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GENE SELECTION OF MENDEL'S RULES

DAVID G. LLOYD

Botany Department, University of Canterbury, Christchurch, New Zealand

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SUMMARY

Evolutionarily stable strategies are examined for genes affecting equal segregation and independent assortment. When a preferentially segregating allele incurs a cost of eliminating the other allele, it can invade a population only if some of the cost is reallocated to offspring containing the overrepresented allele.

Different autosomal genes in one individual may have conflicting fitnesses whenever they do not invariably segregate into the same offspring. Evolutionarily stable strategies are examined for the rest of the genome to "cohabit" with two alleles, α_1 and α_2, which are adapted to different circumstances and thereby provide unique opportunities for their carriers. The ESS for genes which are not linked to such an ecologically maintained polymorphism is for α_1 and α_2 to segregate from $\alpha_1\alpha_2$ heterozygotes in the ratio of their unique opportunities. Additional considerations usually operate to select positively for equal segregation, however. First, the combined effects of linked series of genes with distinct opportunities and linkage to invariably harmful alleles may cause the opportunities for heterozygous blocks of genes to average out towards equality. Second, genes which are linked with α and in linkage equilibrium with its alleles, and genes which cannot detect whether α_1 or α_2 offer more opportunities, have a risk-averting ESS when they cohabit equally with α_1 and α_2. Their cohabitation strategies generate selection for equal segregation and independent assortment.

1. INTRODUCTION

Mendel's First and Second Rules, the Principles of Equal and Independent Assortment, are often seen as automatic and inevitable consequences of "normal" chromosome behaviour. The separation of homologous chromosomes to opposite poles at random and independently of other chromosome pairs leads directly to Mendel's Rules, seemingly without positive selection pressures other than those that maintain the machinery of cell divisions.

There is no compelling reason why chromosomes should behave in a democratic manner, however. It is well known that certain pairs of alleles do *not* segregate equally *e.g.*, Sex Ratio and Segregation Distorter genes in *Drosophila* (Charlesworth and Hartl, 1978; Crow, 1979), *t*-alleles in mice (Andrews and Goodfellow, 1982) and "pollen killer" in *Nicotiana* (Cameron and Moav, 1957). The total number of genes and chromosomes that are known to segregate unequally is quite considerable. But when one considers the innumerable crosses involving hundreds of species of plants and animals that are examined each year, the occasional reports of unequal segregation stand out as exceptions to the general pattern of obedience to Mendel's Rules.

A number of mathematical models have been proposed to account for unequal segregation ratios. When a preferentially segregating allele has no, or relatively little, disadvantage to its carriers, it will readily be incorporated into a population (Prout, 1953). If such an allele is not subject to a frequency-dependent selective force that limits its increase, it becomes fixed in the population. But if frequency-dependent selection is operating, as

when the allele that is overrepresented among the segregating progeny of heterozygotes suffers a disadvantage when it is homozygous, the continued spread of a preferentially segregating allele may be arrested, resulting in a persistent polymorphism (Prout, Bundgaard and Bryant, 1973; Charlesworth and Hartl, 1978). The fates of genes that modify unequal segregation ratios have also been analysed. Segregation modifiers can exist in a stable two-locus polymorphism in which there is permanent linkage disequilibrium (Prout *et al.*, 1973; Charlesworth and Hartl, 1978; Wu, 1983). In certain circumstances, linkage modifiers may select for decreased recombination between the two loci (Thomson and Feldman, 1974).

The selection models proposed to date have been primarily aimed at explaining the precise properties of polymorphisms such as the SD system in *Drosophila* and *t*-alleles in mice. The models are centred on specifications of the viability and fertility of particular genotypes at the segregating loci, and often the effects of particular genotypes at modifying loci as well. These models are of only limited value in explaining why non-Medelian alleles that lack severe fertility or viability effects do not invade populations more often and are not encountered more frequently, either in inter-population crosses or in natural polymorphisms. At present, we lack general principles, apart from secondary adverse effects of the non-Mendelian alleles themselves, which can explain why Mendel's Rules are obeyed so often. Liberman and Feldman (1980) demonstrated that the stability of a single-locus polymorphism that is maintained by overdominance is greatest when the alleles segregate equally, but their model utilised group selection and the result applies only when the two homozygotes have equal fitnesses. The prevailing pattern of equal segregation shown by most heterozygous loci remains as a "major paradox in the evolution of genetic systems" (Bell, 1982).

