Theor Appl Genet (1986) 73:102–112

Linkage disequilibrium and gametophytic self-incompatibility

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Received April 24, 1986; Accepted May 6, 1986
Communicated by H. F. Linskens

Summary. The approach to linkage equilibrium of a locus linked to the locus determining gametophytic self-incompatibility (*S*) is considered. For the simplest case of three alleles at the *S* locus and two at the linked locus it is necessary to consider 3 measures of linkage disequilibrium. These are found to approach their equilibrium value of zero in one of three ways: 1) steadily declining to zero; 2) oscillating as decline proceeds; 3) a combination: 2) followed by 1). Linkage equilibrium may be established before genotype frequencies reach their expectation under random crossing. Earlier studies (Li 1951; Moran 1962) of the approach to *S* allele equilibrium have been based on the assumption that all types of pollen take part in fertilizations equally frequently. Such an assumption leads to simpler expressions for changes in *S* gene frequencies but is extremely unrealistic and, in particular, leads to a different rate of approach to equilibrium from the more comprehensive model. It is shown that even in the absence of selection it is not possible to predict the equilibrium gene frequency of a linked locus until *S* allele equilibrium is reached. This frequency may be either higher or lower than that calculated from a gene count in the starting genotype pool. However, these two gene frequencies may stabilize long before linkage equilibrium is achieved. An examination of selection against one genotype at the linked locus is undertaken. If linkage is complete, lethality can be less effective at reducing the gene frequency than is less intense selection (in only a few generations of selection). Here too linkage equilibrium may be established with selection still effective in bringing about a decline in gene frequency. An examination of the analysis and conclusions of Rasmuson (1980) shows that because these were based on the inadequate formulae previously discussed and exclude phenomena discussed above, they are misleading. The possibility of a gametophytic self-incompatibility system providing a sufficient condition for the sheltering of lethals in the absence of the condition of complete linkage to the *S* locus ($r = 0$) is shown to be unlikely.

Key words: Linkage – Linkage disequilibrium – Gametophytic self-incompatibility – Sheltering of lethals

Introduction

In random mating populations in the absence of selection, the joint genotypes at linked loci ultimately reach frequencies expected on the basis of independence, i.e. loci appear unassociated. In population-genetical studies, it is sometimes useful to know the number of generations required to approach this equilibrium configuration to any given extent. For two autosomal loci this is a relatively simple problem and for X-linked loci the problem, although more complex, has also been solved (Bennett et al. 1965). In this paper we look at the rate of approach to linkage equilibrium of two linked loci, one of which is a locus which determines gametophytic self-incompatibility (*S*), where all genotypes are of equal fitness. The analysis is extended to include differential fitness of the genotypes at the linked locus with a view to assessing the rate at which incompatibility systems might be expected to accumulate linked deleterious, possibly lethal genes.

Muller (1914) first demonstrated balanced systems of lethal factors and since that time a number of writers have taken the view that enforced heterozygosity is sufficient to explain the accumulation of lethals in the sheltered chromosomes. This can be seen in a very simple form if we compare the equilibrium frequencies of lethal recessives for autosomal and X-linked genes: if the rate of mutation to the lethal allele is μ, the equilibrium frequencies are μ and 3μ for the autosomal and X-linked cases, respectively. The higher autosomal frequency occurs because two doses of the gene are necessary for lethality, whereas in the heterogametic sex only one dose is needed.

It has long been suggested that genetical systems in plants (which may vary from complete self-fertilization to obligate outcrossing) determine the amount of heterozygosity found in natural populations of plants (Darlington 1958). However, Fisher (1935) demonstrated that, by itself, enforced heterozygosis does not shelter lethal mutations in such a way as to explain their accumulation from this cause alone. Further, Strobeck (1980) considering a system of heteromorphic self-incompatibility showed that the mating system affects the proportion of heterozygous individuals only at those loci which are directly adjacent to the S locus, and Ellstrand (1978) observed that the amount of variation maintained in populations of ring-forming species of *Oenothera* (i.e. those with balanced lethal factors), is not much different from non-ring-forming species.

We compare the rate of approach to equilibrium under the restrictive condition imposed by the self-compatibility system with the situation of X-linkage which might be regarded as a special (non-reciprocal) case of a self-incompatibility system. As with the X-linked case, measures of linkage disequilibrium can only be determined in terms of genotypic frequencies not the simpler commonly used form involving haplotype frequencies appropriate for autosomal loci.

This approach to the problem, deemed necessary to give a true representation of a population of plants, leads to results involving the approach to S allele equilibrium different from those previously described by Li (1951) and Moran (1962) and used by Rasmuson (1980). A re-evaluation of these results is given.

Table 1. Legitimate crosses and their progeny with three S alleles

		Male parent		
		S_1S_2	S_1S_3	S_2S_3
	S_1S_2	–	$\frac{1}{2}S_1S_3\,\frac{1}{2}S_2S_3$	$\frac{1}{2}S_1S_3\,\frac{1}{2}S_2S_3$
Female	S_1S_3	$\frac{1}{2}S_1S_2\,\frac{1}{2}S_2S_3$	–	$\frac{1}{2}S_1S_2\,\frac{1}{2}S_2S_3$
parent	S_2S_3	$\frac{1}{2}S_1S_2\,\frac{1}{2}S_1S_3$	$\frac{1}{2}S_1S_2\,\frac{1}{2}S_1S_3$	–

Methods

Self-incompatibility may be defined as the failure of self or cross pollination by reason of genetical similarity within an otherwise freely interbreeding group (Darlington and Mather 1949). The case considered here is that of gametophytically determined self-incompatibility in which pollen tube growth in the stylar tissue is controlled by the incompatibility genes in the pollen. Pollen grains are unable to grow in styles which possess the same gene as that carried by the pollen, i.e. individuals must always be heterozygous at the S locus. A minimum of three alleles is necessary for the system to survive, and with three alleles S_1, S_2, S_3 at the incompatibility locus, three genotypes S_1S_2, S_1S_3 and S_2S_3 will exist in the population.

