Ecology of Infectious Diseases in Natural Populations

EDITED BY

B. T. Grenfell and A. P. Dobson

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ECOLOGY OF INFECTIOUS DISEASES

IN NATURAL POPULATIONS

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Dedicated to the memory of Anne Keymer

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Introduction

A.P. Dobson and B.T. Grenfell

1 Introduction

The epidemiology of infectious diseases is one of the great triumphs of applied ecology. In particular, the public health importance of parasites has lead to a large literature, exploring their impact on the population dynamics, population genetics and evolutionary biology of human populations. An important milestone was the Dahlem Conference on population biology of infectious diseases, held in 1981. The resulting book (Anderson and May 1982) lucidly summarised the contemporary state of parasite ecology and epidemiology. The meeting was also important in bringing together theoretical and empirical workers from a range of relevant disciplines. Their deliberations, in a series of group reports, set the scene for many developments in parasite ecology over the following decade.

Following the advent of HIV/AIDS, there has since been a particular flowering in the quantitative epidemiology of human infections (Anderson and May 1991). By contrast, work on diseases of naturally fluctuating animal and plant populations has had a lower profile. Although there are large bodies of published research on theoretical and empirical aspects of the ecology of infectious diseases in naturally fluctuating host populations, there has been no recent attempt to bring these together systematically. This is partly happenstance but, as we shall see, probably also arises from a lack of empirical knowledge about the details of many interactions. The Isaac Newton Institute programme on epidemic models, held during January–June 1993, provided the ideal venue for addressing this gap between theory and practice. This volume is based on a workshop which we convened during the second week of March 1993. We followed the Dahlem pattern, bringing together a collection of experts to provide overviews of the subject and produce group reports on important issues. This was a highly interdisciplinary group, ranging from biomathematicians to plant pathologists, veterinarians and wildlife managers. Their collective deliberations led to the synthesis which makes up the remaining chapters of this book.

Before summarising the structure and relationship of these contributions, we explore some broad philosophical issues.

2 What is R_0?? Who is Arnold?

The transfer of infection is fundamentally a contact process. The central quantity here is the speed of spread of infection through a host population under optimal conditions. This parameter is usually demoted by the symbol R_0, which can be defined in a variety of ways, depending on the nature of the host-parasite interaction (Heesterbeek and Roberts, Roberts *et al.* this volume). As students of theology will know, the naming of such a mystical quantity is always likely to be fraught with difficulty. Various names have been proposed for R_0: the basic reproduction (or reproductive) rate (or number, or ratio). We would not have the temerity to enter this debate, although a recent mistyping of a piece of dictation by one of us (APD) resulted in a new name for R_0 – *Arnold*. Though we hope this usage will spread, we have generally called R_0 the basic reproductive ratio in this volume.

3 How the book is organized

This is not a guide to the aetiology and pathology of infectious diseases. Instead, it provides a synthesis of current knowledge about the quantitative ecology and epidemiology of infections in naturally-fluctuating animal and plant host population. The word 'naturally' is relative here, since few populations have escaped direct or indirect human intervention. Our definition is therefore based on populations whose numbers are relatively unconstrained by humans, so that the impact of parasitism on 'natural' host dynamics (and of hosts on parasite dynamics) can be assessed. The main population dynamic question is obviously whether parasites tend to 'regulate' host abundance (i.e., reduce the tendency for unconstrained growth or fluctuation in numbers; see Anderson and May (1978) Holmes (1982)) or 'destabilise' it, contributing to variations in host population density (May and Anderson 1978). Which effect predominates in a particular interaction depends crucially on the nature of density dependent (nonlinear) processes in the host-parasite interaction (Roberts *et al.* this volume).

The background chapters present reviews of the current state of theoretical and empirical knowledge about the dynamics of infectious diseases in natural populations. During the meeting, we also convened working groups on four specialist areas: the population biology of microparasites and macroparasites, spatial dynamics of parasitism and genetic and evolutionary issues. Their deliberations are summarized by the four groups reports presented between the background papers below. The volume concludes with a glossary, which gives brief definitions of widely used technical terms, from both theoretical and empirical branches of the subject.

In terms of broad taxonomic and functional classification, we adopt the

standard division of pathogens into *microparasites* (viruses, fungi, bacteria, protozoa) and *macroparasites* (helminths and arthropods) (May and Anderson 1979, Anderson and May 1979). The biological and theoretical bases of this division are discussed extensively in the group reports on microparasites and macroparasites (Dye *et al.* this volume, Smith *et al.* this volume).

The group reports and background chapters are divided between three sections. We use the micro/macroparasite division in the first section, titled *Broad patterns and Processes*, which considers both observed patterns and techniques for modelling them. As these papers tend to focus on pathogens of vertebrate hosts, a number of important groups of interactions are not covered in detail in this sections (plant pathogens, vector borne-infections and insect micropathogens) We therefore devote the second section, *Pathogens, Insects and Plants*, to reviews of interactions between pathogens and non-vertebrate hosts. The main aim of this section is to draw out the special features of these interactions.

