Title

Selection of *Lactiplantibacillus* strains for the production of fermented table olives

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Table S1. Reaction mixture and PCR-program for the amplification of partial 16S rRNA gene.

Reagents	**Reaction mixture concentration (50 μL)**	**Amplification program ***
Deionized water	-	Initial denaturation: 95°C for 5 minutes
Reaction buffer (WonderTaq, Euroclone)	1x	
Primer forward 27F-ND	0.5 μM	30 cycle of: denaturation (95°C, 45 sec.), annealing (54°C, 45 seconds) and extension (72°C, 45 seconds)
Primer reverse 1492R-ND-L	0.5 μM	
Taq (WonderTaq, Euroclone)	0.025U/μL	
DNA	50 ng/μL	Final extension: 72°C for 7 minutes

* PCR was carried out in a T100™ Thermal Cycler Bio-Rad (Bio-Rad Laboratories Srl, Segrate, Milan, Italy); PCR products (1535 bp) were separated (90 min at 100 V) on 1.5% w/v agarose gel, stained with 0.05 μL/mL of GelRed™ (10,000*x* in water; Botium Inc., Fremont, California) and visualized using GelDoc XR system (Bio-Rad Laboratories).

Table S2. List of genes involved in phenolic compound metabolism, used to verify the occurrence in publicly available genomes of *Lactiplantibacillus paraplantarum*, *Lpb. plantarum* and *Lpb. pentosus*.

Gene annotation	COG categories*	Strain	Accession n.	Locus tag (symbol)	Size (bp/aa)	References
β-glucosidase/6-phospho-β-glucosidase	G (COG 2723)	*Lpb. plantarum* WCFS1	CCC78348	lp_0906 (pbg2)	1503 bp/500 aa	[1]
aromatic acid carboxylase, subunit B	H (COG 0163)	*Lpb. plantarum* WCFS1	CCC77798	lp_0271 (*lpdB*)	564 bp/187 aa	[1, 2]
3-octaprenyl-4-hydroxybenzoate carboxy-lyase, UbiD family	H (COG 0043)	*Lpb. plantarum* WCFS1	CCC80016	lp_2945 (*lpdC*)	1473 bp/490 aa	[1-3]
aromatic acid carboxylase, subunit D	-	*Lpb. plantarum* WCFS1	CCC77799	lp_0272 (*lpdD*)	411 bp/136 aa	[1, 2]
phenolic acid decarboxylase	Q (COG 3479)	*Lpb. plantarum WCFS1*	CCC80619	lp_3665 (*padA*)	537 bp/178 aa	[1, 4]
transcriptional regulator of phenolic acid metabolism, PadR family	K (COG 1695)	*Lpb. plantarum* WCFS1	CCC80618	lp_3664 (*padR*)	546 bp/181 aa	[1]
tannase (tannin acyl hydrolase)	I (COG 0657)	*Lpb. plantarum* WCFS1	CCC80022	lp_2956 (*tanLp1*, $tanB_{Lp}$)	1410 bp/469 aa	[1-3, 5, 6]
hypothetical protein (with tannase-like activity)	-	*Lpb. plantarum* ATCC 14917	KRL35904	HMPREF0531_11477 ($tanA_{Lp}$)	1881 bp/626 aa	[1, 6-8]
carboxylesterase	Q (COG 1647)	*Lpb. plantarum* WCFS1	CCC78257	lp_0796	750 bp/249 aa	[5]
esterase	I (COG 0657)	*Lpb. plantarum* WCFS1	CCC80020	lp_2953	750 bp/249 aa	[2]
alpha/beta hydrolase	I (COG 0657)	*Lpb. plantarum* JDM1	WP_015825406	JDM1_1092	885 bp/295 aa	[6, 9]

* G: carbohydrate transport and metabolism; H: coenzyme transport and metabolism; Q: secondary metabolites biosynthesis, transport and catabolism; K: transcription; I; Lipid transport and metabolism. In bracket COG family.

Table S3. Exopolysaccharides (EPS) production and antimicrobial activity of strains.

