DELETERIOUS MUTATIONS AS AN EVOLUTIONARY FACTOR. II. FACULTATIVE APOMIXIS AND SELFING

ALEXEY S. KONDRASHOV
Research Computer Centre of the Academy of Sciences of the USSR, 142292 Pushchino, Moscow Region, USSR

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ABSTRACT

A population with $u$ deleterious mutations per genome per generation is considered in which only those individuals that carry less than a critical number $k$ of mutations are viable. Besides a large number of loci subject to mutation and selection, the genome contains one or two special loci responsible for the mode of reproduction. Amphimixis vs. apomixis and amphimixis vs. selfing are considered separately. In the first case, the genome degradation rate $v (= u/\sqrt{k})$ is found to play the decisive role, as in the case of recombination. When $v > 1.25$, obligate amphimixis is established. If $v$ decreases below this value, the alleles with first low and then larger penetrance are fixed, until alleles conferring obligate asexual reproduction become advantageous. The proportion of resources allocated to produce seeds also increases with decrease of $v$. These results are unlikely to depend on the genetic basis of the mode of reproduction. The result of competition between outcrossing and selfing depends on both $u$ and $k$, as well as on whether the mutations are recessive. The alleles for selfing with low penetrance are selected against if the mutations are at all recessive. The fitness of alleles with high penetrance depends primarily on $u$, decreasing when $u$ increases. There may exist conditions when only the alleles providing intermediate selfing rates can be fixed in a population. In other cases a population may exist with either obligate outcrossing or selfing at a high rate. Thus, truncation selection against deleterious mutations may be a factor supporting obligate or facultative sex despite the twofold advantage of apomixis or selfing.

SEXUAL reproduction is characteristic of a great majority of eucaryotes despite an obvious advantage of parthenogenesis. The twofold advantage (see, for instance, Lloyd 1980a), as well as a number of additional advantages (Daly 1978; Lewis 1983), has been widely discussed.

However, there is no agreement about what makes sexual reproduction so ubiquitous. The chief results of sex are the destruction of the parental genotypes (that have already been tested by selection) and the creation of new gene combinations. These processes can be advantageous (not involved with an additional cost) only when the genotype/environment correspondence is being violated in a number of successive parthenogenetic generations with sufficient rapidity (Maynard Smith 1978).

Such a violation may result from a change in both environment and geno-
type. Hence, the hypotheses of the advantage of sexual reproduction can be divided into environmental and mutational hypotheses. The former are more numerous. Different hypotheses presume environmental changes that are either population-independent or population-induced. The first case implies that sexual reproduction is favorable for adaptation either to irreversible changes of environment (Fisher-Muller hypothesis, see Griffin 1983; hitchhiking and Red Queen, see Maynard Smith 1978, chapters 4 and 7) or to fluctuations of environmental properties in time (Maynard Smith 1980) or in space (Tangled bank, Bell 1982, chapter 2). The second case assumes that organisms degrade the environment of genetically similar individuals (sib competition, Bulmer 1980; Young 1981; some other models, Price and Waser 1982; Rice 1983). Some environmental hypotheses encounter major difficulties (Maynard Smith 1978, chapter 6; Bell 1982; Case and Bender 1981; Moore and Hines 1981). Others may have explained the advantage of sex only under special assumptions (Bulmer 1980; Price and Waser 1982). The rest can explain the advantage of sex in the long run but still do not explain what protects sexual population against invading asexual clones (Griffin 1983).

Mutational hypotheses are attractive because of the ubiquity of mutation processes. A large part of the genome was reported to be under purifying selection (see Kreitman 1983), so that most mutations are probably deleterious irrespective of environmental conditions. However, it was shown that, with independent selection against mutations at different loci, the fitness of a stationary infinite population is equal to $e^{-u}$ under both sexual and asexual reproduction, where $u$ is mutation rate per genome per generation. Thus, sexual reproduction can enjoy an advantage due either to stochastic mechanisms operating only in small populations (Muller ratchet, see Maynard Smith 1978, chapter 3; Manning 1976, 1982a,b, 1983) or because sexual females can choose males with a smaller number of mutations (Manning 1984). Both these mechanisms are not likely to be responsible for the wide occurrence of sex.

If the mode of selection is truncation and not exponential, sex enjoys a considerable advantage of a deterministic nature (Kondrashov 1982) because here the fitness of a sexual population increases (Crow and Kimura 1979) while that of an asexual population remains $e^{-u}$ (Kimura and Maruyama 1966). Truncation selection against deleterious mutations can also account for recombination (Kondrashov 1984a) and cyclical parthenogenesis (Kondrashov 1984b). Note that the mutational explanation of cyclical parthenogenesis was first introduced by Manning and Jenkins (1980). However, under exponential selection as adopted in their model, the oscillations of the intensity of selection against mutations that lead to alternation of sex and apomixis can appear only under a rather artificial assumption.

The present paper deals with other combinations of sexual and asexual features of reproduction; namely, facultative apomixis and selfing. These forms of reproduction are particularly significant in plants (Jain 1976), although our models can be applied to any population.

Selfing differs from various forms of automixis (see Templeton 1982) in that it involves fusion of meiotic products from different cells. Nevertheless,
population characteristics of these modes of reproduction may be similar. Apo-
mixis is the production of single cells identical to those of the parent (neglect-
ing new mutations). Vegetative reproduction is probably similar to apomixis,
although it allows intercellular selection in the course of creating a new or-
ganism. We will further use the terms “sexual reproduction,” “outcrossing” and
“amphimixis” as synonyms.

