

Supplementary Data

Supplementary Table 1. Genome information of the six *Lactobacillus acidophilus* strains from NCBI database

| Strain | Assembly | Taxon ID | Length | Genes | Reference |
|-----------|-------------|----------|-----------|-------|---|
| NCFM | ASM1198v1 | 272621 | 1,993,560 | 1,963 | Pfeiler et al. [21] |
| La14 | ASM38967v2 | 1314884 | 1,991,579 | 1,978 | Complete Genome Sequence of Probiotic Strain Lactobacillus acidophilus La-14 |
| FSI4 | ASM93462v1 | 1579 | 1,991,969 | 1,977 | Complete Genome Sequence of Lactobacillus acidophilus FSI4, Isolated from Yogurt |
| ATCC53544 | ASM222430v1 | 1579 | 1,991,906 | 1,977 | Genome of Lactobacillus acidophilus strain ATCC 53544 |
| LA1 | ASM228621v1 | 1579 | 1,991,195 | 2,002 | Complete genome sequence of Lactobacillus acidophilus LA1 |
| DSM20079 | ASM304706v1 | 1579 | 2,009,973 | 2,020 | The whole genome sequencing and assembly of Lactobacillus acidophilus DSM 20079T strain |

NCBI, National Center for Biotechnology Information Center.

Supplementary Table 2. Significant evolutionarily accelerated genes identified in dN/dS analysis (the branch-site model) and related information for *Lactobacillus acidophilus* C5