EPS production				Antimicrobial activity	
Strains	**G-MRS** [a]	**M-MRS** [a]	**S-MRS** [a]	***Y. lipolytica*** [b]	**halo** [c]
B15 (Lpl)	+	+	+	CNRZ1890 (Lpl)	23.0
38AA (Lpl)	+	+	+	WCFS1 (Lpl)	18.1
B7N23 (Lpl)	+	+	+	MT2D6S (Lpl)	18.1
MTD12L (Lpl)	+	+	+	MT2D7S (Lpl)	17.9
MTNTA3S (Lpl)	+	+	+	MTC13L (Lpl)	17.2
MT2D6S (Lpl)	+	+	+	1513 (Lpl)	13.1
MT2D7S (Lpl)	+	+	+	872 (Lpl)	13.4
MTC13L (Lpl)	+	+	+	4TP (Lpe)	19.0
MT2S (Lpl)	+	+	+	954 (Lpl)	20.3
MTF13S (Lpl)	+	+	+	4TG (Lpe)	15.0
MTF1L (Lpl)	+	+	+	O4 (Lpl)	8.6
MTF28L (Lpl)	+	+	+	O19 (Lpe)	12.1
MTF9L (Lpl)	+	+	+	O20 (Lpe)	14.5
2TP (Lpe)	+	+	+	OM53 (Lpe)	11.6
5TP (Lpe)	+	+	+	OM52 (Lpe)	10.5
O4 (Lpl)	+	+	+		
O18 (Lpe)	-	+	-		
O19 (Lple)	+	+	+		
OM50 (Lpe)	-	-	+		
OM53 (Lpe)	-	-	+		

[a] G-MRS, M-MRS, S-MRS: MRS with 20 g/L maltose (M-MRS), or 20 g/L glucose (G-MRS), or 50 g/L sucrose (S-MRS) as carbon source (+, EPS-positive strains; -, EPS-negative strains); [b] *Y. lipolytica:* inhibitory activity of strains against *Yarrowia lipolytica* YL-12 (Deferred Antagonism Assay [10]); [c] halo: the size of inhibition zone (mm) was measured with a caliper. In brackets: Lpl, *Lpb. plantarum*; Lpe, *Lpb. pentosus.*

