magnetization indicative of magnetization in strong fields are about 3.9–3.6 gigayears (Gyr) old. The fields are smaller than, but of the same order of magnitude as, the geomagnetic field. With one possible exception, older and younger samples were probably magnetized in fields at least an order of magnitude smaller. Samples magnetized in strong fields include mare basalts probably carrying a primary thermoremanent magnetization acquired during the initial cooling of large masses of rock, and impact melt rocks from the highlands. The most strongly magnetic rocks are the breccias (shock-welded lunar soil and rock) that contain far more iron than the crystalline rocks. This is consistent with Hood's model. But the samples also suggest that Hood's model is not complete, because mare basalts that are not antipodal to young basins are also magnetized.

The surface magnetometer data⁵ and the orbital data from the fluxgate^{6,7} and back-scattered electron experiments⁸ reveal that the principal magnetic anomalies are in the highlands. In contrast, the lunar mares are generally magnetically subdued, with younger ones having weaker anomalies than the older ones.

Craters do not have particular magnetic expression. The orbital data also provide the key observation that the main crustal anomalies are roughly antipodal to four relatively young, large impact basins: Imbrium, Orientale, Serenitatis and Crisium. It is interesting that the ages of these basins (3.9–3.6 Gyr) are the same as those of the various rock samples that were probably magnetized in strong fields. It would have been a nice economy of theory had Hood's model explained all aspects of lunar magnetism, but it leaves some of them unresolved, such as the magnetization of the mare basins. □

1. Hood, L.L. *Geophys. Res. Lett.* **14**, 844–847 (1987).
2. Lin, R.P., El-Baz, F., Hood, L.L., Runcorn, S.K. & Schultz, P. *Lunar planet. Sci.* **11**, 626–627 (1980).
3. Srnka, L.J. *Proc. 8th Lunar Sci. Conf.* 782–795 (1977).
4. Cisowski, S.M., Dunn, J.R., Fuller, M., Rose, M.F. & Wasilewski, P. *Proc. 5th Lunar Sci. Conf.* 2841–2858 (1974).
5. Dyal, P., Parkin, C.W. & Sonett, C.P. *Apollo 12. Preliminary Sci. Rep. NASA Spec. Publ.* **235**, 55–73 (1970).
6. Coleman, P.J., Lichtenstein, B.R., Russell, C.T., Sharp, L.R. & Schubert, G. *Proc. 3rd Lunar Sci. Conf.* 2271–2286 (1972).
7. Russell, P.J., Coleman, P.J., Soderblom, L.A., Stuart-Alexander, D.E. & Wilhelm, D.E. *Proc. 8th Lunar Sci. Conf.* 1171–1185 (1977).
8. Anderson, K.A., Lin, R.P., McGuire, R.E. & McCoy, J.E. *Space Sci. Instr.* **1**, 439–444 (1974).

Mike Fuller is at the Department of Geological Sciences, University of California, Santa Barbara, California 93106, USA.

Evolutionary biology

Winning against history?

Paul H. Harvey and H.C.J. Godfray

In the opening address at a recent meeting*, A.J. Cain (Liverpool University) declared that "nature never evolved to be researched on, while humans never evolved to do research". If he is right, the ensuing talks demonstrated that evolutionary history has had little influence on current progress. In particular, we are no longer short of ingenious but testable explanations for the short-term evolutionary advantages of sex and genetic recombination.

Why is genetic recombination so widespread in nature? The 'red queen' explanation depends on continuously coevolving biotic interactions between competitors, pathogens and hosts or predators and prey. In support of this theory, G. Bell (McGill University) has demonstrated for the first time that cross-species comparisons within various taxa, including *Carex* sedges, seed plants, Orthopteran insects and mammals, reveal a positive relationship between one measure of chiasma frequency and the richness and intensity of negative biotic interactions such as parasitism, herbivory and predation. Such comparative tests do not exclude the possibility that other con-

found factors produce the relationship, but it is more difficult to conceive of these factors when the same relationships are demonstrated in diverse taxa.

Apparently allied to recombination, sex itself has always been a problem for evolutionary biologists. Two novel treatments of the topic were presented at the meeting. B. Levin (Amherst University) discussed the occurrence of sex and recombination in bacteria. Sex in this group is not coupled with reproduction and, with this point in mind, Levin asked how transformation, plasmid-mediated recombination and phage-mediated gene transfer evolved. He concluded that group-selection explanations are particularly appealing for the evolution of transformation in colonial bacteria. After excluding explanations involving parasitic DNA and individual selection, he argued that genetic recombination could have evolved coincidentally during phage- and plasmid-mediated gene transfer, possibly as a by-product of the need for DNA repair. In contrast to the situation in bacteria, sex in eukaryotes is coupled with reproduction, causing Levin to be sceptical about generalizing his arguments. This may be one of the few cases where what is true for *Escherichia coli* is not true for elephants. □

Where Levin's treatment divorces sex from reproduction, a new theory for the evolution of sex in eukaryotes divorces sex from recombination. A. Grafen (Oxford University) suggested that, if centrosomes replicate with error, an offspring might test whether the maternal or paternal centrosome is more efficient at microtubule initiation. The best centrosome could be chosen, resulting in non-mendelian inheritance. The ensuing best-of-two advantage could almost overcome the famous twofold cost of sex. Grafen gave clear criteria for testing his theory; the relevant information should not be long in coming.

When sexual reproduction has evolved, sex must be determined. Haplo-diploid sex determination is of particular interest because it is found in the hymenoptera, and has been implicated in the evolution of eusociality in this insect group. Under haplo-diploidy, unfertilized eggs develop into haploid males. An apparently functional equivalent occurs when males lose the paternal contribution to their genome during development. It has been thought that haplo-diploidy has the advantage over paternal genome loss because mothers can determine the sex of their offspring by deciding whether or not to fertilize their eggs (Bull, J.J. *Evolution of Sex-Determining Mechanisms* Cummings, Menlo Park, 1983). M. Sabelis (Leiden University) demonstrated that this theory cannot hold for phytoseiid mites, which have paternal genome loss, because he has shown experimentally that mothers can influence the sex ratio of their offspring.

From these considerations, two further questions arise. First, what is passed on to the egg which results in the eventual loss of the paternal genome? Sabelis and others suggest maternally transmitted enzymes or parasites. Second, why transfer the paternal genome at all? Sabelis speculates that the spare DNA could be used for repairing double-strand damage.

Despite the interest in sex and recombination, R.C. Lewontin (Harvard University) heralded the identification of DNA sequences as evolutionary biology's New Jerusalem. It is here, he argued, that the age-old controversy about the relative importance of identity by descent (evolutionary history) and identity by kind (selection) will be settled. But it was also with DNA sequences that Gabor Vida (Budapest University) warned British participants that their days on the international stage seem to be numbered. UGC, he pointed out, is just one mutational step from the stop codon. □

Paul H. Harvey is in the Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK, and H.C.J. Godfray is in the Department of Pure and Applied Biology, Imperial College, Silwood Park, Ascot, Berkshire SL5 7PY, UK.

*Founding Congress of the European Society for Evolutionary Biology organized by S.C. Stearns and A.J. van Noordwijk. Basel, Switzerland, 26–30 August 1987.