**Table 1. The major differences between insect pests of plants and animals**

| Insect pests of plants | Insect pests of animals |
|---|---|
| Most damage is done directly | Although some damage is done directly (e.g. myiasis) most is caused by spreading disease |
| Vector species are almost exclusively limited to vectors of viruses | Insects are vectors of a wide range of animal pathogens including viruses, bacteria, protozoa and helminths |
| Almost exclusively controlled with insecticides | Insecticide control is supplemented with vaccines and drugs |
| Pheromones have been used in control programmes for many years | Pheromones have only recently been introduced into control programmes |
| Repellents and antifeedants are in development | Repellents and antifeedants are already widely used |
| Transgenic hosts are widely used (e.g. Bt crops) | Transgenic hosts have not been developed |
| Transgenic vectors are not being developed | Transgenic vectors are in development |

(Frank Collins, University of Notre Dame, Indiana, USA). An analogy can be drawn with the explosion of new information that became available following the development of gene transfer technology in *Drosophila*. This was demonstrated by Julian Dow (University of Glasgow, UK) who uses these techniques to investigate the integrative physiology of *Drosophila*.

### Bluetongue

Several talks concerned the recent outbreak of bluetongue in southern Europe. This viral disease of sheep is transmitted by *Culicoides* midges. By far the most important vector of bluetongue virus (BTV) in the Old World is *Culicoides imicola*. Although BTV has occasionally invaded parts of southern Europe, until 1998 it was unable to establish itself, and had been absent for >20 years. The current outbreak has now been running for four years and >250 000 sheep have died. Areas affected include Majorca, Sardinia, Sicily, Rhodes, Lesbos, the Greek mainland and Turkey; and the disease still appears to be spreading. Perhaps the most worrying aspect of this outbreak is that, according to Philip Mellor (Institute for Animal Health, Pirbright, UK), the virus has been found in areas that appear to be free of *C. imicola*. This could mean that BTV has acquired a new vector. The most likely candidate is *Culicoides obsoletus*, which has a much wider distribution in Europe than *C. imicola*.

### Modelling

Emma Whitmann (Institute for Animal Health, Pirbright, UK) described how vector surveys have been combined with remote sensing of climate data to produce a model that predicts areas of Europe suitable for colonization by *C. imicola*. This empirical approach provides a powerful tool for producing risk maps, particularly when linked to process-based models. Steve Lindsay (University of Durham, UK) described the combined use of climate data and a mathematical model of the relationship between larval development and temperature for mapping the distribution of the principal vectors of malaria in Africa. This combined approach relies on accurate process-based models of insect abundance, and Cynthia Lord (University of Florida, USA) reviewed recent attempts to incorporate seasonality and behaviour into these models. On the plant side of things, Mike Jeger (Imperial College at Wye, Ashford, UK) described a variety of epidemiological models of disease dynamics and control interventions for insect-transmitted plant viruses. As process-based models continue to incorporate more realistic assumptions, predictions of insect distribution and abundance will continue to improve. This will be of considerable benefit to entomologists studying pests of both animals and plants.

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# So what if parasites vary?

Mark E. Viney and Andrew F. Read

**The British Society for Parasitology Autumn Symposium was held on 14 September 2001 at the Linnean Society of London, UK, only a few yards from the room in which Darwin and Wallace presented their joint papers on organic variation. Fittingly, the symposium – Parasite variation: immunological and ecological significance – considered the consequences of parasite variation.**

Like all animals – protozoan and helminth parasites vary. The molecular biology revolution has led, at least in some cases, to detailed descriptions of variation in parasite species and, in a subset of these cases, to detailed descriptions of the mechanism of the variation. However, the immunological and ecological consequences of all parasite variation are far from understood.

### Antigenic diversity in the Protozoa

Antigenic diversity can be generated by diverse alleles at a single locus, in which case it is a property of a population and this is called polymorphism. Diversity can also be generated by alleles at different loci in the same clonal lineage, and this is called antigenic variation. David Conway (London School of

 1471-4922/02/$ – see front matter  PII: S1471-4922(01)02194-8

Hygiene and Tropical Medicine, UK) asked why is it that polymorphic antigens are found on the surface of invasive stages whereas antigenic variants are found on host cell surfaces? Is polymorphism a precursor to variation controlled by multi-gene families? Unable to answer these questions, he went on to demonstrate how theoretical advances in evolutionary genetics make it possible to recognize regions of highly polymorphic antigen loci that are the target of immune selection [1]. This non-experimental approach raises the prospect that comparative genome data can detect epitopes that are, or have been, under immune selection.