The evolution of facultative apomixis (MARSHALL and BROWN 1981; HARPER
1982) and selfing (LLOYD 1979; WELLS 1979) has been discussed by a number
of authors. It has been shown that, without natural selection, these forms of
reproduction always replace outcrossing due to an autoselection mechanism
(BELL 1982) which, in a limit case of obligate apomixis or selfing, results in
the twofold cost of amphimixis. However, when apomixis or selfing leads to a
considerable decrease of fitness, then facultative or even obligate outcrossing
can be established. While a decrease of fitness under selfing may be due to
inbreeding depression, the cause of such a decrease with apomixis is obscure.
Strange as it may seem, apomixis is more rare than selfing (MARSHALL and

In this paper we do not arbitrarily assign to the progeny produced by dif-
ferent reproductive modes any difference in fitnesses. This differences is to
arise in the model as a result of selection against deleterious mutations.

MODEL

As before, consider an infinite population with discrete generations having
the life cycle: mutation-reproduction-selection-mutation (KONDRASHOV 1982,
1984b). An individual genome contains a large number of loci subject to
mutation and selection and, in addition, one or two special loci that determine
the mode of reproduction. (In a previous paper, one such locus influences the
frequency of recombination which is assumed here to be free.) Mutations occur
independently at all the loci, except the special ones, with rate \( u \) per genome
per generation. Individuals carrying \( k \) or more mutations die. Without taking
into account the special loci, and assuming that mutations at all the loci are
rare and never occur in homozygous state, the equations from KONDRASHOV
(1982) describe selection on both the haploid and diploid stages of the life
cycle. In the first case, sexual reproduction begins with mating and fertilization
followed by meiosis and recombination; in the second case, this process takes
the reverse course. Considering the special loci, it is important to know the
ploidy of the selectable stage since, in the case of, say, one diallelic locus,
haploids will have two and diploids will have three genotypes. Therefore, both
haploids and diploids will be considered in the case of apomixis. Selfing is only
possible with diploids. Furthermore, the term “genotypes” will be applied only
to the special loci. The rest of the genome is characterized by the numbers of
heterozygous and homozygous mutations.

Let us assume that, without alleles for apomixis or selfing, all the individuals
are hermaphrodites belonging to the same sexual class (cosexuality according
to LLOYD 1980a,b). The competition between sexual reproduction with apo-
mixis and that with selfing will be considered separately. Under apomixis, an
individual of $k$-th genotype allocates to the production of amphimictic ovules, apomictic seeds and pollen $\frac{1}{2}(1 - z)$, $\frac{1}{2}(z_x + yz_x)$ and $\frac{1}{2}(1 - yz_x)$ portions of its resources, respectively. Here, $z$ may be regarded as an apomixis rate and $y$ as a pollen discount. In a model for selfing, the place of apomictic seeds is taken by selfed seeds. Thus, without the genes of apomixis or selfing, the resources are allocated equally to the production of seeds and pollen (Charnov 1982). We shall consider only the main twofold cost of amphimixis and shall assume the total resources to be equal for all reproductive individuals, selection being only due to different viabilities of individuals with various numbers of mutations.

Our model allows other interpretations. We may assume that an individual of $k$-th genotype reallocates to production of apomictic or self-pollinated seeds all the resources from amphimictic seeds and pollen with probabilities $z_x$ and $yz_x$, respectively. Here, $z$ is apomixis (or selfing) penetrance rather than its rate. Alternatively, individuals may be assumed to have two sexes: individuals of $k$-th genotype who were initially females become apomictic females with probability $z_x$ and males become apomictic females with probability $yz_x$. It is important, however, that the mode of an individual’s reproduction should not depend on the way that individual was produced. This seems reasonable; however, some populations do not satisfy this assumption (Jain 1976).

To describe population dynamics in the case of apomixis, it is sufficient to know $q_i$, $q_i'$ and $q_i''$; that is, the frequencies of individuals with $i$ mutations before mutation, reproduction and selection, respectively (Kondrashov 1984b). In the diploid case, all the mutations are assumed to be in the heterozygous state. This assumption is not valid for selfing that requires the functions $q_{ij}$; that is, the frequencies of individuals with $i$ mutations in heterozygous and $j$ mutations in homozygous states. We shall analyze both models simultaneously, denoting similar variables by the same symbols. The frequency of the $k$-th genotype among the individuals with a specified number of mutations will be $x_i(k)$ for the case of apomixis and $x_{ij}(k)$ for selfing.