The present paper examines two separate factors that can restrict the spread of preferentially segregating alleles. One factor is structural—the developmental cost of eliminating the under-represented allele in terms of a reduction in the number of progeny produced by the parent. The second factor is ecological and occurs when the two alleles in a heterozygote provide distinct and limited opportunities for the progeny. The emphasis is placed on conditions that determine whether alleles for non-Mendelian behaviour are able to establish themselves in a population, rather than on the particular fitnesses of all possible genotype combinations that determine whether the alleles will continue to increase until they are fixed. Hence the models examine segregation ratios and coassortment frequencies as evolutionarily stable strategies (Maynard Smith, 1974) of particular genes.

2. Driven unequal segregation with a cost of elimination

A "non-Mendelian" gene, A, has two alleles. In the segregating progeny of heterozygotes, one allele, A_0, is overrepresented while the other, A_u, is underrepresented compared with equal segregation. The inequality may arise in the segregation of either male or female gametes, or in both. The inequality may result from an unequal representation in the products of meiosis (meiotic drive *s.s.*, or by gene conversion—Lamb and Helmi, 1982) or from differential viability of gametes, or from their differential fertilization success. The unequally segregating alleles have no ecological effects; that is their carriers are equally well or poorly adapted in all environments.

We consider conditions under which the driven allele is able to increase when it is rare. When A_0 is rare, it is assumed to occur only in A_0A_u individuals and to participate only in matings with A_uA_u individuals. Then all the progeny of A_0A_u that carry A_0 are A_0A_u, and the progeny that inherit A_u from the heterozygote are A_uA_u. The post-segregation fitnesses of the A_0-carrying and A_u-carrying progeny are p_0 and p_u respectively. The bulk of the population are A_uA_u and produce $2n$ offspring each. The unequal segregation in A_0A_u heterozygotes is achieved by an "elimination" of a number of gametes or zygotes, so the heterozygotes produce $n-e$ progeny containing A_u. Of the resources initially allocated to the A_u gametes or progeny that are eliminated, a proportion a is reallocated to A_0-carrying gametes or progeny, so a heterozygote produces $n+ea$ progeny that carry A_0. The total number of progeny that heterozygotes produce is therefore $2n-e+ea$, where $e(1-a)$ is the "cost of elimination" measured in numbers of progeny. The progeny of A_0A_u that carry A_u and A_0 are then in the ratio $r_0 : r_u = n+ea : n-e$. If A_0A_u produces as many offspring as A_uA_u, $a=1$ and there is no cost of elimination.

The fitness of each copy of the A_u allele (in A_uA_u individuals, ignoring the effect of rare A_0A_u individuals) in whichever sex or sexes show unequal segregation,

$$w_u = np_u.$$

The fitness of each copy of the A_0 allele (in A_0A_u, and in whichever sex or sexes show unequal segregation),

$$w_0 = (n+ea)p_0.$$

The A_0 allele can initially increase in the population if $w_0 > w_u$, *i.e.*,

$$(n+ea)p_0 > np_u. \tag{1}$$

In the special case of a driven allele with no cost of elimination ($a=1$), conditions for invasion simplify to $r_0p_0 > \frac{1}{2}p_u$. A parallel result was derived by Prout (1953). If the overrepresented allele has no post-segregation disadvantage ($p_0 = p_u$) as well as no cost of elimination, the inequality invariably holds and the non-Mendelian allele can always invade the population. But if the over-represented allele also imposes a disadvantage on its diploid carriers, ($p_0 < p_u$), it can invade the population only if the over-representation at segregation outweighs the post-segregation disadvantage.

If there is a cost of elimination ($a<1$), conditions for the driven allele to invade the population become much more stringent. Even if a cost-incurring allele segregates in 100 per cent of A_0A_u progeny ($e=n$) and has no post-segregation disadvantage ($p_0 = p_u$), it is not automatically selected. It can invade the population only if there is a sufficient reallocation of parental resources, so that the absolute number of A_0-carrying offspring is greater than the number of offspring left by copies of the competing allele in the bulk of the population. And if a cost-incurring allele that is over-represented at segregation has a post-segregation disadvantage, invasion is even more difficult.

