calculated two-dimensional diffraction patterns of the various conformers are very different. Table 1 compares the models to the experimental data (Fig. 2). The data eliminate conformers (ii) and (iii), in which the molecular arrangements are such that the amide groups are interlinked by hydrogen bonds along the a- or c-axis. Even rotating the chain about the C2—C3 bond by ±5° does not improve the fit for these two models (see the calculated intensities in brackets). Their calculated intensities I(h,k,l) using the model atomic (x, z) coordinates (see Table 1) do not match the experimental results. In particular, conformer (iii) would be associated with a very large (0, 1) peak, contrary to observation. Conformer (i) gives a good match to the observed intensities, in particular after the final section of the chain was rotated around the C8—C9 bond by 7.5° from the all trans conformation. The (0, 1) reflection is not expected to be detectable because of higher background intensity at low 2θ values. The 8:1 intensity ratio of the two observed peaks indicates a value of $U = 0.25 \AA^2$ for the average isotropic thermal parameter (for all atoms). This temperature factor seems reasonable considering that the average isotropic thermal parameter is 0.14 $\AA^2$ for crystalline deoxyxysophosphatidylcholine monohydrate. The reflectivity data (Fig. 4a) was analysed by fitting to it the calculated reflectivity of a simple model of the monoclinic monoclinic cell (Fig. 4b). The resulting layer thickness of 26.6 ± 1.0 Å is shown in Fig. 4b and compares well with the layer thickness of 27.2 ± 0.2 Å provided by X-ray powder diffraction data of crystalline palmitoyl-(R)-lysine (measured by P. Speik of Rigaku Co.). This, in turn, matches the layer thickness calculated for the model molecule (27.4 Å), as indicated in Fig. 3B. Note that the layer thicknesses quoted here include van der Waals radii totalling 2.6 Å and are not simply the distance between extremal non-hydrogen atom centres. The calculated model density of the monolayer is then 0.96 Mg m$^{-3}$ compared with the measured density of crystalline palmitoyl-(R)-lysine of 1.03 Mg m$^{-3}$. If there were three-dimensional crystallites at the air-water interface then they would be platelets lying with the (010) face parallel to water. One would then detect the extremely intense (020) reflection ($d = 27.2 \AA$) at $\theta = 10.6\,$ in the reactivity curve. This was never observed. Thus the monolayer diffraction peaks observed must arise from two-dimensional structure. The diffraction results indicate that the packing arrangement of the amino acid head groups in the monolayer is very close to that found in α-glycerine and several hydrophobic α-amino acids. This explains the fact that the monolayer at the air-water interface induces epitaxial nucleation of these amino acids in solution. The ability to determine the size and structure of small domains will perhaps enable determination of the smallest domain size of the monolayer required to induce crystallization as well as the structure and size of the smallest nucleating crystal. Eventually we hope to monitor the process of nucleation of α-glycine onto the monolayer by real-time experiments involving the reflectivity and in-plane diffraction measurements. The possibility of inducing large monolayer domains (perhaps 4–5 mm$^{-2}$) would allow for a less ambiguous ‘single crystal’ structure determination of the α-amino surfactant. It would also permit the direct assignment of its absolute configuration by simply noting the absolute angular sequence of the diffraction peaks, as was pointed out previously.

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Short-term selection for recombination among mutually antagonistic species

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The recombination of genes is clearly disadvantageous in a uniform and predictable environment where a single multilocus genotype is optimal. But heterogeneity or unpredictability do not necessarily imply a short-term advantage for recombination, which will be created only if the correlation between adaptively important features of the environment frequently changes sign. Another way of expressing this conclusion is to say that genes causing non-zero rates of recombination will tend to spread only if selection often favours a change in the sign of linkage (gametic phase) disequilibrium. Because it is difficult to imagine that the physical environment often behaves in this fashion, recent theoretical work on the maintenance of sex, recombination, and outcrossing has speculated that sexual interactions may be important 5–8. May and Anderson analysed a two-locus haploid model of the coevolution of host and parasite, similar to that considered here, and showed that the mean fitness of a population with recombination is typically higher than that of a population without, although they did not explicitly consider changes in the frequency of genes affecting recombination. Hutton and Lawand Bell8 suggested that the crucial feature of antagonistic interactions between species is the effect on the current fitness of a genotype of its frequency in previous generations; such time-lagged frequency-dependent selection tends to destabilize both genotype frequencies and linkage disequilibrium, whose oscillation has been shown to fuel the spread of high-recombination alleles in explicit genetic models. In this paper, we shall show how the mutual antagonism of two species can lead to a cyclical game in which high-recombination alleles can have a large short-term selective advantage in a fully defined genetic model.

Because the parasite-host interaction is often highly specific and has major effects on fitness, we shall refer to the two antagonists as ‘host’ and ‘parasite’, although in principle our
model applies equally well to competitors or to predators and prey. Both parasite and host are sexual haplonts with a single chromosome bearing three loci arranged in the order R−A−B. The A and B loci determine viability or fecundity through the host–parasite interaction, whereas the only effect of alleles at the R locus is to alter the probability of crossing-over, with a dominant allele R* causing free recombination between the three loci and a recessive R− completely suppressing recombination. The effects of changing these assumptions about the R locus are described below.