Much of the progress in parasite population biology in the last 15 years has been in analyzing the impact of various *heterogeneities* in the host or parasite population (Anderson and May 1984,1985, Nold 1980, Anderson and Gordon 1982, Burdon *et al.* 1989, Kallen *et al.* 1985, Dwyer 1991, Pacala *et al.* 1990, Barlow 1991). A variety of distinct, but not necessarily mutually exclusive, processes produce important heterogeneities in host parasite systems. We have classified them loosely under the following four headings: *immunological*, *spatial*, *genetic* and *ecological*. The final group of chapters focus on the effects these important heterogeneities have on host-parasite interactions in naturally fluctuating host populations.

4 The balance between theoretical and empirical research

A central implicit question for the meeting was: *what balance of new theory and empirical work do we need to advance the subject?* A major thrust of this book is that, currently, we particularly need to improve our empirical knowledge of interactions and our ability to manipulate them experimentally. New theoretical tools are also required – particularly in dissecting the dynamics of immunity (Grenfell *et al.* this volume), spatial infection processes (Bolker *et al.* this volume) and host-parasite population genetics (Read *et al.* this volume). However, these processes are often so complex that the models are best extended by reference to detailed empirical studies of particular systems (Gulland, Dobson and Hudson, Hudson and Dobson, all this volume). Constantly confronting new theoretical developments with empirical data allows the assumptions underlying the structure of new models to be examined from an empirical perspective. It also keeps theoreticians focused on real prob-

lems and encourages empiricists to have their results and biological insights clarified using the analytical perspective afforded by well-posed models.

We can divide the requirement for new empirical work into two broad areas. First, we need simply to know more about the diversity of host-parasite interactions – in particular, a greater empirical understanding of the impact of parasites on host-population dynamics is required if we are to resolve the endless 'compensatory versus additive' mortality debate (Holmes 1982, Gulland this volume). Such information is not won easily and depends crucially on a combination of long term detailed studies, controlled experiments, and, ideally, notification schemes for disease incidence. Unfortunately, there are only a limited number of National Centers which act as clearing houses and information centers for long-term data on infectious diseases in natural populations. The Center for Wildlife Diseases at Madison, Wisconsin provides an important model for this in the United States, but other countries – or groups of countries – need to examine the possibility of setting up similar centralized facilities. Only with this sort of information can our comparatively strong theoretical understanding of host-parasite population dynamics be tested and extended, for example, to provide more accurate predictions of the epidemiological impact of anthropogenic effects such as global-climate change.

Second, we require new technologies to dissect the dynamics of individual host parasite interactions. This is particularly important in terms of host immunity and host-parasite population genetics. For example, if sufficient variability can be discerned in molecular genetic studies of helminth parasite transmission stages, such as eggs, this could provide a method for non-destructively monitoring the dynamics of adult norm burden. Such developments would revolutionise epidemiological studies of many parasite groups.

5 A brief overview

This section synthesises the wealth of information and opinion generated in the background papers and group reports, in order to draw out common themes.

5.1 Microparasites

The empirical review of microparasite incidence concentrates on vertebrate examples (Dobson and Hudson this volume), whilst the chapter by Gulland surveys the impact and potentially regulatory role of pathogens in wild animal populations. The paper by Briggs *et al.* provides examples from studies of pathogens of insects, while Swinton and Anderson deal with plant pathogens. Heesterbeek and Roberts and Barlow provide respectively, an introduction

to mathematical models for microparasites and a 'field guide' to models that have been used in studies of infectious disease of wildlife. The microparasite group report (Dye *et al.* this volume) focused on the following major issues.

5.1.1 Persistence of infection in populations

Persistence is emerging as a problem in reconciling models for microparasites with observed patterns of empirical data. The group reports on microparasites and spatial processes and the background papers on observed patterns and impact all examine this problem from a variety of perspectives. Numerous recent studies emphasize the importance of spatial heterogeneity in perpetuating epidemic infections in host metapopulations (Bolker *et al.*, Dye *et al.* this volume). Though this insight is not new (Bartlett 1957), the development of individual-based models (and the computing technology necessary to implement them) has recently highlighted the importance of geographical and social space.

However, a careful balance is needed between emphasizing this particular heterogeneity and examining other biological phenomena which may be equally important, but less topical. For example, recrudescence of latent infections is probably very important in the persistence and re-emergence of herpesvirus infections (Grenfell and Smith 1990). Each of the discussions on this problem emphasizes the importance of sequentially adding ecological and epidemiological information to mathematical models. Similarly, we need to acknowledge the empirical fact that many microparasites persist in host species that live at low density, in social systems where contacts between individuals or social groups are minimal. In this case, we are likely to need individual-based models that more accurately reflect actual contact patterns, as determined by the host's social system.

