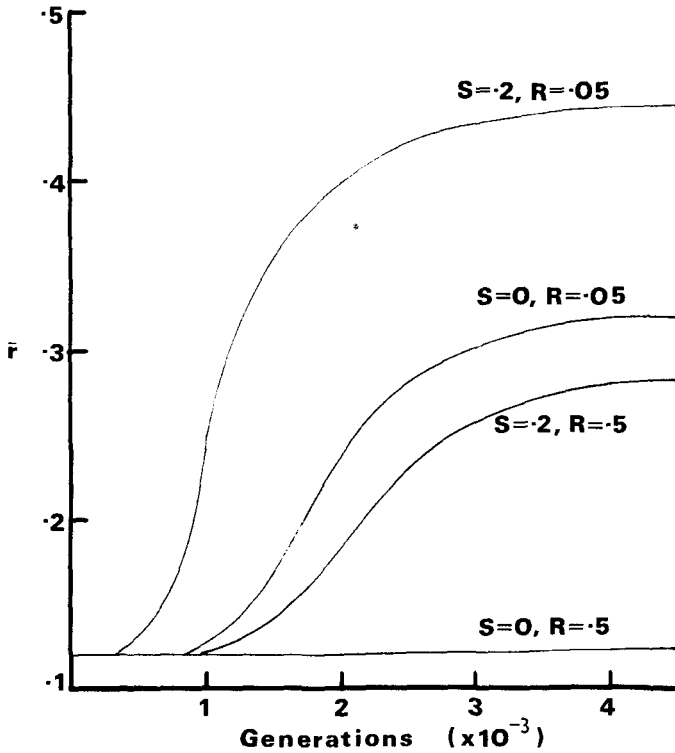


FIGURE 2.—Effects of linked and unlinked modifier genes on the mean recombination rate (\bar{r}) in populations with different levels of selfing. R denotes the recombination fraction between the modifier of recombination and the selected loci (R_{BC}).

the genes, such that the gametes Ab and aB are selected for, and there is heterozygote advantage at each locus. If the population were exposed indefinitely to this environment, the variability would be maintained, and furthermore there would be linkage disequilibrium of opposite sign to that which would be found under a regime of permanent fluctuation between environments C and D.

The results of simulations of this system are similar to those of the previous model. Table 4 gives a typical parameter set used. With no selfing, and with 10

TABLE 3

Fitness matrices used in the simulations of the model of CHARLESWORTH (1976)

| | | $A_1 A_1$ | $A_1 A_2$ | $A_2 A_2$ |
|-----------|-----------|-----------|-----------|-----------|
| Matrix 1. | $B_1 B_1$ | 0 | 0.75 | 0.7 |
| | $B_1 B_2$ | 0.9 | 1 | 0.9 |
| | $B_2 B_2$ | 0.7 | 0.75 | 0 |
| Matrix 2. | $B_1 B_1$ | 0.7 | 0.75 | 0 |
| | $B_1 B_2$ | 0.9 | 1 | 0.9 |
| | $B_2 B_2$ | 0 | 0.75 | 0.7 |

generations spent in each environment, an unlinked modifier that increases the recombination frequency between loci *A* and *B* from zero to 0.5 (with a value of 0.25 for the heterozygotes at the modifier locus) rises quite rapidly, so that the population's mean recombination frequency is above 0.2 by 2,500 generations. The equilibrium value is uncertain, but is below 0.5. When the original recombination frequency between the *A* and *B* loci is 0.12, the modifier rises in frequency much more slowly than this, so that no appreciable change in the population mean occurs over many thousands of generations. With selfing, the changes produced are faster; for example, with 80% selfing, the mean recombination fraction in the population rises from 0 to 0.5 in approximately 1,250 generations. Selection is also faster when the modifier gene is linked to *A* and *B*. Finally, as shown by CHARLESWORTH (1976) for his system, the time-course of the environmental changes affects the strength of selection for recombination. With the present parameter system, a cycle of 6 generations (2 generations spent in each of environments C, D and E in turn) generates weak selection for recombination, and the final equilibrium value attained by the population is below 0.06, though above zero, even with 80% selfing, and a tightly linked modifier (1% recombination fraction). With a cycle of 15, selection is considerably stronger, and a mean value for the population of 0.5 is reached with zero selfing and an unlinked modifier. Longer cycles again give weaker selection. In these simulations, the linkage disequilibrium between loci *A* and *B* was consistently negative, although the size of *D* varied as the environment changed. In other words, the negative sign of *D*, which was generated by the interaction in environment E, was never entirely abolished during the periods spent in the other environmental states. Thus selection for recombination could be demonstrated without change in the sign of *D*.