In the model of apomixis, the mutation process is described by (Kondrashov 1984b, equation 2):

$$q_i = e^{-u} \sum_{n=s_i}^{\infty} q_n \frac{u^{i-n}}{(i-n)!}$$

$$x_i'(k) = (q_i')^{-1}e^{-u} \sum_{n=s_i}^{\infty} q_n x_n(k) \frac{u^{i-n}}{(i-n)!}$$

The second equation must be repeated $k$ times for all the genotypes. In the model of selfing, assuming that mutations only appear in those loci that are homozygous for normal alleles, the equations will be the same as (1) but with doubly indexed $q$ and $x$. To describe reproduction, it will be convenient to introduce several auxiliary values. For apomixis they are

$$F_o = \frac{1}{2} \sum_i q_i' \sum_x x_i'(k)(1 + z_x y_x); \quad F_o = 1 - F_o$$

that is, proportions of population resources allocated to produce all the ovules and pollen;

$$\beta_i = \frac{1}{2} F_o q_i' \sum_x x_i'(k)(1 - z_x); \quad \gamma_i = \frac{1}{2} F_o q_i' \sum_x x_i'(k)(z_x + y_x z_x);$$
that is, proportions from $F_\delta (\beta$ and $\gamma$) or $F_\delta (\rho)$ that comprise the resources allocated to produce amphimictic ($\beta$) and apomictic ($\gamma$) seeds and pollen ($\rho$) by individuals with $i$ mutations;

$$g_i(\kappa) = x'_i(\kappa)(1 - z_e)(\sum x'_i(\kappa)(1 - z_e))^{-1}; \quad a_i(\kappa) = x'_i(\kappa)(z_e + y_e z_e).$$

$$\cdot \left( \sum x'_i(\kappa)(z_e + y_e z_e) \right)^{-1}; \quad h_i(\kappa) = x'_i(\kappa)(1 - y_e z_e)(\sum x'_i(\kappa)(1 - z_e y_e))^{-1}$$

that is, proportions of resources of the $\kappa$-th genotype with $i$ mutations allocated to produce amphimictic ovules ($g$), apomictic seeds ($a$) and pollen ($h$) from all the resources allocated to the same function by individuals with $i$ mutations.

In the model for selfing, the respective values are given in a similar way, for example:

$$F_\theta = \frac{1}{2} \sum_i \sum_j q_{i,j} \sum_k x'_{i,j}(\kappa)(1 + y_e z_e).$$

The proportion of individuals with $i$ mutations among the progeny from individuals with $n$ and $l$ heterozygous mutations is

$$b_i(n, l) = \begin{cases} \left( \frac{n + l}{i} \right) \left( \frac{1}{2} \right)^{n+i}, & i \leq n + l \\ 0, & i > n + l \end{cases}$$

Under apomixis an individual with $n$ mutations produces progeny with $i$ mutations with probability

$$s_i(n) = \begin{cases} 1, & i = n \\ 0, & i \neq n \end{cases}$$

Let $R_\kappa(\xi, \zeta)$ and $T_\kappa(\xi)$ be the probabilities that an individual of $\kappa$-th genotype will appear after mating of $\xi$-th with $\zeta$-th genotype ($R$) or will appear by apomixis from an individual of $\xi$-th genotype ($T$). It is clear that $T = 1$ if $\kappa = \xi$ and $T = 0$ if $\kappa \neq \xi$. The function $R$ is easy to determine from Mendelian laws for any number of special loci.

We will assume for selfing that most individuals in the population are not related and, because mutations at any locus are rare, the amphimictic progeny will carry mutations in heterozygotes only. Then, with probability

$$b_{i,j}(n, \nu, l, \lambda) = \begin{cases} \left( \frac{n + l}{i - \nu - \lambda} \right) \left( \frac{1}{2} \right)^{n+i}, & \nu + \lambda \leq i \leq n + l + \nu + \lambda, \\ 0; \quad \text{otherwise} \end{cases}$$
an individual with \(i\) and \(j\) mutations will appear in a mating between an individual with \(n\) mutations in heterozygous state and \(v\) mutations in homozygous state and another individual with \(l\) and \(\lambda\) mutations. Under selfing, homozygous loci do not change, while heterozygous loci become homozygous at a normal or mutant allele with probability 0.25. Therefore,

\[
s_{i,j}(n, v) = \begin{cases} 
\binom{n}{i}\binom{n-i}{j-v}(\frac{1}{2})^{2n-i} & ; \; i \in (0, n), \; j \in (v, v+n) \\
0 & \text{otherwise.}
\end{cases}
\]

The transformation operators for the genotypes are easy to find from Mendelian laws, \(R\) being the same as before, while \(T\) becomes nonidentical.

Now we can write the equations that describe reproduction. For apomixis:

\[
q_i^{*} = \sum_n \sum_l \beta_n \rho_l b_i(n, l) + \sum_n \gamma_n s_i(n)
\]

\[
x_i^{(\kappa)}(\kappa) = (q_i^{*})^{-1} \sum_n \sum_l \beta_n \rho_l b_i(n, l) \sum_\xi \sum_\zeta g_n(\xi) h_l(\xi) \cdot R_s(\xi, \zeta) + \\
+ \sum_n \gamma_n s_i(n) \sum_\xi a_n(\xi) T_s(\xi).
\]

The second equation must be taken \(\kappa\) times for all the genotypes. The equations of the model for selfing are to be obtained from (2) by substituting doubly indexed functions for the singly indexed ones and by summation by additional indices.

In the apomictic model, selection is given by

\[
Q_i = q_i^{*} \tilde{w}^{-1}; \quad X_i(\kappa) = x_i^{(\kappa)},
\]

where capital letters stand for the next generation and the second equation is repeated \(\kappa\) times (Kondrashov 1984b). The proportion of surviving progeny \(\tilde{w} = \sum_i q_i^{*} \tilde{s}_i\) can be regarded as an average population fitness. We will consider the function \(s_i = 1 - \left(\frac{i}{k}\right)^\alpha\) where \(\alpha = 1, 2\) and \(\infty\) correspond to linear, intermediate and threshold selection, respectively (Kondrashov 1982). In the model for selfing, the probability of survival of an offspring should depend on the number of both heterozygous and homozygous mutations in its genome. This can be achieved in the following way:

\[
s_{i,j} = 1 - \left(\frac{i + d j}{k}\right)^\alpha
\]

Here, \(d = 2\) means that dominance is absent and the effect of a mutation in a homozygote is twice the effect of that in a heterozygote; however, under large \(d\), homozygous mutations are lethal.

