

## Supporting Information

# Contribution of YthA, a PspC family transcriptional regulator to *Lactococcus lactis* F44 acid tolerance and nisin yield: a transcriptomic approach

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**Table S1** Significantly changed genes in FythA in other pathways

<b>Gene name</b>	<b>Log2 Ratio*</b>	<b>Description</b>
<b><i>Translation, ribosomal structure and biogenesis</i></b>		
<i>cysS</i>	2.13	cysteinyl-tRNA synthase
<i>asnC</i>	2.01	asparaginyl-tRNA synthase
<i>argS</i>	1.64	arginyl-tRNA synthetase
<i>trpS</i>	1.54	tryptophanyl-tRNA synthase
<i>lysS1</i>	1.52	lysyl-tRNA synthetase
<i>ylgC</i>	3.49	RNA methyltransferase
<i>rpmG3</i>	2.85	50S ribosomal protein L33
<i>rpsN2</i>	2.55	30S ribosomal protein S14
<b><i>Signal transduction mechanisms</i></b>		
<i>kdpD</i>	2.08	histidine kinase
<i>kdpE</i>	1.80	PhoP family transcriptional regulator
<i>tcsK7</i>	1.88	histidine kinase
<i>tcsR7</i>	1.82	two-component system regulator
<i>yheB</i>	1.64	oligoribonuclease
<i>lepA</i>	1.81	GTP-binding protein LepA
<i>radA</i>	1.58	DNA repair protein RadA
<i>cstA</i>	-2.0	carbon starvation protein CstA
<i>uspA2</i>	-1.5	universal stress protein A
<i>yahB</i>	-1.5	universal stress protein A
<i>yjaB</i>	-1.5	universal stress protein family
<b><i>Transcription</i></b>		
<i>argR</i>	1.62	arginine catabolic regulator
<i>scrR</i>	2.79	LacI family transcriptional regulator
<i>yebF</i>	2.82	RpiR family transcriptional regulator, glv operon transcriptional regulator
<i>yfdD</i>	2.83	regulatory protein spx
<i>ybjK</i>	2.03	PadR family transcriptional regulator, regulatory protein PadR
<i>yfdC</i>	1.89	regulatory protein spx
<i>rex</i>	1.81	redox-sensing transcriptional repressor
<i>rlrG</i>	1.68	LysR family transcriptional regulator, hydrogen peroxide-inducible genes activator
<i>rcfB</i>	2.03	Crp family transcriptional regulator
<i>zitR</i>	1.55	zinc transport transcription regulator
<i>yohC</i>	-3.02	transcription regulator
<i>ysgA</i>	-2.01	transcriptional regulator
<i>rarA</i>	-1.53	transcriptional regulator
<i>tcsR8</i>	-2.29	Two-component system, response regulator, LytTR family
<i>hrcA</i>	-2.4	heat-inducible transcription repressor HrcA

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**Carbohydrate transport and metabolism**

<i>scrB</i>	2.49	sucrose-6-phosphate hydrolase
<i>pgi</i>	1.96	glucose-6-phosphate isomerase
<i>yrjI</i>	1.82	phosphoglycerate mutase
<i>gapA</i>	-7.8	glyceraldehyde 3-phosphate dehydrogenase
<i>enoA</i>	-1.7	enolase
<i>glk</i>	-1.9	glucokinase
<i>mtsA</i>	3.71	manganese ABC transporter substrate-binding protein
<i>mtsB</i>	2.70	manganese ABC transporter ATP binding protein
<i>mtsC</i>	3.29	membrane protein

**Inorganic ion transport and metabolism**

<i>era</i>	1.80	GTPase Era
<i>ybaB</i>	1.71	heme ABC transporter ATP-binding protein

**Secretion**

<i>secE</i>	3.00	preprotein translocase subunit SecE
<i>secY</i>	1.86	preprotein translocase subunit SecY
<i>secA2</i>	1.72	preprotein translocase subunit SecA
<i>secA1</i>	1.55	preprotein translocase subunit SecA

**Chaperones**

<i>grpE</i>	-3.1	molecular chaperone GrpE
<i>groES</i>	-2.0	molecular chaperone GroES
<i>groEL</i>	-1.9	chaperonin GroEL
<i>dnaK</i>	-2.7	molecular chaperone DnaK

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\*represents fold change in log<sub>2</sub>-scale

