
Figures and figure supplements

Regional sequencing collaboration reveals persistence of the T12 *Vibrio cholerae* O1 lineage in West Africa

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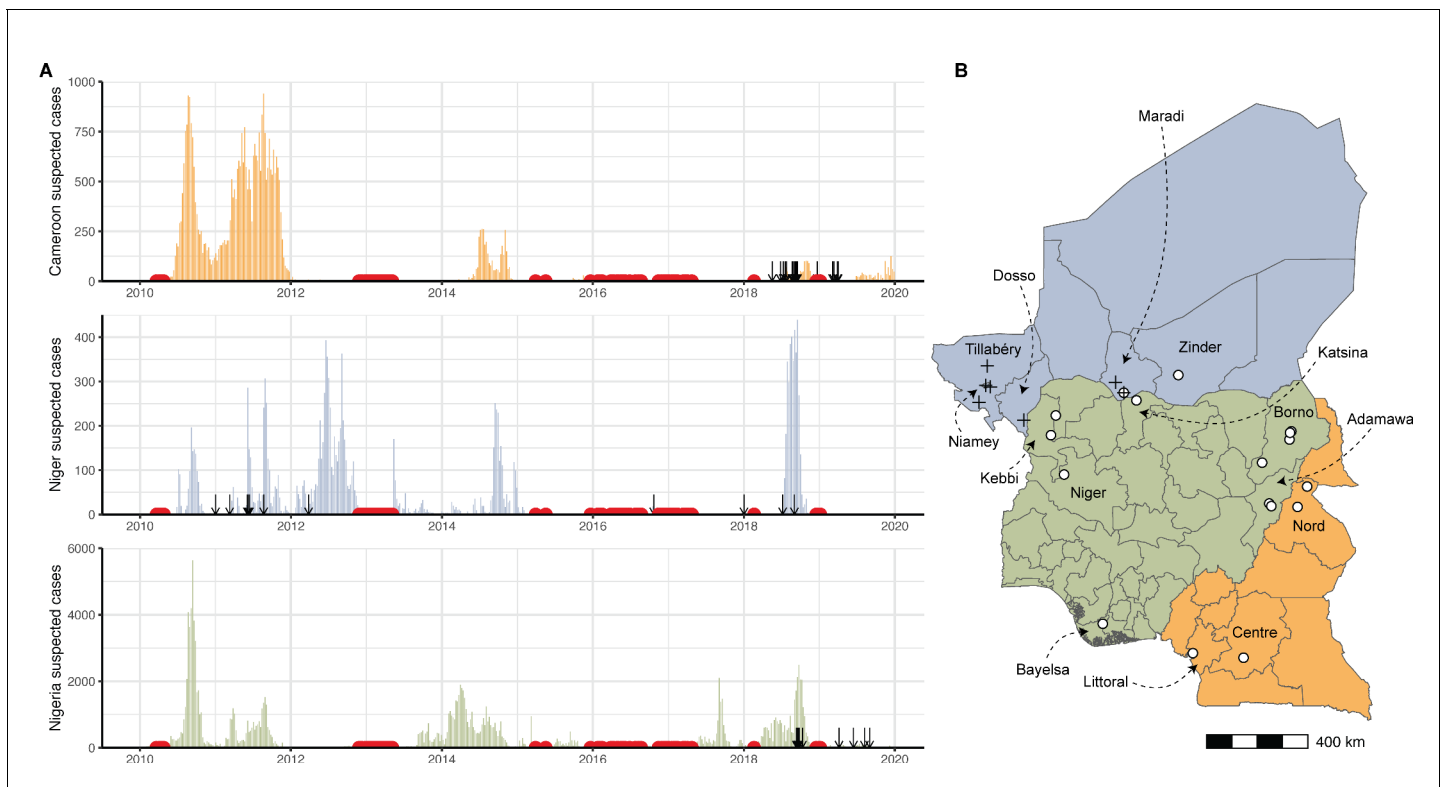


Figure 1. Cholera cases and sequenced isolates. (A) Weekly suspected cholera cases for Cameroon (orange), Niger (blue), and Nigeria (green) from 2010 through 2019 ('Regional Cholera Platform in West and Central Africa,' n.d.) (**Figure 1—source data 1**). Suspected cases are defined as recommended by the World Health Organization (**Global Task Force on Cholera Control Surveillance Working Group, 2017**). Red points: weeks with no more than five suspected cases reported across all three countries. Arrows: collection dates of isolates sequenced. Collection dates provided as year only (n=2) are plotted on January 1 of their given year. (B) Map of Cameroon, Niger, and Nigeria. Colors are as in (A). White points: location of sequenced isolates collected in 2018 and 2019 (**Figure 1—source data 2**). Black crosses: location of sequenced isolates collected prior to 2018. One isolate with unknown sub-country location is not shown.