A cost of elimination therefore constitutes a powerful force opposing the selection of non-Mendelian alleles, and it may well be the principal reason why Mendel's First Rule is obeyed so often. A preferentially segregating locus could incur a cost of elimination whenever the preference is

obtained by stopping the development of gametes or zygotes that would normally proceed. On the maternal side, this is likely to happen whenever the development of eggs or megaspores is arrested (Zimmering *et al.*, 1970; Grant, 1975 give examples). On the paternal side, unequal segregation usually arises from the non-functioning of normally functioning cells (*e.g.*, Segregation Distorter in *Drosophila*, Crow, 1979; pollen aborting genes in tobacco and wheat; Cameron and Moav, 1957, Scoles and Kibirge-Sebunya, 1983). This abortion will incur a cost whenever the fitness of the parent is limited by its gamete production, as it is likely to be if there is sperm or pollen competition among paternal parents.

The cost of elimination is similar to the constraint operating on the selection of unequal sex ratios when the primary sex ratio is equal and the fitnesses of sons and daughters depends differently on parental investment. Maynard Smith (1980) showed that selection of unequal ratios is then restricted by the amount of lost resources (equivalent to e above). The situation considered here for unequally segregating loci in general is different in that the inequality is derived from non-Mendelian behaviour of the alleles rather than from a difference in the expense of raising males and females. Hence it is not possible to produce more of the over-represented allele merely by cutting investment in the other allele, and some degree of reallocation of resources, not considered by Maynard Smith, is necessary before the driven allele is selected.

The model presented above analyses only the conditions for a non-Mendelian gene to spread initially in a population. If A_0 has the same segregation success in $A_0A_u \times A_0A_u$ and $A_0A_u \times A_0A_0$ crosses that it has in $A_0A_u \times A_uA_u$ crosses, and A_0A_0 homozygotes are as fit as the heterozygotes, any conditions that allow A_0 to invade a population will also permit its continued spread and eventual fixation. But if A_0 has less success in the genotype combinations which appear only when its frequency becomes appreciable, its further spread may be arrested. It is then necessary to employ a full genotypic model of selection that specifies the fitness of each genotype and the outcome of every possible mating.

Previous genotypic models of the selection of non-Mendelian genes have defined precisely the necessary conditions for protected polymorphisms (*e.g.*, Prout *et al.*, 1973; Charlesworth and Hartl, 1978). Some of these models have in effect incorporated the equivalent of the cost of elimination considered here, but this has been included in terms for the fitness or fertility of particular genotypes, and the cost of elimination has not hitherto been identified explicitly as a constraint on the selection of non-Mendelian genes.

3. Segregation ratios of alleles that provide unique opportunities

An entirely different situation exists at a polymorphic locus at which each allele provides its carriers with unique opportunities to increase their fitness. We consider whether it is advantageous for genes in heterozygotes for such alleles to modify the segregation ratio towards or away from equality. The models assume there is no cost of elimination and examine alleles that operate in a haploid phase of a life cycle. Parallel results may well pertain to diploids, but the calculations required to examine selection

in a diploid generation would be considerably more complicated and are not considered here.

The ESS models analyse the fitnesses of *alleles* that affect genetic recombination, rather than the fitnesses of the *individuals* that carry the recombining genes. The principal reason for examining gene selection is that a particular pattern of recombination may have divergent consequences for different genes in the same individual. Whenever two genes in an individual are not invariably inherited together, there is a potential conflict between them over the frequency that is most advantageous for each gene to associate or "cohabit" with the other in the progeny. Any gene may therefore be selected for its own cohabitation strategies that control the segregation ratio at another locus or coassortment frequencies between loci.

