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0521019443 - Pattern and Process in Host-Parasitoid Interactions

Bradford A. Hawkins

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How is the staggering biodiversity of the parasitoid insects maintained? This book explores patterns in host–parasitoid interactions, including parasitoid community richness, the importance of parasitoids as mortality factors and their impact on host densities as determined by the outcomes of parasitoid introductions for biological control.

It documents general patterns using data sets generated from the global literature and evaluates potential underlying biological, ecological and evolutionary mechanisms. A theme running throughout the book is the importance of host refuges as a major constraint on host–parasitoid interactions. Much can be learnt from the analysis of broad patterns; a few simple rules can go a long way in explaining the major components of these interactions.

This book will be an invaluable resource for researchers interested in community ecology, population biology, entomology and biological control.

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Preface

In January 1986 I arrived at the University of York in northern England as an NSF-sponsored post-doctoral fellow to conduct a field experiment involving insects on bracken. One day in February, while waiting to begin the real work in the summer, John Lawton stopped me in the hallway and asked me if I thought it would be possible to use the parasitoid–host literature to examine patterns in the number of parasitoid species that individual herbivore species support, in much the same way as he and others had analyzed herbivore species richness patterns on plants. My response was immediate and self-assured: No! Everyone knows that the records are too fragmented and the data too piecemeal and biased to have any chance of finding any meaningful results. But after returning to my office and thinking it over for a while, I decided that it could not hurt to try, particularly since the Yorkshire winter is ideal for this type of research. The following day I made the first of what was to become many trips to the library to search the literature.

Looking back, I suspect that my response to John's question may have been overly pessimistic. The initial analysis of the parasitoids of British insects revealed a number of potentially interesting patterns, but it raised far more questions than it answered. A follow-up analysis of North American patterns of parasitoid diversity produced results surprisingly similar to those found in Britain, but, again, there were nagging doubts about what they really meant. In a continuing effort to test and expand the results, the research snowballed. Now, seven years later, with my reputation as a data miner firmly established, and my papers on this topic beginning to clutter-up the literature, the time seems appropriate to publish in a single work the sum of the interrelated projects that have used this comparative approach and to synthesize the results. This is what this monograph does.

As with any such project of this scale, it is important to acknowledge my friends and colleagues who have contributed data and ideas that have shaped

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Preface

the final outcome. First, I thank those with whom I have collaborated at various stages in the research: Richard Askew, Raymond Gagné, Paul Gross, Michael Hochberg, John Lawton and Mark Shaw. I have learned a great deal from them. Correspondence, discussion and occasionally heated debate with a number of other workers have also been stimulating and invaluable; particularly helpful have been Ian Gauld, Charles Godfray, Nick Mills, John Noyes, Peter Price, William Sheehan, Chris Thomas and Jeff Waage. I also thank my wife, Ada, who spent untold hours in front of photocopy machines generating grist for the analytical mill. I am especially grateful to the staff of the National Lending Library, Boston Spa (UK) for their patience, and to the CAB International Institute of Biological Control for providing a copy of their biological control data base. Phases of this research were supported financially by the National Science Foundation, the Leverhulme Foundation and the NERC Centre for Population Biology. Finally, I thank Paul Gross, John Lawton, Gabor Lövei, Nick Mills, Peter Price, Mark Shaw, William Sheehan and Teja Tschamntke for their trenchant critiques of all or parts of this manuscript. All errors of fact or interpretation that remain are entirely their fault!

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