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## EVOLUTION OF SEXUAL REPRODUCTION: IMPORTANCE OF DNA REPAIR, COMPLEMENTATION, AND VARIATION

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An evolutionary explanation for the widespread occurrence of sexual reproduction must clarify which of its functions are most generally important for its selective maintenance. Evolutionary biologists have, by and large, concentrated on one particular aspect of sexual reproduction: the production by recombination of genetically varied progeny. Since Fisher (1930) and Muller (1932) first suggested situations in which such variation could accelerate evolution, this theme has been pursued in evolutionary biology and now exists in a number of different forms.

Our goal is not to criticize these explanations, but only to suggest that the general view is too narrow since the production of genetically varied progeny is only one consequence of the sexual cycle. Also of fundamental importance in the evolution of sexual reproduction are, we believe, (1) DNA repair and (2) complementation of gene function. The possible importance of DNA repair in the evolution of sexual reproduction was first raised in the literature (to our knowledge) by Felsenstein (1974). He posed the question of whether recombination exists because it is "intrinsically" beneficial, or because it is the result of some "extrinsic" process. The implication was that the production of variability is intrinsic to the sexual cycle, whereas DNA repair is extrinsic. The basis for making this distinction is not evident to us, and we have taken the view that DNA repair, complementation, and variability all provide basic selective advantages. Recent work in molecular biology has begun to clarify the role of recombination in DNA repair. We believe that a better understanding of the evolution of sex can come about when both the molecular and phenotypic consequences of the sexual cycle are viewed in a synthetic framework. We do not claim to present such a framework, but hope to broaden the traditional evolutionary view of sexual reproduction to include these other aspects.

The fossil record is ambiguous concerning the first appearance of eucaryotic organisms (Knoll and Barghoorn 1975). However, fossil evidence has been presented (Schopf 1972) of sporelike bodies arranged in a tetrahedral configuration similar to an arrangement commonly found after meiosis in extant plants. Although subject to alternative interpretation (Oehler et al. 1976), this evidence may

indicate that meiosis was present by about 900 million yr ago (Schopf 1978). It is sometimes assumed that sexual reproduction is largely restricted to eucaryotic organisms. However, sexual reproduction probably existed even prior to its occurrence in eucaryotes capable of a recognizable meiosis. In procaryotes, ordered processes such as bacterial conjugation and transformation as well as viral mating involve exchange of genetic material (see Lewin 1977 for review). Such mechanisms appear to be common among those present day bacteria and bacteriophage studied in the laboratory. In addition, it has been shown in natural bacterial populations that these sexual mechanisms can be adaptively important (Graham and Istock 1979). Since sexual reproduction appears to be common in extant microorganisms, it also may have existed among the early procaryotes in the period preceding the emergence of the eucaryotes. Thus sexual reproduction could have come into existence as early as 2.5–3.5 billion yr ago with the emergence of protocellular and early procaryotic organisms (Schopf 1978; Sklarew and Nagy 1979).

The details of the sexual cycle vary greatly among species. To facilitate further discussion it is useful to outline the main steps of the cycle that appear to be of general occurrence. These steps are: (1) Two genomes, or in some cases parts of genomes, come together within a shared cytoplasm. The genome of most organisms is composed of DNA, but in at least one recombining organism, polio virus, it is composed of RNA (Cooper 1968). (2) The genomes become aligned or synapsed, so that homologous sequences are in close register. (3) Accurate exchange, or recombination, of genetic material can occur between the two genomes. The accuracy of the exchange process is such that ordinarily there is no net gain or loss of nucleotides in the formation of the recombinant genome. (4) This exchange is followed by the separation of the products of the interaction. A product genome, or its replica, can then join with the product of another exchange as in step (1). Often, as in meiosis, these events are intimately coupled with DNA replication.

If, as we suppose, the sexual cycle is fundamentally a cycle of events at the nucleic acid level, it is unlikely that the early stages of this process have been preserved intact in the fossil record. Thus, in attempting to understand the origin and early evolution of sexual reproduction, a reasonable approach is to try to deduce the course of events from our knowledge of mechanisms of sexual reproduction in contemporary organisms.

