CORRESPONDENCE

Reemergence of Cholera in Haiti

TO THE EDITOR: Cholera was absent from Haiti until an inadvertent introduction by United Nations security forces in October 2010. The ensuing epidemic sickened 820,000 people and caused 9792 reported deaths.[1] The last confirmed cholera case in Haiti was recorded in January 2019, and in February 2022, cholera was declared to have been eliminated in Haiti.[2] In late September 2022, a new outbreak began in Port-au-Prince and rapidly expanded to include 11,953 suspected cases by late November, more than 1000 of which were confirmed by culture.[3] We conducted a genomic and phenotypic analysis of the *Vibrio cholerae* isolated from a stool specimen obtained on September 30, 2022, from an index patient — a child who presented with watery diarrhea and severe dehydration — to begin to address the origins of the epidemic.

The 2022 *V. cholerae* isolate shares phenotypes with the 2010 outbreak strain. Both strains are *V. cholerae* serogroup O1 (El Tor biotype) of the Ogawa serotype and have similar antimicrobial resistance profiles, including resistance to trimethoprim–sulfamethoxazole and low-level resistance to ciprofloxacin (Table S1 in the Supplementary Appendix, available with the full text of this letter at NEJM.org). This resistance profile is consistent among 130 isolates from the current outbreak, which suggests that the strain that was isolated from the index patient is representative of the ongoing epidemic.

To decipher the relationship between the current outbreak strain and other toxigenic O1 El Tor strains from the ongoing seventh pandemic of cholera, we sequenced the isolate obtained on September 30, 2022, along with four isolates obtained in 2021 and 2022 from Dhaka, Bangladesh (Table S2). Phylogenetic analysis of more than 1200 isolates revealed that the 2022 Haiti isolate was closely related to the 2010 Nepal isolate that was the origin of the initial outbreak. The 2022 isolate belongs to a subclade of Haiti *V. cholerae* isolates that originated in 2013 during the previous epidemic and is divergent from 2013 strains from Mexico that were thought to have spread from Haiti, as well as from currently circulating Bangladesh isolates. Haiti isolates from 2022 and 2010 have identical *ctxB* (*ctxB7*) and other virulence factors (Table S3) and produce similar quantities of cholera toxin (Fig. 1).

These analyses suggest that the reemergence of cholera in Haiti in 2022 was caused, at least in part, by a descendant of the *V. cholerae* strain that caused the 2010 epidemic. However, no cases of cholera were confirmed between 2019 and 2022, despite ongoing surveillance. Several explanations for the recrudescence of this strain are possible. The first is that toxigenic *V. cholerae* O1 persisted in Haiti through subclinical infections in humans and has recurred in the context of waning population immunity coupled with a crisis in lack of clean water and sanitation. Another nonexclusive possibility is that this *V. cholerae* strain has persisted in environmental reservoirs. Finally, because the 2010 outbreak in Haiti was ultimately transmitted to other countries in Latin America,[4] a third potential explanation is that the current strain could have been reintroduced to Haiti from a nearby country; however, this explanation is less likely than the others, given the phylogenetic evidence and the absence of recent cholera cases in the region. These findings, along with the resurgence of cholera in several parts of the world[5] despite available tools to fight it, suggest that cholera control and prevention efforts must be redoubled.