Legitimate crosses and the progeny they yield are set out in Table 1. Considering two alleles A_1A_2 at the linked locus leads to 12 possible genotypes (Table 2) which can cross according to the constraints outlined in Table 1.

Linkage disequilibrium is defined as the difference in genotypic frequency between the two classes of double heterozygotes. Thus three measures of linkage disequilibrium are necessary to describe this, the simplest, case involving a gametophytic self-incompatibility system.

These are

$$D_1 = y_2 - y_5 \colon \frac{S_1A_1}{S_2A_2} - \frac{S_1A_2}{S_2A_1}$$

$$D_2 = y_4 - y_7 \colon \frac{S_1A_1}{S_3A_2} - \frac{S_1A_2}{S_3A_1}$$

$$D_3 = y_{11} - y_{10} \colon \frac{S_2A_2}{S_3A_1} - \frac{S_2A_1}{S_3A_2}.$$

In order to obtain these measures it is necessary to consider the 12×12 matrix of matings involving the 12 genotypes and collect up the 36 terms which contribute to each new genotype frequency in each generation. An example, the expectation for the genotype $\frac{S_1A_1}{S_1A_2}$, is given in Table 3.

It is unfortunate that this set of equations does not lead to simple expressions for D_i in each generation so that only numerical solutions may be obtained by repeated iteration. (We have attempted simplification by the use of the MACSYMA algebraic computer package but no useful results were obtained.)

Many different starting frequencies for the 12 genotypes were considered and similar patterns emerged. The ones described here in detail are i) the same for the three S genotypes as those considered by Li (1951) and ii) sets which satisfy the conditions specified by Rasmuson (1980), so that comparisons may be presented in a later section.

Conditions i) were examined for recombination frequencies r = 0, 0.01, 0.1, 0.2, 0.3, 0.4, 0.5 and fitness values of s = 1, 0.9, 0.5 and 0 for the A_1A_1 homozygote at the linked locus and conditions ii) at r = 0 and fitness either 0 or 0.5.

Table 2. Genotypes possible with 2 alleles linked to the S locus

Genotype	$\frac{S_1A_1}{S_2A_1}$	$\frac{S_1A_1}{S_2A_2}$	$\frac{S_1A_1}{S_3A_1}$	$\frac{S_1A_1}{S_3A_2}$	$\frac{S_1A_2}{S_2A_1}$	$\frac{S_1A_2}{S_2A_2}$	$\frac{S_1A_2}{S_3A_1}$	$\frac{S_1A_2}{S_3A_2}$	$\frac{S_2A_1}{S_3A_1}$	$\frac{S_2A_1}{S_3A_2}$	$\frac{S_2A_2}{S_3A_1}$	$\frac{S_2A_2}{S_3A_2}$
Frequency	y_1	y_2	y_3	y_4	y_5	y_6	y_7	y_8	y_9	y_{10}	y_{11}	y_{12}

Table 3. The frequency of $\frac{S_1A_1}{S_2A_1}$ (y_1^1) after one generation of crossing

$$
\begin{aligned}
&\frac{1}{2}\Big\{[y_1y_3+2y_3y_9+y_1y_9]\\
&\quad+\frac{1}{2}[y_2y_3+2y_3y_{11}+y_1y_7+2y_7y_9+y_5y_9+y_1y_{11}]\\
&\quad+\frac{(1-r)}{2}[y_3y_5+2y_3y_{10}+y_1y_4+2y_4y_9+y_2y_9+y_1y_{10}]\\
&\quad+\frac{r(1-r)}{2}[y_2y_4+2y_4y_{11}+y_5y_7+2y_7y_{10}+y_5y_{10}+y_2y_{11}]\\
&\quad+\frac{(1-r)^2}{2}[y_4y_5+2y_4y_{10}+y_2y_{10}]\\
&\quad+r^2[y_2y_7+2y_7y_{11}+y_5y_{11}]\Big\}\Big/\sum_{i=1}^{12}y_i
\end{aligned}
$$

Results

Approach to linkage equilibrium in the absence of selection

As noted by Li (1951), the frequencies of the *S* genes approach their equilibrium values of 1/3 in an oscillating fashion. This oscillating pattern is also observed in the approach to equilibrium frequencies of X-linked genes. However, in the case considered here, the D values may also oscillate, either giving a "saw tooth" approach to equilibrium values of zero without change in sign or oscillating in sign. Such behaviour was not found in the X-linked cases studied (Bennett et al. 1965). These oscillations are more likely to persist for larger values of the recombination frequency (r); for small values of r they tend to cease at *S* allele equilibrium, a condition which is always reached after relatively few (4–8) generations. Table 4 gives examples of these points.

For a given set of conditions at least one pair of the D values tend to be highly correlated. This correlation is greater for increasing values of r and may extend to all three D values.

We have found that it is not possible to predict the equilibrium frequencies of the genes at the linked locus from a gene count in the genotypes of the starting population. Although the equilibrium gene frequency is determined after relatively few generations of mating (at about the same time as *S* allele equilibrium), its value for a given set of starting genotype frequencies differs for different values of r. It may either increase or decrease with r and may be more or less than the original value obtained from a gene count. Figure 1 illustrates these points.

The case where $r = 0.5$ reflects the behaviour of any gene in the genome unaffected by the constraints of the incompatibility system; under these conditions linkage equilibrium and *S* allele equilibrium are coincident and rapid: always in less than 10 generations.