The above equations could neither be simplified nor studied analytically.
Therefore, we investigated them with a computer EC 10–40 in the Research Computer Center, USSR Academy of Sciences.

RESULTS

Before studying general equations it is helpful to consider some special cases. Let us consider a haploid diallelic locus \( M \). Individuals with allele \( m \) are obligate amphimicts, while those with allele \( M_{z,y} \) (which has frequency \( p \)) are facultative apomicts or selfers (which makes no difference here) that have parameters \( z \) and \( y \) (see above). As was shown by Harper (1982), the contribution to the next generation by an individual who allocates \( \varphi \), \( \sigma \) and \( \mu \) portions of its resources to produce amphimictic ovules, apomictic (or self-pollinated) seeds, and pollen, respectively, is proportional to \( 2\sigma + \varphi + \mu \cdot r \), where \( r \) is a ratio of the resources allocated by the population to produce amphimictic ovules and pollen. As \( \varphi = \mu = \frac{1}{2} \), \( \sigma = 0 \) for individuals with allele \( m \); and \( \varphi = \frac{1}{2}(1 - z) \), \( \sigma = \frac{1}{2}(z + yz) \), \( \mu = \frac{1}{2}(1 - yz) \) for individuals with allele \( M_{z,y} \); and, furthermore, \( r = (1 - pz)(1 - pyz)^{-1} \); then the relative fitness of allele \( M_{z,y} \) may be written as

\[
\frac{z + 3yz}{1 - (1 - pz)/(1 - pyz)}
\]

(see Table 1). The results for \( p = 0 \) and \( p = 1 \) are to be interpreted as the limits of the value \( w \) at small and large \( p \), respectively.

Now let us consider mutations and find a stationary state of the population under obligate amphimixis. Obviously, both models in this case coincide with the model from Kondrashov (1982).

Let us consider the question: how will the fitness of a stationary amphimictic population change after one or several generations of obligate apomixis or selfing? In the first case, the ratio of population fitness after one generation of apomixis to fitness of the initial population is \( \sum \hat{q}_i s_i / \sum \hat{q}''_i s_i \), where \( \hat{q}_i' \) and \( \hat{q}''_i \) are the characteristics of a stationary sexual population. This ratio is given in Figure 1. In the subsequent apomictic generations, the population fitness decreases monotonically to the limit \( e^{-z} \). In the first generation, the fitness mainly depends on the genome degradation rate, \( v = u/\sqrt{k} \), and not on \( u \) and \( k \) taken

<table>
<thead>
<tr>
<th>( \gamma )</th>
<th>0.0</th>
<th>0.2</th>
<th>0.4</th>
<th>0.6</th>
<th>0.8</th>
<th>0.9</th>
<th>1.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>( p )</td>
<td>1.0</td>
<td>1.56</td>
<td>1.63</td>
<td>1.71</td>
<td>1.83</td>
<td>1.91</td>
<td>2.00</td>
</tr>
<tr>
<td>0.0</td>
<td>1.60</td>
<td>1.67</td>
<td>1.77</td>
<td>1.90</td>
<td>2.09</td>
<td>2.23</td>
<td>2.40</td>
</tr>
<tr>
<td>0.2</td>
<td>1.70</td>
<td>1.78</td>
<td>1.88</td>
<td>2.04</td>
<td>2.30</td>
<td>2.50</td>
<td>2.80</td>
</tr>
<tr>
<td>0.4</td>
<td>1.80</td>
<td>1.86</td>
<td>1.97</td>
<td>2.12</td>
<td>2.42</td>
<td>2.70</td>
<td>3.20</td>
</tr>
<tr>
<td>0.6</td>
<td>1.90</td>
<td>1.94</td>
<td>2.01</td>
<td>2.12</td>
<td>2.39</td>
<td>2.71</td>
<td>3.60</td>
</tr>
<tr>
<td>0.8</td>
<td>1.95</td>
<td>1.97</td>
<td>2.01</td>
<td>2.08</td>
<td>2.26</td>
<td>2.52</td>
<td>3.80</td>
</tr>
<tr>
<td>1.0</td>
<td>2.00</td>
<td>2.00</td>
<td>2.00</td>
<td>2.00</td>
<td>2.00</td>
<td>2.00</td>
<td>2.00</td>
</tr>
</tbody>
</table>
A. S. KONDRASHOV

FIGURE 1.—A change of fitness after one generation of obligate apomixis. Threshold (1) and linear (2) selection, $k = 20$.

separately (data not presented). The same is true for a stationary amphimictic population (Kondrashov 1984b).