| Gene_ID | Start | End | Length | Strand | COG | Gene product | diff_InL.2 | Chisqu test | FDR | #AA Change (#Sig) |
|------------|-----------|-----------|--------|--------|-----|---|------------|-------------|----------|-------------------|
| C5_1_00009 | 15,595 | 16,678 | 1,084 | - | S | Putative membrane protein YdgH | 17.03 | 3.68E-05 | 3.79E-03 | 4 (0) |
| C5_1_00026 | 32,426 | 33,881 | 1,456 | - | S | hypothetical protein | 26.01 | 3.39E-07 | 1.04E-04 | 4 (1) |
| C5_1_00138 | 148,018 | 148,726 | 709 | - | S | hypothetical protein | 25.81 | 3.77E-07 | 1.04E-04 | 13 (7) |
| C5_1_00140 | 150,441 | 150,660 | 220 | - | R | hypothetical protein | 20.45 | 6.11E-06 | 7.20E-04 | 20 (10) |
| C5_1_00253 | 242,731 | 243,085 | 355 | - | G | Oligo-1,6-glucosidase | 11.04 | 8.91E-04 | 4.90E-02 | 6 (2) |
| C5_1_00257 | 244,712 | 245,525 | 814 | - | K | Catabolite control protein Ad | 22.97 | 1.65E-06 | 2.49E-04 | 8 (1) |
| C5_1_00352 | 336,963 | 337,302 | 340 | + | S | hypothetical protein | 14.27 | 1.59E-04 | 1.14E-02 | 8 (4) |
| C5_1_00359 | 341,349 | 341,709 | 361 | - | P | H(+)/Cl(-) exchange transporter ClcA | 12.48 | 4.11E-04 | 2.51E-02 | 5 (1) |
| C5_1_00647 | 613,927 | 616,276 | 2,350 | + | L | Transcription-repair-coupling factor | 12.04 | 5.20E-04 | 3.06E-02 | 1 (1) |
| C5_1_00767 | 705,460 | 705,760 | 301 | + | O | tRNA N6-adenosine threonylcarbamoyltransferase | 30.80 | 2.85E-08 | 3.65E-05 | 15 (11) |
| C5_1_00898 | 817,770 | 818,112 | 343 | + | G | Fructose-bisphosphate aldolase | 20.67 | 5.47E-06 | 7.18E-04 | 57 (6) |
| C5_1_00919 | 832,019 | 832,469 | 451 | + | U | hypothetical protein | 13.04 | 3.04E-04 | 2.01E-02 | 2 (2) |
| C5_1_01000 | 914,379 | 914,928 | 550 | + | J | tRNA dimethylallyltransferase | 12.78 | 3.51E-04 | 2.23E-02 | 4 (2) |
| C5_1_01133 | 1,057,899 | 1,058,238 | 340 | + | G | Glucose uptake protein GlcU | 24.85 | 6.20E-07 | 1.40E-04 | 11 (6) |
| C5_1_01292 | 1,210,451 | 1,211,291 | 841 | + | R | hypothetical protein | 28.23 | 1.08E-07 | 5.94E-05 | 16 (9) |
| C5_1_01372 | 1,295,364 | 1,295,751 | 388 | - | G | hypothetical protein | 18.19 | 2.00E-05 | 2.20E-03 | 8 (6) |
| C5_1_01457 | 1,376,297 | 1,376,813 | 517 | - | E | L-cystine import ATP-binding protein TcyC | 24.68 | 6.78E-07 | 1.40E-04 | 13 (8) |
| C5_1_01510 | 1,441,239 | 1,449,198 | 7,960 | - | R | Levansucrase | 15.96 | 6.47E-05 | 5.93E-03 | 12 (2) |
| C5_1_01536 | 1,481,347 | 1,481,662 | 316 | - | D | Putative fluoride ion transporter CrcB | 22.95 | 1.66E-06 | 2.49E-04 | 30 (22) |
| C5_1_01553 | 1,496,724 | 1,497,633 | 910 | - | P | Sodium, potassium, lithium and rubidium/H(+) antiporter | 15.17 | 9.81E-05 | 8.09E-03 | 4 (0) |
| C5_1_01571 | 1,510,462 | 1,510,822 | 361 | - | S | hypothetical protein | 11.72 | 6.19E-04 | 3.52E-02 | 4 (3) |
| C5_1_01724 | 1,659,667 | 1,661,095 | 1,429 | - | M | Penicillin-binding protein 2B | 14.31 | 1.55E-04 | 1.14E-02 | 6 (2) |
| C5_1_01764 | 1,697,228 | 1,698,386 | 1,159 | - | L | Putative defective protein IntQ | 13.87 | 1.96E-04 | 1.35E-02 | 2 (2) |
| C5_1_01782 | 1,713,305 | 1,713,773 | 469 | - | T | Signal transduction histidine-protein kinase BaeS | 20.60 | 5.66E-06 | 7.18E-04 | 5 (5) |
| C5_1_01796 | 1,723,378 | 1,723,753 | 376 | - | U | hypothetical protein | 15.58 | 7.91E-05 | 6.87E-03 | 3 (3) |
| C5_1_01799 | 1,724,814 | 1,725,501 | 688 | - | K | putative transcriptional regulatory protein | 27.25 | 1.79E-07 | 7.38E-05 | 6 (3) |
| C5_1_01889 | 1,820,193 | 1,821,627 | 1,435 | - | G | Phosphoenolpyruvate-protein phosphotransferase | 16.33 | 5.34E-05 | 5.18E-03 | 4 (0) |
| C5_1_01983 | 1,909,806 | 1,910,190 | 385 | + | L | hypothetical protein | 29.95 | 4.43E-08 | 3.65E-05 | 8 (6) |
| C5_1_02023 | 1,944,357 | 1,944,594 | 238 | - | K | HTH-type transcriptional repressor YvoA | 24.30 | 8.24E-07 | 1.51E-04 | 13 (11) |
| C5_1_02081 | 2,003,239 | 2,003,548 | 310 | + | K | hypothetical protein | 14.77 | 1.22E-04 | 9.56E-03 | 6 (5) |

dN/dS, the ratio of nonsynonymous to synonymous substitution COG, Clusters of Orthologous Groups; FDR, false discovery rate; ATP, adenosine triphosphate; S, function unknown; R, general function prediction only; G, carbohydrate transport and metabolism; K, transcription; P, inorganic ion transport and metabolism; L, replication, recombination and repair; O, posttranslational modification; U, intracellular trafficking, secretion, and vesicular transport; J, translation, ribosomal structure and biogenesis; E, amino acid transport and metabolism; D, cell cycle control, cell division, chromosome partitioning; M, cell wall/membrane/envelope biogenesis; T, -Signal transduction mechanisms.