#### THE ORIGIN OF RECOMBINATION AS A DNA REPAIR PROCESS

Bernstein (1977) has presented the view that sexual reproduction originated as a recombinational repair process and has retained this function throughout the course of evolution. The concept that rejuvenation of the germ line occurs by DNA repair during meiosis has also been discussed by Martin (1977), Walker (1978), and Bernstein (1979). In addition, Maynard Smith (1978, p. 7) has speculated that “long before the origin of eucaryotic sex, the procaryotes had acquired the capacity for genetic recombination—that is the pairing, breaking and

rejoining of homologous lengths of DNA. It seems clear that the original function was not the generation of evolutionary novelty, but the repair of damage."

In early organisms there probably were strong selective pressures to develop means of protecting DNA. Sagan (1973) examined the flux of solar UV light penetrating the primitive reducing atmosphere of the earth. He concluded that a mean lethal dose at 2,600 Å would be delivered to unprotected microorganisms of the type existing today in  $\leq 0.3$  s, and that this could have posed a major problem for the early evolution of life. In general, the accumulation of lesions that arise spontaneously (such as depurinations [Lindahl 1977]) or through the action of environmental chemicals and radiation would have affected survival of early organisms by interfering with the expression and replication of their genetic material. Thus we think that the sexual cycle arose as a recombinational repair process in primitive microorganisms to protect their DNA against damage. Unfortunately, however, data are not available, even for extant organisms, to assess the level of damage to DNA in natural populations caused by environmental agents or arising endogenously.

There are two main processes by which lesions in DNA can be repaired: excision repair and recombinational repair. Excision repair is a process by which a lesion in one strand of DNA is removed, and the resulting gap filled by copying from the other intact strand (for a recent review see Grossman and Riazuddin 1978). This process, which makes use of the redundancy of information in the two complementary strands of DNA, probably evolved before the more complex process of recombinational repair which requires two homologous duplexes. Various types of excision repair processes are effective against different types of single strand lesions.

However, there are a number of ways in which both complementary strands can become damaged at approximately the same position. In these cases we might expect that excision repair would be of limited use since neither strand can be employed as an accurate template for repairing the other. Double stranded lesions occur through the action of UV light which introduces DNA crosslinks (Marmur and Grossman 1961) or ionizing radiation which can cause double strand breaks (Krasin and Hutchinson 1977). Furthermore, the large number of chemical agents which cause single strand lesions can also generate defects nearby in opposite strands, a situation equivalent to a double strand lesion. Such events might occur much more frequently than expected by chance, since DNA, even in the prokaryotic cell, is in a highly ordered, compact form (Worcel and Burgi 1972; Griffith 1976), and different regions of DNA probably differ in their vulnerability to extrinsic agents as has been shown for the chromosomes of at least one higher organism (Ramanathan et al. 1976a, 1976b). In addition, when a replicative DNA polymerase with 3' to 5' exonucleolytic "proofreading" activity arrives at a UV-induced thymine dimer in the template strand, it may idle (i.e., incorporate nucleotides opposite the lesion and then excise them by its exonuclease which removes incorrectly paired bases (Villani et al. 1978). Eventually the polymerase can skip over this lesion leaving a gap in the newly synthesized complementary daughter strand (Rupp and Howard-Flanders 1968), which would then create a

situation equivalent to a double strand lesion. Presumably, postreplicative gaps are also formed opposite other types of lesions besides thymine dimers.

When both strands of DNA are defective at the same or nearby positions, information in that region is lost to the duplex. However, it can be accurately recovered from another homologous chromosome by recombinational exchange (as pointed out by Bernstein [1977] and Martin [1977]). This probably involves the replacement of a damaged DNA sequence with intact DNA by physical transfer of a single stranded segment from the undamaged homologue. The donor duplex can recover the information in the gap left by the donated segment by copying from its other intact strand. By this view recombinational repair is a stimulated event at the site of a lesion, and the distribution of such events throughout the genome should reflect the distribution of lesions. There is evidence in a variety of organisms that recombinational repair can be used for overcoming different types of DNA lesions induced by chemicals and radiation (see Bernstein 1977 for review). Thus we think that the original function of the primitive sexual cycle was to allow recombinational repair to overcome double strand lesions which could have been introduced in various ways. Once developed, recombinational repair may have come to be used for repair of single strand lesions, as an alternative to excision repair. The unraveling of the chromosome which occurs during synapsis may also have come to promote excision repair because of the increased accessibility of the DNA to repair enzymes.

