CHAPTER 5

SEX AND THE EVOLUTION OF RECOMBINATION

Joseph Felsenstein

INTRODUCTION

Over a decade ago, I wrote two papers (Felsenstein, 1974; Felsenstein and Yokoyama, 1976) on models for the evolution of recombination. The central concern of those papers was to demonstrate the relationship between various models that had previously been proposed for the evolution of recombination and to present some simulation and theoretical results. The problem has continued to be of interest to evolutionary biologists, although they seem particularly entranced by it when it is called "the evolution of sex" rather than, more accurately, "the evolution of recombination." When books are written on the subject, the noun in their title is inevitably "sex" rather than "recombination." One wonders how many fewer people would buy a book on this subject if the word "sex" were not in the title.

Recently, interest in the subject seems to be increasing. In his monograph, Williams (1975, p. v) has declared that "I hope at least to convince [readers] that there is a kind of crisis at hand in evolutionary biology, and that my suggestions are plausible enough to warrant serious consideration." Crises in evolutionary biology have been declared quite frequently recently, although it has been noticeable that the biologist declaring one usually just happens to have completed a piece of work that is thought to solve it. These crises seem comparable in importance to the "constitutional crises" that used to be declared daily by the press during the Watergate hearings of 1973. After a time, it became clear that a constitutional crisis was somewhat less serious than a flat tire on your car.

This year, the sex crisis seems to have returned. Shortly after I finished a short review on this subject for a volume in honor of John Maynard Smith

(Felsenstein, 1985), I was asked by two different editors to write similar articles for volumes on the evolution of sex, and there is talk of at least one conference as well. What has happened? Has a new source of data or a new kind of experiment been discovered that will help us resolve the controversies? Has the failure to arrive at a consensus here become a barrier to further progress in some other area?

There is a continuing flow of new theories and variants of existing theories, but there seems to be no major new source of data, no illuminating new experiment, no barrier to progress in other fields. The problem has simply flared up again and will probably gutter out after a while. Biologists will once again all become convinced that they know the answer, but once again there will be no unanimity as to what the answer turned out to be.

TWO DISTINCTIONS

The issue of "the evolution of sex" covers at least four distinguishable phenomena: differentiation of the sexes, anisogamy, outcrossing, and recombination. Most of the work under that heading is actually on the last two phenomena. In this chapter, I provide an overview of the main categories of theories for the evolution of outcrossing and recombination. Note that for haploid organisms the absence of recombination has in effect the same consequences as the absence of outcrossing.

Explanations for the origin and maintenance of recombination are of two kinds. The crucial difference between them is whether or not they argue that recombination exists because of its action in reducing the extent of linkage disequilibrium. For example, Bernstein, Hopf, and Michod (in this volume) argue that recombination acts as a repair mechanism near the site of the chiasma. In that argument, the recombination between outside markers does not play an important role. Models in which the proper functioning of the chromosomes in meiosis depend on the presence of recombinations fall into the same class. By contrast, in the classical models of Fisher (1930) and Muller (1932), the essential function of recombination is to remove nonrandom associations between genotypes at different loci, or linkage disequilibrium. Unfortunately, the distinction I am making is not quite the same as that made by Maynard Smith (1978, p. 73), between "physiological" and "genetic" theories of the evolution of recombination. Maynard Smith defined the physiological theories as those in which recombination is maintained to ensure "the proper functioning of meiosis." The repair theory and the classical theory would both have been called "genetic" by Maynard Smith, although one involves local effects and the other outside markers.

My intention here is to comment on the theories that invoke linkage disequibrium, leaving it to others to cover the other theories.

IS LINKAGE DISEQUILIBRIUM A BAD THING?