At a polymorphic locus, two alleles, α_1 and α_2, adapt their carriers to environments that are non-overlapping in part or in their entirety. The environments are uniformly spread throughout a population so the haploid families of all $\alpha_1\alpha_2$ zygotes or diplophase individuals experience the same frequencies of different environments. The α_1 progeny of each diploid "parent" have access to u_1 "unshared" sites per parent in which they can succeed but α_2 individuals cannot, and to s "shared" sites per parent in which both α_1 and α_2 progeny compete on an equal basis. Similarly, the α_2 progeny of an $\alpha_1\alpha_2$ parent have access to u_2+s appropriate sites per parent. The progeny of a parent are distributed over an area such that the progeny of N parents compete at each site. The α_1 and α_2 alleles are distributed evenly through the population in frequencies f_1 and f_2, where $f_1+f_2 \leqq 1$. It is shown in the Appendix that there is a stable polymorphism that is at equilibrium when the allele frequencies are proportional to the unique opportunities which the alleles confer on their carriers, *i.e.*,

$$f_1 : f_2 = u_1 : u_2.$$

We first consider the fitness of an allele, G_i, which is present as a single copy in the heterozygote $\alpha_1\alpha_2$ and controls the segregation ratio of α_1 and α_2, $a_1 : a_2$, where $a_1 + a_2 = 1$. The fitness of G_i is the sum of the fitnesses it obtains while cohabiting with α_1 or with α_2 in the progeny of $\alpha_1\alpha_2$. The fitness G_i obtains from cohabiting with either α allele is equal to the sum of the opportunities available to progeny containing that allele multiplied by the proportion of progeny of $\alpha_1\alpha_2$ that contain G_i among the total number of individuals competing for each site. If G and α are not linked, G_i cohabits with α_1 and α_2 in the ratio in which they segregate, $a_1 : 1 - a_1$. Then if the $2n$ progeny of one parent are dispersed widely so they compete with those from many other parents ($N \to \infty$), the fitness of G_i,

$$w_i = \frac{1}{2} \cdot \frac{2nN}{2nN}\left[\frac{a_1 u_1}{f_1} + \frac{a_2 u_2}{f_2} + \frac{(a_1 + a_2)s}{f_1 + f_2}\right].$$

Putting $a_2 = 1 - a_1$ gives

$$\frac{\partial w_i}{\partial a_1} = \frac{1}{2}\left[\frac{u_1}{f_1} - \frac{u_2}{f_2}\right].$$

If the frequencies of α_1 and α_2 are at equilibrium, $f_1 : f_2 = u_1 : u_2$ (Appendix (I)), and

$$\frac{u_1}{f_1} = \frac{u_2}{f_2}.$$

Therefore

$$\frac{\partial w_i}{\partial a_1} = 0. \tag{2}$$

When the progeny of many parents compete, the fitness of a gene is unaffected by the segregation ratio at an unlinked gene whose alleles provide unique opportunities.

If the progeny of only a limited number of parents compete with each other ($N < \infty$), the total number of α_1 or α_2 individuals in a competition pool containing the progeny of an $\alpha_1\alpha_2$ parent is influenced by the segregation ratio. The fitness of G_i in $\alpha_1\alpha_2$ parents when G and α are unlinked,

$$w_i = \frac{1}{2} \cdot \frac{2nN}{2n}\left[\frac{a_1 u_1}{f_1(N-1)+a_1} + \frac{a_2 u_2}{f_2(N-1)+a_2} + \frac{(a_1+a_2)s}{(f_1+f_2)(N-1)+a_1+a_2}\right].$$

When

$$\frac{\partial w_i}{\partial a_1} \neq 0, \qquad \frac{a_1}{a_2} = \frac{f_1}{f_2}. \tag{3a}$$

Therefore

$$\frac{a_1}{a_2} = \frac{u_1}{u_2}, \tag{3b}$$

since at equilibrium $f_1 : f_2 = u_1 : u_2$ (Appendix (I)). The second derivative is always negative, so equations (3a) and (3b) specify an ESS. The fitness of G_i is maximised when α_1 and α_2 segregate in the proportions of the unshared opportunities they confer on their carriers. If a series of G alleles variously modify the segregation ratio of the α alleles, the G allele that specifies the ratio closest to that in equation (3a) and (3b) will be selected.