A difficulty with this model is that the environments must occur in approximately equal frequencies, in order to maintain the variability. In particular, long sequences of environment C or D would lead to fixation at the selected loci. We have simulated cycles containing excess of environment C, for example, and have shown that the selection for recombination is considerably weakened, with

TABLE 4

Fitness matrices used in the simulations of STURTEVANT and MATHER's model

| | | $A_1 A_1$ | $A_1 A_2$ | $A_2 A_2$ |
|-----------|-----------|-----------|-----------|-----------|
| Matrix C. | $B_1 B_1$ | 1.0 | 0.7 | 0.4 |
| | $B_1 B_2$ | 0.7 | 0.49 | 0.28 |
| | $B_2 B_2$ | 0.4 | 0.28 | 0.16 |
| Matrix D. | $B_1 B_1$ | 0.16 | 0.28 | 0.4 |
| | $B_1 B_2$ | 0.28 | 0.49 | 0.7 |
| | $B_2 B_2$ | 0.4 | 0.7 | 1.0 |
| Matrix E. | $B_1 B_1$ | 0.3 | 0.75 | 0.6 |
| | $B_1 B_2$ | 0.9 | 1.0 | 0.9 |
| | $B_2 B_2$ | 0.6 | 0.75 | 0.3 |

or without selfing. Excess of environment E intervening for short periods between C and D, however, tended to strengthen the selection, though long periods in which this type of environment remained constant would of course lead to selection against recombination.

MODEL OF SELECTION FOR DECREASED RECOMBINATION

This type of system was simulated in the same way as the model of the previous section, except that a single fitness matrix was employed throughout a run.

Using the upper fitness matrix of Table 3, at equilibrium before the introduction of the recombination modifier, there is linkage disequilibrium, whatever the value of the recombination fraction between the *A* and *B* loci. A value of 0.5 was chosen for the unmodified recombination fraction, and the modifier was assumed to decrease this to 0.25 in heterozygotes ($C_1 C_2$), and to zero in homozygotes ($C_2 C_2$). When the *C* locus was unlinked to the *AB* region, selfing increased the rate at which the frequency of C_2 increased in the population. With the same fitness matrix but with a linked modifier ($R_{BC} = 0.01$), similar results were obtained, except that the modifier increased fastest at intermediate levels of selfing, and was as slow to increase when there was a high rate of selfing as when selfing was rare. These results are summarized in Table 5.

The second fitness matrix we tested was the one used by LEWONTIN (1974, p. 293). The essential difference from the system of Table 3 is that the advan-

TABLE 5

Results of simulations of modifiers for reduction of recombination

| Fitness matrix | R_{BC} | Selfing rate | Frequency of modifier gene (C_2) after | |
|----------------|----------|--------------|--|----------|
| | | | 150 gens | 400 gens |
| 1 | 0.5 | 0 | 0.00072 | 0.00365 |
| | | 0.5 | 0.00268 | 0.12454 |
| | | 0.8 | 0.00577 | 0.73299 |
| | 0.01 | 0 | 0.00231 | 0.07776 |
| | | 0.5 | 0.00709 | 0.97651 |
| | | 0.8 | 0.00383 | 0.48892 |
| 2 | 0.5 | 0 | 0.00025 | 0.00025 |
| | | 0.5 | 0.00664 | 0.95330 |
| | | 0.8 | 1 | 1 |
| | 0.01 | 0 | 0.00025 | 0.00025 |
| | | 0.8 | 0.27107 | 1 |
| | | 0.95 | 0.00025 | 0.00025 |
| 3 | 0.5 | 0 | 0.00025 | 0.00025 |
| | | 0.8 | 0.00094 | 0.01216 |
| | | 0.95 | 0.00510 | 0.72225 |

Fitness matrices.

1: Upper matrix of Table 3.

2: Matrix of LEWONTIN (1974, p. 293).

3: Multiplicative fitnesses (see text).

