1. Record Nr.	UNINA9910798280503321
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Titolo	The evolution and emergence of RNA viruses / / Edward C. Holmes
Pubbl/distr/stampa	Oxford, England : , : Oxford University Press, , 2009 2009
ISBN	0-19-154941-X
Descrizione fisica	1 online resource (267 p.)
Collana	Oxford Series in Ecology and Evolution
Disciplina	579.25
Soggetti	RNA viruses Viruses - Evolution Viral genetics Virus diseases
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Contents; 1 Introduction; 1.1 Why study RNA virus evolution?; 1.1.1 Ways to study viral evolution; 1.1.2 The scope of this book; 1.2 RNA viruses and evolutionary biology; 1.2.1 The RNA virus world; 1.3 The basics of viral biology; 1.3.1 A cursory history of virology; 1.3.2 Virology 101; 1.3.3 Exploring the virosphere; 2 The origins of RNA viruses; 2.1 Introduction; 2.1.1 The perils of deep viral phylogeny; 2.2 Theories for the origin of RNA viruses; 2.2.1 The regressive origin theory; 2.2.2 RNA viruses as escaped genes; 2.2.3 RNA viruses and the RNA world; 2.2.4 Eigen's paradox 2.2.5 The taxonomic distribution of RNA viruses2.2.6 Conserved protein structures; 2.3 Deep phylogenetic relationships among RNA viruses; 2.3.1 The 'higher-order' relationships of RNA viruses; 2.3.2 Phylogenies based on genome organization; 2.3.3 Phylogenies based on protein structure; 2.4 RNA viruses and the evolution of the genetic code; 3 The mechanisms of RNA virus evolution; 3.1 The evolutionary dynamics of RNA viruses; 3.1.1 Mutation rates in RNA viruses and their determinants; 3.1.2 A comparison of substitution rates in viruses; 3.1.3 Differences in viral generation time 3.1.4 Slowly evolving RNA viruses?3.1.5 Rapidly evolving ssDNA viruses; 3.1.6 What sets the rate of RNA virus evolution?; 3.1.7 Trade-

offs and the evolution of mutation rates; 3.1.8 Mutation rates and mutational loads; 3.1.9 Are RNA viruses trapped by high mutation rates?; 3.2 Recombination and reassortment in RNA virus evolution; 3.2.1 Recombination frequency in RNA viruses; 3.2.2 Detecting recombination in RNA viruses; 3.2.3 What determines the rate of recombination in RNA viruses?; 3.2.4 Recombination and deleterious mutation

3.3 Natural selection, genetic drift, and the genetics of adaptation3.3.1 Effective population sizes in viral evolution; 3.3.2 Transmission bottlenecks; 3.3.3 The dynamics of allele fixation: estimating selection coefficients; 3.3.4 The importance of hitch-hiking; 3.3.5 Patterns of synonymous and nonsynonymous evolution; 3.3.6 Natural selection and transmission mode; 3.3.7 Escape from intrinsic immunity; 3.3.8 Strictly neutral evolution in RNA viruses?; 3.3.9 Determinants of codon bias (and nucleotide composition) in RNA viruses; 3.4 Deleterious mutation and RNA virus evolution

3.4.1 Deleterious mutation and intra-host genetic diversity3.4.2 The importance of defective interfering particles and complementation; 3.4.3 Complementation may be commonplace in RNA viruses; 3.5 Epistasis in RNA virus evolution; 3.5.1 Epistasis and robustness; 3.5.2 The importance of RNA secondary structure; 3.5.3 Convergence and pleiotropy; 3.6 The importance of intra-host viral diversity; 4 The RNA virus quasispecies; 4.1 What is a quasispecies?; 4.2 The great quasispecies debate; 4.2.1 What's in a name: quasispecies or polymorphism?

4.2.2 Is quasispecies theory different from 'classical' population genetics?

Sommario/riassunto

While the study of viral evolution has developed rapidly in the last 30 years, little attention has been directed toward linking the mechanisms of viral evolution to the epidemiological outcomes of these processes. This book intends to fill this gap by considering the patterns and processes of viral evolution at all its spatial and temporal scales.

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Record Nr.	UNINA9910679284903321
Titolo	International journal of business and society
Pubbl/distr/stampa	Sarawak, Malaysia : , : Faculty of Economics and Business, Universiti Malaysia Sarawak, , 2000-
Descrizione fisica	1 online resource
Disciplina	338.005
Soggetti	Industries - Social aspects Social responsibility of business Business ethics Entreprises - Responsabilité sociale Morale des affaires Periodicals.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Periodico
Note generali	Refereed/Peer-reviewed