We propose that double strand lesions of the types described above occur frequently in contemporary organisms and that, in fact, recombinational repair is still an important adaptive function of sex. Possibly the most frequent type of lesion in need of recombinational repair is that in which there is a postreplication gap formed opposite a single strand lesion. The basis for this surmise is that a significant proportion of thymine dimers in *Escherichia coli* induced by UV light cause formation of postreplicative gaps which are subsequently repaired by a recombinational process (Rupp et al. 1971). In this case, the type of recombinational repair that most often occurs involves interaction between the daughter DNA duplexes produced by replication in nonmating cells. However in higher organisms, recombinational repair of thymine dimers between daughter chromatids appears to be much less frequent than in *E. coli* (Lehman 1978; D'Ambrosio and Setlow 1978). This may be because chromosomes of higher organisms are far more complex, and special structures (such as the synaptonemal complex formed during meiosis [see Gillies 1975 for review]) ordinarily may be needed for orderly synapsis and genetic exchange.

In extant organisms recombinational repair is most well understood with respect to psoralen-plus-light-induced DNA crosslinks in *E. coli* (Cole et al. 1978), X-ray-induced double strand breaks in *E. coli* (Krasin and Hutchinson 1977), UV-induced thymine dimers in *E. coli* (Rupp et al. 1971), and nitrous acid-induced lesions in phage T4 (Nonn and Bernstein 1977). Other evidence from both prokaryotes and eucaryotes has been summarized by Bernstein (1977). Recent experiments with cells from individuals having the inherited condition Fanconi's anemia suggest a recombinational repair mechanism specific for double strand lesions, such as crosslinks, in humans (Sasaki 1978).

## THE EVOLUTION OF DIPLOIDY AND THE CONSEQUENCES OF COMPLEMENTATION

In the previous section we proposed that the sexual cycle evolved because it promotes repair of DNA lesions. In this section we consider the evolution of diploidy as a modification of the sexual cycle. Here mutations rather than lesions play the dominant selective role. The distinction between lesions and mutations should be stressed. Lesions include any steric deformation in the DNA structure. If a lesion is not recognized and removed by repair enzymes it may prevent DNA replication and transcription, or it may induce mutation upon replication of the deformed template strand. Mutations are most often point alterations of a type (such as base-pair substitutions, or base-pair additions or deletions) that do not alter the regularity of the DNA structure. As such, mutations represent changes in the informational content of DNA. While lesions can be eliminated directly from the DNA, mutations can be eliminated only through the consequences of their expression on fitness.

Initially the stage of the sexual cycle in which homologous genomes occurred together in a common cytoplasm was probably transient, taking only as long as required by the recombinational repair process. However, the presence of two chromosomes of different parental origin in a common cytoplasm allows complementation to occur. Thus, if one of the genomes contains mutations leading to defects in one or more gene products, these deficiencies can be compensated for by the other genome which nevertheless may have its own defects in other genes. In some fungi the advantage of complementation probably promoted the evolution of systems similar to heterokaryons found in many contemporary species such as *Neurospora crassa*. But in the great majority of higher organisms diploidy has arisen as an important or predominant stage of the sexual cycle. Possibly the shift from haploidy to diploidy has occurred many times.