It is worth repeating here some of the fundamental properties of linkage disequilibrium in the presence of selection, since it is one of the most abstruse population genetic phenomena and many evolutionists have little feel for it. Imagine first that we have a diploid population with two loci (a haploid version of the argument is easily constructed as well). At locus A there are two alleles, A and *a*, and at locus B there are two alleles, *B* and *b*. Now suppose that the population is in linkage equilibrium, meaning that there is no association between the presence of any genotype at the A locus and the presence of any genotype at the B locus. Then the fraction of *BB* genotypes among individuals who are *AA* is the same as the overall fraction of *BB* genotypes. Thus if *P*(AA) is the overall fraction of *AA* genotypes in the population, and *P*(*BB*) the fraction of *BB* genotypes,

$$P(AA\ BB) = P(AA)\,P(BB) \tag{1}$$

At the gametic or haplotype level, too, the presence of an *A* allele is independent of the presence of a *B* allele if there is linkage equilibrium:

$$g(AB) = p(A)\,p(B) \tag{2}$$

Natural selection acting on only one of these loci (say, the B locus) will not change the gene or genotype frequencies at the other. If, say, half of the *bb* and one-eighth of the *Bb* individuals die, irrespective of their genotypes at the A locus, then we can see that the chance that an individual dies is independent of its genotype at the A locus, and hence that the gene and genotype frequencies at the A locus are unchanged. Furthermore, after those deaths, the A locus and the B locus continue to be in linkage equilibrium.

Now suppose that a similar mortality occurs at the A locus, irrespective of the genotype at the B locus. It does not change the gene or genotype frequencies at the B locus, and it too leaves the population still in linkage equilibrium. Thus the effect of linkage equilibrium is that natural selection can go on independently at each locus, without affecting the rate or outcome at the other.

If in a generation we impose viability selection first at the A locus and then at the B locus, the effect will be the same as if a selection regime were imposed according to which the fitness of each genotype is the product of fitnesses at the A locus and at the B locus. Thus if the fitnesses of *AA*, *Aa*, and *aa* are 1:0.9:0.7, and fitnesses of *BB*, *Bb*, and *bb* are 1:0.8:0.4, then a multiplicative fitness scheme in which the fitness of *AaBb* is $0.9 \times 0.8 = 0.72$ will have exactly the same effect as two successive bouts of selection, one at each locus. This follows because the chance of surviving both rounds of selection is the product 0.9×0.8 of the chances of surviving each of them. If fitnesses are multiplicative, then linkage disequilibrium will be preserved and selection at each locus will not affect selection at the other. Even if the fitnesses are fertilities rather than viabilities, multiplicative determination of the multilocus fitnesses is the relevant condition.

I showed (Felsenstein, 1965) that, with multiplicative selection, linkage disequilibrium (departure from linkage equilibrium) will not arise if it does not already exist. In fact, the effect of recombination, at least at the population genetic level, is to reduce linkage disequilibrium towards zero by creating gametes that contain genes randomly assembled from different gametes of the previous generation. If the population is already in linkage equilibrium, then it does not matter whether recombination occurs or not—the genetic composition of the population is unaffected by it. Individuals are affected, but the numbers of various kinds of genotypes and gametes created and eliminated exactly cancel out as long as there is linkage equilibrium.

If there is linkage disequilibrium, then this affects the rate of response of each locus to natural selection. For instance, if a population has alleles A and *B* associated with each other, then *a* and *b* will also be nonrandomly associated. By virtue of the association, natural selection eliminating *a* alleles will also concurrently tend to eliminate *b* alleles as well. Thus natural selection at each locus will change gene frequencies at the other. If the favored alleles A and *B* are associated (in "coupling" linkage disequilibrium), then selection on each speeds the change of gene frequencies at the other. Coupling linkage disequilibrium increases the rate at which the population responds to natural selection. Association between A and *b* alleles (and correspondingly between *a* and *B* alleles) causes selection at the two loci to conflict. Of course, the terms "coupling" and "repulsion" require us to specify which alleles at each locus are to be regarded as comparable: in the present case, the favored alleles are those denoted by capital letters.

