

Table S6. MLST properties of the *Vibrio cholerae* non-O1, non-O139 populations analyzed in this study.

| | | Total ^a (n = 108) | Environmental ^a (n = 98) | Baltic Sea ^a (n = 48) | North Sea (n = 50) | Clinical (n = 10) | PubMLST ^b |
|----------------------------------|----------------------------------|---------------------------------|--|-------------------------------------|-----------------------|----------------------|----------------------|
| Alleles | | | | | | | |
| <i>adk</i> | n _t (p _t) | 32 (13.0%) | 31 (13.1%) | 22 (14.4%) | 18 (14.0%) | 6 (14.3%) | 105 (9.9%) |
| | n _n (p _n) | 20 (62.5%) | 19 (61.3%) | 12 (54.5%) | 11 (61.1%) | 4 (66.7%) | |
| <i>gyrB</i> | n _t (p _t) | 30 (12.2%) | 30 (12.7%) | 18 (11.8%) | 18 (14.0%) | 5 (11.9%) | 116 (10.9%) |
| | n _n (p _n) | 17 (56.7%) | 17 (56.7%) | 8 (44.4%) | 10 (55.6%) | 3 (60.0%) | |
| <i>mdh</i> | n _t (p _t) | 25 (10.2%) | 25 (10.5%) | 17 (11.1%) | 14 (10.9%) | 4 (9.5%) | 121 (11.4%) |
| | n _n (p _n) | 14 (56.0%) | 14 (56.0%) | 7 (41.2%) | 10 (71.4%) | 1 (25.0%) | |
| <i>metE</i> | n _t (p _t) | 56 (22.8%) | 51 (21.5%) | 30 (19.6%) | 25 (19.4%) | 8 (19.0%) | 270 (25.5%) |
| | n _n (p _n) | 44 (78.6%) | 40 (78.4%) | 23 (76.7%) | 19 (76.0%) | 7 (87.5%) | |
| <i>pntA</i> | n _t (p _t) | 38 (15.4%) | 37 (15.6%) | 28 (18.3%) | 18 (14.0%) | 7 (16.7%) | 154 (14.5%) |
| | n _n (p _n) | 19 (50.0%) | 19 (51.4%) | 13 (46.4%) | 9 (50.0%) | 4 (57.1%) | |
| <i>purM</i> | n _t (p _t) | 20 (8.1%) | 20 (8.4%) | 12 (7.8%) | 14 (10.9%) | 5 (11.9%) | 96 (9.1%) |
| | n _n (p _n) | 14 (70.0%) | 14 (70.0%) | 9 (75.0%) | 9 (64.3%) | 2 (40.0%) | |
| <i>pyrC</i> | n _t (p _t) | 45 (18.3%) | 43 (18.1%) | 26 (17.0%) | 22 (17.1%) | 7 (16.7%) | 198 (18.7%) |
| | n _n (p _n) | 34 (75.6%) | 32 (74.4%) | 19 (73.1%) | 17 (77.3%) | 5 (71.4%) | |
| total | n _t (p _t) | 246 (100%) | 237 (100%) | 153 (100%) | 129 (100%) | 42 (100%) | 1060 (100%) |
| | n _n (p _n) | 162 (65.9%) | 155 (65.4%) | 91 (59.5%) | 85 (65.9%) | 26 (61.9%) | |
| Sequence types | | | | | | | |
| n _t | | 74 | 66 | 42 | 25 | 8 | 718 |
| n _n (p _n) | | 71 (95.9%) | 63 (95.5%) | 40 (95.2%) | 24 (96.0%) | 8 (100.0%) | |

n, number of isolates; n_t, total number of alleles/sequence types; p_t, proportion of n_t of locus X as a percentage of n_t of all loci of the respective *V. cholerae* population; n_n, number of new alleles/sequence types; p_n, proportion of n_n as a percentage of n_t.

^a Two *V. cholerae* strains from the Baltic Sea, VN-00455 and VN-00477, were excluded from the analyses due to failing *pyrC* amplification.

^b PubMLST database as of November 5, 2018.