For the case $r = 0$ a consideration of linkage equilibrium is uninformative as in the absence of recombination changes in gene arrangement can only occur through gene conversion, mutation or other rare processes. In this case the population reaches a steady state in which large values for the D's may persist. These D's stabilize at *S* allele equilibrium. Table 5 illustrates these points.

Selection

Rasmuson (1980) has held that a tightly linked deleterious gene cannot be eliminated from a population in the absence of mutation. This is only true for the case $r = 0$, not for $r > 0$. The case $r = 0$, $s = 1$ results in a stable state with the deleterious gene still present in heterozygotes, i.e. in such a case the lethal is sheltered. This stable state coincides with *S* allele equilibrium.

However, with $r = 0.01$, $s = 1.0$ a deleterious gene can be eliminated as selection is still effective after *S* allele equilibrium and also after linkage equilibrium. See Figs. 2 and 3 for illustrations.

In general, after linkage equilibrium is reached the approach of the frequency of A_1 to zero should be the same as the standard infinite population case, i.e. $\Delta q = \frac{-sq^2(1-q)}{1-sq^2}$. This proves to be the case. Thus, in a population with a self-incompatibility system, once the population is in linkage equilibrium the effect of selection is independent of that system. This also militates against the notion of sheltering of lethals by the incompatibility system per se if $r > 0$. If selection is imposed on a population at linkage equilibrium, the changes in gene frequency as a result of selection are independent of the recombination fraction between the selected locus and the *S* locus.

Rasmuson also claimed that when selection is relaxed the frequency of *aa* (in this case A_1A_1) increases rapidly. We have shown this not to be the case; even if selection is relaxed before *S* allele equilibrium is reached the population soon stabilizes again. See Table 6.

Sheltering of lethals

Consider a population which has reached *S* allele equilibrium and suppose that all chromosomes carry

Table 4. Approach to equilibrium of y_1, D_1, D_2, D_3, A_1, S_1 from the initial set of frequencies $(D \times 10^3)$

1) 0.2 0.3 0.04 0.08 0.1 0.2 0.03 0.01 0.01 0.01 0.01 0.01
to the equilibrium set of frequencies
0.09371 0.08303 0.09371 0.08303 0.08303 0.07356
0.08303 0.07356 0.09371 0.08303 0.08303 0.07356 with $r = 0.4$ $s = 0.0$

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
1	0.07572	−32.45192	3.60577	35.45673	0.52855	0.27885
2	0.09698	−9.60235	−8.03049	2.61858	0.53026	0.34515
3	0.09283	−3.67518	−0.13398	3.40702	0.53022	0.33028
4	0.09386	−0.96509	−0.72923	0.25490	0.53023	0.33409
5	0.09367	−0.36616	−0.02043	0.34364	0.53023	0.33314
6	0.09372	−0.09691	−0.07208	0.02508	0.53023	0.33338
7	0.09371	−0.03657	−0.00212	0.03442	0.53023	0.33332
8	0.09371	−0.00970	−0.00720	0.00250	0.53023	0.33334
9	0.09371	−0.00366	−0.00021	0.00344	0.53023	0.33333
10	0.09371	−0.00097	−0.00072	0.00025	0.53023	0.33333
11	0.09371	−0.00037	−0.00002	0.00034	0.53023	0.33333
12	0.09371	−0.00010	−0.00007	0.00003	0.53023	0.33333
13	0.09371	−0.00004	0.00000	0.00003	0.53023	0.33333
14	0.09371	−0.00001	−0.00001	0.00000	0.53023	0.33333
15	0.09371	0.00000	0.00000	0.00000	0.53023	0.33333

2) 0.2 0.3 0.04 0.08 0.1 0.2 0.03 0.01 0.01 0.01 0.01 0.01
to the equilibrium set of frequencies
0.09498 0.08295 0.09498 0.08295 0.08295 0.07245
0.08295 0.07245 0.09498 0.08295 0.08295 0.07245 with $r = 0.45$ $s = 0.0$

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
1	0.07531	−26.14183	10.36659	36.20793	0.53320	0.27885
2	0.09908	−2.97655	−2.88539	0.58789	0.53379	0.34515
3	0.09384	−1.24589	0.51133	1.72833	0.53379	0.33028
4	0.09524	−0.07660	−0.15272	−0.07340	0.53379	0.33409
5	0.09491	−0.05735	0.03426	0.09148	0.53379	0.33314
6	0.09499	−0.00029	−0.00969	−0.00939	0.53379	0.33338
7	0.09497	−0.00285	0.00232	0.00516	0.53379	0.33332
8	0.09498	0.00016	−0.00063	−0.00079	0.53379	0.33334
9	0.09498	−0.00015	0.00016	0.00031	0.53379	0.33333
10	0.09498	0.00002	−0.00004	−0.00006	0.53379	0.33333
11	0.09498	−0.00001	0.00001	0.00002	0.53379	0.33333
12	0.09498	0.00000	0.00000	0.00000	0.53379	0.33333

3) 0.0005 0.0 0.0 0.0 0.0 0.0 0.0 0.49975 0.0 0.0 0.0 0.49975
to the equilibrial set of frequencies
0.0 0.00034 0.0 0.00034 0.00034 0.33265
0.00032 0.33267 0.0 0.00034 0.00032 0.33267 with $r = 0.1$ $s = 0.0$

