**Table S1.** Primers employed in MLST of *L. fermentum*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **Primera** | **Sequence****(5' to 3')** | **Size of****amplicon** **(bp)** | **Size of****sequence fragment****(bp)** |
| ATP-dependent Clp protease ATP-binding subunit | *clpX*/F | CGC ACG GAA GCA GAA AC | 659 | 453 |
| *clpX*/R | GAG TCG GTC CCA AAC CC |
| chaperonin GroEL | *groEL*/F | CCG ACA ACG ACA AGA TGG | 663 | 458 |
| *groEL*/R | CCA AGG CAG GGA TAA CG |
| CTP synthetase | *pyrG*/F | TCA TTG GGT CGG CTG TT | 709 | 532 |
| *pyrG*/R | GGT CCA TCC CTT GCT TTT G |
| chromosomal replication initiation protein | *dnaA*/F | ACC CGC TCC TGA TTT ACG | 589 | 258 |
| *dnaA*/R | GCC TCG GTA GCC AGT TTG |
| DNA-directed RNA polymerase subunit beta | *rpoB*/F | GAA GTT CCG CCG CTC TA | 715 | 467 |
| *rpoB*/R | GGT CCC ATC TGG CAT GTA C |
| excinuclease ABC subunit C | *uvrC*/F | TCG TCA CCT CCT CCA ATA A | 748 | 518 |
| *uvrC*/R | TGG TTC GGT AAT CCC TCC |
| molecular chaperone DnaK | *dnaK*/F | GAC AAC GGT CCG CTC CAC T | 734 | 519 |
| *dnaK*/R | TCG GCT TCT TCC TTC TTC TTC T |
| recombinase A | *recA*/F | ATT GCC GAC GCC CTG AT | 647 | 483 |
| *recA*/R | TGC GGT TCG CCT TCC TT |
| UDP-N-acetylmuramate-L-alanine ligase | *murC*/F | TTT GAA GCC GAC GAA TAC C | 745 | 602 |
| *murC*/R | CGA TGT CCT CGC TAC CC |
| UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase | *murE*/F | CTA CCG CCA GCA CTT CTT | 659 | 426 |
| *murE*/R | GGT CCA TCT GGG TGT TTA GC |
| x-prolyl-dipeptidyl aminopeptidase | *pepX*/F | AAA GAA GAC GAG CAA CCA ACC | 724 | 580 |
| *pepX*/R | CGG AGT CCT TAG TCC CGA TT |

a Primers based on study of Dan et al., [2015].