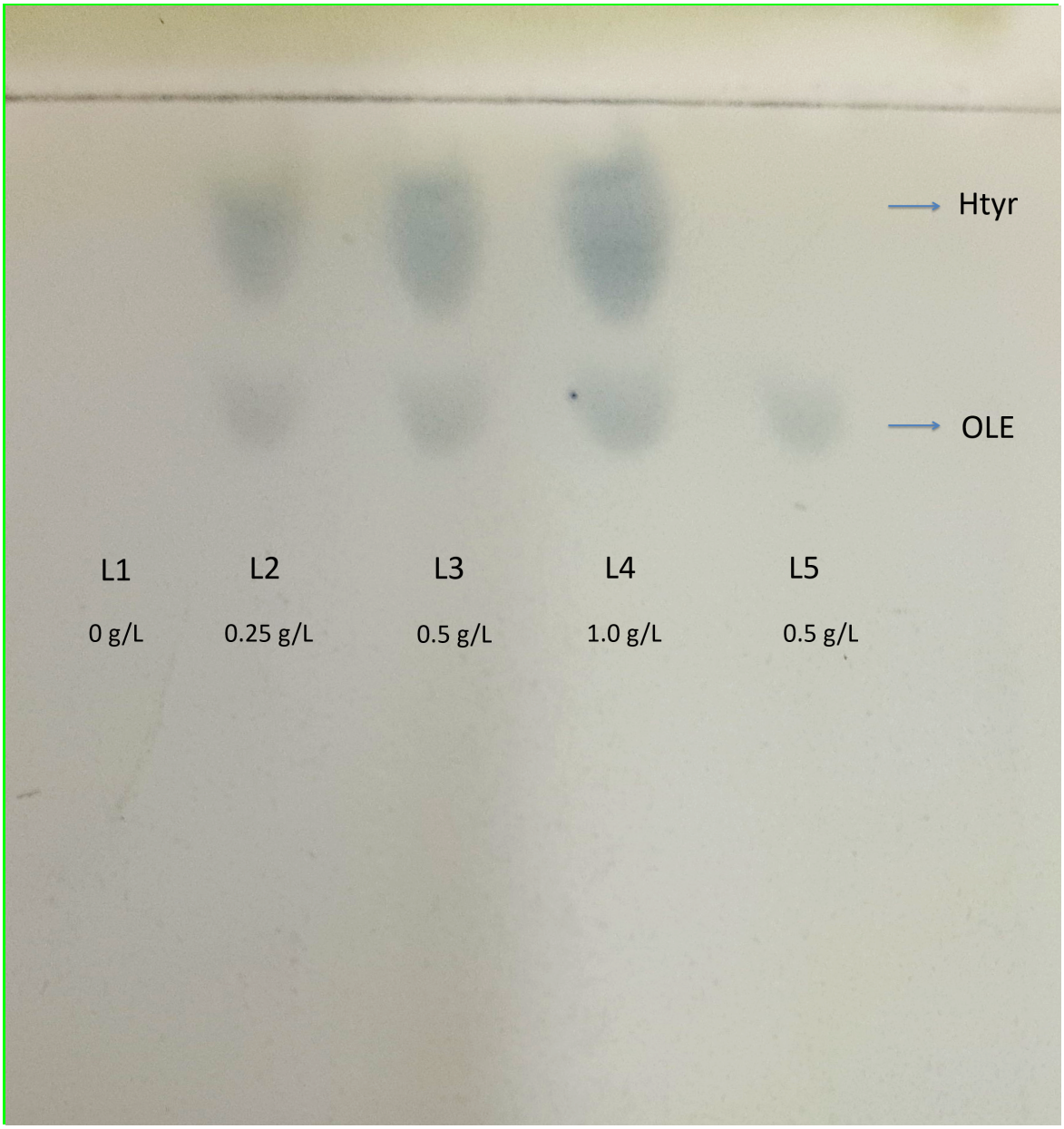

Figure S1. Thin Layer Chromatography (TLC) of MRS samples ([11]; *section 2.3*) unsupplemented (lane 1, L1) and supplemented with 0.25 g/L of oleuropein (OLE) and hydroxytyrosol (Htyr; L2), or with 0.5 g/L of OLE and Htyr (L3) or with 1 g/L of OLE and Htyr (L4) or only with 0.5 g/L of OLE (L5).

Table S4. Qualitative evaluation of oleuropein degradation and hydroxytyrosol formation using Thin Layer Chromatography (TLC).

Strains	Oleuropein (OLE) TLC spot		Hydroxytyrosol (Htyr) TLC spot	
	presence	absence	presence	absence
Lpb. paraplantarum B7N26 *Lpb. plantarum* WCFS1, ISLCPT68, PA20S, PE2S, B7N23, MT2A11S, B161, O1, O13; *Lpb. plantarum* subsp. *plantarum* B15, C17, 1069, DKO22, S85, UBS3, P1.5, MTNTA3S, DCU101, 38AA, FSM170, S12, MT2D6S, 954, UT2.1, US3.1, S2A19LPa; *Lpb. plantarum* subsp. *argentoratensis* CNRZ1890, DK36, FSL170, MTC13L *Lpb. pentosus* 2TP, 4TP, 4TG, 5TP, P13.3, OM24, OM53, OM52, OM62, OM50, OM13, OM14, OM35, O12, O17, O18, O19, O20, O24	OLE degradation ability		Htyr formation ability	
Lpb. paraplantarum MTG30L, MTG8L *Lpb. plantarum* MT2D3S, O4; *Lpb. plantarum* subsp. p*lantarum* NCIMB8826, MTD12L, MT2D20S, ISLCPT57, MT2D7S, MT2D25L, MT2S, MTF13S, MTF1L, MTF28L, MTF9L, LM3; *Lpb. plantarum* subsp. *argentoratensis* NCIMB12120 *Lpb. pentosus* LPL, O5, O11, O15	OLE degradation ability			Htyr formation inability
Lpb. paraplantarum F10 *Lpb. plantarum* subsp. *plantarum* 1505, 1513, 872, 1089, NCFB340		OLE degradation inability		Htyr formation inability