**Table S2** Sequence of the putative promoter regions used to motif scanning

Operon	Gene name	Log2 Ratio *	The putative promoter regions
<i>argGH</i>	<i>argG</i>	8.62	ATAAACTTTCAATTTTATTATATTTATAACTACTACCTTGCAAAAAGTGGTAGTTTTTTTCATCAACGAAAATT TTTTTGAATAAAAAAACCTCCTGACGTAATCTTATACAGTCAGGAGGAAAAGGAGTAAGCGTATTGGTCACT GGATTTTCTATAATTTTTTCAAATAGGGTAGAAAAATCTATTTATAAAAGGAGTCAAGGGGATTTGAACCCCT GCGCCGCTTTACACGGTTCGACGGATTTGAGTCCGCTGCATTACCACTCTGCCATGGCTCCACTCCTTTATC TAAATTAATTATATCACAGTTGATTCTCTTCTTGAAATAATATGAAATTGCTAGAATGAAAATAAACGCATATT TATACAAAAATGTTGACAAATGAATAAATATGCTGTACAATTGCATTTATATTAATTTGAAAGAAGAAAAATGA TGGGAAACAAAAAAATTGCTTTGGCATAATCGGGTGGATTGGATACAAGTGTGCTGTAATAATGGTTGACTG ATAAAGGATTTGACGTCATTGCTG
	<i>argH</i>	7.67	
<i>gltPQ</i>	<i>gltP</i>	6.32	CAGAATAAAAAAACTCCAATTATGGAGTTTTTATTTATTTTCAATTAATTATTATACATTAATTGTTGTATTTTTA TACTTTTTATATTATAATTATGCTATTGTTTTTATAAAAATAGAAATTATAAACAGAAAAGAGAAAATATGAA CTTTGATTTTTTACCGAAATATCTGCCCTATTTTAATGACGGGA
	<i>gltQ</i>	4.45	
<i>pyrR</i>	<i>pyrR</i>	4.41	AAAATAATTTTTGACAAGTGGCGAGAACTTTGCTATAATCTATCTAACCTTTAAGATTGTCCAGAGAGGCAGG CAAGGTCAGAAATTAATAATGTAATAATATGATGGATACTGTCCATTTTCTGATACCTACCTGCATTCTTTTTG AGTGCAGGTTTTTTGTATGTTAATGGACAACCTTAGAAATGGAAGCTAAATCGCTAAATGAAAGATTTGTTAGT TACTGACCAATTGATCATCAAGAATGAAAGGAGCCACAATGGCTAGAAAAGAAATTATTGACGAAATCACA ATGAAACGTGCAATTACACGTATCACTTACGAGATTATTGAACGTAATAAAG
<i>gltS-argE</i>	<i>gltS</i>	3.58	TTAATAATTAATAAAAAATTCCTCATTGAGTGAATTTTTATTTTGAATCAAGTATAAAAGTACAGTTTTTATCTA AAAAICTTTGTTTATTAATAATTATAATATAAATATGCAAAAATCTTGACAAAATAATTTTAAAATGTATAATT ATACTTATTCTATTTATAAAAGAGGTTTAAAGGATGAACAAGAAGATGAAAAAATTAGCATTGGGAATGGTCGG TTTGGCCGCAGTAGCAACATTAGCAGCTTGTGGAAATGGAAAATCGGCTACTAATCAAGTGGATAAAGTAA GACTTGCAAATCTGGCTCAAGTTTGTAACTAATAACAATATAACTTTTAACTAGTCCAGAGAGGGCTAG CAAGGTTGAAATCAGGAAAAATTGATTCTATTTTTACTGACAGGATTTTCTGTGTCAGTAAAAGTGAATTTGTTT TGATACTTTTTACACTTGCTAGGATTCTTGCAAGTGTTTTTTATTGCTGACAACCTACCAGGATTGGACTGCA
	<i>argE</i>	3.45	
<i>pyrE</i>	<i>pyrE</i>	3.30	

