

## Genetic and Phenotypic Variability Among the Vibrio Cholerae O1 Isolates of India

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**Abstract :** Cholera is still a global public health burden and is caused by Vibrio cholerae O1 and O139 serogroups. Evidence from recent outbreaks in Haiti and Yemen suggested that circulating V. cholerae O1 El Tor variant strains are continuously changing to cause more ruinous outbreaks worldwide, and most of them have emerged from the Indian subcontinents. Therefore, we studied the changing virulence characteristics along with the antibiotic resistance profile of V. cholerae O1 strains isolated from seasonal outbreaks in three cholera endemic regions during 2018, Gujarat and Maharashtra in Western India (87 strains), and to compare those features with the isolates of West Bengal in Eastern India (48 strains) collected during the same period. All the strains from Western India were of Ogawa serotype, polymyxin B-sensitive, hemolytic, and contained a large fragment deletion in VSP-II genomic region similar with Yemen outbreak strains and carried more virulent Haitian genetic alleles of major virulence associated genes ctxB, tcpA, and rtxA. Conversely, 14.6% (7/48) of the strains from Eastern India were belong to the Inaba serotype, polymyxin B-resistant, non-hemolytic, harbored intact VSP-II region, classical ctxB, Haitian tcpA, and El Tor rtxA alleles. Interestingly, resistance to tetracycline and chloramphenicol was seen in isolates from both regions, which are not very common among V. cholerae O1 isolates in India. Therefore, this study indicated West Bengal as a diverse region where two different types of El Tor variant hypervirulent strains are co-existed, probably competing for their better environmental survival, which may result in severe irrepressible disease outcome in the future.

**Keywords :** cholera, vibrio cholerae, polymyxin B, Non-hemolytic, ctxB, tcpA, rtxA, VSP-II

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