The easiest way to see the effect of disequilibrium is to consider haploids where the fitnesses at the loci are multiplicative, so that the fitnesses of *AB*, *Ab*, *aB*, and *ab* are in the ratios $(1+s)^2{:}1+s{:}1+s{:}1$. This is the situation in which at each locus the capital letter allele is favored with a selection coefficient of *s*, and the loci do not interact. If the gene frequencies happen to be identical at the two loci, then the most extreme coupling disequilibrium that could exist would be for the population to consist entirely of *AB* and *ab* gametes. Their fitnesses are in the ratio $(1+s)^2{:}1$. The coupling disequilibrium means that A-bearing gametes and *a*-bearing gametes differ more strongly in fitness than 1+s:1, and that will speed the change of the A locus by natural selection. The most extreme repulsion disequilibrium would be to have all *aB* and *Ab* gametes. Both of these types have the same fitness, $1+s$, so that the repulsion disequilibrium results in selection being completely stalled: selection favoring A exactly counterbalances selection favoring *B*.

Maynard Smith (1968) drew from these facts the implication for theories of the evolution of recombination. If a population starts in linkage equilibrium and undergoes natural selection with multiplicative fitnesses, then it will remain in linkage equilibrium at all times. The rate of change at each locus will be

the same regardless of the amount of recombination, since all that recombination could do would be to restore linkage equilibrium, and that already exists. One can go farther than Maynard Smith and show that a modifier gene affecting the rate of recombination will not undergo any change of gene frequencies in this situation.

The broader implication of the argument is that if we are to see any effect of recombination on the rate of evolution or the genetic equilibria in a population, we must have either nonmultiplicative fitnesses or some other force creating linkage disequilibrium. From the point of view of natural selection, it is departure from multiplicative combination of fitnesses that constitutes "interaction," although this conflicts with a statistical tradition that associates interaction with departure from additivity. The way to reconcile these two views seems to be to think not of the fitness of a genotype, but of the logarithm of its fitness. Additivity on a logarithmic scale is multiplicative interaction on the original fitness scale. Provided that we are talking of the logarithm of fitness, "interaction" in the (log) fitnesses is the condition for selection to cause departure from linkage equilibrium.

It is worth noting that Maynard Smith's argument invalidates the earliest genetic argument for the evolution of recombination, that advanced by East (1918). That argument is also the one commonly found in textbooks, which tend to be a bit out of date (in this case, by over 50 years). East argued that recombination creates new genotypes. So it does. An *AB/ab* parent will have among its gametes not only the two types that formed it, *AB* and *ab*, but also *Ab* and *aB* if there is recombination between the two loci. But if the population is in linkage equilibrium, then somewhere else an *Ab/aB* parent will be undergoing recombination, which will remove *Ab* and *aB* gametes and replace them by *AB* and *ab*. These two processes will exactly cancel each other if the two types of double heterozygote, coupling (*AB/ab*) and repulsion (*Ab/aB*) are equally frequent. This will happen precisely when the population is in linkage equilibrium. In that case no new genotypes arise by recombination.

In some cases, of course, new genotypes are disadvantageous. This will happen, for example, when natural selection favors particular multilocus genotypes. For example, suppose that natural selection favored genotypes that had as many capital letters (*A* and *B*) as lowercase letters (*a* and *b*). If we have a population consisting only of the genotypes *Ab/Ab*, *Ab/aB*, and *aB/aB*, then recombination will be deleterious to the population. It will produce *AB* and *ab* gametes from the heterozygotes. Except for the rare case of these two combining with each other, all other genotypes resulting from this recombination will have too many or too few capital letters.