The fitness loci bear the pairs of alleles A, a and B, b, which determine the response of parasite to host and vice versa. This interaction can be modelled in two ways, depending on the properties of the repulsion genotypes Ab and aB. The first is to assume that resistance and virulence depend on the sum of effects across loci, with the alleles contributing larger or smaller effects to a total score. The crucial feature of this 'quantitative' model is that Ab and aB have identical properties. The second possibility is that genes at one locus in either partner are specifically antagonized by genes at a corresponding locus in its antagonist, leading to a 'gene-for-gene' mode of interaction.

The crucial feature of the gene-for-gene model is that Ab and aB have opposite properties. The matrices defining the response of the antagonists to one another in both models are shown in Fig. 1. To calculate overall fitness in either case, we assume that a host is infected by only one type of parasite, with probability proportional to the frequency of that type in the parasite population, and that the overall fitness of a given type of host is equal to the sum of its responses to all the parasite types, weighted by their frequencies. The fitness of parasite genotypes is calculated in the same way. We shall show results for both quantitative and gene-for-gene models in which gene effects are additive, using the parameter values given in Fig. 1.

These assumptions have been investigated by computer simulation, starting with a low frequency of the R* allele (10^-3) in both species, with the frequencies of the fitness alleles close to 0.5. Initial gamete frequencies had a small random departure from linkage equilibrium: replicate runs showed that the results are not altered qualitatively by this variation in initial conditions.

Fig. 1 The response of host and parasite types when challenged by antagonists. The two upper tables define a quantitative model in which A, B have unit genotypic value and a, b zero, with response depending on the absolute difference between the summed genotypic values of the two antagonists; consequently, Ab and aB have the same (unit) phenotype. The two lower tables define a 'gene for gene' model in which each gene in one species is specifically antagonized by a gene in the other; as a result Ab and aB have opposite phenotypes. Note that gene effects are additive in both models, which have been set up so as to give a twofold range in response; so long as the additive property is preserved, the direction of selection on the R* gene does not depend on the particular numerical values used.

Fig. 2 Selection for recombination in a quantitative model. These diagrams illustrate changes in the 'parasite' population over 100 generations. The bottom diagram shows the oscillation of mean phenotype, with the changing genotype frequencies given above. Note that Ab and aB are both always abundant, with selection alternately favouring ab and Ab. The next diagram (second from top) shows how this flux of genotypes results in an oscillation of the correlation between loci (expressed as the correlation between genotypic values, to avoid the dependence on gene frequency of the coefficient of linkage disequilibrium). Finally, the top diagram shows the correlated spread of the R* gene, from its initial frequency of 10^-5 to a final frequency of >0.25. The spread of R* is much more regular and more rapid than in the gene-for-gene model.

Simulation of a quantitative model is shown in Fig. 2. In this model, the performance of a given parasite infecting a given host type is determined by the absolute value of the difference between their phenotypes, with ab having a phenotype of 0, aB and Ab of 1, and Ab and 2. Its performance is greatest when infecting a host with the same phenotype. The performance of a host type is likewise determined by the absolute difference between its phenotype and that of the parasite type with which it is interacting, but host susceptibility is least when this difference is greatest. These assumptions satisfy the conditions for a cyclical game^10, and create a divergent oscillation of mean phenotype in both host and parasite. The R* allele always spreads in the parasite and is lost from the host (we emphasize that 'host' and 'parasite' refer, respectively, to the species that is fittest when most different from its antagonist, and to the species that is fittest when most similar). The response matrix of the pathogen implies that selection is generally stabilizing, so that most of the time there is an excess of Ab and aB individuals, whose phenotype is intermediate. It is therefore
often the case that the population consists mainly of a more or less equal mixture of \( ab \) and \( Aa \), while selection is favouring a phenotype of zero (or 2) and thus \( ab \) (or \( AB \)). Selection at these times favours a change in the sign of the linkage disequilibrium, and the \( R^+ \) allele increases in frequency, essentially because the progeny of \( R^+ \) parents are closer to linkage equilibrium than the majority of the population. In the host population, selection alternately favours the two extreme genotypes \( AB \) and \( AB \). The population comes to consist almost entirely of these two genotypes. There is no selection for a change in the sign of the linkage disequilibrium, and the frequency of the \( R^+ \) allele declines to zero. These conclusions, that \( R^+ \) decreases in the host and increases in the parasite, are insensitive to the intensity of selection.

