

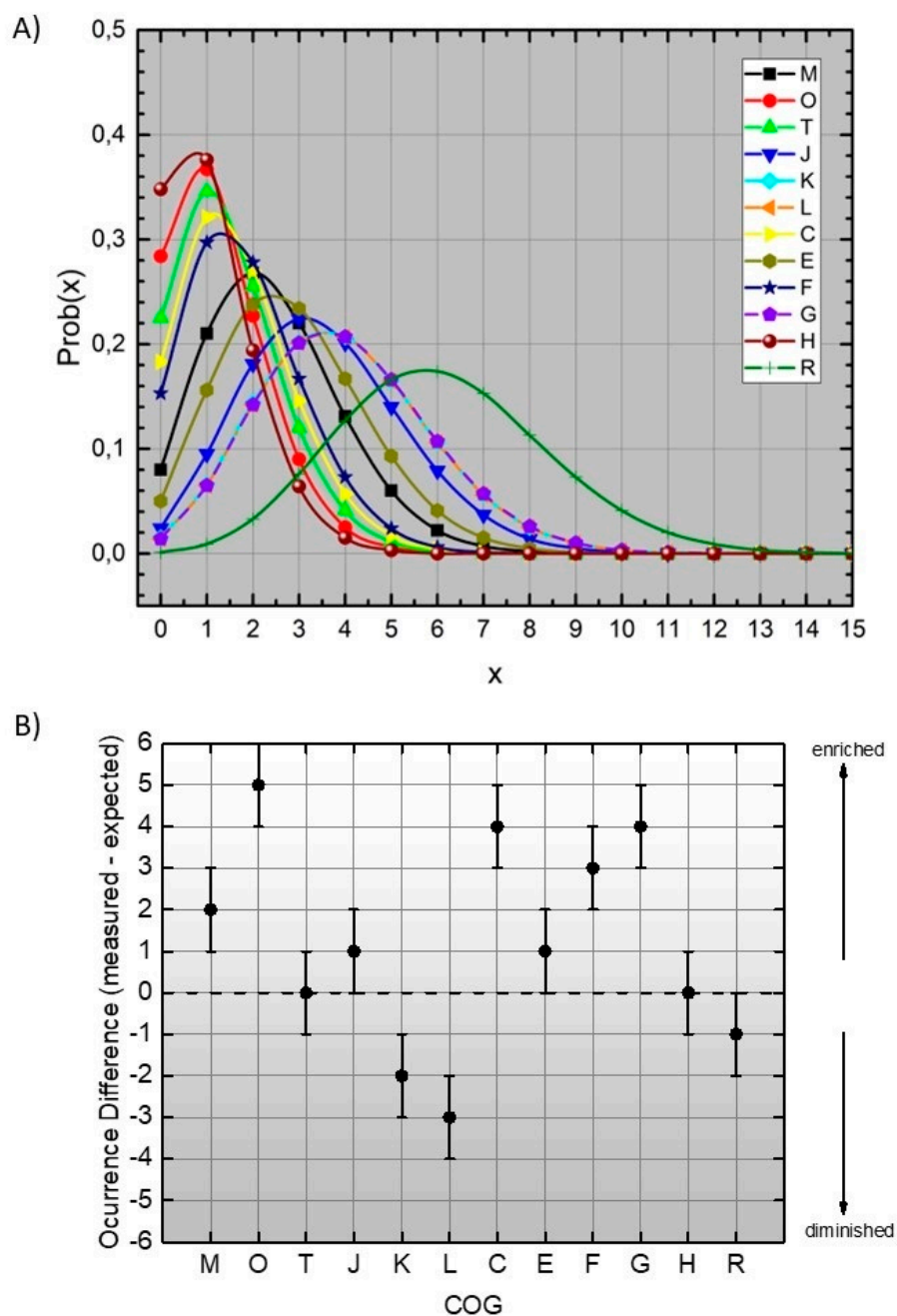
*Supplementary Materials*

# **Role of curing agents in the adaptive response of the bioprotective *Latilactobacillus curvatus* CRL 705 from a physiologic and proteomic perspective**

