TABLE S1 Sources of isolation and general genome features of *L. plantarum* strains. The previously determined genomes of WCFS1 (1, 2) and *L. plantarum* type strain DSM20246, *L. plantarum* subsp. *plantarum* DSM20174 and *L. plantarum* subsp. *argentoratensis* DSM16365 (3) are indicated by #.

Sources	**Accession No.**	**Strains**	**GC content (%)**	**Size (bp)**	**Number of Subsystems**	**Number of Coding Sequences**
Fermented Rice	LEBT00000000	*L. plantarum* K35	44.1	3,492,709	330	3345
	LEBW00000000	*L. plantarum* K36	44.5	3,211,684	332	3042
	LEBS00000000	*L. plantarum* T10	44.2	3,494,222	337	3387
Pla Pang Dang (Fermented fish)	LEBV00000000	*L. plantarum* P14	44.3	3,346,627	335	3257
	LEBR00000000	*L. plantarum* P22	44.3	3,303,556	327	3123
	LEBQ00000000	*L. plantarum* P26	44.4	3,275,958	326	3052
	LEBP00000000	*L. plantarum* P31	44.5	3,264,053	334	3095
	LEBO00000000	*L. plantarum* P42	44.5	3,343,255	334	3100
	LEBN00000000	*L. plantarum* P62	44.5	3,237,213	334	3089
	LEBM00000000	*L. plantarum* P67	44.4	3,238,093	326	3052
	LEBL000000000	*L. plantarum* P73	44.4	3,310,440	335	3146
	LEBK00000000	*L. plantarum* P76	44.3	3,343,255	328	3197
	LEBJ00000000	*L. plantarum* P86	44.4	3,237,213	323	3057
Fermented food (Pickled cabbage)	LEAW00000000	*L. plantarum* TISTR875	44.4	3,225,632	329	3055
Shrimp intestine	LEBI000000000	*L. plantarum* MHO2.4	44.5	3,207,275	329	3047
	LEBH00000000	*L. plantarum* MHO2.5	44.4	3,349,544	337	3195
	LEBG00000000	*L. plantarum* MHO2.9	44.3	3,338,588	333	3190
Marine fish	LEBF00000000	*L. plantarum* A3	44.2	3,394,509	336	3237
infant feces 8 months	LEBE00000000	*L. plantarum* I08	44.4	3,313,485	330	3170
infant feces 6 months	LEBU00000000	*L. plantarum* I61	44.4	3,314,417	330	3167
Infant feces 5 months (aerobic)	LEBD00000000	*L. plantarum* CIF17A2	45.1	3,105,497	330	2945
	LEBC00000000	*L. plantarum* CIF17A4	45.1	3,107,640	329	2932
	LEBB00000000	*L. plantarum* CIF17A5	45.1	3,106,602	329	2939
Infant feces 5 months (anaerobic)	LEBA00000000	*L. plantarum* CIF17AN2	45.1	3,128,930	330	2942
	LEAZ00000000	*L. plantarum* CIF17AN8	45.1	3,107,439	330	2942
Human	LEAV00000000	*L. plantarum* 299V	44.4	3,304,086	330	3134
Pickled cabbage	LEAY00000000	*L. plantarum* DSM2601	44.5	3,199,427	329	3020
	#	*L. plantarum* DSM20174	44.5	3,208,905	335	3060
Plant material	LEAX00000000	*L. plantarum* DSM20246	44.4	3,242,593	331	3063
Fermented cassava roots	#	*L. plantarum* DSM16365	45	3,201,989	334	2999
Human (oral cavity)	NC_004567.2	*L. plantarum* WCSF1	44.5	3,308,274	330	3013

Fig. S1 Pan and core genome of 28 *L. plantarum* strains isolated from various sources.