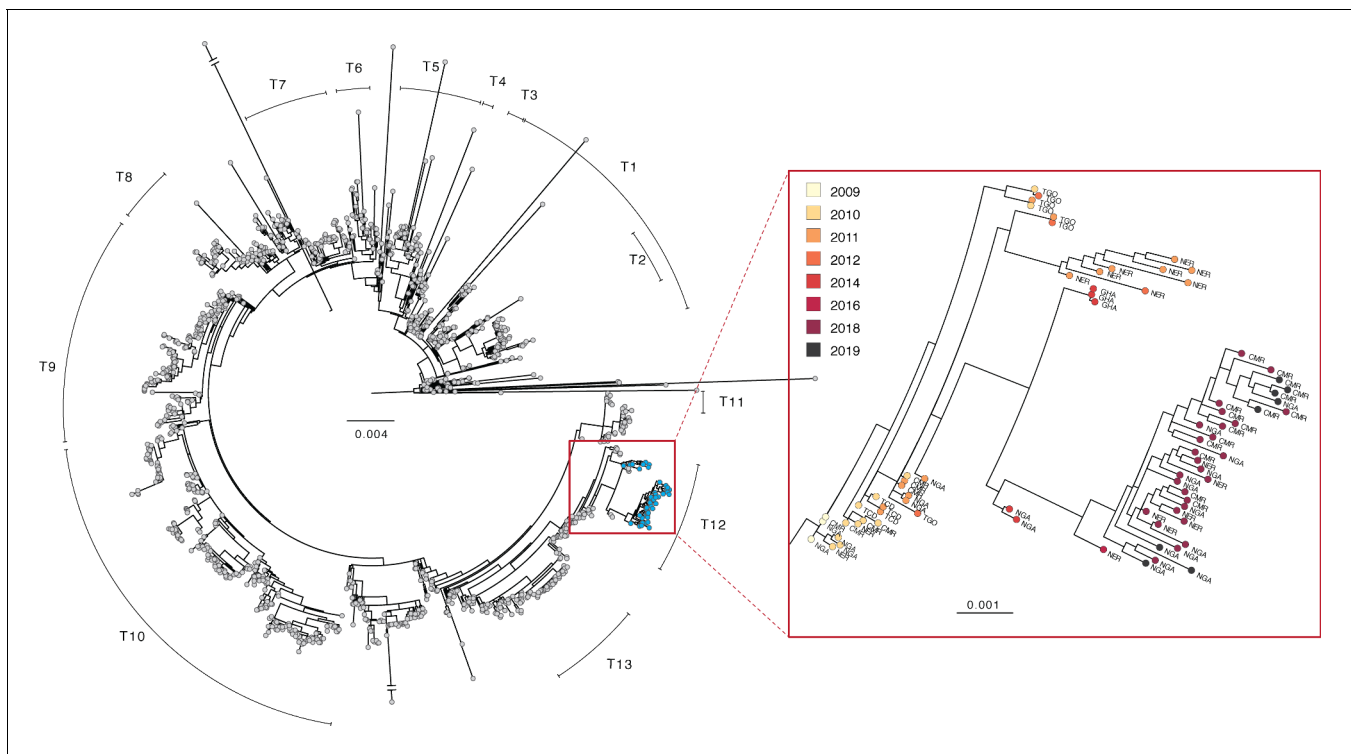


Figure 2. Phylogenetic tree of *V. cholerae* O1 sequences. Left: maximum likelihood tree of global *V. cholerae* isolates. Samples generated in this study are shown in blue (see also, **Figure 2—source data 1**). Right: zoom view of a portion of the T12 lineage containing *V. cholerae* genomes generated in this study. Country codes: TGO, Togo; NER, Niger; GHA, Ghana; CMR, Cameroon; NGA, Nigeria; TCD, Chad. Scale bar unit: nucleotide substitutions per site.