The reason for the ESS segregation ratio specified by equations (3) is that the local competition pools for the unique opportunities provided by the α alleles cause the fitness gains from increasing the proportion of either segregating allele to diminish as that proportion increases. The ESS occurs at the point where the marginal gains for G_i from cohabiting with the two α alleles are numerically equal (*i.e.*, $\partial w_i/\partial a_1 = -\partial w_i/\partial a_2$). The stability of the segregation ratio is similar to that conferred on sex ratios or sex allocations by local mate competition or local resource competition (Charnov, 1982). The deviations in the segregation ratio analysed here are caused by differences in the *heights* of the fitness curves obtained by graphing w_i against a_1 or a_2. The heights are determined in turn by the sizes of the unique opportunities, u_1 and u_2. The shapes of the two fitness curves are identical, since the same numbers of parents contribute to the competition pools for individuals carrying α_1 or α_2. With local mate competition or local resource competition, on the other hand, the unequal sex ratios or allocations are caused by sex differences in the sizes of the competition pools, *i.e.*, by the relative *shapes* of the male and female fitness curves (Charnov, 1982).

The opportunities shared by progeny containing α_1 and α_2 do not affect the position of the equilibrium segregation ratio, since the shared opportunities can be taken equally and interchangeably by either allele. A stable ESS is reached as long as the opportunities do not overlap completely, but the stability of the ESS increases as the extent of non-overlap increases.

Equation (3b) suggests that any unlinked modifying gene that can modify the segregation ratio at a polymorphism maintained by spatial heterogeneity is favoured if it causes the ratio to match the relative opportunities available to carriers of the alleles. However, there are three further considerations which may limit deviations and cause stabilising selection for equal segregation ratios.

First, no gene segregates by itself. The α alleles will be linked to alleles of other loci, β, γ, δ, etc. Various heterozygous loci linked to α in $\alpha_1\alpha_2$ may favour a preponderance of the chromosome containing α_1 at some loci and that containing α_2 in others, either because one chromosome carries a deleterious allele or because there are other ecologically maintained polymorphisms. The summation of diverse effects in the block of genes surrounding α may lead to an averaging out of selective forces so that a segregation ratio at or near equality will be favoured overall *i.e.*, $a_1 \doteqdot a_2$.

Second, a different selective force operates on segregation modifiers linked to α. Suppose G and α are linked and in linkage equilibrium. When G_i is represented as a single copy (in G_iG_j) in the heterozygote $\alpha_1\alpha_2$, it is equally likely to be coupled with α_1 or α_2. The ESS for G_i is then to favour equal segregation of α_1 and α_2 as a risk-averting strategy, regardless of the relative numbers of opportunities they confer. This can be seen most easily in the extreme case when G and α are so closely linked that the fitness contributions of recombinants among the $2n$ progeny of $G_iG_j\alpha_1\alpha_2$ heterozygotes can be ignored. The average fitness of G_i coupled equally often with α_1 and α_2 (omitting shared environments, which have no effect) is then

$$\bar{w}_i = \frac{1}{2}\left[\frac{1}{2}\cdot\frac{2nNa_1u_1}{2n[f_1(N-1)+a_1]}+\frac{1}{2}\cdot\frac{2nNa_2u_2}{2n[f_2(N-1)+a_2]}\right].$$

Putting $a_2 = 1-a_1$ gives when $\partial\bar{w}_i/\partial a_1 = 0$,

$$a_1 = a_2. \tag{4}$$

The second derivative is negative, so equal segregation is evolutionarily stable.

Thirdly, equal segregation also operates as a risk-averting strategy when G_i can cause a segregation ratio $a_1 : a_2$ to deviate from equality in either direction, but it cannot determine in any instance whether it would be more profitable to increase a_1 or a_2. The expected fitness of G_i, w_i^*, in circumstances when opposite deviations are equally likely to be beneficial is the average of the fitnesses for either outcome. Again omitting shared environments, for all cohabitation (recombination) frequencies between α and G alleles (c),

$$w_i^* = \frac{1}{2}\cdot\frac{2nN}{2n}\left\{\frac{1}{2}\left[\frac{a_1cu_1}{f_1(N-1)+a_1c}+\frac{(1-a_1)(1-c)u_2}{f_2(N-1)+(1-a_1)(1-c)}\right]\right.$$
$$\left.+\frac{1}{2}\left[\frac{(1-a_1)cu_1}{f_1(N-1)+(1-a_1)c}+\frac{a_1(1-c)u_2}{f_2(N-1)+a_1(1-c)}\right]\right\}.$$

When

$$\frac{\partial w_i^*}{\partial a_1} = 0, \qquad a_1 = a_2. \tag{5}$$

The second derivative is negative. Hence if a modifying gene cannot discern which direction of deviation should be preferred in a particular individual, the ESS is to be strictly neutral and favour neither.