**Lucrecia C. Terán, Alejandra Orihuel, Emilse Bentencourt, E, Raúl Raya and Silvina Fadda \***

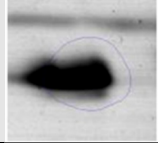
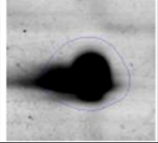
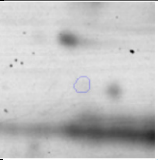
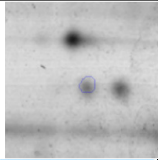
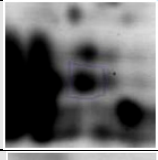
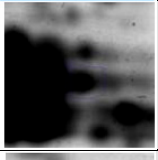
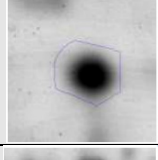
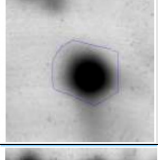
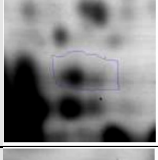
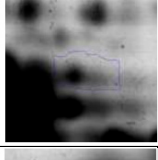
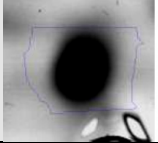
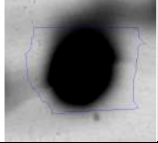
Centro de Referencia para Lactobacilos, Consejo Nacional de Investigaciones Científicas y Técnicas (CERELA CONICET), Chacabuco 145, T4000ILC, San Miguel de Tucumán, Tucumán, Argentina; lucreteran@gmail.com (L.C.T.); rraya@cerela.org.ar (R.R.)

\* Correspondence: sfadda@cerela.org.ar (S.F.)

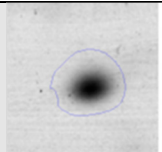
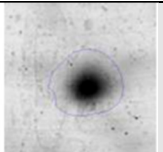
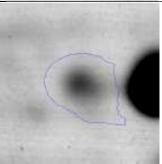
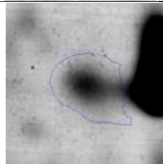
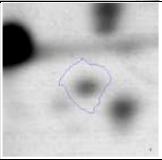
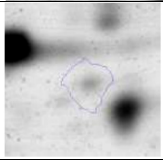
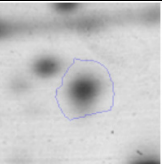
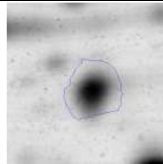
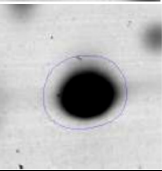
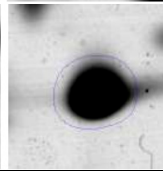
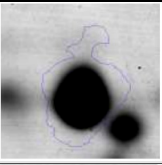
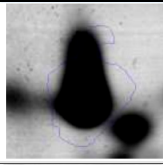
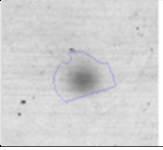
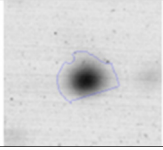


**Figure S1. A)** Hypergeometric distribution for the probabilities (Prob) of finding a certain COG functional category a certain number of times “x” of the differentially expressed proteins of *L. curvatus* CRL 705 while growing in CDM with and without additives at 25 °C. The highest value of the y axis (Prob) for each of the curves represents the higher probability of the times of occurrence of proteins from a certain COG. **B)** Differences between measured and expected occurrence for the proteins of each COG category, where 0 represents no differences in occurrence and separates potentially enriched categories (positive values) from the potentially impoverished categories (negative values).

