

Preface

More than 150 years ago the cholera-causing pathogen *Vibrio cholerae* was discovered and knowledge on its characteristics, biochemistry, physiology and genetics is growing incessantly. Many of its unique features give feast for research and frustration in managing the disease. Though our understanding of the features and behaviour of *V. cholerae* are remarkable, suffering from its infection in the form of cholera is still continuing, mostly in Asian and African countries. Owing to lack of surveillance and timely reporting of cholera in endemic regions due to economic and other disincentives, the overall cholera scenario has not changed substantially. The *raison d'être* of its persistence in nature is mainly attributed to age old factors such as contaminated or inadequate water supply, sanitary conditions, congregation of people due to natural calamities or political unrest and by and large the poor health practises.

During the last three decades, intensive research has been made to understand the virulence properties of the organisms, genes that support the colonization and survival in the gut as well in the environments and their contribution in the epidemiology of cholera. How cholera spreads around the globe and what determines its seasonal peaks in endemic areas are not well known. These features of cholera have been hypothesized primarily due to the biotic and abiotic environmental factors and such findings are acknowledged all over the world. However, utilization of such important information still remains a gray area.

Recently, studies have also been made on the adaptive mechanisms of *V. cholerae* in the environments. The phenotypic and genetic studies showed that *V. cholerae* is relentlessly flex, resulting in instantaneous adaptation to the environment as well as in the human host. Detection of strain diversity at the molecular level and its impact of disease dynamics are the other important components in the molecular epidemiology. This field of research is growing fast facilitated by recent technological developments. However, on account of its broad spectrum of pathogenic potential, *V. cholerae* still remains as a paradigm of human pathogen.

Many cholera monographs have been published in the past describing the history of the disease and developments in the research during that time. We have kept away our sights on this erstwhile information to avoid redundancy and to focus on current developments. We hope that this book will be an abridgment for researchers in the

field of cholera and other enteric diseases. We acknowledge the generous time and effort that the authors have devoted for their manuscripts and also for patience to see their great chapters in print.

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