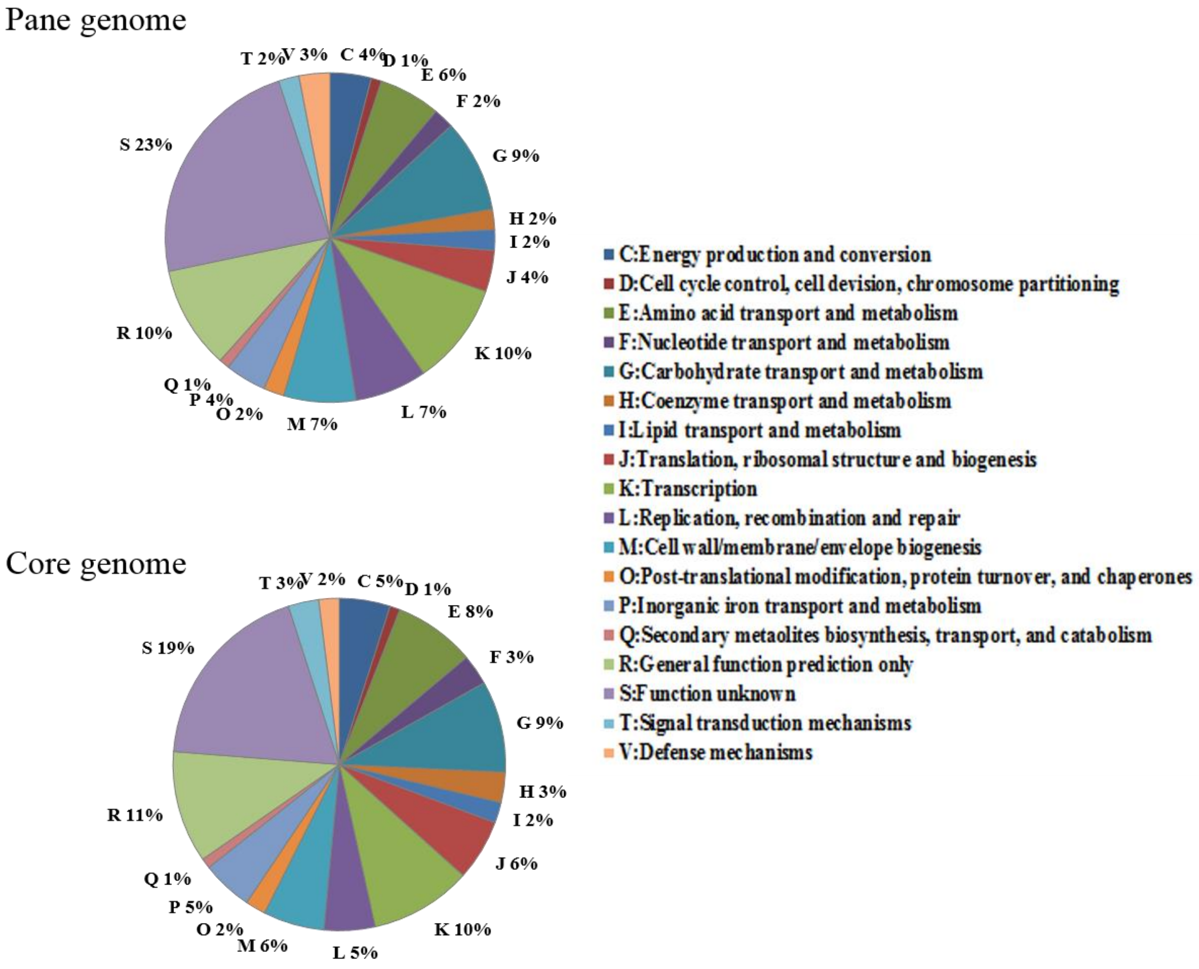


Fig. S2 Analysis of genome diversity based on carbohydrate gene presence and absence in *L. plantarum* isolated from various sources by using Mega 6 programme, dark orange colour: gene presence in the genome, white orange colour: gene absence in the genome. The PTS and other transport and metabolic genes for the following carbohydrates were identified: 1: Trehalose biosynthesis; 2: Sucrose utilization; 3: Fructooligosaccharide (FOS) and raffinose utilization; 4: Lactose utilization; 5: Moltose and moltodrextrin utilization; 6: Beta-glucoside metabolism; 7: Trehalose uptake and utilization; 8: Lactose and galactose uptake utilization; 9: Mannose metabolism; 10: D-Tagatose and galactitol utilization; 11: D-gulconate and ketogluconates metabolism; 12: Fructose utilization; 13: D-ribose utilization; 14: L-rhamnose utilization; 15: D-sorbitol (D-glucitol) and L-sorbose utilization; 16: L-arabinose utilization; 17: Glycerol and glycerol-3-phosphate uptake and utilization; 18: Mannitol utilization; 19: Inositol catabolism.