Antigenic variation in protozoa is currently being scrutinized by molecular biologists. There was some disagreement about just how good the understanding of the mechanisms of control actually is, but all agreed that we understand little about the immunological or ecological consequences of antigenic variation. For both malaria (Chris Newbold, University of Oxford, UK) and trypanosomes (Mike Turner, University of Glasgow, UK), it is assumed that antigenic variation is favoured by natural selection because this enhances transmission, probably by prolonging infections. Multi-gene families are indeed unlikely to be maintained by natural selection if they contribute nothing to transmission, but there are remarkably few data on the fitness benefits of antigenic variation. Such data can only come from *in vivo* studies of parasites whose antigenic repertoires and rates of antigen switching have been experimentally altered. One study, involving two mutants, found that antigenically invariant *Plasmodium chabaudi* (rodent malaria parasite) is unable to form chronic infections [2]. However, in the rodent model, the chronicity of wild-type parasites contributes trivially to total gametocyte numbers and hence, presumably, relatively little to transmission.

Repertoires of *Plasmodium* variants are ~50 per clonal lineage. Why 50? How variable is repertoire size? How much overlap is there between the antigen repertoires of genetically distinct clonal lineages? If these antigens are under intense immune selection, why are they there at all? Across a wide range of taxa, the rates of switching are remarkably similar ($10^{-4}$–$10^{-2}$ per parasite per generation): why? Given such high switch rates, many variants must appear early in an infection. Why are they not killed? Are differences in rate of switching to particular variants sufficient to account for the sequential way in which antigens appear during the course of a trypanosome infection? Because antigenic phenotypes are, by definition, transient states, investigation of the population-level behaviour and the consequences of this behaviour are particularly challenging. If we had a better understanding of their genetic control we could perhaps, as has been done for malaria, begin to measure immune selection genetically and thereby infer epidemiological significance.

### Worms vary too

Reviews of examples of variation in filarial and intestinal nematode infections showed that when variation in patterns of infection or molecular variation in parasite molecules of immunological interest are specifically sought, then it is readily found (Rick Maizels, University of Edinburgh, UK; Derek Wakelin, University of Nottingham, UK), but it is also rarely followed up [3]. For example, data on agglutination patterns (analogous to the data that underpinned studies of antigenic diversity in protozoa) points to antigenic diversity in filarial worms [4]. Diversity of immunological significance even turns up in the laboratory: lines of *Trichuris muris* derived from the same ancestral laboratory stock in the 1960s have diverged into one line that is highly immunogenic and rapidly expelled from the host, and another line that generates chronic infections. Not only does this diversity capture much of the variation found across nematode species, it also makes possible experimental analysis of the genetics of immunomodulation. Variation between isolates of *Trichinella* in their infections in mice is probably the best known example of helminth variation. This variation between parasite isolates is only seen in some host (mouse) strains but not others. Thus, the environment used to observe parasite variation could determine the nature of observed variation.

### Variation in immunity and parasite countermeasures

Differing assumptions about the effect of the host immune response on an infectious organism can alter the predicted epidemiological pattern of infection within a population, which varies between stable, endemic infection in a population and unstable, periodic epidemics (Graham Medley, University of Warwick, UK). Other theoretical analyses challenge common assumptions of the behaviour of the host immune response, by emphasizing that selection acts on host immunity to enhance host fitness. This generates the inevitable conclusion that in some situations, host fitness is greatest when the host immune response does not act to remove or ameliorate an infection [5]. Such issues could, at least in part, explain why immunity to helminths is slow to develop, particularly when compared with the rapidity and effectiveness of immune responses to most micro-parasites.