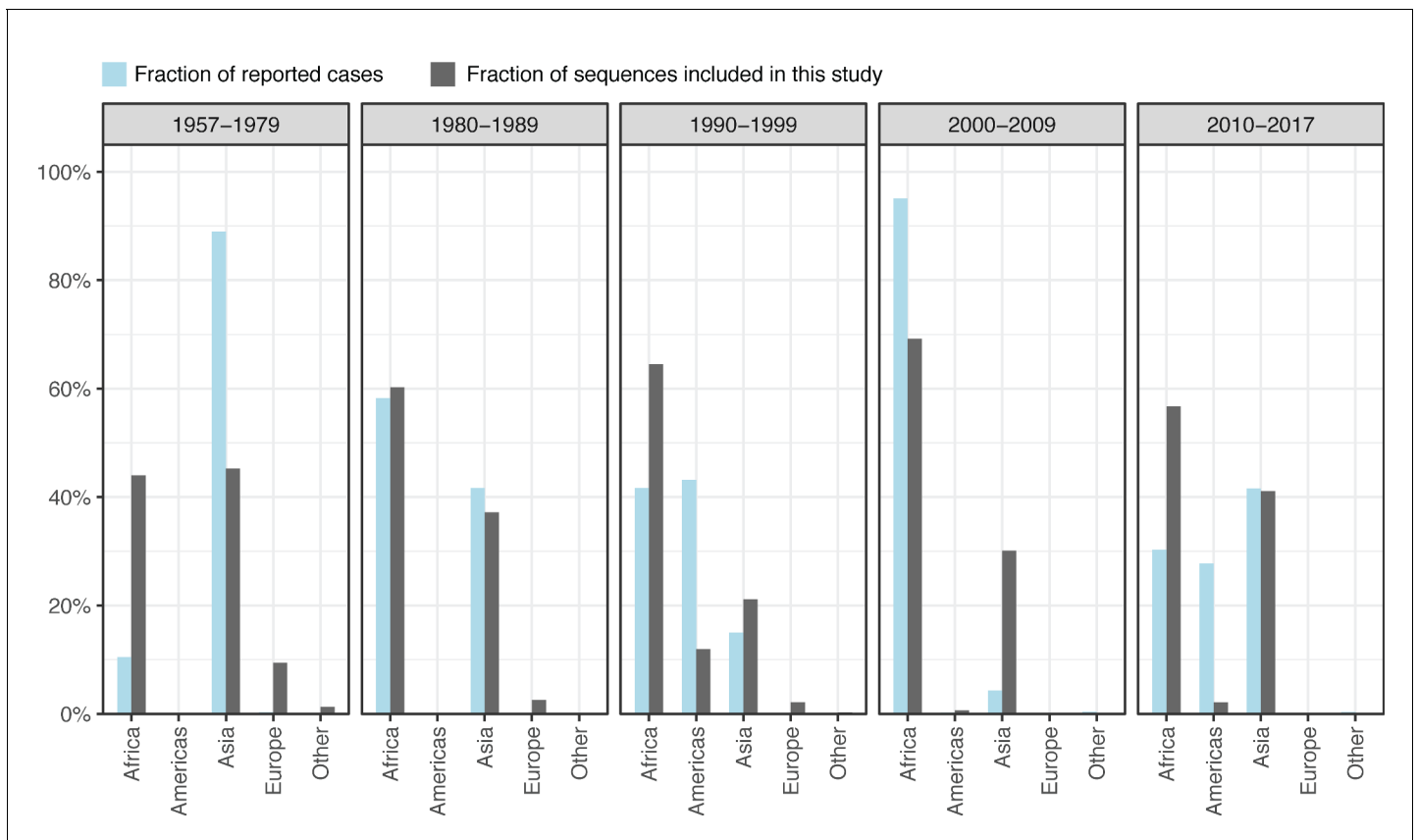


Figure 2—figure supplement 1. Proportion of reported cholera cases and *V. cholerae* sequences by continent. For each decade, the proportion of cholera cases reported to the World Health Organization from each continent (blue bars) and proportion of *V. cholerae* sequences included in this study from each continent (gray bars).