Thus when the population comes to equilibrium under selection regimes involving multilocus interaction, there will be linkage disequilibrium. This disequilibrium increases the fitness, and its disruption by recombination will be deleterious. Such an argument was made by Lewontin (1971). But it is by no means obvious that an argument based on mean population fitness will convince

a modifier gene altering recombination frequency to be a good sport and change its frequency. Nei (1967) made an approximate argument and Feldman (1972) a more exact argument that the modifiers would usually do the honorable thing. Many references to work since then can be found in the interesting recent paper by Feldman and Libermann (1986) and in the chapter by Brooks in this volume. I have assumed and will assume throughout this chapter that the modifiers will behave themselves and be selected in the direction that improves the fitness of the population. But this is not invariably so; I am being intellectually lazy, and there is no substitute for a genuine analysis of a model having modifier loci.

We have the anomalous situation that a detailed population genetic analysis reveals not only that the standard explanation for the evolution of recombination will not work, but also that there is a good evolutionary reason for believing that modifiers will be selected to eliminate recombination.

TWO THEORIES OF THE EVOLUTION OF RECOMBINATION

To have a theory that predicts that recombination will be favored, or at least not eliminated from a population, a necessary part of that theory will be a source of linkage disequilibrium. Without it, recombination will have no effect on the genetic composition of the population, and modifiers increasing or decreasing its frequency will not be selected.

Two major classes of theory have been proposed, differing in the evolutionary source of the disequilibrium. For each of these, a variety of biological mechanisms have been suggested. When people talk of "a theory" for the evolution of recombination they usually are referring to the biological scenario rather than to the combination of evolutionary forces. I have been concerned with understanding the theories in the latter sense. Once we ask what forces are at work, it turns out that there are only these two distinguishable theories.

We may call these the Fisher–Muller theory and the varying selection theory. Fisher (1930) and Muller (1932) argued, in very similar terms, that recombination was advantageous to a population because it enabled favorable mutations that occurred in different individuals in the population to be fixed in the same gene pool. Without recombination the two favorable mutations could at best compete with each other and could not both be incorporated into the same genome.

How can we understand Fisher and Muller's theory in terms of linkage disequilibrium? I have argued (Felsenstein, 1974, 1985) that in their theory the source of linkage disequilibrium is genetic drift. For example, if two favorable mutants happen to occur in the same generation in a diploid population of size N, one at the A locus and one at the B locus, then the chance that these will occur in different gametes is $1 - 1/(2N)$. They will occur in the same gamete $1/(2N)$ of the time. Either way the population will be in linkage disequilibrium. The disequilibrium is random and a result of the finiteness of the population size. If the population were of infinite size, each mutant would recur many

times and would arise at a frequency μ. A fraction μ^2 of the gametes would be double mutants, so that the population would be at linkage equilibrium.

The varying selection theory is the work of Sturtevant and Mather (1938). They imagined natural selection that favored in some generations coupling gametes (*AB* and *ab*) and, not long after, repulsion gametes (*aB* and *Ab*). If natural selection has favored the coupling types for some time, then the only way of generating repulsion gametes will be to have them produced by recombination. A population having recombination could come up with the appropriate recombinant types, while one that had no recombination might have lost them.

One can immediately see the similarity of the two theories—they both appeal to recombination as a means of coming up with absent gamete types. Both thus envisage linkage disequilibrium, but have different forces producing the disequilibrium. The two theories are one of the dimensions—the horizontal—of the classification used by Maynard Smith in this volume.

VARIANTS OF THE FISHER–MULLER THEORY

A number of other theories have been proposed that turn out to be variants of one or the other of these two. Muller (1964, p.8) pointed out "that an asexual population incorporates a kind of ratchet mechanism, such that it can never get to contain, in any of its lines, a load of mutations smaller than that already existing in its at presently least-loaded lines." Once every asexual genome contains deleterious mutants, one can never get back to a genome that has no deleterious mutants, except by back-mutation. With recombination, however, a mutant-free gamete can be produced from two parental gametes having different mutants. The asexual lineages will thus accumulate deleterious mutants at a higher rate than sexual ones. This seems at first to be a theory wholly different from the two I have just cited. In fact, it involves linkage disequilibrium randomly generated by genetic drift, as I have pointed out (Felsenstein, 1974). If the population contains mutants at a large number of loci, if it is finite, every gamete is likely to contain at least one mutant. But if it were infinite, then all possible gametic types would exist in their linkage equilibrium proportions, including the gamete that lacks all these deleterious mutants.