Analogous data for obligate selfing are given in Table 2. To make $v$ and, consequently, the fitness of the initial population independent of $k$, different $u$ values are taken for various values of $k$. Different columns correspond to the genome degradation rates 0.316, 0.632, 0.949 and 1.265. As the fitness in the early generations is not always monotonic, we present the data for several generations. The fitness always decreased monotonically after the fifth to tenth generation. With $d > 2$, the fitness in the first selfed generation always decreased markedly. In subsequent generations, after a moderate rise with a maximum in the fourth to tenth generations, the fitness gradually decreased. With $d = 2$, the fitness in the first generation was close to that with obligate outcrossing. In the next few generations a small increase occurred with some values of $u$ and $k$, but the main trend was a slow decrease. By the 100th generation the fitness was close to stationary under obligate selfing, although, in this case, convergence was slower than under apomixis. In a stationary self-pollinated population there was a polymorphism in the number of mutations even under threshold selection. This is due to the fact that under selfing there is a probability of a decrease in the number of mutations in a heterozygote without an increase in their number in a homozygote. If not for this process one could have concluded, following the idea of Kimura and Maruyama (1966), that the fitness of a stationary selfed population would be $e^{-(u)}$. Figure 2, based on the data of Table 2, shows that the fitness of a stationary self-pollinated population is determined mainly by $u$ and is sufficiently close to the lower limit $e^{-(u)}$. Most of the individuals in such a population have close to a maximum number of mutations in a homozygote, which is why the number of heterozygous loci is small under all conditions (no more than three to four for an individual; data not presented).
We shall now proceed to analyze the general model of apomixis. First, consider the results for a haploid diallelic locus $M$ with alleles $m$ and $M$, under $k = 20$. Table 3 shows the values of $v$ when $m$ fixation, which is stable at larger $v$ (the upper value), and $M$ fixation, which is stable at smaller $v$ (the lower value), change their stabilities. If both the fixations are unstable at some value of $v$, a polymorphism is maintained; when both are stable, the final state depends on the initial allele frequency. With small $z$, fixation of $m$ is unstable at $v < S = 1.25$. The data at other $k$ values show that selection at locus $M$ depends on $v$ in all cases except for $z = y = 1$, which was considered previously (KONDRASHOV 1982). Under other types of selection, the difference is a certain widening of the fixation zones of alleles $M$. Thus, at $k = 20$, with small $z$ and under linear selection, $\nu \approx 1.5$. Considering the diploid case when heterozygote $Mm$ has intermediate characteristics yields no qualitatively new results (data not presented).

Table 4 gives the results of the experiments with a haploid polyallelic locus.
Figure 2.—Fitness of a stationary selfed population under $k = 10$ (1), $k = 20$ (2) and $k = 40$ (3) with threshold selection. The function of $e^{\theta_{\text{th}}}$ is also present (4).

### Table 3

*Competition of alleles m and $M_{\text{th}}$, when locus M is diallelic*

<table>
<thead>
<tr>
<th>$\gamma$</th>
<th>$\nu$</th>
<th>0.0</th>
<th>0.33</th>
<th>0.66</th>
<th>1.0</th>
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<tr>
<td>0.33</td>
<td>1.19</td>
<td>1.16</td>
<td>1.14</td>
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</tr>
<tr>
<td>0.66</td>
<td>1.10</td>
<td>1.05</td>
<td>0.98</td>
<td>0.90</td>
<td></td>
</tr>
<tr>
<td>1.00</td>
<td>1.00</td>
<td>0.90</td>
<td>0.76</td>
<td>0.18</td>
<td></td>
</tr>
</tbody>
</table>

### Table 4

*Alleles fixed at the single locus controlling apomixis*

<table>
<thead>
<tr>
<th>$\nu$</th>
<th>Alleles</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.125</td>
<td>$M_{0.66}$, $M_{0.66,0.66}$ (34%) (66%)</td>
</tr>
<tr>
<td>0.250</td>
<td>$M_{0.66}$, $M_{0.66,0.66}$ (34%) (66%)</td>
</tr>
<tr>
<td>0.375</td>
<td>$M_{0.66}$, $M_{0.66}$, $M_{0.66,0.66}$ (35%) (65%)</td>
</tr>
<tr>
<td>0.500</td>
<td>$M_{0.66}$, $M_{0.66,0.66}$ (35%) (65%)</td>
</tr>
<tr>
<td>0.625</td>
<td>$M_{0.66}$, $M_{0.66,0.66}$ (35%) (65%)</td>
</tr>
<tr>
<td>0.750</td>
<td>$M_{0.66,0.66}$, $M_{0.66}$ (35%) (65%)</td>
</tr>
<tr>
<td>0.875</td>
<td>$M_{0.33}$, $M_{0.33,0.66}$</td>
</tr>
<tr>
<td>1.000</td>
<td>$M_{0.33,0.66}$</td>
</tr>
<tr>
<td>1.125</td>
<td>$M_{0.33,0.66}$</td>
</tr>
<tr>
<td>1.250</td>
<td>$m$</td>
</tr>
</tbody>
</table>
M. The population contains an allele m and 12 alleles Mz,y, each characterized by a combination of values of z = 0.33, 0.66, 1.0 and y = 0, 0.33, 0.66, 1.0. Those alleles that are fixed in the population are presented in the table. Where a stationary state is polymorphic, the frequencies are also given.

In Table 5 analogous data are shown for a model with two special loci. The locus Z determines the value of z and the locus Y determines the value of y of its owner. We considered a haploid population with four alleles at both loci. These alleles set up the values of z and y at 0, 0.33, 0.66 and 1.0. Like Table 4, Table 5 gives the characteristics of a stationary state of the population. In the case of v = 0.875, the result depends on the initial conditions: in some cases alleles z0.33 and y1 are fixed; in other cases at locus Z allele z0.66 is fixed while at locus Y there appears polymorphism with alleles y0.66 and y1.

