CONTENTS

List of Contributors xiii
Preface xv

1 THE UNIQUENESS OF BATS
Paul A. Racey 1
1.1 Introduction 1
1.2 Flight 2
1.3 Echolocation 4
1.4 Communication 5
1.5 Foraging, Diet, and Ecosystem Services 5
1.6 Heterothermy, Daily Torpor, and Hibernation 7
1.7 Reproduction 8
1.8 Life History Strategies 9
1.9 Roosting Ecology 9
1.9.1 Caves 9
1.9.2 Trees 10
1.9.3 Houses 10
1.9.4 Foliage 10
1.9.5 Roosts of other species 11
1.9.6 Roost fidelity 11
1.10 Migration 11
1.11 Climate Change 12
1.12 Disease-Related Mortality 13
1.13 Conservation and Disease Surveillance 14
Acknowledgment 14
References 15

2 VIRUSES IN BATS: A HISTORIC REVIEW
Charles H. Calisher 23
2.1 Introduction 23
2.2 Knowledge of Bats, Background 25
2.3 Early, Somewhat Random Bat Virus Discoveries 25
2.4 More Recent Bat Virus Discoveries 27
2.4.1 Marburg and Ebola viruses (order Mononegavirales, family Filoviridae, genera Ebolavirus and Marburgvirus, respectively) 27
2.4.2 Hendra and Nipah viruses (order Mononegavirales, family Paramyxoviridae, genus Henipavirus), and other paramyxoviruses 28
2.4.3 Coronaviruses (order Nidovirales, family Coronaviridae, genus Coronavirus) 30
2.4.4 Other viruses detected in bats 31
2.5 Summary 36
Acknowledgments 41
References 41

3 BAT LYSSAVIRUSES 47
Ivan V. Kuzmin and Charles E. Rupprecht
3.1 Lyssavirus Genus 47
3.2 Pathobiology 54
3.3 Surveillance and Diagnosis 57
3.4 General Biological Considerations on Bat Rabies 59
3.5 Global Distribution of Bat Lyssaviruses 62
  3.5.1 The Americas 62
  3.5.2 Africa 69
  3.5.3 Eurasia 72
  3.5.4 Australia 78
3.6 Public Health and Veterinary Significance of Bat Rabies 80
3.7 Conclusions 84
References 85

4 BAT PARAMYXOVIRUSES 99
Danielle E. Anderson and Glenn A. Marsh
4.1 Introduction to the Paramyxoviridae 99
  4.1.1 Virus structure 100
  4.1.2 Genome organization 101
  4.1.3 Paramyxovirus replication 103
4.2 Bats as a Major Source of New Paramyxoviruses 105
  4.2.1 Sampling methods 105
  4.2.2 Methodologies utilized in the detection and characterization of paramyxoviruses 106
4.3 Known Bat Paramyxoviruses 109
  4.3.1 Hendra virus (HeV) 109
  4.3.2 Nipah virus (NiV) 111
  4.3.3 Menangle virus (MenPV) 112
  4.3.4 Cedar virus (CedPV) 113
  4.3.5 Mapuera virus (MprPV) 114
  4.3.6 Porcine rubulavirus (PorPV) 114
  4.3.7 Tioman virus (TioPV) 114
4.3.8 Achimota viruses (AchPV) 114
4.3.9 Tukoko viruses (ThkPV) 115
4.3.10 Sosuga virus (SosPV) 115
4.3.11 Other paramyxoviruses 115

4.4 Risks, Control, and Prevention 116
4.4.1 Risk of spillover 116
4.4.2 Reservoir host management 117
4.4.3 Vaccines 117

4.5 Conclusions 118
Acknowledgments 118
References 118

5 BAT CORONAVIRUSES 127
Xing-Yi Ge, Ben Hu, and Zheng-Li Shi

5.1 Introduction 127
5.2 Human Diseases Related to Bat Coronaviruses 134
5.2.1 SARS 134
5.2.2 Middle East respiratory syndrome (MERS) 140
5.3 Genetic Diversity of Bat Coronaviruses 142
5.3.1 Alphacoronaviruses 142
5.3.2 Betacoronaviruses 145
5.3.3 Gammacoronaviruses 146
5.3.4 Classification of coronaviruses 146
5.4 Conclusions 147
Acknowledgments 148
References 148