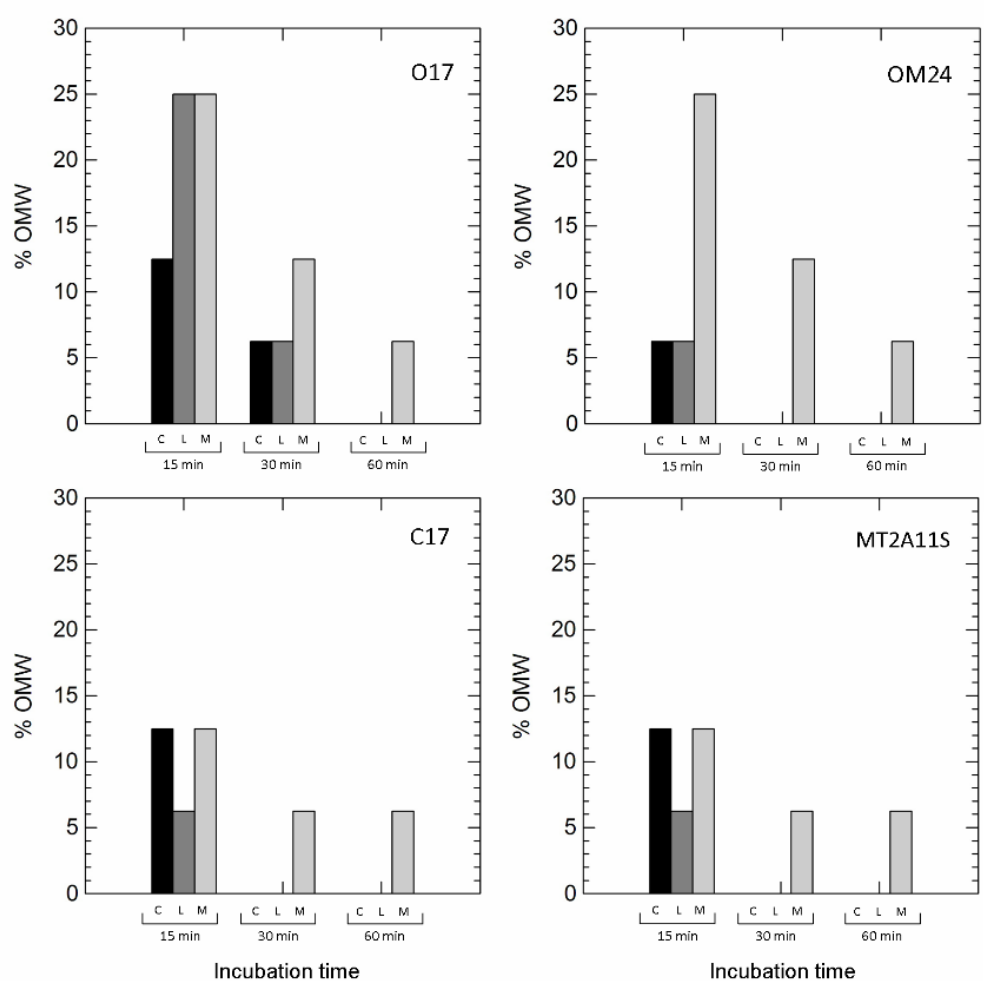

Figure S2. Survival of *Lpb. pentosus* O17, OM24 and *Lpb. plantarum* C17, MT2A11S to different concentrations (from 50% to 6.12% v/v) of *Leccino*, *Coratina* and *Cima di Melfi* OMWs after 15, 30, 60 and 120 minutes of incubation at 30°C.

Table S5. Occurrence analysis of genes involved in degradation and metabolism of phenolic compounds in *Lactiplantibacillus pentosus* genomes.

Strains	**Sequencing status**	**Isolation source**	***pbg*** [a]	***padA*** [b]	***padR*** [c]	***Carboxyl-esterase***	***lpdB*** [d]	***lpdC*** [e]	***lpdD*** [f]	***Esterase***	***tanA*** [g]	***tanB*** [h]
Lpb. pentosus 1.2.11, 1.2.13, 1.2.7, 1.8.18, 1.8.6, 14.2.16, 14.2.3, 14.8.42, 3.2.36, 3.2.37, 3.8.24, 3.8.45, 7.2.11, 7.2.15, 7.2.20, 7.2.23, 7.8.2, 7.8.46, LA0445, MU0445	Permanent draft	Cucumber fermentation	1	1	1	1	1	1	0	1	1	1
Lpb. pentosus ZFM222	Finished	Fermented vegetables										
Lpb. pentosus SLC13	Finished	Mustard pickles										
Lpb. pentosus BGM48	Finished	Olive fermentation										
Lpb. pentosus 3.2.8	Permanent draft	Cucumber fermentation	1	1	1	1	1	1	1	1	1	1
Lpb. pentosus 1.8.9	Permanent Draft	Cucumber fermentation	1	0	1	1	1	1	0	1	1	1
Lpb. pentosus DSM 20314	Finished	Corn silage	1	1	1	1	1	1	0	1	1	0
Lpb. pentosus FL0421	Permanent draft	Temperate deciduous forest biome soil	1	1	1	1	1	1	0	1	0	0
Lpb. pentosus KCA1	Permanent draft	Vagina of a healthy Nigerian woman	1	1	1	1	1	1	0	1	0	1
Lpb. pentosus O17	Draft (this study)	Brine from treated table olives (*Cerignola* cv.)	1	1	1	0	0	1	0	1	1	1

[a] *pbg: β*-glucosidase; [b] padA: p-coumaric acid decarboxylase; [c] *padR*: Transcriptional regulator PadR; [d] *lpdB*: Gallate decarboxylase subunit B; [e] *lpdC*: Gallate decarboxylase subunit C; [f] *lpdD*: Gallate decarboxylase subunit D; [g] *tanA*: Tannase subunit A; [h] *tanB*: Tannase subunit B. 1: gene presence; 0: gene absence.

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