

## Notes from the Field

## Cholera Caused by a New Clone of Serogroup O1 *Vibrio cholerae* — Beijing Municipality, China, June 2021

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Several lineages have been identified in the population of serogroup O1 *Vibrio cholerae* (*V. cholerae*) (1–3). The strains, which were responsible for the ongoing seventh cholera pandemic, were in Lineage 2. Nearly all the *V. cholerae* strains in this lineage carried genes coding cholera toxin (*ctxAB*) (1–2). Lineage 3b consists of strains isolated from different continents and the vast majority of strains in this lineage lack the *ctxAB* genes.

In China, toxigenic serogroup O1 *V. cholerae* strains were rarely isolated after 2010 (4). However, 2 serogroup of O1 *V. cholerae* that possessed the *ctxAB* genes were isolated from patients in June 2021. The first and second case were found after visiting doctors in the same hospital in Beijing on June 19 and 21, 2021, respectively. Both patients complained of abdominal pain and watery diarrhea about 5 times a day, which started on June 17 and 18, respectively. No erythrocytes and leukocytes were observed by stool microscopy. There was no epidemiological connection between these two cases. Neither patient had a common history of exposure or had a common travel history. The first patient stayed in Beijing and the second one traveled to Tianjin 3 days before onset of symptoms. No contacts of the two patients complained of having diarrhea symptoms. Both patients recovered after receiving antibiotic therapy. Real-time polymerase chain reaction (PCR) assay showed that the fecal specimens were positive for the *ctxAB* and *rfb* gene of O1 *V. cholerae* (5). *V. cholerae* strains (named BJVC202101 and BJVC202102) were obtained on June 20 and 22 from the specimens of the first and second cases, respectively, and both were serogroup O1, serotype Ogawa.

Genome sequencing analysis indicated that both of these 2 genomes harbored 2 tandem copies of CTX prophage (6), which both carried genes for *rstR*<sup>class</sup> and *ctxB*<sup>10</sup> (Figure 1C). *Vibrio* pathogenicity island 1 (VPI-1) and VPI-2 were detected but *Vibrio* seventh pandemic island 1 and 2 were absent in them. These 2 genome sequences were combined with a representative

global serogroup O1 *V. cholerae* genome collection (1–3,7) for phylogenetic analysis using a pipeline in the China Pathogen Identification Net (China PIN). These 2 strains formed a cluster, and it was most closely related to the *V. cholerae* isolated in Ukraine and Russia (8) in the phylogenetic tree based on the non-repetitive, non-recombinant core genome single nucleotide polymorphisms (SNPs) (Figure 1A). We reconstructed a phylogenetic tree based on the non-repetitive, non-recombinant core genome SNPs of 18 (including these 2 genomes) most closely related genomes (Figure 1B). The SNP number between these 2 isolates was 8, and varied from 894 to 2,231 between this cluster and the Ukraine and Russia isolates. Therefore, these 2 strains were genetically closely related but remotely related to the Ukraine and Russia ones.

In conclusion, these 2 strains were most closely related to the genomes in Lineage 3b. We prefer to take these isolates as a new clone. The existence of *ctxAB* indicated the potential of this clone to cause cholera outbreaks. Moreover, no epidemiological connection between the 2 patients was observed, which may indicate the wide distribution of this clone of *V. cholerae*. Therefore, surveillance on this clone should be carried out.

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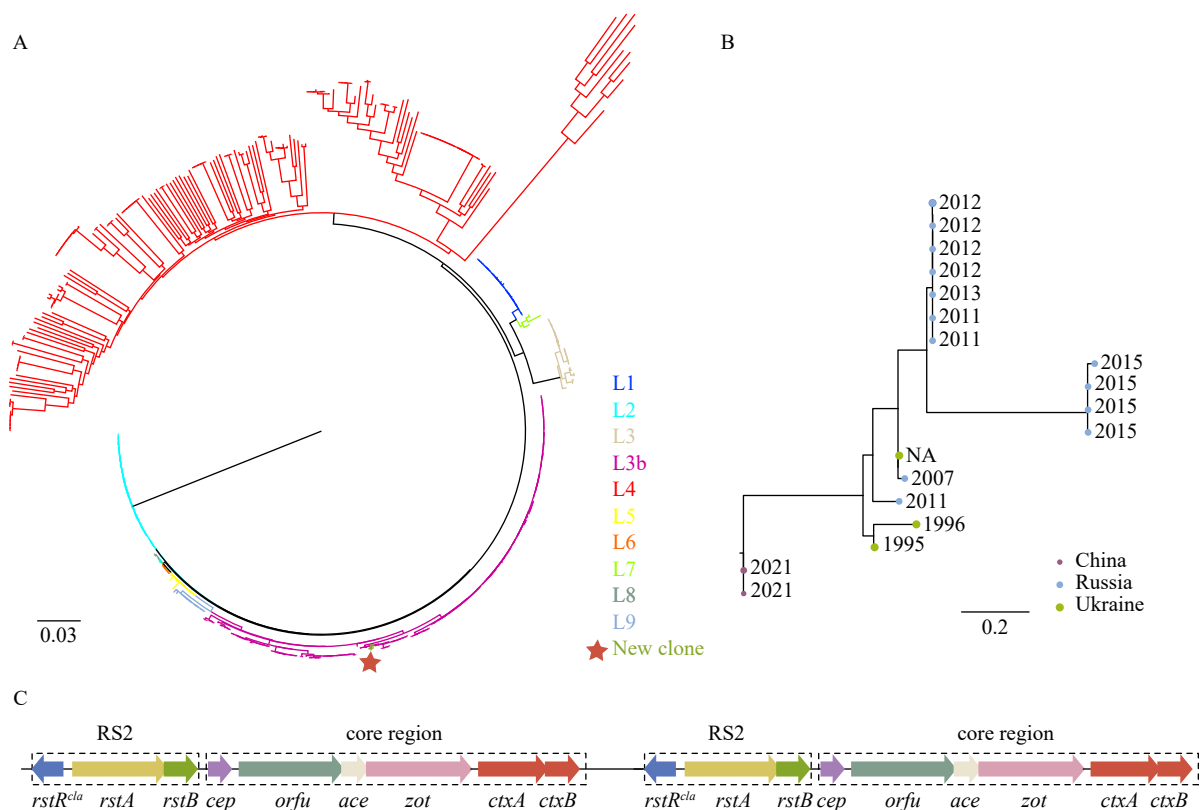


FIGURE 1. Phylogenetic analysis and CTX prophage structure of these two *V. cholerae*. (A) Maximum-likelihood tree constructed for SNPs identified in the non-repetitive, non-recombinant core-genome of the genome collection. (B) The maximum-likelihood tree was constructed on the SNPs identified in the non-repetitive, non-recombinant core-genome of the 18 most closely-related genomes including the 2 Beijing *V. cholerae* strains isolated in 2021. (C) Schematic diagram of the CTX prophages identified in *V. cholerae* BJVC202102.

Notes: Branches were colored according to the lineages they belonged to in Figure 1A. The isolation time was labelled and the tips were colored according to the isolation countries in Figure 1B. Schematic diagram of the CTX prophages were identified in *V. cholerae* BJVC202102.

Abbreviations: SNPs=single nucleotide polymorphisms.

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