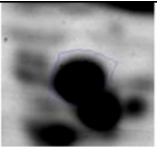
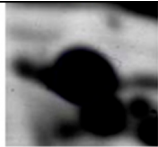
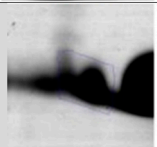
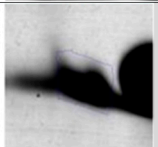
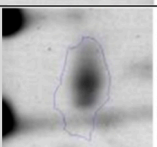
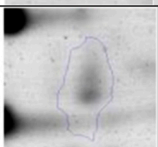
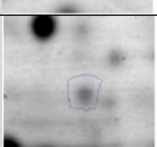
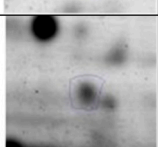
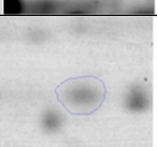
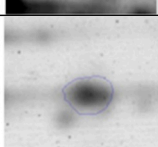
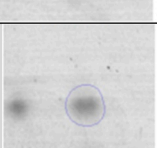
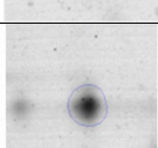
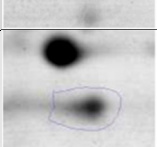
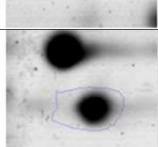
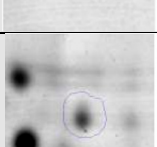
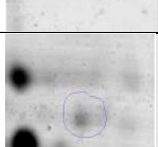
**Table S1.** Differentially expressed proteins by *L. curvatus* CRL 705 during growth in CDM with (CDM<sup>+CA</sup>) and without (CDM<sup>-</sup>) the presence of curing additives (CA) at 25°C

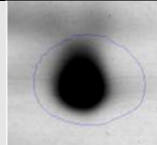
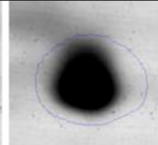
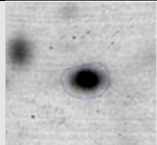
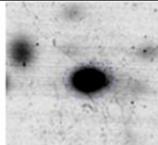
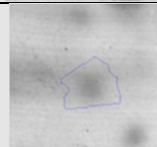
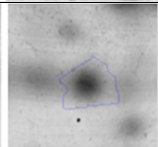
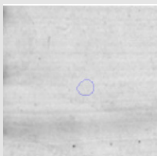
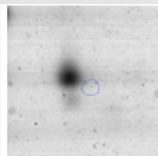
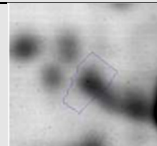
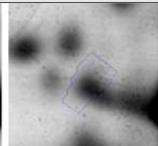
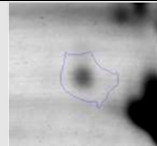
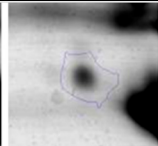
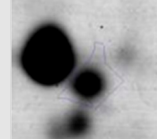
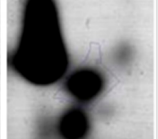
Biological process	COG <sup>a</sup>	Spot N <sup>qb</sup>	UniProt entry	Name of the protein and abbreviation	MASCOT Score <sup>c</sup>	# matching peptides <sup>d</sup>	MM/pI <sup>f</sup>	Fold changes <sup>g</sup>	Detailed 2DE gel showing differentially expressed spot in:	
									CDM <sup>+CA</sup>	CDM <sup>-</sup>
TRANSLATION AND MODIFICATION OF PROTEINS	O	LT04	A0A3R5V4Y6	Trigger factor Tig WP_004271115.1	218	7	47903/ 4.43	-1.5		
	O	LT08	A0A385ACP8	ATP-dependent Clp protease ATP-binding subunit DT351_03000 WP_004265761.1	136	4	81331/ 5.06	-3.0		
	J	LT12	A0A385ACG4	Glutamyl-tRNA(Gln) amidotransferase subunit A GatA WP_004270872.1	408	12	51771/ 4.90	-1.2		
	J	LT16	A0A1B2A539	50S ribosomal protein L10 RplJ WP_064777478.1	350	8	17832/ 4.97	-1.3		
	J	LT25	A0A1X7QIK5	Elongation factor Tu TufA WP_004271118.1	112	2	43183/ 4.70	-1.2		
	J	LT40	A0A1B2A552	50S ribosomal protein L7/L12 RplL WP_004270851.1	413	4	12639/ 4.43	-1.5		