6 BAT FILOVIRUSES 157
Gael Darren Maganga, Virginie Rougeron, and Eric Maurice Leroy

6.1 Introduction 157
6.2 Marburgvirus Outbreaks 158
6.3 Ebolavirus Outbreaks 159
6.3.1 Ebolavirus and Sudan ebolavirus 159
6.3.2 Tai Forest and Bundibugyo ebolaviruses 160
6.3.3 Reston ebolavirus 160
6.4 Filoviruses in Yinpterochiropteran Bats 160
6.4.1 Ebolaviruses 161
6.4.2 Marburgvirus 161
6.5 Filoviruses in Yangochiroptera Bats 163
6.5.1 Ebolaviruses 163
6.5.2 Marburgvirus 163
6.5.3 Cuevavirus 163
Contents

6.6 Ecological and Epidemiological Patterns in Bats
6.6.1 An extended natural geographic distribution
6.6.2 Bats as drivers of filoviruses emergence and spillover?
6.6.3 Uncertainty surrounding the identification of the Lloviu virus reservoir
6.7 Bat Filovirus Characterization
6.7.1 Filovirus isolation
6.7.2 Filovirus RNA detection
6.7.3 Filovirus antigen detection
6.7.4 Whole genome amplification
6.8 Conclusions
Acknowledgments
References

7 BATS AND REVERSE TRANSCRIBING RNA AND DNA VIRUSES
Gilda Tachedjian, Joshua A. Hayward, and Jie Cui

7.1 Introduction to Reverse Transcribing RNA and DNA Viruses
7.1.1 Retroviruses
7.1.2 Hepadnaviruses
7.2 Endogenous Retroviruses in Bats
7.2.1 Endogenous retroviruses: A transposable element subclass
7.2.2 Endogenous retroviruses originate from exogenous retroviruses
7.2.3 Endogenous retrovirus nomenclature
7.2.4 Role of transposable elements and endogenous retroviruses in disease and host evolution
7.2.5 Endogenous retroviruses as fossil records of ancient exogenous retroviruses
7.3 Gammaretroviruses in Bats of Different Suborders
7.3.1 Gammaretroviruses: host range and diseases
7.3.2 Discovery of gammaretroviruses in bats
7.4 Betaretroviruses in Bats of Different Suborders
7.4.1 Betaretroviruses: host range and diseases
7.4.2 Betaretroviruses in bat transcriptomes and genomes
7.4.3 Extensive diversity among bat betaretroviruses
7.5 Pathogenic Hepadnaviruses Related to HBV in Bats
7.6 Bat Metagenomics Studies
7.7 Bats as Potential Reservoirs for Retroviral and Hepadnaviral Zoonoses
7.8 Conclusions
Acknowledgments
References
8 BAT REOVIRUSES
Claudia Kohl and Andreas Kurth

8.1 Introduction
8.1.1 Background
8.1.2 Reovirus taxonomy and disease epidemiology
8.2 Orthoreoviruses of Bats and Humans
8.2.1 Nelson Bay orthoreovirus
8.2.2 Other bat-related orthoreoviruses
8.3 Bat Orbiviruses
8.4 Bat Rotaviruses
8.5 Zoonotic Potential of Bat Reoviruses
Acknowledgments
References

9 OTHER BAT-BORNE VIRUSES
Krista Queen, Mang Shi, Larry J. Anderson, and Suxiang Tong

9.1 Introduction
9.2 RNA Viruses
9.2.1 Influenza viruses
9.2.2 Alphaviruses
9.2.3 Bunyaviruses
9.2.4 Flaviviruses
9.2.5 Arenaviruses
9.2.6 Picornaviruses
9.2.7 Astroviruses
9.2.8 Caliciviruses
9.3 DNA Viruses
9.3.1 Adenoviruses
9.3.2 Herpesviruses
9.3.3 Poxviruses
9.3.4 Polyomaviruses
9.3.5 Parvoviruses
9.3.6 Papillomaviruses
9.4 Conclusions
References

10 ANTHROPOGENIC EPIDEMICS: THE ECOLOGY OF BAT-BORNE VIRUSES AND OUR ROLE IN THEIR EMERGENCE
Jonathan H. Epstein and Hume E. Field

10.1 Introduction
10.2 The Bat–Human and Bat–Livestock Interface:
The Importance of Disease Ecology
10.3 Approaches to Understanding the Ecology of Bat-Borne Viruses