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
1	0.0	0.0	−0.74888	−0.74888	0.00100	0.37488
2	0.0	0.0	−0.18002	−0.18002	0.00098	0.32502
3	0.0	0.0	−0.41971	−0.41971	0.00101	0.33552
4	0.0	0.0	−0.22492	−0.22492	0.00100	0.33279
5	0.0	0.0	−0.25352	−0.25352	0.00100	0.33347
6	0.0	0.0	−0.18481	−0.18481	0.00100	0.33330
7	0.0	0.0	−0.17076	−0.17076	0.00100	0.33334
8	0.0	0.0	−0.13795	−0.13795	0.00100	0.33333
9	0.0	0.0	−0.12004	−0.12004	0.00100	0.33333
10	0.0	0.0	−0.10019	−0.10019	0.00100	0.33333
11	0.0	0.0	−0.08559	−0.0.8559	0.00100	0.33333
12	0.0	0.0	−0.07217	−0.07217	0.00100	0.33333
13	0.0	0.0	−0.06130	−0.06130	0.00100	0.33333

continued overleaf

Table 4 (continued)

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
14	0.0	0.0	−0.05186	−0.05186	0.00100	0.33333
15	0.0	0.0	−0.04397	−0.04397	0.00100	0.33333
16	0.0	0.0	−0.03723	−0.03723	0.00100	0.33333
17	0.0	0.0	−0.03155	−0.03155	0.00100	0.33333
18	0.0	0.0	−0.02671	−0.02672	0.00100	0.33333
19	0.0	0.0	−0.02264	−0.02264	0.00100	0.33333
20	0.0	0.0	−0.01918	−0.01918	0.00100	0.33333

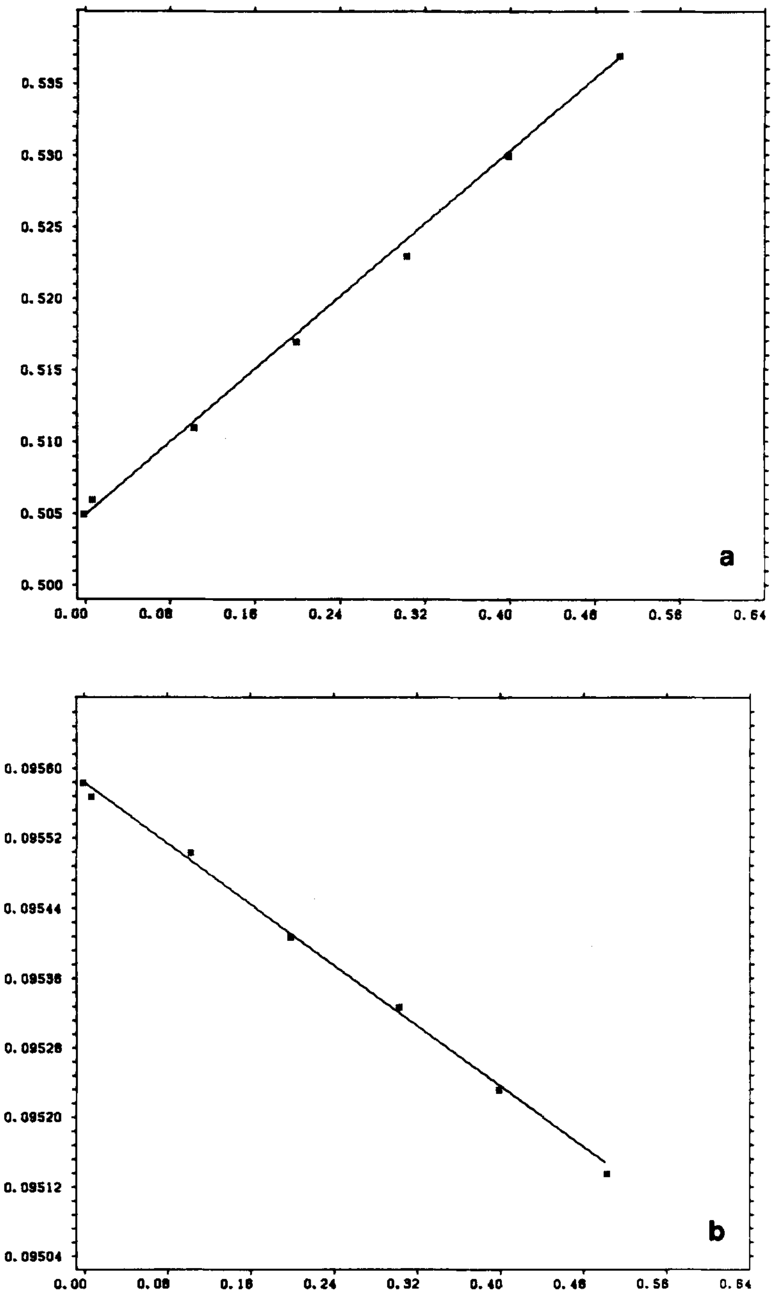

Fig. 1. Relationship between equilibrium frequency at the linked locus and recombination frequency between loci (**a**) initial gene frequency = 0.515 (**b**) initial gene frequency = 0.094

Table 5. Approach to equilibrium of y_1, D_1, D_2, D_3, A_1, S_1 from the initial set of frequencies 0.2 0.3 0.04 0.08 0.1 0.2 0.03 0.01 0.01 0.01 0.01 0.01 to the equilibrium set of frequencies ($D \times 10^3$)

1) 0.09629 0.08287 0.09629 0.08287 0.08287 0.07131
0.08287 0.07131 0.09629 0.08287 0.08287 0.07131 with $r = 0.5$ $s = 0.0$

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
1	0.07482	−19.83173	17.12740	36.95913	0.53786	0.27885
2	0.10152	2.74162	1.27051	−1.47111	0.53748	0.34515
3	0.09498	−0.27916	−0.05789	0.22128	0.53748	0.34515
4	0.09662	0.03626	0.01002	−0.02624	0.53747	0.33409
5	0.09621	−0.00449	−0.00116	0.00332	0.53747	0.33314
6	0.09631	0.00056	0.00015	−0.00041	0.53747	0.33338
7	0.09629	−0.00007	−0.00002	0.00005	0.53747	0.33332
8	0.09629	0.00001	0.00000	−0.00001	0.53747	0.33334
9	0.09629	0.00000	0.00000	0.00000	0.53747	0.33333