At present, it is difficult to estimate the numbers of ecologically maintained polymorphisms in populations and the potential for modifying genes to influence their segregation ratios. Even where the opportunities offered by two alleles of one locus are markedly unequal, ever-changing linkage relationships with alleles of other polymorphisms and with disadvantageous alleles are likely to preclude the selection of deviant ratios. Uncertainties in the direction of selection will create a widespread selective pressure for modifying genes to be actively neutral towards all other genes and maintain equal segregation ratios throughout the genome as a whole. Selection for equal segregation is easily put into effect, since it requires only that chromosome divisions and cell functions operate efficiently and without bias during meiosis, fertilisation and embryogenesis.

4. Independent assortment as a cohabitation strategy

Suppose that selection of cohabitation strategies by genes such as G_i has resulted in selection of a stable (equal or unequal) segregation ratio in the heterozygote $\alpha_1\alpha_2$, as described in the previous section. It can be further shown that the evolutionary stable co-assortment strategy for a gene G_i is to assort independently of α rather than to be linked with it. Let the co-assortment in the double heterozygote $G_iG_j\alpha_1\alpha_2$ be such that a fraction c_1 of progeny containing G_i also contain (cohabit with) α_1, and a fraction $c_2 = 1 - c_1$ cohabit with α_2. Haploid progeny containing α_1 compete for u_1 unshared and s shared sites per parent, and α_2 progeny compete for $u_2 + s$ sites per parent. The relative frequencies of α_1 and α_2 in the population are f_1 and f_2, where $f_1 + f_2 \leqq 1$. When the progeny of a limited number of parents compete for each site ($N < \infty$), the fitness of G_1,

$$w_i = \frac{1}{2} \cdot \frac{2nN}{2n}\left[\frac{c_1 u_1}{f_1(N-1)+c_1} + \frac{(1-c_1)u_2}{f_2(N-1)+1-c_1} + \frac{(c_1+1-c_1)s}{(f_1+f_2)(N-1)+c_1+1-c_1}\right].$$

When $\partial w_i / \partial c = 0$,

$$\frac{c_1}{c_2} = \frac{f_1}{f_2}, \quad \text{which from equation (3a)}$$

$$= \frac{a_1}{a_2}. \tag{6}$$

The second derivative is negative, so the ESS for G_i is to cohabit with α_1 and α_2 in the ratio in which they have been selected to segregate, whether the ratio is equal or unequal. This can be achieved only when α and G assort independently. If there are additional loci, β, γ, etc., whose alleles also provide distinct opportunities for fitness independently of the opportunities for α_1 and α_2, then G_i should assort independently of each of these loci. Moreover, the fitness of G_i is maximised when α, β, γ, etc. assort independently of each other. Thus G_i capitalises fully on the separate fitness

opportunities provided by various loci by cohabiting with their alleles randomly in all possible combinations.

The maximum utilisation of ecological opportunities may help to explain a long-standing puzzle in genetics, why the genome does not "congeal" (Turner, 1967). Geneticists have repeatedly pointed out that whenever sets of genes interact epistatically with each other, there is selection for increased linkage between the genes (Maynard Smith 1977, 1978). A number of factors promoting recombination between loci have been proposed, including spatially or temporally varying environments (Maynard Smith, 1971; Slatkin, 1975; Charlesworth, 1976), spatial heterogeneity with sib competition (Williams, 1975; Maynard Smith, 1976), and hitch-hiking (Strobeck, Maynard Smith and Charlesworth, 1976), but they all lack adequate generality (Maynard Smith, 1977).

The present model invokes spatial heterogeneity and sib competition, as do the "lottery models" (Young, 1981) developed by Williams (1975) and subsequently quantified by Maynard Smith (1976), Taylor (1979) and Bulmer (1980). Lottery models depend on inter-*family* selection based on the probabilities that families of different parents provide the fittest genotype in a competition pool. The present model, however, incorporates inter-*sib* competition within local areas, which causes diminishing fitness gains for a gene continuing to cohabit with any other gene that adapts its carriers to a part of the total environment. The present model therefore belongs to the "elbow-room" class of sib competition models (Young, 1981), together with local mate competition and local resource competition models for sex ratios (Hamilton, 1967; Clark, 1978) and the "tangled bank" hypothesis for sex (Ghiselin, 1974; Bell, 1982).