To obtain the data presented in Tables 4 and 5, we first studied five to ten initial states of a population with all the alleles involved. If there were alleles that were quickly eliminated in all the cases, they were not considered further. For the rest of the alleles, we particularly estimated whether their fixations were stable. Therefore, it seems doubtful that there could be other final population states besides those presented in Tables 4 and 5, although we cannot exclude such a possibility.

Let us now consider selfing. In Table 6 the data for selfing are given under threshold selection. The individuals contain a single diallelic locus μ. The mm individuals are obligate outcrossers; μz,y, μz,s are selfers with parameters z and y; and heterozygotes have parameters z/2 and y/2. The experiment was confined to the case z = y. In every run an allele m and one of the alleles μz,y with z = y = 0.1, 0.3, 0.5, 0.7, 0.9 and 1.0 were present in a population. Under k = 10, allele m was always ousted. Data for k = 20 are given in Table 6. If in some cases there is only one letter m (or μ) it means that, under these conditions, sexual reproduction (or selfing) always won. With larger k, the
Alleles fixed at the locus controlling selfing

<table>
<thead>
<tr>
<th>u</th>
<th>2/√2</th>
<th>4/√2</th>
<th>6/√2</th>
<th>8/√2</th>
</tr>
</thead>
<tbody>
<tr>
<td>z</td>
<td>d = 2</td>
<td>d = 3</td>
<td>d = 4</td>
<td>d = 2</td>
</tr>
<tr>
<td>0.1</td>
<td>m</td>
<td>m</td>
<td>m</td>
<td>m</td>
</tr>
<tr>
<td>0.3</td>
<td>m</td>
<td>m</td>
<td>m</td>
<td>m</td>
</tr>
<tr>
<td>0.5</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
</tr>
<tr>
<td>0.7</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
</tr>
<tr>
<td>0.9</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
<td>μ</td>
</tr>
<tr>
<td>1.0</td>
<td>μ</td>
<td>μ</td>
<td>m</td>
<td>m</td>
</tr>
</tbody>
</table>

computations were too tedious for our computer. Investigation of other forms of selection gave similar results (data not presented).

DISCUSSION

First, we shall consider separately the factors favoring amphimixis and those acting against it. An advantage of apomixis or selfing is due to the fact that, under these modes of reproduction, the seed has twice the number of the mother's genes as compared to amphimixis. This twofold advantage has been discussed by a number of authors (Maynard Smith 1978; Lloyd 1980a; Charlesworth 1980; Bell 1982; Harper 1982). Note that the ability of natural selection sensu stricto (that is, variations of fertility and viability) to compensate for this advantage does not contradict the "prophecies of parthenogenesis" (Templeton 1982). The advantage of allele M responsible for apomixis or selfing is set by (4). It is easy to show that, under small pZ, when the sex ratio is close to 1:1, the relative fitness of M is 1 + \( \frac{z}{2} + \frac{yZ}{2} \); that is, reallocation of resources to production of nonamphimictic ovules from amphimictic ovules or pollen is equally advantageous. When y = 1, so that M individuals do not produce pollen, \( w = 1 + z \) under any p. When \( y \neq 1 \), \( w \) always increases along with z and p; at small pZ it also increases along with y. At y = 0, \( w = 1 + \frac{z}{2-pZ} \), that is, the advantage of pathenogenesis approaches twofold with increasing pZ; it does not disappear as was stated by Price and Waser (1982). This can be explained by the fact that, under large frequency of \( M_{1,0} \), pollen of M individuals takes no noticeable part in pollination, although the production of pollen does not considerably increase the number of genes that are transferred to the progeny by \( M_{1,0} \) individuals. As a result, allele \( M_{1,0} \) has a twofold advantage, because \( M_{1,0} \) females transfer to their progeny two \( M_{1,0} \) alleles and M females give each of their progeny one \( M_{1,0} \) allele and one m allele. However, with large pZ, it is too wasteful to allocate one-half of the resources to the competition with M pollen. Therefore, with large pZ, w reaches
a maximum under $0 < y_0 < 1$. When $pz$ increases, $y_0 \to 1$ and $w_{\text{max}} \to 4$ (see Table 1). To illustrate this, consider the case when allele $M_{1,1-\epsilon}$ occurs with frequency $1 - \epsilon^2$, where $\epsilon$ is a small number. Then almost all $m$ ovules are fertilized by $M_{1,1-\epsilon}$ pollen, so that an $m$ individual will transfer an $m$ allele and an $M_{1,1-\epsilon}$ allele to its progeny through seeds, while $M_{1,1-\epsilon}$ individuals will give $4 - 2\epsilon$ $M_{1,1-\epsilon}$ alleles. This consideration shows that the costs of meiosis and production of males (LLOYD 1980a,b) do differ because, as in the above case, $m$ individuals have to pay them both. It is clear that it is useful here for $m$ individuals to reallocate all their resources to production of ovules, which will result in a twofold decrease in the advantage of $M_{1,1-\epsilon}$. This is consistent with an observation of HARPER (1982) about a connection between selection on the mode of reproduction and on sex allocation; but a detailed discussion of this question is beyond our aim.