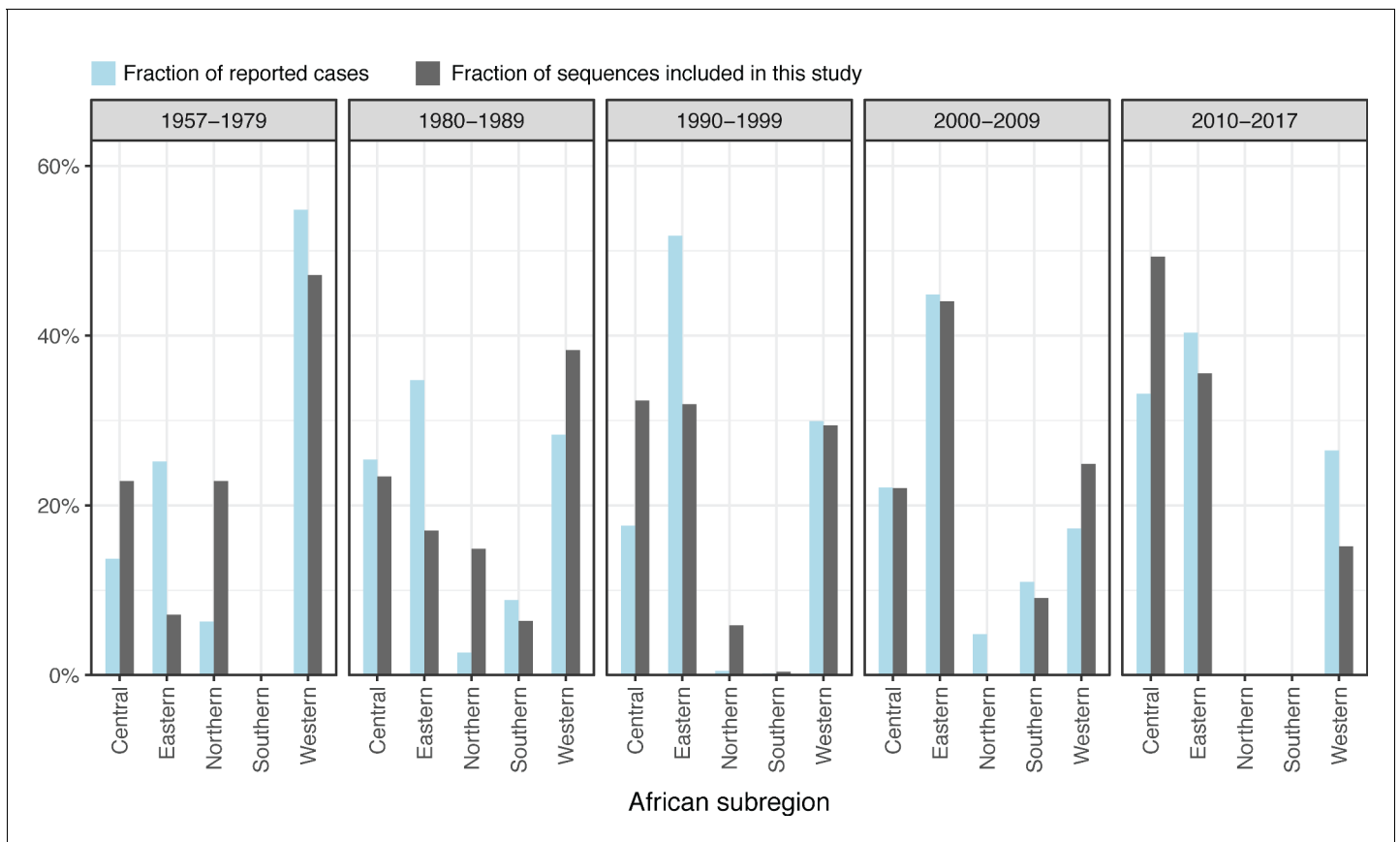


Figure 2—figure supplement 2. Proportion of reported cholera cases and *V. cholerae* sequences by African region. For each decade, the proportion of cholera cases reported to the World Health Organization from each African subregion (blue bars) and proportion of *V. cholerae* sequences included in this study from each African subregion (gray bars).