Muller's ratchet is thus a variant of the Fisher–Muller theory. It assumes that the favorable alleles being substituted start out at very high frequencies, instead of at very low frequencies, for the simple reason that the favorable alleles are the preexisting "wild-type" alleles rather than new advantageous mutations. The ratchet mechanism is a particularly plausible biological scenario, although Haigh (1978) has shown that the ratchet will be a fairly weak force favoring recombination under many of the possible combinations of parameters. Nevertheless, the universality of occurrence of deleterious mutations makes it an appealing explanation. Charlesworth (1978) has made a particularly interesting application of it to explain the genetic inactivation of Y chromosomes. Heller and Maynard Smith (1978) have argued that it would also operate in selfing species.

Another theory that turns out to be identical to the Fisher–Muller theory is that of Williams (1975; Williams and Mitton, 1973). I have argued elsewhere (Felsenstein and Yokoyama, 1976; Felsenstein, 1985) that Williams's "short-term" theory of selection in patches presents another biological scenario for the classical Fisher–Muller theory. The theory of Ghiselin (1974, p. 57) seems to be closely related to Williams's theory. Strobeck, Maynard Smith, and Charlesworth (1976) have put forward "hitchhiking" as a force acting to favor modifiers promoting recombination. I have argued (Felsenstein and Yokoyama, 1976) that this too is equivalent to the Fisher–Muller theory. Manning (1983) has emphasized the potential importance of hitchhiking effects.

VARIANTS OF THE VARYING SELECTION THEORY

A number of interesting biological scenarios have been proposed that would lead to the kinds of patterns of natural selection envisaged by Sturtevant and Mather (1938). One class of these is the parasite–host models, in which, if the loci A and B interact, a predominance of coupling hosts could select for a mixture of parasites adapted to those hosts. In the next few generations this might make repulsion genotypes favorable. This negative correlation between the disequilibrium favored in one generation with that favored in the next seems to require selection strong enough to cause rapid change of the parasite mix, as well as interactions between the loci so that coupling and repulsion gametes have significantly different parasite resistances. Theories of this sort have been put forward by Bremermann (1979), Glesener (1979), Hamilton (1980), and Price and Waser (1982).

Another situation that could lead to an appropriate conflict between selection for coupling and repulsion gamete types is Maynard Smith's (1980) optimum selection scheme. He supposes that natural selection is selecting for an intermediate optimum value of a phenotype, one controlled additively by a number of loci. This is likely to be a quite common pattern of selection. One of its normal effects is to create negative (repulsion) linkage disequilibrium, so that if *A* and *B* are alleles that increase the phenotype, *Ab* and *aB* gametes will be favored. Maynard Smith also assumes that the position of the optimum continually shifts back and forth. As we have already seen, when *A* and *B* are both being favored, the response to selection is fastest, and the fitness of the population highest when *A* and *B* are in coupling disequilibrium. Maynard Smith suggests, and shows by simulation, that this pattern of selection does in fact select for modifiers that increase the frequency of recombination. The generality of the pattern of selection makes this hypothesis particularly attractive, even if the strength of selection on the modifiers seems to be rather weak.

For some other biological scenarios, particularly Bell's (1982) "tangled bank" theory, I cannot easily tell whether they are versions of the Fisher–Muller theory

or the varying selection theory, or whether they represent some completely new theory. The matter is worth investigation. This can be done most efficiently by the author of each scenario before its publication.

