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Genome Sequences from a Reemergence of *Vibrio cholerae* in Haiti, 2022 Reveal Relatedness to Previously Circulating Strains

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After more than 3 years without a documented cholera case, the Republic of Haiti reported its first resurgent case on 30 September 2022 (1–3). As of 18 February 2023, more than 27,000 cholera cases have been hospitalized and 594 deaths confirmed from all 10 departments (4). Here, we describe *Vibrio cholerae* isolates first characterized by the Laboratoire National de Santé Publique (LNSP) and include both genotypic and phenotypic antimicrobial resistance profiles. Whole-genome sequencing (WGS) analysis was compared with recently circulating cholera toxin-producing *V. cholerae* O1 in a maximum likelihood phylogeny.

LNSP sent 17 isolates collected from Centre, Grand-Anse, and Ouest departments between 30 September and 31 October 2022 to the Centers for Disease Control and Prevention (CDC) for species and toxin confirmation, antimicrobial susceptibility testing, and WGS analysis. CDC confirmed 16 isolates as toxigenic *V. cholerae* serogroup O1; 15 were serotype Ogawa, and one was Inaba. One isolate was confirmed as *Escherichia coli*. DNA libraries were prepared using Illumina reagents; sequencing was performed on the MiSeq and assessed for quality. Quality metrics for WGS analysis included a minimal Q-score of ≥30, average *de novo* coverage of ≥40×, and genome length of ≥4 Mb. *De novo* assembly of 2010EL-1786 was performed using SPAdes v.3.14.0, and this strain served as the reference for a high-quality single nucleotide polymorphism (SNP) analysis using Lyve-SET (v1.1.4f). A phylogeny was visualized on iTOL.

Antimicrobial susceptibility testing by broth microdilution using CMV5AGNF panels (Sensititre, Westlake, OH) was performed according to the manufacturer's instructions and interpreted based on CLSI guidance (5). Reduced susceptibility to ciprofloxacin was defined as a MIC of ≥0.25 μg/mL (6). Resistance determinants from sequences were found with the ResFinder database and by interrogating *gyrA* and *parC* genes (7). Isolates showed resistance to sulfisoxazole and trimethoprim-sulfamethoxazole, conferred by *sul2* and *dfrA1*, and reduced susceptibility to ciprofloxacin was attributed to *gyrA*(S83I) and *parC*(S85L) mutations. Susceptibility to azithromycin, chloramphenicol, and tetracycline was observed despite the detection of chloramphenicol resistance determinants (*catB9* and *floR*). Streptomycin resistance determinants were also observed [*aph(3")-Ib* and *aph(6)-Id*]. Phenotypic and genotypic resistance findings are consistent with the Haiti 2010 outbreak strains (6, 8).

Haiti 2022 Outbreak genomes were compared with historical isolates from the CDC and genomes available on NCBI Pathogen Detection (9) closely related to the reference sequence 2010EL-1786 (Fig. 1) (8). All Haiti 2022 outbreak strains were very closely related to one another (0 to 3 SNPs apart). Furthermore, these strains were most closely related to 2016 isolates (3 to 10 SNPs apart) and other clinical and environmental isolates between

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