Modifier was introduced at a frequency of 0.00025.

tage of heterozygosity increases with the level of background heterozygosity. With this fitness matrix there is linkage disequilibrium at equilibrium only when the recombination fraction is less than 0.08125, in a random-mating population. With the same modifier action as before, starting at an initial recombination fraction of 0.5, a modifier reducing recombination is therefore not selected for, when selfing is zero; starting with a recombination fraction of less than 0.0815, there will be weak selection for such a modifier. With selfing, modifiers reducing recombination increase in frequency, in either situation. Table 5 shows some examples of cases with an initial recombination fraction of 0.5, so that there was no linkage disequilibrium when the modifier was introduced.

The third type of fitness matrix which we have studied was a multiplicative one, with the same fitness values at both the *A* and *B* loci. Both loci were assumed to be heterotic, with homozygotes having fitnesses equal to 0.7 of the values for the heterozygotes. No linkage disequilibrium is generated by this system, under random mating, unless the recombination fraction is less than 0.0225. With an initial recombination fraction of 0.5, and random mating, a modifier reducing recombination does not change in frequency, whereas, as Table 5 shows, there can be a large change in a selfing population.

The results described here suggest that increased levels of selfing on the whole favor a higher intensity of selection for reduced recombination in constant-environment models with two heterotic loci. It is therefore most unlikely that this type of model can account for increased recombination rates in selfers, and it seems highly probable that its effects work in the opposite direction.

DISCUSSION

The results of the simulations described in this paper show that in selfing populations there are complex effects acting on genes that alter recombination frequencies between other genes. First, when there is selfing, the rarity of double heterozygotes may limit the rate of change in frequency of such modifiers. In situations which favor recombination, however, the fact that double heterozygotes are rare may increase the level of recombination favored by selection. These two factors oppose one another, so that it is impossible to predict the outcome beforehand.

Similarly, when there is selection in a constant environment favoring reduction in recombination rates, there may also be an opposition of two factors with respect to the effects of increased selfing. One factor is the effect of reduced double heterozygote frequencies, as above, which will retard the spread of a modifier reducing recombination. This effect can be seen in the results for a linked modifier with the first fitness matrix of Table 5. On the other hand, in situations involving several linked heterotic loci, the intensity of selection against recombinant genotypes may be higher with increased selfing. This can be viewed intuitively as follows. In the extreme case of complete selfing, the average fitness of the progeny of multiple heterozygotes is the only factor affecting the intensity of selection against recombination. The chance that an individual is homozygous at a given locus, in the selfed progeny of a heterozygote, is increased if the individual is homozygous at a linked locus which was also heterozygous in the parent

(HALDANE 1949). The closer the linkage, the greater the effect. The selective deaths due to homozygosity at the second locus will therefore have less impact the tighter the linkage between the loci, since they are occurring more frequently in individuals due to be eliminated in any case as a result of selection at the first locus. This effect creates a selection pressure for reduced recombination, even in the absence of linkage disequilibrium between the two loci, but can obviously only operate when there is some degree of self-fertilization or other form of extreme inbreeding. Its intensity will obviously increase, the higher the level of inbreeding, provided the loci do not become fixed. This factor probably accounts for the increased rates of selection for modifiers reducing recombination with increased selfing, shown in Table 5.

It is thus apparent that the question of how selfing will affect selection on recombination rates is an extremely complicated one. Matters are yet further complicated by the fact that a real chromosome may carry not only gene pairs that generate selection for recombination, or against it, but both types together, and these will very likely be interspersed among one another, so that the net effect on modifiers of recombination will depend on the whole complex situation. From the results of the computer simulations described earlier, it seems likely that selfing will tend to increase the selective advantage of some genes that decrease recombination and may do so also for others that increase recombination rates. The fact that recombination appears empirically to be promoted in selfing species suggests that forces promoting recombination come into play in selfing populations, which are strong enough to outweigh the increase in selection against recombination. These considerations show that it is an oversimplification to equate increased selfing with reduced recombination when trying to understand how selection acts on recombination and selfing rates. There has been a tendency in the literature to make this equation (*e.g.*, KAHLER, CLEGG and ALLARD 1975).