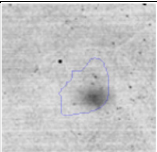
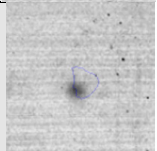
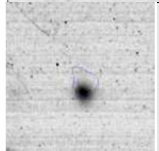
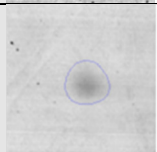
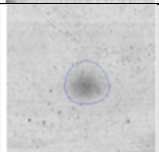
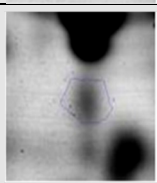
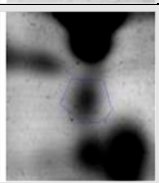
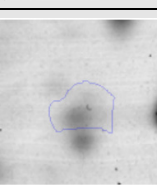
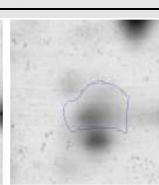
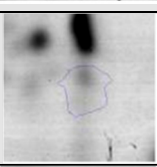
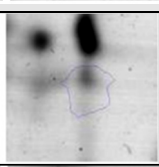
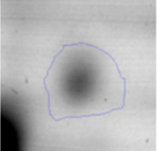
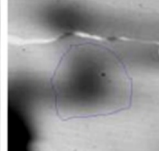
CARBOHYDRATES METABOLISM AND ENERGY  
PRODUCTION

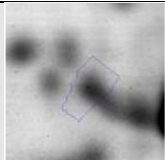
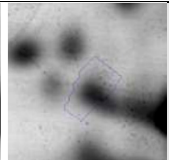
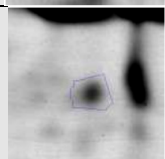
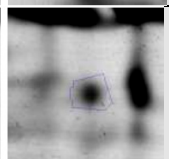
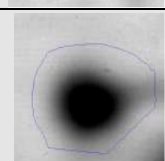
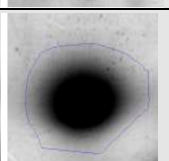
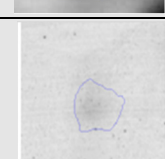
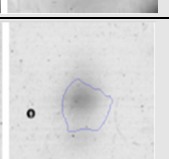
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G	LT09	A0A0B2XPK6	2,3-diphosphoglycerate- dependent phosphoglycerate mutase GpmA WP_039098080.1	111	2	258382/ 5.13	-1.5		
G	LT10	UPI000230F3DE	sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC WP_004266075.1	161	3	40966/ 5.36	+2.3		
G	LT26	UPI000230F588	PTS mannose transporter subunit IIAB ManX WP_004270728.1	279	7	35347/ 5.34	-1.3		
G	LT27	A0A0B2XK70	(ATP dependent) 6-phosphofructokinase PfkA KHO12221.1	234	6	33664/ 5.26	-1.5		
G	LT30	A0A1B2A4B2	2,3-diphosphoglycerate- dependent phosphoglycerate mutase GpmA WP_004271006.1	345	8	25868/ 5.04	-1.5		
G	LT31	A0A1B2A408	Histidine phosphatase LCU_08255 WP_004266073.1	300	9	24829/ 6.08	-1.8		

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C	LT32	A0A1B2A5E8	L-lactate dehydrogenase Ldh WP_004270763.1	298	7	33664/ 5.26	-1.4		
G T	LT36	UPI000230EFAA	Pyruvate kinase Pyk WP_004270411.1	271	8	62980/ 5.27	-1.4		
C	LT41	A0A385ADR5	L-lactate oxidase DT351_03565 WP_004265223.1	220	1	39721/ 5.36	+1.7		
C	LT43	UPI000B5E1B86	Dihydrolipoyl dehydrogenase LpdA ASN60289.1	103	1	49610 49330/ 5.07	-1.4		
F	LT02	A0A4U0E4L1	Dihydroorotase FCF11_02690 WP_004270425.1	226	8	46224/ 5.45	-2.8		
F	LT07	A0A4U0E0K0	CTP sintetase FCF11_05720 WP_004270634.1	314	7	58991/ 5.44	-2.7		
E	LT11	UPI000230F388	Type I glutamate--ammonia ligase GlnA WP_004265314.1	382	9	50544/ 5.40	-2.3		
E H	LT19	UPI0006F0BB97	Pyruvate oxidase Pox KRK92661.1	240	9	61527/ 5.06	+1.6		

