

Table S1 Identification of the five genes in 19 lactobacilli strains and sequence conservation similarity

Group	Strains	Genes ID (accession No.) and similarity with the PM1 strain <sup>a</sup>				
		Fructokinase	6-phosphofructokinase	Glucose 6-phosphate isomerase	Fructose 1,6-diphosphate aldolase	Triosephosphate isomerase
I	<i>L. acidophilus</i> 30SC	650745597 (YP_004286346), 44.97%	650746564 (YP_004292051)	650746372 (YP_004291861), 69.25%	650747281 (YP_004292767), 71.80%	650746322 (YP_004291811), 40.31%
	<i>L. amylovorus</i> GRL 1112	650724351 (YP_004030817), 8.22% 650724347 (YP_004030813), 44.97%	650725350 (YP_004031755)	650725157 (YP_004031565), 69.25%	650726109 (YP_004032513), 71.80%	650725087 (YP_004031495), 40.31%
	<i>L. crispatus</i> ST1	646761531 (YP_003600490), 41.95%	646762585 (YP_003601479)	646762330 (YP_003601227), 68.14%	646763201 (YP_003602094), 70.49%	646762284 (YP_003601181), 41.47%
	<i>L. delbrueckii bulgaricus</i> 2038	N.F.	650390714 (ADY84901) 650391575 (ADY85687)	650390580 (ADY84772), 67.55%	650391374 (ADY85510), 69.18%	650390527 (ADY84719), 40.31%
	<i>L. gasseri</i> ATCC 33323	639671876 (YP_813869), 44.82%	639672737 (YP_814708)	639673092 (YP_815060), 67.77%	639672325 (YP_814303), 66.56%	639673139 (YP_815107), 42.02%
	<i>L. helveticus</i> DPC 4571	641310735 (YP_001576600), 37.20%	641311598 (YP_001577401)	641311408 (YP_001577214), 67.48%	641312090 (YP_001577892), 71.15%	N.F.
	<i>L. johnsonii</i> DPC 6026	651136969 (AEB92353), 44.15%	651138043 (AEB93408)	651138189 (AEB93552), 67.77%	651137472 (AEB92841), 66.23%	651138237 (AEB93600), 42.41%
	<i>L. kefiranofaciens</i> ZW3	650904929 (YP_004563251), 43.29%	650904173 (YP_004562509)	650904375 (YP_004562710), 68.14%	650903657 (YP_004561994), 71.80%	650904413 (YP_004562748), 39.92%
	<i>L. ruminis</i> ATCC 27782	2521929235, 46.62%	2521929885	2521930531, 71.02%	2521930559, 66.32%	2521929706, 39.30%
	<i>L. salivarius</i> CECT 5713	648250961 (ADJ79471), 48.31%	648250462 (ADJ78994)	648250176 (ADJ78713), 70.58%	648250105 (ADJ78668), 66.21%	648250709 (ADJ79239), 38.91%
II	<i>L. casei</i> ATCC334	N.F.	639664304 (YP_806584)	639664077 (YP_806359), 67.70%	639663308 (YP_805630), 27.52% 639663408 (YP_805730), 55.07% 639665611 (YP_807862), 29.29%	639663926 (YP_806209), 39.69% 639665610 (YP_807861), 15.44%
	<i>L. plantarum</i> WCFS1	637387577 (NP_784016), 20.55% 637390475 (NP_786830), 28.82%	637389046 (NP_785441)	637389578 (NP_785941), 72.79%	637387703 (NP_784142), 59.31%	637388111 (NP_784536), 43.19%
	<i>L. rhamnosus</i> GC	645012628 (YP_003170153), 41.84%	645013595 (YP_003171120)	645013306 (YP_003170831), 67.92%	645012414 (YP_003169939), 28.38% 645012634 (YP_003170159), 27.72% 645012635 (YP_003170160), 30.97% 645012745 (YP_003170270), 54.73%	645013156 (YP_003170681), 40.86%
	<i>L. sakei sakei</i> 23K	637796403 (YP_396403), 60.80%	637795615 (YP_395644)	637795762 (YP_395789), 69.45%	637796116 (YP_396141), 59.31%	637795189 (YP_395221), 39.69%
III	<i>L. brevis</i> ATCC367	639654318 (YP_796245), 73.63%	N.F.	639653487 (YP_795446), 73.67%	N.F.	639652851 (YP_794837), 40.47%
	<i>L. buchneri</i> NRRL B-30929	2505384060, 75.69%	N.F.	2505384064, 75.66%	N.F.	2520958147, 43.97%
	<i>L. fermentum</i> CECT5716	648249646 (ADJ4163), 81.29%	N.F.	648249647 (ADJ41632), 77.88% 648248900 (ADJ40936), 77.66%	N.F.	648248902 (ADJ40938), 51.94%
	<i>L. reuteri</i> JCM 1112	642584601 (YP_001841850), 28.23% 642584602 (YP_001841851), 29.93%	N.F.	640590226 (YP_001271026), 88.27%	640590034 (YP_001270845), 82.64%	642583870 (YP_001841158), 62.26% 642583938 (YP_001841224), 64.37% 642584103 (YP_001841379), 41.63%
	<i>L. sanfranciscensis</i> TMW 1.1304	2511696944, 56.42%	N.F.	2511696945, 73.07%	N.F.	2511696895, 40.47%

<sup>a</sup> Each gene was searched in DOE Joint Genome Institute (<http://www.jgi.doe.gov/>) and similarity with the PM1 strain was analyzed at the UniProt database (<http://www.uniprot.org>). Gene ID is from DOE joint Genome Institute and accession No. is from Genbank  
N.F. not found