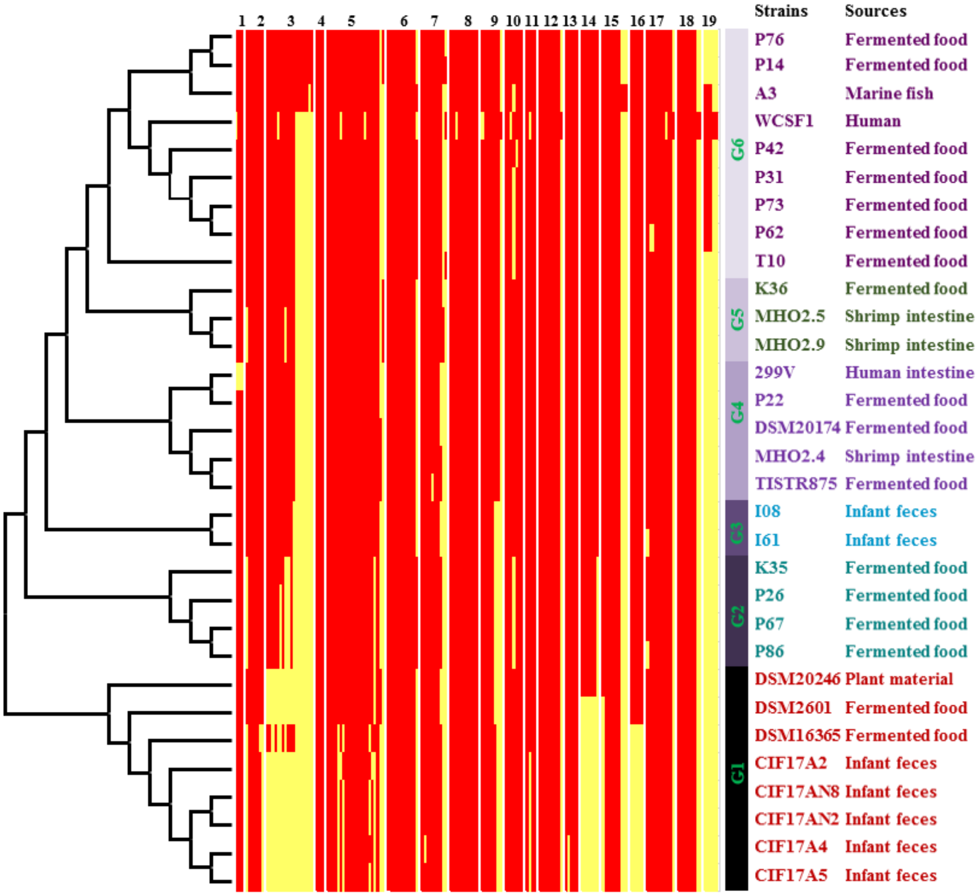


Fig. S3 Genes involved in carbohydrate metabolism in the RAST-annotated genomes of the *L. plantarum* strains.