We believe that diploidy almost inevitably must evolve in complex higher organisms in response to the effects of complementation. An essential, underlying assumption of our argument is that an increasingly complex environment puts a selective premium on new gene functions and hence on an increase in the informational content of the genome. As the haploid genome expanded during early evolution, it incurred a corresponding rise in vulnerability to deleterious mutation because of the increased number of vital gene functions present. Initially the expression of these deleterious mutations would select for a reduction in the mutation rate per base pair per replication so that the rate per genome per replication remained low. This hypothesis is supported by the data analyzed by Drake (1974) for the bacteriophage  $\lambda$  and T4, the bacteria *Salmonella typhimurium* and *E. coli*, and the fungus *N. crassa*. With increasing genome size over a 1,000-fold range among these organisms, there is a corresponding decrease in mutation rate per base pair per replication, so that the mutation rate per genome per replication remains relatively constant at about 0.001 to 0.003 for the five organisms. As an example of these relationships, the mutation rate per base pair per replication is 60-fold higher in phage  $\lambda$  than in *E. coli* (e.g.,  $240 \times 10^{-10}$  compared to  $4.0 \times 10^{-10}$ ) whereas the genome size is 80-fold smaller ( $4.7 \times 10^4$  compared to  $380 \times 10^4$  base pairs). Although selection for reduction in mutation

rate per base pair may have been successful over a wide range, such reduction probably could not continue indefinitely with increasing genome size. This is suggested by the finding that although there is a ninefold increase in genome size from *N. crassa* to *Drosophila melanogaster* there is no decrease in mutation frequency per base pair per replication. There are two reasons for thinking that the mutation rate per base pair could not be reduced indefinitely.

First, improvements in accuracy are probably obtainable only by investing additional genetic information in upgrading the replicative and repair machinery of the cell or by slowing down the rate of replication. The replicative apparatus of even as simple an organism as phage T4 involves, in addition to the DNA polymerase, six other associated proteins (Liu et al. 1978), all of which appear to have a role in determining replication accuracy (Mufti 1979). Thus in haploid organisms reduction in mutation rate per base pair below some critical level may become excessively costly when the cost in terms of committed genetic information, cellular processes, or replication rate is balanced against the benefit of further reducing the frequency of disadvantageous mutations. The critical level would appear to be in the range of  $4 \times 10^{-10}$  (the rate for *E. coli* [Drake 1974]) and  $0.8 \times 10^{-10}$  (the rate for *D. melanogaster*). This interpretation is supported by the experiments in phage T4 of Gillin and Nossal (1976) who showed that a DNA polymerase antimutator mutant (which causes a general reduction in spontaneous mutation) produces a polymerase that copies the DNA template more slowly than the wild-type enzyme. This implies that in wild-type, natural selection favors a rate of replication that causes a higher mistake frequency than could be achieved by a slower, more deliberate rate.

Second, there are long term costs associated with vanishingly small mutation rates. Some finite level of mutation per base pair has to be maintained to provide the beneficial mutations on which evolutionary advance is based. Whether the mutation rate represents a compromise between selection for a reduced rate (since most mutations are deleterious) and selection for a higher rate (to facilitate evolutionary advance, as suggested by the work of Cox and Gibson [1974]), or whether the rate is simply as small as possible in an imperfect world is a question of considerable debate in evolutionary biology (Kimura 1960, 1967; Williams 1966; Leigh 1970, 1973, to list only a few). We do not wish to deal at any length with this topic except to note that lines of descent in which the rate approached zero could not be competitive in a changing environment with those that would mutate at an adequate level.

In summary, the increasing haploid genome, with its benefits of new gene functions, has an associated cost in terms of an increasing mutation rate per genome per replication. As discussed above this mutation load was avoided initially by improving the replication and repair machinery, thereby reducing the mutation rate per base pair and keeping the genome wide rate approximately constant. The remarkably low rate attained attests to the selective significance of these deleterious mutations. However as the mutation rate approached its lower limit, deleterious mutations would begin to accumulate as the genome continued to expand.

