Technical Appendix

Primers for 5 variable number of tandem repeat loci in *Vibrio cholera*:

<table>
<thead>
<tr>
<th>Gene</th>
<th>Basepair 1</th>
<th>Basepair 2</th>
<th>Primer (5′ → 3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>VC0147</td>
<td>136981</td>
<td>137461</td>
<td>TTGTCATGGCTTGGATTGG</td>
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<td></td>
<td>137461</td>
<td>137461</td>
<td>TGTCGATCACCAGTGCTGG</td>
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<td>VC0436-7</td>
<td>466861</td>
<td>467401</td>
<td>CGTGGTACTAGTTCCACGC</td>
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<tr>
<td></td>
<td>467401</td>
<td>467401</td>
<td>CGTTTTTACCACGCCTCCGCTTC</td>
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<td>VC1650</td>
<td>1778221</td>
<td>1778701</td>
<td>CTACCAAGGCCGGTTAGCAGCTG</td>
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<td>1778701</td>
<td>1778701</td>
<td>TGGGCAACCTGCTGGTAGC</td>
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<td>VCA0171</td>
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<td>188101</td>
<td>GCATCATCCACACGTTTGG</td>
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<td>188101</td>
<td>GCTGAAGCCTTTCCGATCC</td>
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<td>VCA0283</td>
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<td>304201</td>
<td>GTACATTCAAAATTGCTCACC</td>
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<tr>
<td></td>
<td>304201</td>
<td>304201</td>
<td>ACTTCAAAAACTATTGCCAC</td>
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</tbody>
</table>

Standard conditions were a 30-μL reaction containing 100 μmol/L of each dNTP, 1.5 mmol/L MgCl₂, 1× PCR buffer (Invitrogen, Carlsbad, CA, USA), and 1 unit of Taq DNA polymerase (Invitrogen); cycling was 30 times at 95°C for 30 s, annealing (at 50°C or 55°C) for 30 s and 72°C for 30 s.

ClustalX (*I*) alignment of 6 sequences derived from *Vibrio cholerae* isolates to determine distinct alleles. Each row represents a single isolate. Each base is a different color. The repeating unit is the hexamer: AACAGC. The dashes mark bases missing relative to the longest repeat in the first row.

Row 1 = allele 1; rows 2, 3, and 4 = allele 2; rows 5 and 6 = allele 3
Distribution of sequence types by serotype and source in Bakerganj and Mathbaria. For each sequence type, the source is indicated by a C for clinical or an E for environmental, the number of isolates follows after n=, and the month(s) when it was isolated. The arrows indicate sequence types found at both locales, while the barbells indicate sequence types found in both clinical and environmental samples within a locale.

<table>
<thead>
<tr>
<th>Bakerganj</th>
<th>Mathbaria</th>
</tr>
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<tbody>
<tr>
<td>O1</td>
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</tr>
<tr>
<td>Inaba</td>
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<tr>
<td>O1</td>
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</tr>
<tr>
<td>Ogawa</td>
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</tr>
</tbody>
</table>

C: clinical isolate; E: environmental isolate

: indicates genotypes are found in both clinical and environmental isolates

: indicates genotypes found in both Bakerganj and Mathbaria