10.3.1 Observational study design

10.3.2 Mathematical models

10.3.3 Outbreak response and long-term ecological study

10.4 Anthropogenic Activities Drive Zoonotic Disease Emergence from Bats

10.4.1 Agricultural expansion/intensification: Nipah virus

10.4.2 Urbanization: Hendra virus

10.4.3 Wildlife trade: SARS-CoV

10.4.4 Bushmeat hunting: Ebola virus

10.5 Outbreak Mitigation: Managing the Interface

10.6 Conclusions

Acknowledgments

References

11 ARE BATS REALLY “SPECIAL” AS VIRAL RESERVOIRS?
WHAT WE KNOW AND NEED TO KNOW

Kevin J. Olival, Cristin C. Weekley, and Peter Daszak

11.1 Introduction

11.2 What Factors May Make a Host Taxon “Special” as a Viral Reservoir?

11.3 Factors that May Confound Investigations of Whether or Not a Taxonomic Group is “Special”

11.3.1 Research bias towards certain hosts and pathogens

11.3.2 Lack of thorough disease ecology studies

11.3.3 The ability to measure immune responses and detect illness in hosts

11.4 Viral Diversity in Bats Compared to other Mammalian Hosts

11.4.1 Do bats harbor a disproportionate number of viruses?

11.4.2 Do bats harbor a disproportionate number of zoonoses?

11.4.3 Focused literature review of bat viral discovery efforts from the past 7 years

11.5 Life History Traits: Are Bats Unique?

11.6 Distribution and Diversity of Bat Viruses, and Ways to Target Future Discovery Efforts

11.7 Summary and Future Research

References

12 ANIMAL MODELS OF RECENTLY EMERGED BAT-BORNE VIRUSES

Jackie A. Pallister and Deborah J. Middleton

12.1 Introduction

12.2 SARS Coronavirus
12.2.1 Human disease 296
12.2.2 Small animal models 296
12.2.3 Nonhuman primates 298
12.2.4 Spillover hosts 298
12.2.5 Reservoir host 298

12.3 Filoviruses 299
12.3.1 Human disease 299
12.3.2 Small animal models 300
12.3.3 Nonhuman primates 300
12.3.4 Spillover hosts 301
12.3.5 Reservoir host 302

12.4 Paramyxoviruses 302
12.4.1 Human disease 302
12.4.2 Small animal models 303
12.4.3 Nonhuman primates 304
12.4.4 Spillover hosts 305
12.4.5 Reservoir host 305

12.5 Conclusions 306

References 306

13 BAT GENOMICS 315
James W. Wynne and Mary Tachedjian

13.1 Introduction 315

13.2 Genomics 316
13.2.1 The era of bat genomics 316
13.2.2 Phylogenomics 317
13.2.3 Immunity 317
13.2.4 Gene family expansion 319
13.2.5 Longevity 319
13.2.6 Hibernation 320
13.2.7 Echolocation and convergent evolution 320
13.2.8 Genomic adaptations associated with flight 321
13.2.9 Limitations of genome sequencing 321

13.3 Transcriptomics and MicroRNAs 322
13.3.1 Cataloging immune genes 322
13.3.2 Functional genomics of echolocation 323
13.3.3 MicroRNA discovery 323
13.3.4 Bat specific gene discovery through transcriptomics 323

13.4 Conclusions 324

References 324
14 BAT IMMUNOLOGY 327
Michelle L. Baker and Peng Zhou

14.1 Introduction 327
14.2 Immune Tissues and Cells 328
14.3 Innate Immunity 329
  14.3.1 Pattern recognition receptors (PRRs) 329
  14.3.2 Interferon (IFN) family members 330
  14.3.3 Production of IFNs by bat cells 331
  14.3.4 IFN receptors and downstream signaling molecules 333
  14.3.5 Interferon stimulated genes (ISGs) 334
  14.3.6 MicroRNAs 335

14.4 Adaptive Immunity 335
  14.4.1 Immunoglobulins 336
  14.4.2 Antibody mediated immune responses to experimental viral infections 336
  14.4.3 Maternally derived antibody protection 338
  14.4.4 T-cell-mediated immune responses 339
  14.4.5 The major histocompatibility complex (MHC) 340
  14.4.6 Cytokines 340

14.5 Conclusions 341

References 342

Species Index 349

Subject Index 361