

EVOLVING IDENTITY OF EPIDEMIC *VIBRIO CHOLERAE*: PAST AND THE PRESENT

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Vibrio cholerae is the etiological agent of well known disease cholera. Despite several improvements in the therapeutic approaches, the burden of cholera remains several millions each year, mainly in Africa and Asia. Its dual life style has established *V. cholerae* as a free living organism in the environment and successful pathogen in humans. Six pandemics of cholera occurred since 1816 and the ongoing seventh pandemic started in 1961. Serogroup O1 is responsible for the cholera pandemics, in which classical and El Tor biotypes were respectively dominant in sixth and the current seventh pandemics. During the seventh cholera pandemic of cholera, the classical *V. cholerae* O1 became extinct all over the world due to unknown reasons. Genetic rigidity of the pathogen and the host's immunity seems possible explanations for its disappearance. Even though the classical biotype is extinct, some of its signature genes are often detected in El Tor strains, the descendant of classical biotype. Emergence of a new serogroup O139 in the Indian subcontinent and its rapid spread to other Asian countries made an impression that the eighth pandemic has began. Recently, emergence of El Tor variants, which has the ability to produce classical cholera toxin is being considered as a new trend which has several epidemiological implications such as prolonged and wide-spread cholera outbreaks, severity of illness etc. Other than O1 and O139, *V. cholerae* has several serogroups, collectively known as non-O1, non-O139, which are increasingly associated with sporadic cholera-like diarrhoea. Though their virulence features are not correlated precisely with the disease outcome, their appearance in greater numbers in clinical cases is a new trend. Several of these changes in *V. cholerae* have been correlated with modification in environmental conditions, human behaviour, immunogenicity etc. Factors responsible for its environmental persistence and pathogenesis in humans have been studied for many years. Due to appearance of newer clones carrying diverse combinations of phenotypic and genetic properties, the challenge remains the same for researchers and health officials to control cholera. This review highlights significant changes in *V. cholerae* that may have several repercussions in the epidemiology of cholera and cholera-like diarrhoea.