We still need more experimental studies that address the importance of pathogens in regulating host populations and the role they play in determining the geographical range of species, both directly (by exclusion) and indirectly by apparent competition (Price *et al.* 1986,1988). In both these areas, the development of more powerful empirical tools that allow us to differentiate between infection and disease are needed (Gulland this volume). These will considerably strengthen our ability to effectively monitor endemic infections which may lead to disease outbreaks when a population is either stressed, or suddenly increases in density.

5.1.2 Conservation and disease control

The control of infectious diseases in natural population will increasingly become a problem as wildlife become concentrated into National Parks and reserves. The background papers aired the spectrum of opinion about the relative merits of two traditional forms of pathogen control: culling versus

vaccination (Heesterbeek and Roberts, Barlow this volume). Energetic discussion of the issue in the group sessions indicated that the 'best' approach indicated in published studies has usually been a function of model structure, economics, the availability of effective vaccines and public opinion. At present, culling is increasingly replaced by preventive vaccination for domestic animals, while culling continues to be used for wildlife. This asymmetry is changing, as more people emphasize the necessity of reducing human activities that have a detrimental impact on biodiversity. In this context, the widespread success of vaccination in the control of rabies in European wildlife is an excellent example of an ecologically sensitive campaign. In many cases, we need to take this exercise a stage further and examine the role that pathogen control can play in maintaining viable populations of many endangered species (Dobson and May 1986, May 1988, Thorne and Williams 1988, Scott 1988, Spalding and Forrester 1993). The strong consensus to emerge from these studies of pathogens and endangered species is that the small population size of many host species is likely to preclude them from maintaining species specific pathogens that are a major threat to their viability. Instead, the reduced levels of genetic diversity that characterize increasingly rare species may increase their susceptibility to epidemic outbreaks of pathogens acquired from more common species. To understand the epidemiology of these problems fully, we must turn to models for pathogens that infect a range of host species (Begon and Bowers this volume) and studies that examine interactions between pathogens and host genetic diversity (see Lively and Apanius, Read *et al.* this volume).

The properties of multi-species host-parasite models can be examined from two main perspectives: first, what happens when several species of parasite utilize a single host species and secondly, what happens when a single pathogen utilizes a range of hosts species (Holt and Pickering 1985, Hochberg and Holt 1990, Begon and Bowers this volume). A number of important questions remain to be addressed in this area. In particular, it is intriguing that models can be readily constructed that allow a single host population to support a large diversity of macroparasite species (provided each parasite species is sufficiently aggregated in its distribution) (Dobson and Roberts 1994, Roberts and Dobson 1995), while models for multiple microparasite strains usually require the addition of some form of spatial or other heterogeneity in the host population if more than one microparasite is not going to dominate and drive all others to extinction (Nowak and May 1994).

Further development of models for pathogens that infect more than one host species will allow us to examine other problems. In particular, we need to understand the role that 'natural' levels of biodiversity (number of species) in a region play in either buffering epidemic outbreaks, or providing a diversity of hosts species which mediate longer term pathogen persistence.

5.1.3 Microparasites and community structure

Such studies will also address the role that parasites play in food webs – a topic that is almost completely unexplored (Anderson and May 1986, Dobson and Hudson 1986, Dobson and Crawley 1994, Grenfell 1992). Nevertheless, everything we discuss in this book suggests that pathogens may have a bewildering array of potential effects on our understanding of food web structure. For example, counting the numbers of parasites in a food web will increase the numbers of species in an ecological community by a factor between 2 and 5, obviously, this will lead to increases in estimates of the number of species that each species interacts with. Ultimately, this may alter our traditional perspective of a food web as a pyramid of organisms with many producers on the bottom and a few consumers on the top, to a structure that more closely resembles a rhomboid, with each higher level of consumers being consumed by an increasing diversity of parasites. Moreover, there are a number of empirical examples where the introduction of pathogens into already complex communities have led to epidemics that drastically change the abundance of some species. Where these changes in density effect numerically dominant or 'keystone' species they can produce cascade effects that can generate major changes in the relative abundance of other species in the community and significant changes in ecosystem function (Dobson and Hudson 1986, Dobson and Crawley 1994).

5.1.4 The role of vectors

Dye and Williams (this volume) consider the conditions under which indirect transmission (via vectors or other intermediate hosts) will have 'special' dynamical effects, compared to direct transmission. They show that the degree of nonlinearity (density dependence) introduced by the vector, as well as the relative timescales of vector and definitive host components of the parasite life cycle, are crucial. They conclude that the vector component is so fast in its dynamics for microparasites that indirect transmission may not have a qualitative dynamical effect. A different tale may emerge for the more complex life cycles of macroparasites (Smith *et al.* this volume).

5.2 Macroparasites

Hudson and Dobson (this volume) introduce observed patterns of macroparasite infection, whilst the chapter by Gulland concentrates on parasite impact. Roberts, Smith and Grenfell (this volume) review models for host-macroparasite interactions and the paper by Grenfell, Dietz and Roberts considers immuno-epidemiological models in detail. The macroparasite working group (Smith *et al.* this volume) concentrated mainly on how current macroparasite models need to be refined to describe aggregation and other biological complexities. We review these, and other issues which arose, below.