Supplementary materials

Table S1. Detailed information of glucansucrase gene sequences used to construct the phylogenetic tree (Figure 4). These data were obtained from NCBI database.

Accession number (NCBI)	Bacterial strain	Gene	CDS length (bp)
HE972513.1	*Lb. animalis* TMW 1.971	dextransucrase gtf1971	4758
HE972512.1	*Lb. curvatus* TMW 1.624	dextransucrase gtf1624	5094
GU166815.1	*Lb. gasseri* DSM 20077	levansucrase	2960
GU166814.1	*Lb. gasseri* DSM 20604	inulosucrase inuGB	2707
AY697432.1	*Lb. parabuchneri* 33	glucansucrase	5028
MH051191.1	*Lb. reuteri* E81	glucosyltransferase gtfA	5504
EF189716.1	*Lb. reuteri* TMW1.106	dextransucrase gtf106A	5349
AY697434.1	*Lb. sakei* Kg15	glucansucrase	4788
FJ844434.2	*L. citreum* B/110-1-2	dextransucrase	4584
KF360258.1	*L. citreum* NRRL B-1501	alternansucrase asr	6174
MK578555.1	*L. citreum* ABK-1	dextransucrase dex-N	4488
KM083061.2	*L. citreum* ABK-1	alternansucrase	6174
AB362781.1	*L. citreum* HJ-P4	dextransucrase	4861
KF724950.1	*L. citreum* M-3	dextransucrase dsrV	4590
KF360257.1	*L. citreum* NRRL B-1498	alternansucrase asr	6270
MK288168.1	*L. lactis* AV1n	dextransucrase dsr	4900
GQ21391.1	*L. lactis* EG001	glucansucrase	4503
GQ213971.1	*L. lactis* EG001	glucansucrase	4503
KJ000059.1	*L. mesenteroides* LM34	glucansucrase dsr	4503
AJ250173.2	*L. mesenteroides* NRRL B-1355	alternansucrase asr	6174
AY743959.1	*L. mesenteroides* L0309	dextransucrase dsrX	4569
MH684490.1	*L. mesenteroides* MTCC 10508	levansucrase	3033
DQ003207.1	*L. mesenteroides*	levansucrase levS	3069
AY665464.1	*L. mesenteroides*	levansucrase m1ft	1275
KR052819.2	*L. mesenteroides* Lm 17	levansucrase	3069

AB020020.1	*L. mesenteroides*	dextransucrase dsrT	5946
AY504865.1	*L. mesenteroides* IBT-PQ	dextransucrase dsrP	5909
DQ497800.1	*L. mesenteroides* B-1299CB4	dextransucrase dsrBCB4	6077
U38181.1	*L. mesenteroides*	dextransucrase	6253
JX103826.1	*L. mesenteroides* KIBGE-IB-22	dextransucrase dsrN	4722
U81374.1	*L. mesenteroides*	dextransucrase DEX	4907
DQ345760.1	*L. mesenteroides*	dextransucrase dexYG	4584
AF030129.1	*L. mesenteroides*	glucosyltransferase dsrB	6196
AY280636.1	*L. mesenteroides* B-742CB	mutant dextransucrase dsrb742	6193
AY142210.1	*L. mesenteroides*	dextransucrase dsrR	3993
AY017384.1	*L. mesenteroides*	dextransucrase dsrD	5223
AF294469.1	*L. mesenteroides*	dextransucrase dsrb742	6194
KU306933.1	*L. mesenteroides* subsp. *mesenteroides* BD3749	putative glycosyltransferase BD3749_1645	4584
KU306932.1	*L. mesenteroides* subsp. *mesenteroides* BD3749	GH70-family glycosyltransferase BD3749_1323	4542
KU306931.1	*L. mesenteroides* subsp. *mesenteroides* BD3749	glycosyltransferase gsy	4401
GU174476.1	*P. parvulus* CUPV22	glycosyltransferase gtf	1704
EU885339.1	*W. cibaria*	glucansucrase dsrWC	4419
GU237484.3	*W. cibaria* LBAE-K39	dextransucrase dsrK39	4338
KJ173611.1	*W. confusa* VTT E-90392	dextransucrase	4272
GQ46664.1	*W. confusa* MBFCNC-2	fructansucrase	3534
KP729387.1	*W. confusa* Cab3	dextransucrase	4206