Let us now consider selection for amphimixis caused by accumulation of deleterious mutations. Consider first amphimixis vs. apomixis. It is clear from Figure 1 that one apomictic generation leads to a decrease of fitness if $v > v^* \approx 0.6$ and to a more than twofold decrease when $v > v^{**} \approx 1.6$. The selective value of allele $M_{z,y}$ with small $z$ follows from two effects of a single generation of apomixis: its direct effect on fitness, and a change of the genetic background of allele $M_{z,y}$. Since one apomictic generation leads to a growth of average mutation number, obligate amphimixis becomes fixed when $v$ is slightly less than $v^{**}$, as recombination becomes advantageous at $v < v^*$ (KONDRASHOV 1984b).

As for selfing, the effect of one generation of selfing on fitness depends primarily on $d$ (Table 2). This follows from the fact that selfing transfers some of the mutations into the homozygous state without changing their average number in the genome. Therefore, if a homozygote is only twice as harmful as a heterozygote ($d = 2$), the fitness is hardly influenced; otherwise it decreases. The value of the decrease increases along with $k$ (Table 2) for the coefficient of variation of the number of homozygous loci per offspring decreases, as does the probability of appearance of an individual having an acceptable number of such loci. However, the total number of mutations in the genome of an offspring after one generation of selfing at $d > 2$ becomes smaller than that in a stationary sexual population, so that fitness in the next few generations increases and the allele of selfing meets a better genetic background. Consequently, these alleles under small $z$ begin to spread even if one generation of selfing decreases the fitness twofold or slightly more: in this case, in contrast to apomixis and recombination, an allele enjoys an advantage in a wider range of conditions than does an individual. A similar discrepancy in the interests of individuals and their genes has been mentioned for some other conditions (COMINS, HAMILTON and MAY 1980).

Consider now the competition of amphimixis with apomixis, including all factors. With increasing $z$, $y$ and $p$, the probability that allele $M_{z,y}$ will be transferred to several successive generations without amphimixis increases. Consider, for instance, the allele $M_{z,0}$ at small $p$. Its advantage is $1 + \frac{z}{2}$. On
the other hand, selection against this allele is proportional to the frequency of its operation if it is manifested rarely in a succession of generations; otherwise selection increases faster than linearly with increasing $z$. The latter is because, with large $z$, allele $M_{z,y}$ is tightly connected with the consequences of its action, growth of $z$ being similar to the reduction of recombination frequency $r$ (KONDRAKHOV 1984b, p. 201). In any case, selection against $M_{z,0}$ increases along with $v$ (Figure 3).

To put it another way: when $z$ and $y$ increase, the gene pools of individuals carrying alleles $m$ and $M_{z,y}$ (or $u_{z,y}$) become more separated; and when $z = y = 1$ they are separated completely. Thus, coexistence of obligate amphimixis with obligate apomixis (or selfing) is impossible (Table 3). The result of their competition is determined by the fitnesses of a stationary sexual and an apomictic (or selfed) population: amphimixis will win if the latter is no more than 50% of the former.

These arguments allow us to interpret the main features of Tables 3 to 6. It is hardly surprising that selection for apomictic alleles with low penetrance depends mainly on $v$, because their fitnesses are connected with the effect of one generation of apomixis. Figure 3 explains the fact that, under large $v$, obligate amphimixis is advantageous; then, with a decrease of $v$ down to 1.25, first, apomictic alleles with small $z$ are fixed; and a further decrease of $v$ provides for fixation of $M_{z,5}$ alleles with larger $z$ and $y$; then, finally, the population establishes obligate apomixis under fixation of the allele with $z = y = 1$. A comparison of Tables 4 and 5 confirms our belief that this result is not influenced by our unavoidably artificial assumptions about the genetical
basis of apomixis. Some data also suggest that the situation depends principally on $v$, except for the fixation of $M_{1,1}$, which depends separately on $u$ and $k$ (Kondrashov 1982); thus, as $k$ increases, this allele fixes with a smaller $v$. The results for intermediate and linear selection differ only slightly from those for threshold selection.

We shall now proceed to consider selfing. It seems that, to protect amphimixis against selfing, $k$ should be larger than in the case of apomixis, unless $d$ is very large. Under small $z$, selection depends mainly on $d$, and not on $v$ as with apomixis. With $d = 2$, the population is never protected against selfing alleles with low penetrance (Table 6). Selection against such alleles increases along with increasing $d$ and $k$ (see above). On the other hand, selection against $\mu_{1,1}$ is similar to that against $M_{1,1}$. However, in the case of $\mu_{1,1}$, more severe conditions are required; because the fitness of a stationary population with obligate selfing is more than $e^{-z/u}$, it is not equal to $e^{-v}$ as in the case of obligate apomixis. If $d > 2$ and $u$ and $k$ are sufficient to outbalance obligate selfing, it is possible that only alleles $\mu_{z,1}$ with intermediate $z$ can be fixed (Table 6). If $z$ is determined polygenically, so that it cannot change saltatorily, there may exist two stable states of a population under certain conditions ($d > 2$, with moderate $u$): (1) obligate amphimixis or (2) selfing with large frequency, perhaps even obligate selfing. The absence of alleles $\mu_{z,1}$ with small $z$ in the population may be due either to the large value of $d$ or to a competition of the alleles with larger $z$, under small $u$.

