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Titolo	Cholera Outbreaks // edited by G. Balakrish Nair, Yoshifumi Takeda
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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index at the end of each chapters.
Nota di contenuto	Cholera Outbreaks in the Classical Biotype Era -- Cholera Outbreaks in the El Tor Biotype Era and the Impact of the New El Tor variants -- Cholera Outbreaks in India -- Cholera Outbreaks in South East Asia -- Cholera Outbreaks in Africa -- The Cholera Outbreak in Haiti: Where and How Did it Begin?- Role of Phages in the Epidemiology of Cholera -- Circulation and Transmission of Clones of <i>Vibrio cholerae</i> During Cholera Outbreaks -- Modelling Cholera Outbreaks -- Genomic Science in Understanding Cholera Outbreaks and Evolution of <i>Vibrio cholerae</i> as a Human pathogen -- When, How and Where Can Oral Cholera Vaccines be Used to Interrupt Cholera Outbreaks?.
Sommario/riassunto	The most feared attribute of the human pathogen <i>Vibrio cholerae</i> is its ability to cause outbreaks that spread like wildfire, completely overwhelming public health systems and causing widespread suffering and death. This volume starts with a description of the contrasting patterns of outbreaks caused by the classical and El Tor biotypes of <i>V. cholerae</i> . Subsequent chapters examine cholera outbreaks in detail,

including possible sources of infection and molecular epidemiology on three different continents, the emergence of new clones through the bactericidal selection process of lytic cholera phages, the circulation and transmission of clones of the pathogen during outbreaks, and novel approaches to modeling cholera outbreaks. A further contribution deals with the application of the genomic sciences to trace the spread of cholera epidemics and how this information can be used to control cholera outbreaks. The book closes with an analysis of the potential use of killed oral cholera vaccines to stop the spread of cholera outbreaks.