THE COST OF MEIOSIS

Maynard Smith (1971) argued that there was a "cost of meiosis" amounting to one-half. Fisher's (1930) theory of sex ratios showed that outcrossing sexual hermaphrodites would be selected to devote as much reproductive effort to male as to female gametes, even though this would amount to a great overproduction of sperm. If these same individuals were, say, to self-fertilize, they could produce just a few sperm and about twice as many eggs. Competition between the outcrossers and the selfers would favor the selfers by a large margin.

Maynard Smith's argument has attracted much attention, because it is correct, and seems to prove that there is an enormous barrier to the origin of outcrossing and a great benefit to be reaped from its elimination. That in turn seems to put a premium on theories of the evolution of recombination that can show it to be favored by at least a factor of two. I think that the matter is not so simple. As the exchange between Barash (1976) and Maynard Smith and Williams (1976) shows, the argument for the cost of meiosis depends on anisogamy. If sperm are as large and costly as eggs, there will be no cost of meiosis. In an isogamous organism like Chalmydomonas, outcrossing could arise without suffering a factor of two disadvantage.

Once recombination and outcrossing exist, total elimination of the outcrossing will not have any immediate advantage, unless the investment in male gametes is simultaneously reduced. Furthermore, reduction of the amount of recombination will have no advantage; it is outcrossing, not recombination, that incurs the cost. The Maynard Smith argument is an important one, but it would be a mistake to take its implications as being simple. In particular, it would be interesting to have a theory that reworked Parker, Baker, and Smith's (1972) theory of the evolution of anisogamy while at the same time allowing outcrossing and investment in eggs and sperm to be under genetic control. The model of Harper (1982) would provide one possible starting point.

THE HILL–ROBERTSON EFFECT

The hardest part to understand in the major theories is the role of the linkage disequilibrium in the Fisher–Muller theory. Thus it seems worthwhile to devote some attention to explaining its paradoxical nature. After all, the disequilibrium between two loci is generated by genetic drift. On average it is zero, being sometimes positive and sometimes negative. When it is positive, selection at each locus increases the rate of adaptation at the other. When it is negative, selection at the two loci conflicts. Doesn't this lead to the two effects canceling

each other out on average? If so, then we would not expect there to be any natural selection favoring modifiers increasing the rate of recombination.

The two effects do not cancel. Let me try to explain this in two ways. The first is a heuristic argument, the second a (nearly) exact calculation. The heuristic argument involves seeing each locus as a source of random variation of background fitnesses for the other. Suppose first that we consider what happens when two loci are not linked and are substituting in the same population. A basic background fact is that variation from individual to individual in the number of offspring, even when uncorrelated with the genotype at a locus, reduces the effective population size. The extreme case of this is when in each generation one individual is chosen at random to do all the reproducing. It should be obvious in such a case that the effective population size is one rather than the nominal size. When the variation of fitness among individuals is less extreme, the effect is still qualitatively the same: a reduction of effective population size. This in turn means that the probability of fixation of a gene that is being selected is reduced, since that depends on the product $N_e s$ of effective population size and selection coefficient.

When the source of the random variation in fitnesses is the fitness of the genotypes at the other locus, the variation is not quite independent from one generation to another. If a gamete is A and the background locus is B, in the next generation the background locus will not be drawn completely independently. It will be unaltered 50% of the time, so that associations between the two loci persist for an average of two generations. This means that the effect of a random association between the two loci will be slightly larger if it gets to act for two generations before being re-formed at random.

When the loci are tightly linked, the effect should be much more dramatic. Random associations (random linkage disequilibria) will persist much longer and have a much larger effect. The tighter the linkage, the more strongly each locus acts to create large and long-lasting variations of fitness, thereby randomly perturbing gene frequencies at the other locus. The tighter the linkage, the more each locus creates a form of noise that reduces the effectiveness of selection at the other.