CELL WALL BIOSYNTHESIS	F R	LT28	A0A1B2A4E0	IMP dehydrogenase GuaB WP_004265151.1	355	9	52368/ 5.37	-1.5		
	E	LT35	UPI000230EFAA	ABC transporter family protein OppF WP_004265559.1	363	9	36057/ 6.09	-1.8		
	F	LT37	A0A1X7QJJ2	UMP kinase PyrH WP_076800600.1	245	5	25824/ 5.04	-1.5		
	M	LT14	WP_056967123.1	bifunctional UDP-N- acetylglucosamine diphosphorylase/glucosamine-1- phosphate N-acetyltransferase, partial GlmU	240	7	43975/ 5.73	-1.4		
	M	LT22	UPI000B5EB748	D-alanine--D-alanine ligase Ddl ASN59162.1 WP_004271284.1	281	6	38239/ 4.48	-1.5		
	M	LT23	UPI000230D57D	UTP--glucose-1-phosphate uridylyltransferase GalU WP_004271214.1	188	7	33693/ 5.52	-1.7		
	M	LT39	UPI000975D304	dTDP-4-dehydrorhamnose 3,5- epimerase RfbC WP_076638998.1	431	9	21646/ 5.35	-1.4		

RNA RELATED	R	LT13	A0A221RYJ7	GTPase Era Era WP_004270810.1	165	5	34532/ 6.04	-1.7		
	R	LT18	A0A1B2A7I2	Ribonuclease J Rnj WP_065825720.1	239	8	63559/ 5.70	-1.6		
	R	LT38	UPI000230F4ED	Phenylalanine-tRNA ligase/ DUF4479 domain-containing protein PheRS WP_004270340.1	145	1	22224/ 4.34	-1.3		
DNA REPLICATION AND REPAIR	L	LT05	A0A0B2XPH3	Single-stranded DNA-binding protein Ssb WP_004265848.1	367	6	18621/ 4.92	-1.4		
	L	LT20	UPI000230F194	putative endonuclease 4 Nfo EHE85189.1	107	6	32046/ 5.28	-1.5		
REDOX PROCESSES	O	LT06	A0A1B2A4R3	NAD(P)/FAD- dependentOxidoreductase BCY75_02680 WP_004270517.1	173	3	36259 36281/ 5.21	-1.4		
	O C	LT15	A0A0B2XKA6	Thioredoxin TrxA WP_004265032.1	140	9	11555/ 4.57	-1.6		

REDOX PROCESSES	O	LT21	A0A385AFF0	Thioredoxin-disulfide reductase TrxB WP_004265965.1	118	3	32787/ 4.73	-1.3		
	C R	LT29	A0A0B2XMI6	NADP-dependent oxidoreductase OA78_1420 WP_035185948.1	421	9	33766/ 5.13	-1.3		
REGULATION	K	LT03	A0A0B2XPU8	Cold Shock protein CspC WP_004270163.1	178	3	7346/ 4.48	-1.4		
	K	LT17	A0A0B2XP73	MarR family transcriptional regulator OhrR WP_039098448.1	173	6	17636/ 5.97	-2.0		

<sup>a</sup>: Functional category according to COG database where each letter represents the different COG functional categories: O: molecular chaperones and related functions; J: translation, including ribosome structure and biogenesis; G: carbohydrate metabolism and transport; C: energy production and conversion; T: signal transduction mechanisms; K: transcription; E: amino acid transport and metabolism; F: nucleotide transport and metabolism; H: Coenzyme transport and metabolism; M: cell wall structure and biogenesis and outer membrane; L: Replication, recombination and repair; K: Transcription; R: general functional prediction only.

<sup>b</sup>: Spot designations correspond to those of the gels shown in Figure 3