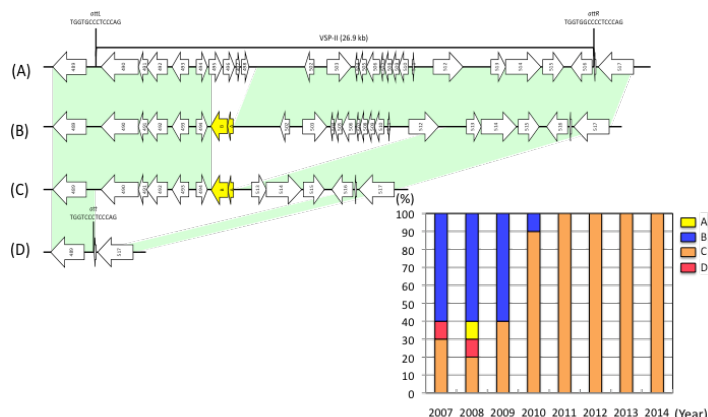


■ Research Highlights

Comparative genomics of epidemic strains from cholera patients reveals evolution of *Vibrio cholerae* O1

Cholera is an acute serious diarrheal disease caused by the bacterial pathogen *Vibrio cholerae* O1, and this infectious disease is a major public health problem in many developing countries. The Bengal region including Kolkata City is considered the epicenter for cholera pandemics. Therefore, to control and prevent the spread of this disease, it is important to clarify and gain greater understanding of the genetic dynamism of the strains from cholera patients in Kolkata, India.



Genetic variation of VSP-II in *V. cholerae* O1 Kolkata strains.

By collaborating with other institutions including the National Institute of Infectious Diseases, Shin-ichi Miyoshi obtained and analyzed the whole genome sequence data of 80 strains isolated between 2007 and 2014 in Kolkata. Miyoshi and members of his colleagues also studied the periodical variation of the heterogeneous genomic region termed the *Vibrio* seventh pandemic island (VSP)-II.

The results of the comparative genomic analysis revealed the heterogeneity of VSP-II in Kolkata strains. Specifically, in 2010 they found the continuous mutation of the VSP-II and the resulting shift of the predominant strain to a virulent strain. These findings demonstrate that the epidemic of cholera in Kolkata was caused by several distinct strains that have been constantly changing within the genetic lineages of *V. cholerae* O1 in recent years.

Reference:

Authors

Daisuke Imamura, Masatomo Morita, Tsuyoshi Sekizuka, Tamaki Mizuno, Taichiro Takemura, Tetsu Yamashiro, Goutam Chowdhury, Gururaja P. Pazhani, Asish K. Mukhopadhyay, Thandavarayan Ramamurthy, Shin-ichi Miyoshi, Makoto Kuroda, Sumio Shinoda, and Makoto Ohnishi.

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Comparative genome analysis of VSP-II and SNPs reveals heterogenic variation in contemporary strains of *Vibrio cholerae* O1 isolated from cholera patients in Kolkata, India.

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