Following Maynard Smith (1978, especially chaps. 3, 11), consider a genome containing  $n$  loci each mutating with rate  $\mu$  to slightly deleterious alleles with

fitness  $1 - s$ . Let  $\mu$  be the lower limit referred to above. Assume multiplicative fitnesses so that the overall fitness of an individual with  $k$  mutations is  $(1 - s)^k$ . According to the DNA repair hypothesis developed above, recombination already exists in these haploid organisms. With free recombination between loci these mutant alleles will reach a frequency of approximately  $\mu/s$  at equilibrium. For  $s$  small, the average fitness  $\bar{W}$  at equilibrium is approximately  $\exp(-\mu n)$  which decreases with  $n$  the genome size. During this period of increasing mutation load, with decreasing  $\bar{W}$ , there is an increasing premium put on complementation and a concomitant increase in the selective advantages of diploidy. An advantage to shifting to diploidy would have existed throughout the early evolution of haploid sexual organisms, since complementation allows the effects of many deleterious alleles to be masked, thereby increasing fitness. However this shift may have been impeded by immediate reproductive costs, if only because the normal functioning of the haploid sexual cycle is thereby interrupted, generating untested mechanical problems. Such costs could postpone the shift to diploidy until the immediate advantage in terms of decreased expression of deleterious alleles outweighs them. We propose that as the mutation rate per base pair reached its lower limit and the mutation load per genome started to increase, the advantages soon outweighed the costs, prompting the shift to diploidy. It is not important to our argument that the deleterious alleles be completely recessive in the diploid state but only that the compensation in fitness accrued be sufficient to overcome any costs involved.

It has been noted previously (Muller 1932; Crow and Kimura 1970, p. 316) that this advantage of diploidy is only transient. Upon the shift to diploidy, the mutant alleles will begin increasing in frequency to a new equilibrium,  $\sqrt{\mu/s}$ . At this new equilibrium allele frequency, the frequency of expression in homozygotes of the mutant alleles is  $\mu/s$  at each locus (assuming recessive alleles)—the same frequency of expression as in the ancestral equilibrium haploid population. Further complicating matters, the mutation load at each locus in both equilibrium populations is the same and equal to  $\mu$ , assuming recessive alleles. However if the alleles are not recessive, the load in diploids is approximately  $2\mu$  over a wide range of dominance—twice that in the equilibrium haploid population (Crow and Kimura 1970). Consequently, though it is clear that in the short run, diploidy through complementation provides advantages over haploidy, it is not clear that anything is gained in the long run.

Of course the long range consequences of evolutionary events are really irrelevant to whether the events will occur. In the case of diploidy the event is most probably irreversible, for once equilibrium is reached, a shift back to haploidy would express all the deleterious alleles which are now at a higher frequency. However, we do believe that certain consequences of diploidy were exploited, enhancing the likelihood that those lines of descent which shifted to diploidy would not become extinct and, in fact, would dominate the future evolutionary scene.

First, the shift to diploidy facilitates further expansion of the genome. We envision expansion of the genome to occur primarily through a process of gene duplication and subsequent accumulation of mutations leading, ultimately, to divergence of function. After the initial establishment of diploidy, complementation

would increase  $\bar{W}$  by masking the effects of deleterious alleles. The associated increase in population size will decrease the probability of extinction. In addition, the rate of evolutionary advance will increase, since the rate of establishment of advantageous alleles and the acquisition of new gene functions depends directly on population size (Maynard Smith 1976). Consequently, the effect of diploidy on these parameters facilitates evolutionary advance in the interim period before equilibrium is reestablished. However before the shift to diploidy, these parameters would be changing in the opposite direction, slowing down expansion of the genome in evolving haploids. Of course, by these considerations, as the mutation load begins increasing anew in the diploid population, evolutionary advance is again slowed. However, it is worth noting that at the new equilibrium more mutations are segregating than before, enlarging the reservoir of variability which can be mobilized as the environment changes. This enhances the prospects that duplicated loci will acquire new functions, again facilitating further expansion of the genome. This may tend to offset the increasing mutation load and allow further evolutionary advance.

Second, the potential in diploidy for gene interaction between loci may increase the range of reactions possible in a changing environment. As noted by Crow and Kimura (1970), if overdominance between alleles is common such effects could be important. Third, Crow and Kimura (1970) note that in complex organisms somatic cell mutations may constrain growth and tissue specialization. Diploidy could protect against the expression of many such mutations in somatic cells.

Consequently there are several possible advantages to diploidy, the most important being, we believe, those associated with increasing genome size. If the above reasoning is correct, then in extant organisms there should be little overlap in genome size from haploid procaryotes and eucaryotes to diploid eucaryotes. According to the data compiled by Sparrow and Nauman (1976) this appears to be the case, even though genome size for all organisms varies over eight orders of magnitude.