There is a striking contrast between the requirement for selection of independent assortment derived above, namely independent action of genes α, β, etc., and the condition leading to selection for increased linkage, epistatic interactions between genes. The linkage relationships among the genes in a genome may represent a complex resolution of these two sets of factors pushing recombination frequencies in opposite directions.

The effects of cohabitation strategies on recombination frequencies have been analysed above only for haploids. The same averaging and risk-averting strategies should also cause equal segregation and independent assortment to be selected in diploid organisms.

5. Discussion

The cohabitation strategies considered here recognise that the selection of recombination frequencies should be considered in terms of the selection of single genes whenever there are conflicts between the ways in which the fitnesses of different genes in an individual are maximised. The concept of "intragenomic conflicts" (Cosmides and Tooby, 1981) between the fitnesses of different genes in the same individual has been recognised to date in two contexts. Fitness conflicts may occur when genes have different patterns of "normal" inheritance, as do genes on male- and female-determining chromosomes (Hamilton, 1967) or nuclear and cytoplasmic genes (Cosmides and Tooby, 1981). Conflicts also occur between "outlaw" genes (those that violate the rules of transmission for nuclear genes) and other genes in the nuclear genome (Leigh, 1977; Alexander and Borgia, 1978; Crow, 1979;

Dawkins 1982; and above). In all these situations, the conflicting genes show different *patterns* of inheritance and therefore their fitnesses are not "maximised in the same way" (Cosmides and Tooby, 1981).

In addition, any two autosomal genes may be subject to different selective forces, even if they both segregate equally. The necessary condition for intragenomic conflict and gene selection must therefore be broadened beyond classes of genes that are inherited in different patterns, the criterion used by Cosmides and Tooby (1981). Selection must be analysed at the level of particular genes *whenever two genes are not invariably transmitted to the same offspring and the behaviour of one affects the fitness of the other.* The model of independent assortment analysed above provides an illustration of the broader conditions requiring consideration of gene selection.

When the behaviour of one gene affects the fitness of another, the concept that the amount of recombination between genes maximises the fitness of the individuals carrying them is not valid. The examination of cohabitation strategies for single genes offers a more accurate alternative framework, at the level of gene selection, for the evolution of the mechanisms of sexual reproduction.

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APPENDIX

Equilibrium at a polymorphism maintained by niche differences in a haploid population:

A haploid population contains two alleles, α_1 and α_2, that enable their carriers to succeed in environments that are wholly or partially distinct. For every individual in the population in one (parental) generation, in the next generation there are u_1 unshared and s shared niche sites available for individuals carrying α_1 to compete for, and u_2 unshared and s shared sites to which individuals carrying α_2 are adapted. The frequencies of α_1 and α_2 are f_1 and f_2, where $f_1+f_2 \leqq 1$. Every site receives a total of x competing progeny carrying α_1 and α_2 in frequencies f_1 and f_2. The fitness of parents carrying either allele is the number of appropriate sites divided by the number of competitors for each site. That is,

$$w_1 = \frac{1}{x}\left[\frac{u_1}{f_1} + \frac{s}{f_1+f_2}\right],$$

and

$$w_2 = \frac{1}{x}\left[\frac{u_2}{f_2} + \frac{s}{f_1+f_2}\right].$$

When the fitnesses of the two alleles are equal,

$$\frac{u_1}{f_1} = \frac{u_2}{f_2},$$

or

$$\frac{f_1}{f_2} = \frac{u_1}{u_2}. \qquad \text{(I)}$$

If $f_1/f_2 > u_1/u_2$, $w_1 > w_2$, and f_1 will decrease in the next generation. Conversely, f_1 will increase if $f_1/f_2 < u_1/u_2$. Hence equation (I) represents a stable equilibrium maintained by the negatively frequency-dependent fitnesses of the two alleles. The equilibrium frequencies of the two alleles are proportional to the unique opportunities they confer on their carriers. Niche overlap between alleles does not affect the equilibrium frequencies, since the shared sites are occupied interchangeably by individuals carrying either allele.