2) 0.08776 0.13734 0.10152 0.12357 0.4220 0.00604
0.04882 0.05942 0.05861 0.07134 0.09172 0.11165 with $r = 0.0$ $s = 0.0$

Gen.	y_1	D_1	D_2	D_3	A_1	S_1
1	0.07632	−82.93269	−50.48077	29.44712	0.49129	0.27885
2	0.08795	−95.28352	−84.80296	17.84504	0.50809	0.34515
3	0.08883	−95.31376	−70.01738	21.31175	0.50464	0.33028
4	0.08691	−94.21442	−77.04496	20.01021	0.50556	0.33409
5	0.08825	−95.68008	−73.63499	20.54234	0.50534	0.33314
6	0.08749	−94.84604	−75.31370	20.30498	0.50540	0.33338
7	0.08789	−95.28872	−74.48078	20.41639	0.50538	0.33332
8	0.08769	−95.06101	−74.89561	20.36249	0.50539	0.33334
9	0.08779	−95.17646	−74.68860	20.38899	0.50539	0.33333
10	0.08774	−95.11834	−74.79200	20.37585	0.50538	0.33333
11	0.08777	−95.14750	−74.74033	20.38239	0.50538	0.33333
12	0.08775	−95.13289	−74.76616	20.37913	0.50538	0.33333
13	0.08776	−95.14020	−74.75324	20.38076	0.50538	0.33333
14	0.08776	−95.13655	−74.75970	20.37995	0.50538	0.33333
15	0.08776	−95.13837	−74.75647	20.38035	0.50538	0.33333
16	0.08776	−95.13746	−74.75809	20.38015	0.50538	0.33333
17	0.08776	−95.13792	−74.75728	20.38025	0.50538	0.33333
18	0.08776	−95.13769	−74.75768	20.38020	0.50538	0.33333
19	0.08776	−95.13780	−74.75748	20.38023	0.50538	0.33333
20	0.08776	−95.13775	−74.75758	20.38021	0.50538	0.33333

A_2 at the closely linked locus. Suppose further that pollen carrying S_1A_1 drifts into the population. The A_1A_1 genotype is lethal.

If there is a 5% contribution to the pollen pool of S_1A_1 we find that the population reaches a new equilibrium with the frequency of A_1 slightly less than 5% depending on the recombination frequency between the A and S loci (Table 7). If this new haplotype is introduced at a very high frequency, e.g. 0.45, the new equilibrium frequency of A_1 is much lower, 0.32, in the case where $r = 0$; this value declines rapidly as r increases (Table 7). Thus unless the condition $r = 0$ is deemed realistic it seems unlikely that a gametophytic self-incompatibility system would provide a sufficient condition for the sheltering of linked lethal genes.

This finding is substantiated by results of small simulated populations of gametophytically self-incompatible plants (see Mayo 1983, for references). However, it does not support either the suggestion that in small populations different outbreeding mechanisms can lead to different frequencies of recessive lethals as discussed for example by Mayo (1981) or the case argued by Rasmuson (1980). Rasmuson argues that with repeated introduction of new S genes, each of which is completely linked to a lethal gene an increasing proportion of the population will become homozygous for this gene. These new haplotypes can only arise by rare processes such as mutation, as mentioned before, and indeed they would seem to be equivalent to new S genes rather than S_1A_1 haplotypes, a different case from that proposed by Rasmuson. In fact the introduction of more S alleles linked to the favourable allele (A_2) would be expected to hasten the decline of the frequency of A_1 at a rate proportional to the

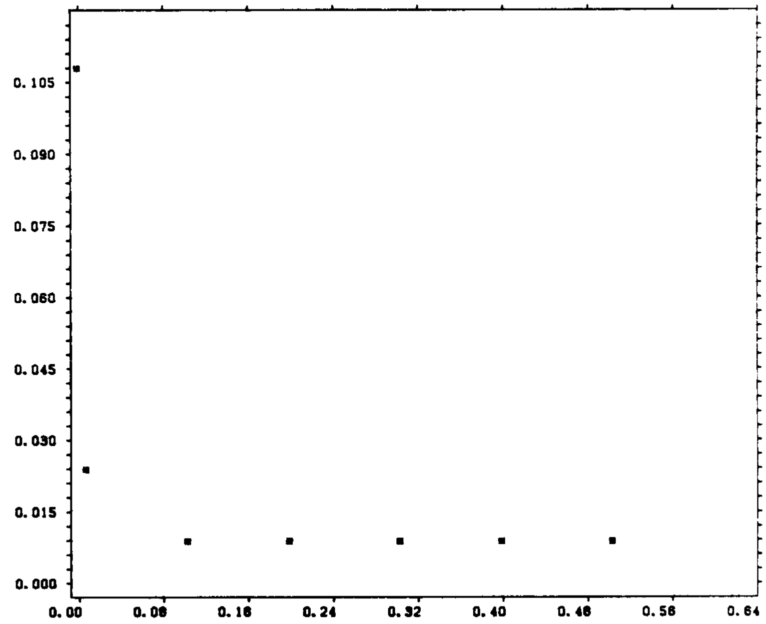

Fig. 2. Relationship between the frequency of a deleterious allele at the linked locus and recombinations frequency between loci