Finally, diploidy has important consequences for the maintenance of sex which were not relevant to its initial establishment. Just as the shift to diploidy is nearly irreversible because of the expression of deleterious alleles, so it prevents the easy abandonment of sex if this entails sudden loss of heterozygosity through inbreeding. Diploidy, which itself evolved as a consequence of sex, in turn helps to preserve sexual reproduction.

#### THE ADVANTAGES OF DNA REPAIR, COMPLEMENTATION, AND VARIATION COMPARED

So far we have argued that the coming together of two homologous genomes in a common cytoplasm provides two advantages; it allows recombination repair to remove lesions in the germ line DNA, and it allows complementation of gene products in the diploid phase. This situation can provide, of course, yet a third major advantage, the production of genetically varied progeny. This is the selective advantage most often considered in the literature, and it has been extensively treated in two recent thoughtful volumes by Williams (1975) and Maynard Smith

(1978). These authors, as well as others, have discussed the conditions in which the production of new gene combinations by sexual reproduction might have immediate adaptive value as well as assist evolutionary advance. A major theme of both volumes is to explain how sexual reproduction can be maintained in the face of the twofold "cost of meiosis" (Williams 1975) or, more generally, the cost of producing males (Maynard Smith 1978). The maintenance of sexual reproduction despite a twofold disadvantage implies that there is a powerful counterbalancing advantage to sex.

Models based on sib-competition (Williams and Mitton 1973), "hitchhiking" (Strobeck et al. 1976), and the "Hill-Robertson effect" all have elements in common (Felsenstein and Yokoyama 1976). In its most generally applicable form, the variation hypothesis for the origin and maintenance of sex argues that recombination accelerates the accumulation of beneficial mutations and the elimination of harmful mutations by breaking down statistical associations between loci and allowing selection to act more freely on net gene effects (Fisher 1930; Muller 1932; Felsenstein 1974; Felsenstein and Yokoyama 1976; Maynard Smith 1978). The generality of this hypothesis relies on the Hill-Robertson effect whereby linkage disequilibrium is generated between functionally independent loci which are undergoing selection in a finite population. These statistical associations which retard selection are broken up by recombination. These considerations have prompted Maynard Smith (1978, p. 36) to write "that recombination itself functions as a form of repair" at the population level. But as he continues to show (Maynard Smith 1978, p. 123), this mechanism can apparently explain only why "some recombination (either a little or 50%) should be favored over no recombination. It does not as yet explain why a lot of recombination should be favored over a little."

It is possible in certain cases tentatively to assess the relative importance of the repair hypothesis and the variation hypothesis in the maintenance of sex. However we will be unable to reach any general conclusions concerning the relative roles played by repair, complementation, and variation.

In haploid organisms both the repair hypothesis and the variation hypothesis require the union of genomes from separate individuals. With the evolution of diploidy, the circumstances permitting the two recombination functions to work diverge. Recombinational repair requires pairing of homologous chromosomes (thus permitting chiasmata formation) during meiosis, but it does not matter whether these chromosomes come from the same parent or from separate parents. The variation and complementation hypotheses suppose, however, that the advantage to recombination is realized only if homologous chromosomes do not carry identical information. Consequently, if recombination were only adaptive as a DNA repair mechanism, the cost of sex could possibly be overcome without disturbing recombination by either reverting (1) to automixis (a form of thelytoky, parthenogenesis, which still depends on meiosis), (2) to obligate self-fertilization (in hermaphrodite organisms), or (3) to close inbreeding (in dioecious species; W. M. Shields, unpublished MS).

Since most organisms do not avoid the cost of sex by these means it would seem that DNA repair cannot be the sole important factor in determining the persistence

of outbreeding sexual systems in diploid organisms. However, it is worth remembering that inbreeding, including automixis as the most extreme expression of it, has a short term cost from the loss of complementation. For this reason it is impressive to us that severe inbreeding, including obligate selfing in hermaphrodite plants, is as common as it is.

