1. Record Nr. UNINA9910814101303321 Autore Holmes Edward C. 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.) Oxford Series in Ecology and Evolution Collana Disciplina 579.25 Soggetti RNA viruses Viruses - Evolution Viral genetics Virus diseases Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Description based upon print version of record. Note generali 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 viruses 2.2.6 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

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## 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.