**S2 Table.** MLST Primers

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | 　 | Primers | Position | Length (bp) |
| *dnaE* | *dnaE*-L-F | TCCTCATCGGCCTCATAAAGCTC | 2012 to 2832 | 821 |
| *dnaE*-L-R | GTTGCGATTCATGATGGTTACACAT |
| *gyrB* | *gyrB*-L-F | CTGCGTGAGCTATCGTTCTTGA | 568 to 1351 | 784 |
| *gyrB*-L-R | TCTTACCTTTCAGTGGTAGGATTGC |
| *recA* | *recA*-L-F | CCGCTGCGCTAGGTCAAAT | 29 to 997 | 969 |
| *recA*-L-R | CTGGTTGAGCTGGAGAAAGTAGCAT |
| *recA*-3F a | ATAACCGCGCAATGGATGTAGAAAC | 89 to 889 | 801 |
| *recA*-3R a | TCTTATCGCCATTGTAGCTGTACCA |
| *dtdS* | *dtdS*-1F(M13)b | tgtaaaacgacggccagtTGGCCATAACGACATTCTGA | 75 to 747  | 673 |
| *dtdS*-L-R | GTTGAATGCCGCTGGGTTAC |
| *pntA* | *pntA*-L-F | CTGGCAGTCTTGGCGCTATC | 569 to 1286 | 718 |
| *pntA*-L-R | GCAGCAGGTGCTACCGATG |
| *pyrC* | *pyrC*-L-F | CGATCGAATTCTGAAAGAGCAGC | 168 to 940 | 773 |
| *pyrC*-L-R | CCGATTTTTCTAGCGTCACCGTAT |
| *tnaA* | *tnaA*-L-F | TCGAAGAACATCTGTGCCATC | 538 to 1192 | 655 |
| *tnaA*-L-R | CACGTCCGAGCAACAATGAG |

a Additional PCR and sequencing primers for recA, when isolates could not be amplified by recA-L-F/R.

b. Primer from *V. parahaemolyticus* MLST scheme (1).

**References**

1. **Gonzalez-Escalona N, Martinez-Urtaza J, Romero J, Espejo RT, Jaykus LA, DePaola A.** 2008. Determination of molecular phylogenetics of *Vibrio parahaemolyticus* strains by multilocus sequence typing. J. Bacteriol. **190:**2831-2840.