It is also relevant to compare the distribution of forms of reproduction which are strictly apomictic and bypass meiosis, with those which can also avoid the cost of sex but continue to rely on meiosis. Apomixis in plants almost always sidesteps meiosis (Gustafsson 1946; Nygren 1954). However, while it is widespread it is also often facultative. Therefore it does not seem difficult to turn off (or on) expression of the necessary genetic machinery for meiosis. Yet in spite of the costs of increased homozygosity, cleistogamy and other forms of predominant selfing, with their associated reduction in the cost of maleness (Cruden 1977), are much more common (Fryxell 1957). We suggest that selfing is more common than ameiotic apomixis, not because apomixis is difficult to come by, but because meiosis is necessary for recombination repair.

In animals apomixis appears to be somewhat more common than automixis (White 1973). Again, this is not surprising since automixis often entails a rapid reduction in heterozygosity, which is maintained unaltered under apomixis (White 1973). Experimental induction of parthenogenesis in animals usually results in automixis with normal meiosis followed by the fusion of haploid nuclei to reconstitute the diploid state in the absence of fertilization. This leads rapidly (sometimes in one generation) to homozygosity and is not often expected to be a successful strategy for this reason. However a significant number of the most successful and conspicuous parthenogens, including at least some parthenogenetic lizards (*Cnemidophorus*), reptiles (*Ambystoma*), fish (*Poeciliopsis*), grasshoppers (*Warramaba*), earthworms, planarians, and spider beetles (*Ptinus*), undergo a premeiotic "endomitotic" doubling in chromosome number followed by formation of bivalents between (presumably) "sister homologues" and an otherwise normal meiosis (Schultz 1971; White 1973). Why should the potential for recombination be maintained in such species when it can occur only between chromosomes which are identical in base-pair sequence? If we are correct in assuming that single-stranded lesions are common and often become double-stranded following replication, and that they require recombinational repair for their elimination, "sister homologues" will be adequate to the task because they will differ in that only one will carry a double-stranded lesion in a particular region of DNA.

In conclusion, we have suggested here that the early evolution of recombination as a repair process was the basis for the later evolution of meiosis in primitive eucaryotes (or "advanced" procaryotes). This in turn provided the basis for the evolution of diploidy which, once evolved in sexual organisms, is not likely to revert back to haploidy because of complementation. In like manner, as pointed out above, the complementation provided by diploidy (and polyploidy) imposes a stiff penalty on many extant organisms experimenting with close inbreeding as a means to overcome the cost of sex. In its origin, then, complementation may be considered a second order phenomenon, but its role in maintaining sex is nonethe-

less real. In addition we have suggested that recombinational repair may have a direct contemporary influence on the maintenance of sex. To argue this compellingly, we would have to show that the accumulation of lesions in the germ line DNA of sexual organisms is rapid enough to give recombinational repair a significant short term advantage. Indeed, there is evidence that the phenomenon of aging is partly a consequence of the accumulation of DNA lesions in somatic cell lines (Hart 1976; Bernstein 1979). Although a direct demonstration is technically unfeasible at the present, it does seem reasonable to us that the accumulation of DNA lesions constitutes a general ecological problem with which life must cope.

#### SUMMARY

We have proposed that sexual reproduction arose in evolution as a DNA repair process which allowed damage in one chromosome to be repaired by the information in another homologous chromosome, and has retained this advantage throughout evolution. Since this process required that two chromosomes be present in a common cytoplasm, additional ways were evolved to take advantage of the redundant information available. The diploid stage of the cycle was probably transient in early organisms, but began to take on a more significant role as genome size increased, since it provided protection against the expression of deleterious mutations. As the diploid stage of the sexual cycle became the predominant stage, genome information content expanded beyond the range of haploid organisms. The shift to diploidy is essentially irreversible, and likewise helps prevent the abandonment of sexual reproduction. A consequence of the DNA exchange reactions that constitute recombinational repair is the reassortment of parental genetic information among progeny. As is widely appreciated, this variation is advantageous in itself under certain conditions. However we argue that a complete evolutionary explanation for the maintenance of sexual reproduction should also include complementation and DNA repair.

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