The interactions between insect hosts and their parasitoids provide a valuable perspective on the evolution of resistance and virulence (Charles Godfray, Imperial College London, UK). Experiments which selected *Drosophila* for increased resistance to either of two species of parasitoids (*Asobara tabida* or *Leptopilina heterotoma*) showed that there was a very considerable response to this selection. This response had no apparent fitness-cost to the host when in a benign environment. Rather, the cost of increased resistance was seen only when food was restricted, apparently as a result of less-efficient larval feeding in the resistant lines. Intriguingly, the fitness costs of the countermeasures by the parasitoids to the increases in host resistance were also seen in terms of competitive ability. Trade offs between resistance and larval feeding could be a result of an embryonic trade off between directing resources to the development of larval feeding organs or to the haemopoietic tissues [6].

### Why so many questions?

A recurrent theme of the meeting was the difficulty of obtaining relevant experimental data about the ecological and immunological significance of parasite variation. Endoparasite variation is hard to work with, even where appropriate animal models exist. Many of the phenotypes are short-lived, and many depend on the precise

environment in which the parasites are present. Several laboratories have worked on a diversity of rodent hosts because these hosts can be easily obtained from suppliers, but almost all laboratories work with a single parasite strain. Part of this is surely habit, but it is difficult to escape the feeling that focusing on parasite variation is to open a can of worms. If we allow that host variation, parasite variation and the environment in which hosts and parasites interact are all important determinants of disease outcome and epidemiology, then we need vast numbers of experimental treatments to make progress. Nonetheless, ignoring complexities is not the way to understand them. Several questions that were raised at this meeting could yield to new approaches to molecular data. Many will also yield to less glamorous, basic parasitology.

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# *Neospora* 2001

David McAllister and Sophia Latham


**Infection with the protozoan parasite *Neospora caninum* is emerging as a major cause of reproductive loss in cattle worldwide. Recent advances in research with the ultimate goal of devising effective and sustainable control measures were discussed at *Neospora* 2001. *Neospora* 2001 was held, 13–15 September 2001, at the Moredun Research Institute, Edinburgh, UK. The international meeting covered many aspects of bovine neosporosis including diagnosis, epidemiology and immunology.**

Neosporosis, caused by the protozoan parasite *Neospora caninum*, is a worldwide problem and a major cause of foetal loss and stillbirths in cattle. In the UK, studies in dairy herds have estimated that neosporosis is responsible for 12.5% of bovine abortions [1], compared with 15–20% in The Netherlands [2] and 20–43% in California [3,4]. Neosporosis is a significant problem in Australasia characterized by a seroprevalence of 30–35% in dairy herds that have had an abortion epidemic. Concurrent infections with other animal pathogens, such as bovine viral diarrhoea virus, increases the risk of *Neospora*-associated abortion significantly (Michael Reichel, Novartis Animal Health, New South Wales, Australia).

There are currently no effective control measures for neosporosis, hence there is an urgent need for more research in order to gain a better understanding of the parasite biology, transmission routes, immune responses and drug efficacy.

## Genetic diversity

Jonathan Wastling (University of Glasgow, UK) gave an excellent overview on the molecular genetics of *Neospora caninum*, and the degree of genetic diversity among different isolates of the parasite. This could be an important consideration for understanding the relative importance of different transmission routes, host specificity and the basis of virulence. Host genetics, however, might also play a role in determining the outcome of an infection. This was highlighted by Chantal Rettigner (University of Liege, Liege, Belgium) whose research with two different strains of mice (CBA/CA and Swiss-White) showed that they were both resistant to *N. caninum* infection, and a Th1-like response was generated in both groups of mice with no visible pathology. However, Esther Collantes-Fernandez (University of Madrid, Spain) presented her results using inbred BALB/c mice infected with the same strain of *N. caninum*, and demonstrated the presence of histological lesions. Data from these combined studies indicated that the host genetic background could influence the outcome of infection.

Little is known on whether the degree of pathology is parasite-strain-dependent or host-dependent. Most laboratory strains of *N. caninum* cause acute infection in *in vivo* models but, during persistent infection, the parasite sequesters into immunoprivileged sites such as the brain. Current culturing techniques using cell monolayers do not replicate the *in vivo* conditions adequately. Andrew Hemphill (University of Bern, Switzerland) has developed an organotypic-slice culture system to study cerebral neosporosis in an environment that can be experimentally modulated,

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