This phenomenon was first described by Hill and Robertson (1966), who were studying the effect of linkage on selection limits. They found, quite generally, that loci that did not interact nevertheless interfered with each other's response to selection as a net effect of random linkage disequilibria. They found that the size of this disequilibrium would be relatively small if $4N_e c$ was large, where c is the recombination fraction. Hill and Robertson discuss the phenomenon in a variety of ways and show by computer simulation how its strength depends on population sizes, selection coefficients, recombination fractions, and gene frequencies. Although their argument is unfortunately not well known, they have identified the common phenomenon underlying all forms of the Fisher–Muller theory.

There is one case in which we can provide a reasonably exact calculation (I am indebted to W.G. Hill for suggesting the approach). Consider a situation where the same selection coefficient s is at the two loci, and where initially the population has one mutant allele at each locus, so that there is exactly one A and one B. If these are placed at random in a diploid population of size N without recombination, then with probability $1/(2N)$ they will occur in the same gamete and with probability $1 - 1/(2N)$ they will occur in different gametes. In both of these cases we can calculate the probability of each locus fixing. In the first case, one gamete is AB and the rest ab. The selective advantage of the AB gamete will be $(1+s)^2 - 1 = 2s - s^2$. In the second case, there are two new gametes, one Ab and one aB, each with a selective advantage of s over the ab gametes. The probability that one or the other of these will fix is simply the probability that a single allele, present in two copies and having a selective advantage of s, will fix. Given that, there is obviously a 50% chance that it is the Ab gamete that ends up fixing.

Kimura (1962) gave an extremely accurate approximation for the probability of fixation in a two-allele case with constant fitnesses. For initial gene frequency p it is:

$$U(p) = \frac{1 - e^{-4Nsp}}{1 - e^{-4Ns}} \tag{3}$$

Moran (1962) has shown that the true fixation probability lies between this value and the value obtained from Equation 3 when s is replaced by $s/(1+s)$. These are very tight bounds in most cases. We can use Equation 3 to give the fixation probabilities in the two cases above. When the selective advantage is $2s-s^2$, the fixation probability of A is the probability of fixation of the AB gametes, whose initial frequency is $1/(2N)$, or

$$U_C = \frac{1 - e^{-2(2s-s^2)}}{1 - e^{-4N(2s-s^2)}} \tag{4}$$

When the two genes are in repulsion, the fixation probability is half the probability of fixing an allele with selective advantage s and initial frequency $2/(2N)$, or

$$U_R = (\tfrac{1}{2}) \frac{1 - e^{-4s}}{1 - e^{-4Ns}} \tag{5}$$

The overall probability that A will fix in the absence of recombination is then

$$U_O = [1/(2N)]U_C + [1 - 1/(2N)]U_R \tag{6}$$

This could be compared with the probability in the presence of free recombination. Unfortunately, we have no formula for that. The best we can do is to pretend that the rather small and fleeting linkage disequilibria formed under free recombination do not exist at all and to compute the probability of fixation

of A as if B were not present at all. This is simply Equation 3 with an initial frequency of $p = 1/(2N)$.

Figure 1 shows the ratio between the fixation probability of A without recombination and with recombination (or at least without any background genetic variation). The ratio drops as s increases. For large N it approaches 0.5 as s increases. This is reasonable: If s is very large and N is large, almost all cases will be of repulsion, in which case even if the favored gametes are certain to fix, only half of those have the A allele. Figure 1 may be compared to the curve for no recombination in Figure 10 of Hill and Robertson (1966). The two differ in that here s is the selection coefficient at both loci, whereas the strength of selection is being varied at only one locus in Hill and Robertson's figure.

The calculations show the reality of the Hill–Robertson effect and also show that it requires relatively strong selection at one locus for it to interfere substantially with selection at another. What cannot be seen from this case is that when many loci are simultaneously under selection, interference between the selection processes at different loci can be substantial. In the simulation results I published (Felsenstein, 1974), fixation probabilities of favorable mutants were noticeably lower when there was complete linkage, with selection coefficients as small as $s = 0.01$, provided that the rate of occurrence of favorable mutants was high enough that several of them would typically be segregating in the same population.