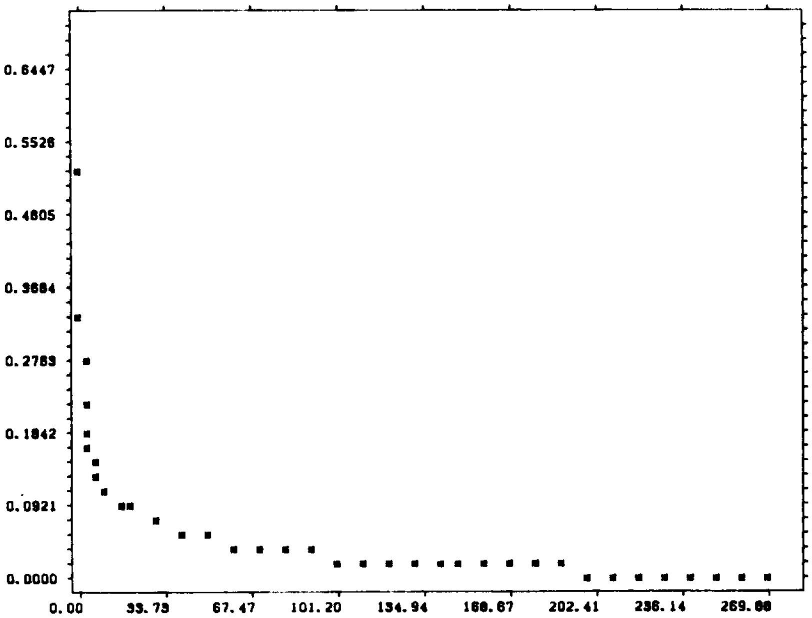

Fig. 3. Change over time in frequency of a lethal gene linked to the self-incompatibility locus

number of S genes so linked even in the case of complete linkage.

Comparison with other previous investigations

Li (1951) considers a population in which there are 3 incompatibility genotypes S_1S_2, S_1S_3, S_2S_3 in arbitrary proportions. He deduces simple and elegant equations for the change in gene frequency of the S alleles between generations and later extends the argument to k alleles arriving at expressions originally given by Wright (1939):

$$q_1' = \frac{(k-2)\,q_1(1-q_1)}{k-3+2q}$$

and

$$\Delta q = \frac{q(1-kq)}{k-3+2q}.$$

These expressions require the assumption that all types of pollen are equally numerous, which may be

Table 6. The effect on genotypic frequencies of relaxation of selection

Genotype	$\frac{S_1A_1}{S_2A_1}$	$\frac{S_1S_1}{S_2A_2}$	$\frac{S_1A_1}{S_3A_1}$	$\frac{S_1A_1}{S_3A_2}$	$\frac{S_1A_2}{S_2A_1}$	$\frac{S_1A_2}{S_2A_2}$	$\frac{S_1A_2}{S_3A_1}$	$\frac{S_1A_2}{S_3A_2}$	$\frac{S_2A_1}{S_3A_1}$	$\frac{S_2A_1}{S_3A_2}$	$\frac{S_2A_2}{S_3A_1}$	$\frac{S_2A_2}{S_3A_2}$	A_1
Initial frequency	0.2	0.3	0.04	0.08	0.1	0.2	0.03	0.01	0.01	0.01	0.01	0.01	0.515
Stable frequency reached with r = 0 s = 1	0	0.10767	0	0.10767	0	0.22567	0	0.22567	0	0	0	0.333	0.10767
Relaxation of selection after stability r = 0 s = 0	0	0.10767	0	0.10767	0	0.22567	0	0.22567	0	0	0	0.333	0.10767
Frequencies at generation 6 r = 0 s = 1	0.00438	0.12211	0.00859	0.12054	0.00715	0.19974	0.01367	0.19155	0.00057	0.00931	0.01877	0.30361	0.15932
												$S_1 = 0.32896$	
Stable frequency after relaxing selection at generation 6 r = 0 s = 0	0.005	0.11948	0.00867	0.1158	0.00838	0.20048	0.0145	0.19431	0.00093	0.01245	0.0223	0.29766	0.16108

appropriate for large numbers of S alleles. If, however, one imagines that pollen can drift into a population from new sources it will not initially do so at the same frequency as existing types which may themselves vary in frequency from generation to generation depending on the frequency of plants with each S allele.

A more complete consideration of the situation requires that both the frequency of the various female parents S_{ij} and the pollen types be taken into account. This leads to the following expression for the gene frequency in any generation derived from the previous one:

$$q_i' = \frac{2q_i(1-2q_i) + \sum_{j\neq i}^{k} S_{ij} \sum_{l\neq i,j}^{k} q_l}{2\left(1-\sum_{i=j}^{k} S_{ij}^2\right)}$$

The case where $k = 3$ leads to the relatively simple formula

$$q_1' = \frac{q_1(1-2q_1) + \sum_{i=1}^{3} q_i(1-2q_i)}{2\left(1-\sum_{i=1}^{3} (1-2q_i)^2\right)}.$$

A comparison of Table 8 given by Li (1951) with that obtained by the above expression (Table 9) shows that they both give an oscillating approach of the S frequencies towards equilibrium, but the rate of change is not simply a halving of the difference from 1/3 in each generation.

The oscillations are less extreme and equilibrium is approached more rapidly than previous formulae would indicate, presumably influenced by the assumption of equal frequencies of all types of pollen despite the considerable differences between the frequency of S_3 compared with S_1 and S_2.

Rasmuson (1980) examined the behaviour of a locus completely linked to the locus determining gametophytic self-incompatibility. She considered the numbers of S alleles linked to A to be N_A and those linked to a to be N_a where $N_A + N_a = N$.