Our results are interesting relative to a number of well-known phenomena connected with selfing and apomixis. Thus, the increase of outcrossing frequency with lengthening intervals between sexual reproductions (in perennials as compared to annuals, and in plants with extensive vegetative reproduction; Lloyd 1980b) may be caused by increasing $u$ and $v$. A similar explanation of increasing recombination frequency in self-pollinators (Holsinger and Feldman 1983) is also possible. Reallocation of resources to produce seeds with an increased frequency of apomixis and selfing (Cruden 1977) is in line with the data of Table 4 and 5. Note that an increase of $z$ and $y$ has almost the same effect on the populational properties of alleles $M_{z,y}$. Therefore, if it is difficult for $y$ to grow because of the physiological cost of reallocation, alleles with smaller $y$ and larger $z$ will spread in the population under the same conditions. Facultative apomixis is likely to be connected with frequent alleles of low penetrance (Maynard Smith 1978, Chapter 4d), and not with coexistence of obligate amphimixis with apomicts (Tables 3 to 5). Higher fitness of self-pollinated progeny in selfers (Lloyd 1979) may be due to reduced numbers of deleterious mutations ($d > 2$) or to selective elimination of less dominant mutations. The latter possibility cannot be addressed in our model.

A wider occurrence of selfing than of apomixis in plants (Marshall and Brown 1981) suggests that variability of the mutation number in selfed progeny is advantageous, notwithstanding the transfer of some mutations into the homozygous state. This means that the genome degradation rate $v$ is large in nature (approximately 1) and, on the other hand, that deleterious mutations
are mostly semidominant. However, simultaneous consideration of all three modes of reproduction is desirable.

Various ecological correlations or reproductive modes (JAIN 1976; BELL 1982, chapter 3) are often difficult to interpret in terms of our hypothesis. This is by no means a drawback: we know so little about the types of selection against mutations in nature, that we cannot estimate the influence of, say, humidity or temperature on \( u \) or \( k \). Still, the striking correlation between parthenogenesis and mutualistic endosymbiosis is easily explained if we assume that endosymbionts living in a supporting environment use only a small part of their genomes, which would lead to a decrease of \( u \) (LAW and LEWIS 1983).

There is a difference between competition of sex with obligate (KONDRASHOV 1982) and facultative apomixis (or selfing). Selection against obligate parthenogenesis or selfing is, in fact, a group selection. Therefore, the advantage of amphimixis accumulates in a number of generations (it may be convenient to call it moderate-time selection; KONDRASHOV 1982, figure 3), so that a sexual population protected against invasion by parthenogenetic clones can have, under a sufficiently high \( k \), viability that is close to 1. This is not so with selection for crossing over and selection against facultative apomixis or selfing, which are intrapopulation processes requiring constantly intensive selection. Such selection must result in 50% of the progeny being excluded from mating in each generation (\( v > 0.5 \)), provided that crossing over is advantageous; the mutation load must be no less than 80% if obligate amphimixis is to be advantageous (\( v > 1.25 \); see KONDRASHOV 1984b, figure 4). Actually, the value of \( v \) protecting obligate amphimixis may be smaller. First, one may suppose that male gametes contain fewer mutations than female gametes (MANNING 1984). This may be due to stronger selection preceding the formation of male gametes at both diploid (for instance, under polygamy if the sex ratio at birth is 1:1) and haploid (for instance, due to competition between pollen grains on the pistil) stages. Competition between spermatozoa is hardly relevant, as their properties are not determined by their haploid genotypes. Note that when directions of selection on haploid and diploid stages coincide, the competition between pollen grains is beneficial to the plant producing them, because its genes would be transferred with fewer deleterious mutations. Similarly, a plant producing ovules also enjoys an advantage due to pollen competition on its pistil and may provide conditions for it.

Another factor that can prevent expansion of facultative apomixis even at \( v < 1.25 \) is physiological difficulties in producing progenies in two different ways. For example, in mice, both maternal and paternal nuclei are necessary for embryogenesis (MCGRATH and SOLTER 1984). Both these factors can hardly counterbalance the twofold cost of sex, but at \( v \approx 1 \) the advantage of apomictic alleles with small \( z \), which are the only possible winners, is very small. It may be presumed, therefore, that obligate amphimixis can exist even when \( v \approx 0.8-1.0 \), which implies a somewhat smaller but still large load. Such a load

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1 In this figure, the abscissa should be labeled \( v \) instead of \( r \). It may be helpful to mention other misprints in this paper. The probability in the third line of page 202 should be \((0.5)^*\). In the sixth line on page 201, \( M_i \) should replace \( M_i \). The value of \( u \) in Table 1 should be 2.0 instead of 0.2.
may seem a drawback of our hypothesis. We believe, however, that any explanation of obligate sex and recombination should require selection of a comparable intensity.

Note that for the modern civilized human population, where low fertility precludes such purifying selection, our hypothesis predicts an accumulation of deleterious mutations. The consequences of this accumulation may only be manifested in the long run. If \( u \) is of the order of \( 10^5 \) and \( k \) of the order of \( 10^6 \) (see Kondrashov 1984b) and improvement of the conditions of life leads to, say, a twofold rise of \( k \), then a new critical mutation number will be reached only after a thousand generations (Crow 1983, p. 102). Recent attempts to measure a mutation component of variability make one hope that experimental data can be obtained on parameters of selection against deleterious mutations in nature (Crow and Denniston 1981). Further investigations may verify our belief that sexual reproduction and other relevant phenomena are “connected with the struggle of organisms to maintain the integrity of their informational molecules” (Manning 1976) under truncation selection.

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LITERATURE CITED


DELETERIOUS MUTATIONS


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