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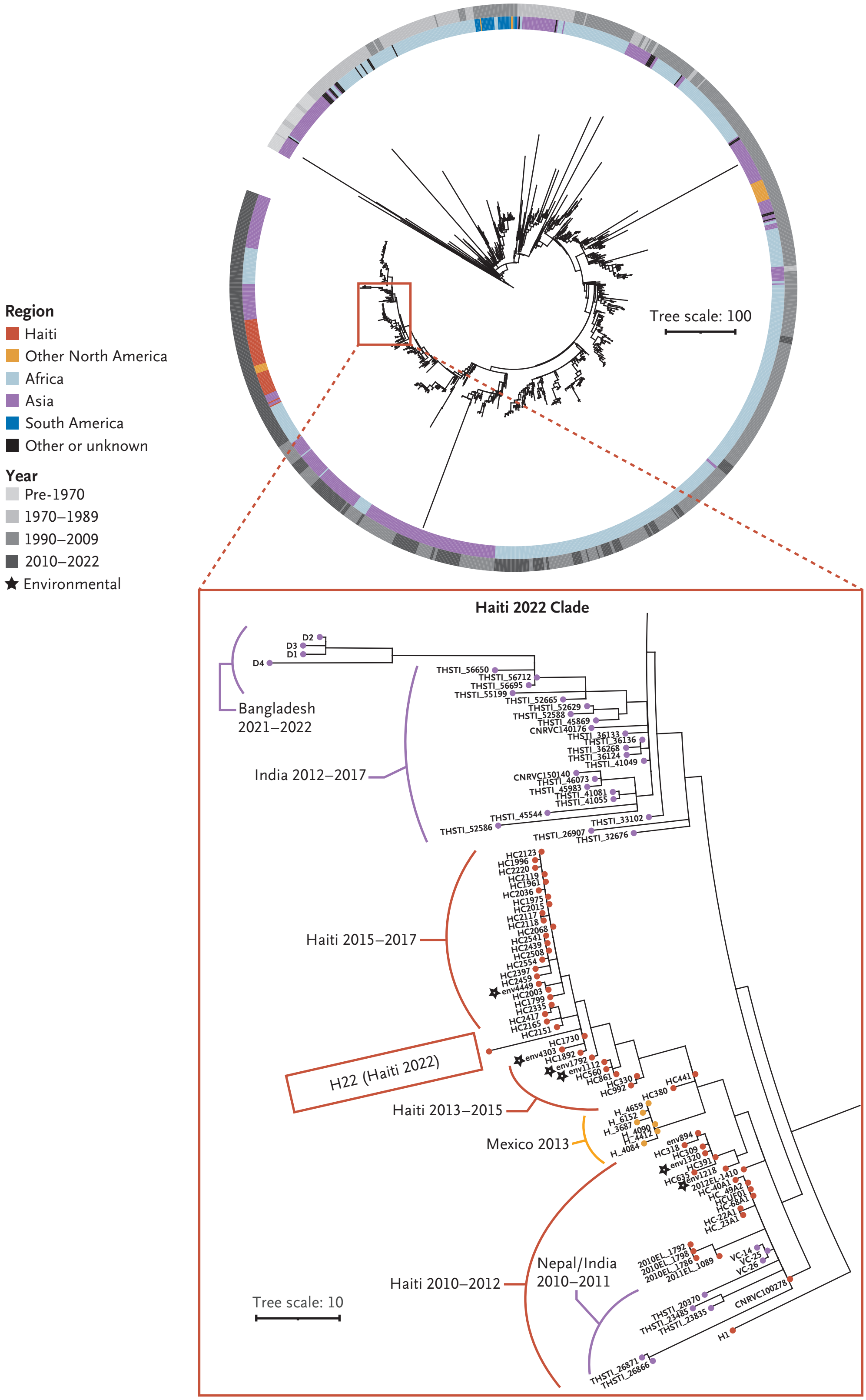
Region
🟥 Haiti
🟧 Other North America
🟦 Africa
🟪 Asia
🟦 South America
⬛ Other or unknown
Year
⬜ Pre-1970
⬜ 1970–1989
⬛ 1990–2009
⬛ 2010–2022
★ Environmental
Tree scale: 100
Haiti 2022 Clade
D2
D3
D1
D4
Bangladesh 2021–2022
THSTI_56650
THSTI_56712
THSTI_56695
THSTI_55199
THSTI_52665
THSTI_52629
THSTI_52588
THSTI_45869
CNRVC140176
THSTI_36133
THSTI_36136
THSTI_36268
THSTI_36124
THSTI_41049
CNRVC150140
THSTI_46073
THSTI_45983
THSTI_41081
THSTI_41055
THSTI_45544
THSTI_52586
THSTI_33102
THSTI_26907
THSTI_32676
India 2012–2017
HC2123
HC1996
HC2220
HC2119
HC1961
HC2036
HC1975
HC2015
HC2117
HC2118
HC2068
HC2541
HC2439
HC2508
HC2554
HC2397
HC2459
env4449
HC2003
HC1799
HC2335
HC2417
HC2165
HC2151
Haiti 2015–2017
HC1730
env4303
HC1892
env1792
env1112
HC560
HC861
HC330
HC992
H22 (Haiti 2022)
Haiti 2013–2015
HC441
HC380
H_4659
H_6152
H_3687
H_4090
H_4412
H_4084
Mexico 2013
env894
HC318
HC309
env1320
HC391
HC635
env1218
2012EL-1410
HC-40A1
HC_49A2
HCUF01
HC-68A1
HC-22A1
HC_23A1
2010EL_1792
2010EL_1798
2010EL_1786
2011EL_1089
VC-14
VC-25
VC-26
Nepal/India 2010–2011
CNRVC100278
THSTI_20370
THSTI_23485
THSTI_23835
H1
THSTI_26871
THSTI_26866
Haiti 2010–2012
Tree scale: 10

Figure 1 (facing page). Phylogenetic Tree of *Vibrio cholerae* from the Seventh Cholera Pandemic.

Shown is a phylogenetic tree of nonrecombinogenic regions from 1270 strains of *V. cholerae* O1, primarily from the current cholera pandemic, which is the seventh cholera pandemic in history. The scale represents single-nucleotide polymorphisms per genome. The inset shows an enlarged image of the *V. cholerae* clade from the 2022 outbreak in Haiti, along with recent isolates from Asia and Mexico.

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