At equilibrium the frequency of genotypes having

$$AA = \frac{N_A(N_A-1)}{N(N-1)}, \quad Aa = \frac{2N_AN_a}{N(N-1)},$$

and

$$aa = \frac{N_a(N_a-1)}{N(N-1)}.$$

Subsequent consideration of x haplotypes where the same S allele is linked to both A and a led to the derivation of a formula for the frequency of aa, namely

$$\frac{x(x-1)q^2 + 2x(N_a-x)q + (N-x)(N_a-x-1)}{N(N-1)},$$

Table 7. Effect of (pollen) immigration of a recessive lethal

Genotype	$\frac{S_1A_1}{S_2A_1}$	$\frac{S_1A_1}{S_2A_2}$	$\frac{S_1A_1}{S_3A_1}$	$\frac{S_1A_1}{S_3A_2}$	$\frac{S_1A_2}{S_2A_1}$	$\frac{S_1A_2}{S_2A_2}$	$\frac{S_1A_2}{S_3A_1}$	$\frac{S_1A_2}{S_3A_2}$	$\frac{S_2A_1}{S_3A_1}$	$\frac{S_2A_1}{S_3A_2}$	$\frac{S_2A_2}{S_3S_1}$	$\frac{S_2A_2}{S_3A_2}$	
Frequency	0	0.05	0	0.05	0	0.28	0	0.29	0	0	0	0.33	(1)
	0	0.43	0	0.45	0	0.03	0	0.02	0	0	0	0.05	(2)

Frequency of A_1 in the population with starting conditions

	(1)	(2)		
No. of generations	20	20	50	100
r = 0 s = 1	0.0498	0.316	0.316	0.316
r = 0.01 s = 1	0.043	0.258	0.173	0.081
r = 0.05 s = 1	0.031	0.107	0.029	0.012
r = 0.1 s = 1	0.028	0.061	0.022	0.010

Table 8. Approach to equilibrium of three self-incompatibility alleles under random mating

	Zygotic proportions			Gene frequencies		
n	S_1S_2	S_1S_3	S_2S_3	S_1	S_2	S_3
0	0.8000	0.1600	0.0400	0.480	0.420	0.100
1	0.1000	0.4200	0.4800	0.260	0.290	0.450
2	0.4500	0.2900	0.2600	0.370	0.355	0.275
3	0.2750	0.3550	0.3700	0.3150	0.3225	0.3625
4	0.3625	0.3225	0.3150			
5	0.31875	0.33875	0.3425			
6	0.340625	0.330625	0.32875			
7	0.3297	0.3347	0.3356			
8	0.3351	0.3327	0.3322			
9	0.3325	0.3336	0.3339			
10	0.3337	0.3332	0.3331			
∞	0.3333	0.3333	0.3333	0.333	0.333	0.333

Table 9. Approach to equilibrium of three self-incompatibility alleles under random mating, without the assumption of equal frequency of all pollen types

	Zygotic proportions			Gene frequencies		
n	S_1S_2	S_1S_3	S_2S_3	S_1	S_2	S_3
1	0.8	0.16	0.04	0.48	0.42	0.10
2	0.2596	0.2981	0.4423	0.279	0.202	0.519
3	0.3517	0.3386	0.3097	0.345	0.331	0.324
4	0.3277	0.3329	0.3394	0.330	0.334	0.336
5	0.3345	0.3337	0.3318	0.334	0.333	0.333
6	0.3331	0.3332	0.3337	0.333	0.334	0.333
7	0.3334	0.3334	0.3332			

Table 10. Approach to equilibrium of the two linked loci in the absence of selection, for 3 different initial sets of genotypic frequencies

	Genotypes												
	$\frac{S_1A_1}{S_2A_1}$	$\frac{S_1A_1}{S_2A_2}$	$\frac{S_1A_1}{S_3A_1}$	$\frac{S_1A_1}{S_3A_2}$	$\frac{S_1A_2}{S_2A_1}$	$\frac{S_1A_2}{S_2A_2}$	$\frac{S_1A_2}{S_3A_1}$	$\frac{S_1A_2}{S_3A_2}$	$\frac{S_2A_1}{S_3A_1}$	$\frac{S_2A_1}{S_3A_2}$	$\frac{S_2A_2}{S_3A_1}$	$\frac{S_2A_2}{S_3A_2}$	A_1
1)	0.25	0	0.25	0	0.125	0	0.125	0	0.25	0	0	0	0.875
2)	0.3	0	0.2	0	0.1875	0	0.625	0	0.25	0	0	0	0.875
3)	0.225	0	0.225	0	0.125	0	0.125	0	0.3	0	0	0	0.875
at equilibrium r = 0 s = 0													
1)	0.22222	0	0.22222	0	0.11111	0	0.11111	0	0.3333	0	0	0	0.88889
2)	0.22475	0	0.22475	0	0.10858	0	0.10858	0	0.3333	0	0	0	0.89142
3)	0.21429	0	0.21429	0	0.11905	0	0.11905	0	0.3333	0	0	0	0.88095

with frequencies of A_1 (a)		A_1A_1 (aa)
	1) 0.88889	= 0.79011
	2) 0.89142	= 0.79463
	3) 0.88095	= 0.77607

predicted value 0.91667

Table 11. Rate of loss of gene against which selection is directed under different selection intensities