The results of the gene-for-gene simulation were highly irregular. If only a single fitness locus is segregating, the effect of the evolutionary lag in the response of one species to another is to cause a divergent oscillation of gene frequency. When both loci are segregating simultaneously, selection at one locus interferes with selection at the other, to create irregular fluctuations in gene frequency. Both populations show rapid shifts from being almost fixed for one genotype to being almost fixed for another, with the sequence of genotypes not obeying any regular pattern. These changes are accompanied by changes in the frequency of the \( R^+ \) alleles. The initial trend is upwards in both host and parasite populations. (The reason for this increase is that from time to time either population may include both \( AB \) and \( AB \) chromosomes while selection is favouring \( AB \) (or \( AB \)). The \( R^+ \) gene then spreads by hitching a ride on the favoured coupling chromosome which it creates by recombination between \( AB \) and \( AB \)). In replicate runs with slightly varying initial conditions, the \( R^+ \) allele increased in both species from an initial frequency of \( 10^{-2} \), but at a very variable rate. After about 2,000 generations, a value of approximately \( 250 \times 10^{-5} \) was reached, and this was maintained in all replicates, with minor fluctuations but with no general trend, for a further 8,000 generations.

In the quantitative model, then, the high recombination allele, \( R^+ \), increases in frequency in one species, the parasitoid, in both decreases in the other, the 'host'. An explanation is that in the parasite there is stabilising selection for a fluctuating optimum, whereas in the host selection is disruptive. In the gene-for-gene model, \( R^+ \) alleles spread in both species, although the increase is slow and irregular. These conclusions were based on simulations in which the initial frequency of the \( R^+ \) alleles was low (\( 10^{-10} \)), and in which there was no recombination in zygotes homozygous for the \( R^+ \) alleles. The conclusions of the quantitative model continue to hold if the initial frequency of \( R^+ \) is 0.6 in both species, and if recombination in the \( R^+ \) homozygote was 0.05 between \( R \) and \( A \), and between \( A \) and \( B \). However, if either of these modifications are introduced into the gene-for-gene model, the general tendency for the \( R^+ \) alleles to increase in frequency disappears.

These models confirm that negative species interactions may be central to the evolution of phenomena such as sexuality, recombination and outcrossing, which ensure that a previously successful strategy is systematically abandoned. Most of the comparative data are consistent with this theory\(^5\), in showing that sexual reproduction is most likely to be lost in environments with relatively few species.

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Comparative evidence supports the Hamilton and Zuk hypothesis on parasites and sexual selection

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Darwin proposed that secondary sexual characters, such as the long tails and bright plumage of many birds, evolved because females use them as cues in male choice. The question of why females should prefer males with such apparently deleterious characters is currently the subject of vigorous debate\(^2,7\). Hamilton and Zuk\(^9\) suggest that females use secondary sexual characters to assess a male's ability to resist parasites. A prediction of this hypothesis is that male brightness should correlate positively with parasite load across species, and the only evidence advanced in support of the model is Hamilton and Zuk's\(^7\) finding that such a correlation exists across North American passerines. But interspecific correlations of this sort can result from phylogenetic associations through common descent or from independent associations with some confounding variable, such as an aspect of behaviour or ecology\(^10-13\). Here, I use data on European passerines and an enlarged data set on North American passerines to demonstrate positive relationships between male brightness and parasite prevalence which remain when the effects of taxonomic, behavioural and ecological variables are removed.

Hamilton and Zuk\(^7\) have proposed that females use colour and other secondary sexual characters to assess a male's ability to resist parasites (defined here to include parasitic viruses, bacteria, protozoa and helminths): males which are more resistant to parasites are assumed to be brighter (or have longer tails) and, if resistance is heritable, a female will increase the viability of her offspring by mating with brighter males. Thus, in species which are particularly susceptible to parasite invasion (and therefore in which variation in parasite resistance is a major heritable component of variation in fitness), sexual selection should favour characters which allow females to judge a male's present and past parasite load. Using parasite prevalence as a measure of a species' susceptibility to infection, the model therefore predicts that, across species, the extent to which such characters are expressed should correlate positively with parasite prevalence. In a preliminary analysis, Hamilton and Zuk found a positive association between brightness and the prevalence of avian haematozoa across 109 species of North American passerines. But there were two major problems with their analysis. First, the correlation could have been due to groups of related species sharing the same traits, not because of convergent evolution, but because of their shared ancestry\(^17\). Second, the positive association between brightness and parasites may exist only because of other variables which are independently associated with both parasite prevalence and brightness\(^12-14\). Here, I use large data sets on the prevalence of avian haematozoa in both North American and European passerines to test the Hamilton and Zuk model after the effects of taxonomy and other potentially confounding variables have been removed.

The colour of each sex of each passerine species during breeding was scored on a six point scale of brightness, with the brightest birds given the highest scores. I used Hamilton and Zuk's\(^9\) brightness scores for the North American species and, for the European birds, brightness ratings used by Baker and Parker\(^15\) in their analysis of bird coloration. Baker and Parker's rankings were determined before the sexual selection and parasite hypothesis had been proposed. They scored seven regions of a bird's body for colour and I averaged these to give a brightness ranking for each species and sex. Data on parasite infestations were taken from surveys of the avian haematozoa.