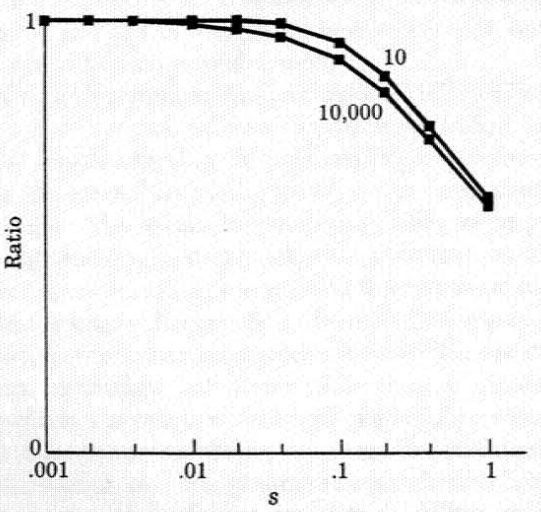

FIGURE 1. Ratio of fixation probability of the favored allele at a locus with complete linkage to that with free recombination, where both loci have the same selection coefficient s and both are present initially as single copies. The horizontal scale is logarithmic. Next to each curve is shown the value of N.

SUMMARY

At the population genetic level, the effect of recombination and outcrossing is to remove linkage disequilibrium (association between genotypes at different loci) from the population. A number of theories have been proposed under which this disequilibrium is deleterious, and modifier loci affecting recombination rates are selected to favor nonzero levels of recombination. These theories fall naturally into two groups, according to whether the linkage disequilibrium is originally produced by natural selection or by random genetic drift. Within these two theories, the detailed proposals of different authors amount to different biological scenarios enabling the action of the same evolutionary forces. In the absence of a comprehensive picture of the evolutionary forces affecting a population, and the genetic variability available, it is unlikely that we can make an informed decision as to which of these theories, if any, is important for the original evolution and subsequent maintenance of outcrossing and recombination. Progress in resolving these questions is likely to continue to be slow. Fortunately, the failure to resolve them does not constitute a crisis in evolutionary biology.

THE EVOLUTION OF RECOMBINATION RATES

Lisa D. Brooks

INTRODUCTION

Recombination is one part of the sexual system. Organisms differ in whether they reproduce asexually or sexually, and how much they outcross. This book contains discussions about the advantages and disadvantages of various aspects of sexual systems. In this chapter I discuss models of how selection acts on recombination, showing what factors are important and over how much of the genome they act. I then discuss evidence about the form of genetic variation for recombination in order to understand how populations can respond to the various types of selection on recombination.

The cost of meiosis argument (Maynard Smith, 1971, 1978; Williams, 1975) shows an advantage for asexual over sexual reproduction. Asexual females produce asexual female offspring. Sexual females produce the same number of offspring as do the asexual females, everything else being equal, but only half of them are female. This results in almost a doubling in frequency of asexual females every generation, a strong selective advantage. A problem for this argument is that many sexual organisms seem to be unaware of the conclusion. One explanation is simply that genetic variation for being asexual may not exist (Williams, 1975), since within most species there is little variation in the mode of reproduction. A stronger test occurs when there is variation for mode of reproduction within a population; that both modes of reproduction are maintained implies there are compensating advantages for sexual reproduction.

Zero recombination over the genome is equivalent to being asexual, with respect to the preservation of gene associations. When outcrossing occurs, though, zero recombination is not the same as being asexual, with respect to mating. Thus, the cost of meiosis argument does not apply to differences in recombination rates. Recombination is relevant to the cost of meiosis argument,

THE EVOLUTION OF SEX

An Examination of Current Ideas

Edited by Richard E. Michod
UNIVERSITY OF ARIZONA, TUCSON

and Bruce R. Levin
UNIVERSITY OF MASSACHUSETTS, AMHERST

SINAUER ASSOCIATES INC. • PUBLISHERS
SUNDERLAND, MASSACHUSETTS