Genotype		$\frac{S_1A_1}{S_2A_1}$	$\frac{S_1A_1}{S_2A_2}$	$\frac{S_1A_1}{S_3A_1}$	$\frac{S_1A_1}{S_3A_2}$	$\frac{S_1A_2}{S_2A_1}$	$\frac{S_1A_2}{S_2A_2}$	$\frac{S_1A_2}{S_3A_1}$	$\frac{S_1A_2}{S_3A_2}$	$\frac{S_2A_1}{S_3A_1}$	$\frac{S_2A_1}{S_3A_2}$	$\frac{S_2A_2}{S_3A_1}$	$\frac{S_2A_2}{S_3A_2}$	A_1	S_1
Initial frequency		0.2	0	0.2	0	0.2	0	0.2	0	0.2	0	0	0	0.8	0.4
Stable frequencies in generation 1															
r = 0 s = 1		0	0	0	0	0.25	0	0.25	0	0.5	0	0	0	0.75	0.25
r = 0 s = 0.5	1	0.1	0	0.1	0	0.2	0	0.2	0	0.4	0	0	0	0.8	0.3
	2	0.06538	0	0.06538	0	0.26154	0	0.26154	0	0.34615	0	0	0	0.73846	0.32692
	3	0.03529	0	0.03529	0	9.28228	0	0.28228	0	0.36486	0	0	0	0.71772	0.31757
	4	0.01874	0	0.01874	0	0.29986	0	0.29986	0	0.36279	0	0	0	0.70014	0.31861
	5	0.00962	0	0.00962	0	0.30786	0	0.30786	0	0.36504	0	0	0	0.69214	0.31748
	6	0.00488	0	0.00488	0	0.31245	0	0.31245	0	0.36534	0	0	0	0.68755	0.31733
	7	0.00246	0	0.00246	0	0.31468	0	0.31468	0	0.36573	0	0	0	0.68532	0.31714
	8	0.00123	0	0.00123	0	0.31583	0	0.31583	0	0.36586	0	0	0	0.68417	0.31707
	9	0.00062	0	0.00062	0	0.31641	0	0.31641	0	0.36595	0	0	0	0.68359	0.31703
	10	0.00031	0	0.00031	0	0.31670	0	0.31670	0	0.36599	0	0	0	0.68330	0.31699
	17	0	0	0	0	0.31699	0	0.31699	0	0.36603	0	0	0	0.68301	0.31699
r = 0 s = 0.2	1	0.13725	0	0.13725	0	0.17157	0	0.17157	0	0.38235	0	0	0	0.82843	0.30882
	2	0.13097	0	0.13097	0	0.20465	0	0.20465	0	0.32876	0	0	0	0.79535	0.33562
	3	0.11131	0	0.11131	0	0.21740	0	0.21740	0	0.34259	0	0	0	0.78260	0.32870
	4	0.09594	0	0.09594	0	0.23423	0	0.23423	0	0.33965	0	0	0	0.76577	0.33018
	5	0.08132	0	0.08132	0	0.24818	0	0.24818	0	0.34099	0	0	0	0.75182	0.32950
	6	0.06842	0	0.06842	0	0.26099	0	0.26099	0	0.34118	0	0	0	0.73901	0.32941
	7	0.05707	0	0.05707	0	0.27213	0	0.27313	0	0.34161	0	0	0	0.72787	0.32920
	8	0.04727	0	0.04727	0	0.28177	0	0.28177	0	0.34191	0	0	0	0.71823	0.32904
	9	0.03892	0	0.03892	0	0.28998	0	0.28998	0	0.34219	0	0	0	0.71002	0.32890
	10	0.03188	0	0.03188	0	0.29691	0	0.29691	0	0.34242	0	0	0	0.70309	0.32879
	20	0.00374	0	0.00374	0	0.32458	0	0.32786	0	0.34347	0	0	0	0.67214	0.32826
	40	0.00004	0	0.00004	0	0.32821	0	0.32821	0	0.34348	0	0	0	0.67179	0.32826
	50	0	0	0	0	0.32825	0	0.32825	0	0.34348	0	0	0	0.67175	0.32826

where q is the frequency of a in the x haplotypes. Figure 1 of her paper does not seem to correspond to the values obtained from this formula as it is shown to give an increasing frequency of aa as the numbers of haplotypes having both S_iA and S_ia increase whilst the frequency of A and a remain constant, whereas the formula above gives a declining value for the frequency of aa as would be expected and as is implied in her discussion: "An increase in the number of S alleles which are linked to the favourable A allele is the only effective way to decrease the segregation of aa."

Though this conclusion is probably true it is not possible to predict the equilibrium value of aa from the starting conditions as may be seen in the set of results presented in Table 10 where the equilibrium value of a is different for each set of conditions.

These cases all involved a population in which $3S$ alleles are segregating, $aa(A_1A_1$ here) is homozygous and into which one new haplotype is introduced, presumably as pollen with a frequency of $A(A_2$ here) $=1/8$ as described by Rasmuson but with the A, $a(A_2,A_1)$ genes differently distributed amongst the S genotypes. Not one of these sets of conditions gives the value of $aa(A_1A_1)$ of 0.91667 which is predicted by Rasmuson's formula. She also states that selection against a locus closely linked to the self-incompatibility locus is different from what occurs in loci under random mating. The allele towards which selection is directed cannot be eliminated.

Three points need to be reiterated finally. Firstly what Rasmuson calls close linkage is in fact complete linkage ($r=0$); if $r \neq 0$ (e.g. $r=0.01$), it is possible to eliminate the allele towards which selection is directed, albeit only after a very long time, and for $r=0.1$ (a value which might well be described as close linkage) elimination may be possible in about 100 generations. Secondly for the case of complete linkage a selection intensity less than 1 is more effective in lowering the gene frequency (Table 11). A selection intensity of $s=0.5$ reduces the gene frequency more in 2 generations than does $s=1$ and after 5 generations the frequency of $a(A_1)$ is 0.69 cf. 0.75. This degree of selection leads to a population with a stable frequency of $a(A_1)$ of 0.683 and it is interesting that for $s=0.2$ the population stabilizes with a frequency of $a(A_1)=0.672$. Thirdly relaxation of selection against $aa(A_1A_1)$ does not lead to a rapid increase in the frequency of $aa(A_1A_1)$.

Acknowledgements. We wish to thank Dr. B. Leach for his assistance with writing program used in the preparation of some of the tables.

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