The calculations presented here do not enable us to rule out any of the models of selection for increased recombination which we have considered, though it is of course possible that none of them plays an important role in real populations. All the models are capable of producing increased selection for recombination with increased levels of selfing, when suitable parameter values are employed.

The first two models studied in this paper both depend on hitchhiking effects. Both can give substantial selection for recombination modifiers even in the absence of selfing, especially in the case of a recessive modifier tightly linked to the selected loci, when the initial recombination fraction is very small. In such cases, selfing increases the selection for the recombination modifier, and the effect on the overall recombination fraction could be big enough to be detectable in a real population. In other cases, the effect of selfing may be in either direction, and in any case even a greatly increased change under selfing is often still too small to be noticeable in any actual study. It also seems unlikely that large effects on a recombination modifier can be generated by these systems except with strong selection on the selected loci. With more than two loci, it is possible that effects might build up along the chromosome, so as to produce bigger differences than those found by us.

The models of selection for recombination in fluctuating environments gen-

erate large differences in the recombination frequency finally attained by the population, depending on the level of selfing. This is true in the long term even with weak selection at the selected loci, though the modifier frequency would change very slowly in such cases. As shown in Figures 1 and 2, this type of model can generate fairly rapid changes in the modifier frequency, even when the starting population has a recombination fraction as high as 12%. These models could therefore adjust the population's recombination fraction in a continuous fashion anywhere between values of 0 and 0.5, as a result of changes in the selfing rate.

LITERATURE CITED

- CHARLESWORTH, B., 1976 Recombination modification in a fluctuating environment. *Genetics* **83**: 181-195.
- CROW, J. F. and M. KIMURA, 1970 *Introduction to population genetics theory*. Harper and Row, New York.
- FELDMAN, M. W. and B. BALKAU, 1972 Some results in the theory of three gene loci. In *Population dynamics*, Edited by T. R. E. GREVILLE. Academic Press, New York.
- FELSENSTEIN, J. and S. YOKOYAMA, 1976 The evolutionary advantage of recombination. II. Individual selection for recombination. *Genetics* **83**: 845-859.
- GARBER, E. D., 1956 The genus *Collinsia*. I. Chromosome number and chiasma frequency of species in the two sections. *Bot. Gaz.* **118**: 71-73. —, 1958 The genus *Collinsia*. VII. Additional chromosome numbers and chiasma frequencies. *Bot. Gaz.* **120**: 55-56.
- GRANT, V., 1958 The regulation of recombination in plants. Cold Spring Harbor Symp. Quant. Biol. **23**: 337-363.
- HALDANE, J. B. S., 1949 The association of characters as a result of inbreeding and linkage. *Ann. Eugen.* **15**: 15-23.
- KAHLER, A. L., M. T. CLEGG and R. W. ALLARD, 1975 Evolutionary changes in the mating system of an experimental population of barley (*Hordeum vulgare* L). *Proc. Natl. Acad. Sci. U.S.* **72**: 943-946.
- LEWIS, K. R. and B. JOHN, 1963 *Chromosome marker*. J. & A. Churchill Ltd., London.
- LEWONTIN, R. C., 1974 *The genetic basis of evolutionary change*. Columbia University Press, New York.
- MATHER, K., 1943 Polygenic inheritance and natural selection. *Biol. Rev.* **18**: 32-64.
- MAYNARD SMITH, J., 1976 A short-term advantage for sex and recombination through sib-competition. *J. Theor. Biol.* **63**: 245-258.
- STEBBINS, G. L., 1950 *Variation and evolution in plants*. Columbia University Press, New York. —, 1958 Longevity, habitat and release of genetic variability in the higher plants. Cold Spring Harb. Symp. Quant. Biol. **23**: 365-377.
- STROBECK, C., J. MAYNARD SMITH and B. CHARLESWORTH, 1976 The effects of hitchhiking on a gene for recombination. *Genetics* **82**: 547-558.
- STURTEVANT, A. H. and K. MATHER, 1938 The interrelations of inversions, heterosis and recombination. *Am. Naturalist* **72**: 447-452.
- WILLIAMS, G. C., 1975 *Sex and evolution*. Princeton University Press, Princeton.
- ZARCHI, Y., G. SIMCHEN, J. HILLEL and T. SCHAAP, 1972 Chiasmata and the breeding system in wild populations of diploid wheats. *Chromosoma (Berl.)* **38**: 77-94.