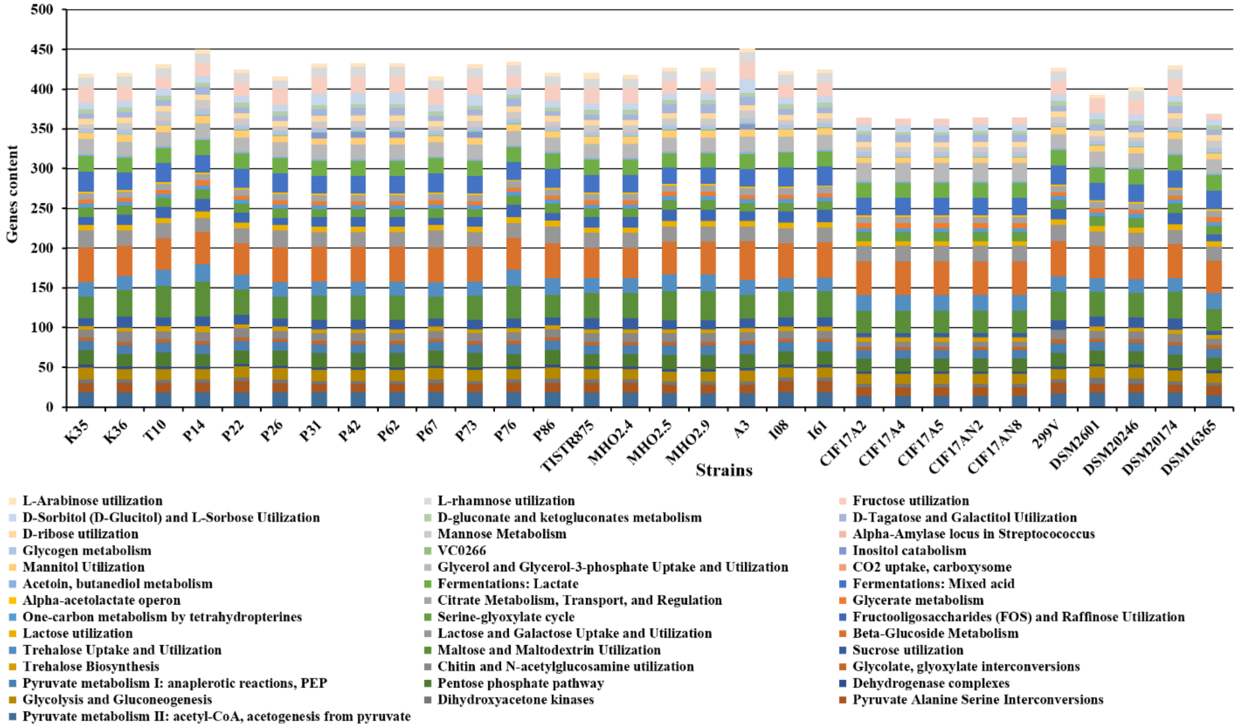
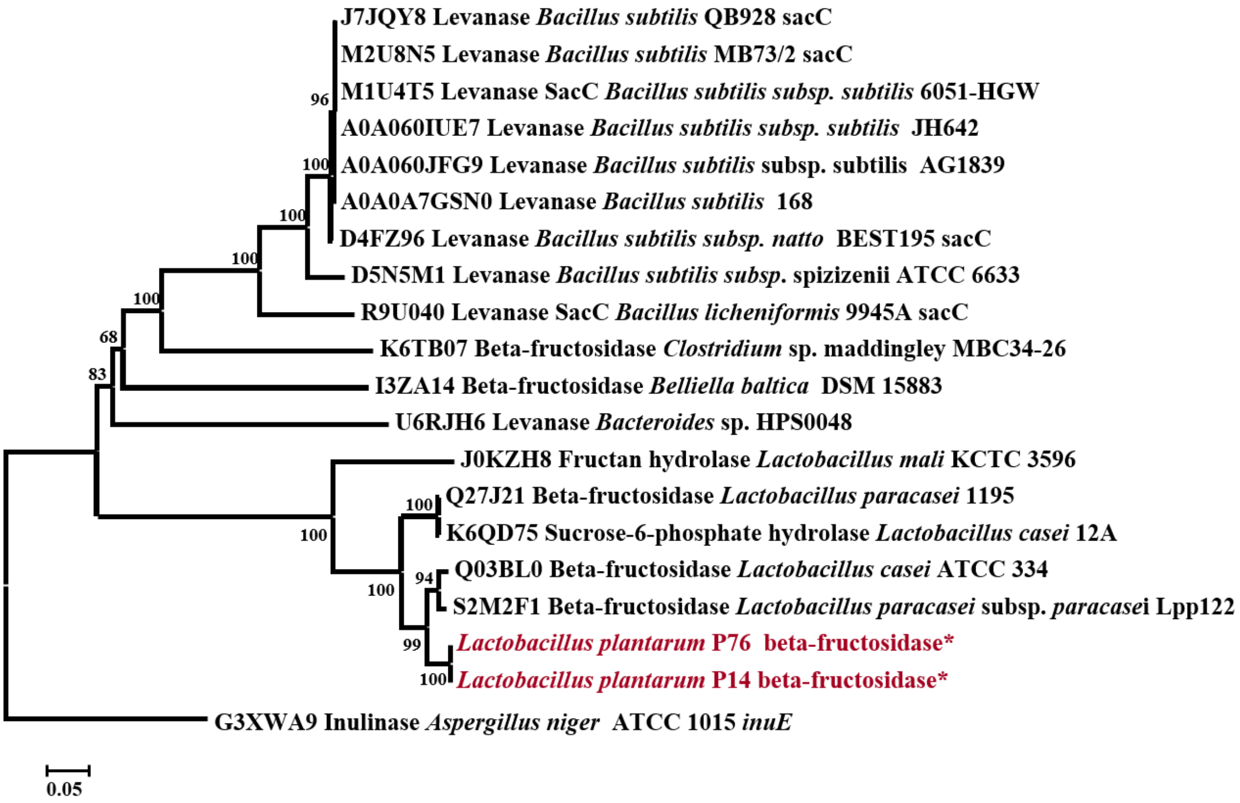


Fig. S4 Phylogenetic tree based on amino acid sequence of beta-fructosidase of *L. plantarum*. The tree was constructed by using MAGA 6 (NJ plot with 1000 bootstraps value, P-distance model).



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