			CGTTATCTATACTCGCTACCGTAGTTCTGTCAGTTCAATATGACCAAAGGGAATTATTGAATCGGTAGAAAA TGAAGTGTGAGCTTTGCTGATGGTTCTGTCAGTAACTAGAAGGAGAAATTATGTCAATATCAAAGCCATT GCTGCAGATTTATTAGAAATTAAGCGGTCAGTCTTTACCAAGTCAACCTTTTACTTGGGCTTCAGGAATTA AGTCGC
<i>pyrB-carA</i>	<i>pyrB</i>	3.29	AAGATTCAAATTACTGACAGAATCGTCAGTAATTAAGGAAAGTGAACCTATAACTGATAGAAATCCTATCG AGATTTCCATCAGTAGATAAAAATTTGTCAGTTTACTGACAAAACAATCAAATATATTGTCAATAAACTGT TGTGACAGAGAGCACACAGTCAGGGTAAAGGAGACCTCATGTGTCAGTAAAAATGGATTAGTTCAACTCGAA AACCTCACAAGTATGGAAAAATTGAGTGTGATGAAGTCATGGGACTTATCAAAGAGCCTCAGCTT
	<i>carA</i>	3.29	
<i>pyrZD</i>	<i>pyrZ</i>	2.89	AAAAATCTTTGACGAATGACACTTTTTTCGTTATAATTTTTAAAACCTTAACTAAGTCCAGAGAGGCTTGC AAGGATACGGAAAATTTAATTTGGTTTACTGACAGCTTAAAGATGAACCTTTTTTAGCGCATTTATTCTGTGAG TAAATTACCAGTTTTTTAGTACACTTGTAAAGTTCTCTTACAAGTGTTTTTTTGTGTCAATTAAGAGTTGCCAG TAAATCTGAACTTTCTGTGTCAGTAAAATGCGATTAACATGAGCATTTTATCGATAAATAAAGAAGGTTTCAGTA AGCTGTAGCTTCTGTCCGAATAAAGAATGGAGAAATAATGCCTAAGTTACAAGAGATGATGACGATTGTGAG CCAACGTGAGGTTGCTTCTAATATTTTCGAGATGGTTCTTAAAGGAGAGCTAGTAGAAGAGATGG
	<i>pyrD</i>	3.22	
<i>aroH</i>	<i>aroH</i>	3.16	TACATAATAAAATTTATGTAAGAAAGAAATTTGAAATAAAATTAAGAAAAATAGATAAATAATTGACAAATC AAAAAATTTAATTATACTAACTAATAATATTAATATCGAGGTTCCAAAATGATTAACAACCTTTAAAAAATTT TATTTTTCTTTATGAATGATCCACATTAGTTTTTGGCTAATAAAATGTGGGTCCTCTTTGATGTTTCGTTAATCA TCTAGGGGATAAAGAAGACGTCCCCTGGGACGTCTTTTTTTATTATAAAGGAGGCACATAAAAAGTAAAATA GAAAAAATTTATTGCAAGTAAAATATTATTAAGTATTTTACTAAAAAATATAGAAAAAAGGTAAAAGATGA CTTTTAAAGAAGTCAAGTAAACAAATTAACATTAAGATGTAAGAGCTAAATCATTAAATGATGAGCAAC GAGAAAAGAAAGAAAAACGTGATA
<i>pfs</i>	<i>pfs</i>	3.19	AGAGTAAAAAGATTAGAAAAAGGTAAAAAATGAAAATAGGAATTATTTGTGCGATGGATGAAGAAATTC GCATACTTGTGAAAACCTTAGAAAATGCAGAAAACATACTCGTCATGGTTTAGTTTTTC
<i>epsGH</i>	<i>epsG</i>	2.86	GAGGAACTAATAGATGAAAATTGCAGTTTTGTTATCAACATTTAATGGAGAAAAGTATCTGAAGGAACAAAT
	<i>epsH</i>	3.01	TGAAAGTATCTTATCTCAGTCACATAAAGATTTAATATTAT
<i>ylgC</i>	<i>ylgC</i>	3.49	AGCAACCCCTCTCATTGATTTTTACTTTTACTATTATAGCAAATTTTTGCTGTTTTCGCTTTGACAAGTTTGATA

			TTGGTCACTCATTTTTAAAAATAATTTCTTTTTTATCAAAAAAATTTAGTTTTCTCTTTACAAAATACAAAAG AAGTGGTATGATATCAATTATATTAATTTGTTTTCAATCTTTCCTGTTATGATTAAGCAAATTAGTCCCCCACT AGACTTCTTGCTGAGATTGACTCCGAGGGGTCTAGTTTTTTTTGTTTTTACTTTAATTAATTTACTGACAGCTC TTCTGCTTATGGTAAAATGTTCTTAAATAATTGCATTTTACTCATAGATTTTTTGATAAGGCTGTCAGTAAAATT TTTGTTATTAAGAAAGTGTATTTTCATGAATCATATTGCTCTTTTTGAACCTCGTATTCATTTCAATACAGGAAAT ATCGCCCGCACTTGTGCGGCTACTAATACCGTTTTACATTTAATTGAAC
	<i>mtsA</i>	3.71	ATTCTTTTCCTCCTTGTGTATATGAAAACGCTATCTAAATATTTCTTACTTGAAGTATAACAAATAATAGTGTAGG AATCCAAACTTATGACTTAAACTTTTTGAGAATAAATTCTGGAATTTAGTATTGAAAGAAAAGTGGTGTAGTTT TCAAATATATTAATAATATTAATAAATAAATAGCTAGTGCAAATATATTGATTTAATTTTTAGGTTCATGCTATAA TCGTGAGAAAGGATTAATTAGTTTTGATTTACTATCATAAGGAGAAAAACAATGATAAATACTAAGAATTTAAA TGTATTCTATAATGAAAATAAAGTCCTGAAAGATATCAACTAGAAGTTATACCTGGGAGAATCACTGGTATTA TCG
<i>mtsBCA</i>	<i>mtsB</i>	2.70	
	<i>mtsC</i>	3,29	
	<i>hrcA</i>	-2.42	ATGAAATTAGCACTCTAATAAAAAGAGTGCTAATTTTTATGTCTTTTTGCTTGACAAGGTATAAACAAAGGGT TATAATCAATTTGTTAGCACTTAGAGATGAAGAGTGCTAAAACAGAAAAAAGCTTGATAGATACTAAACAGAA GTCAAAGCTCAAGAAATTTTTGAGCTTGCGAAAGAAGTTTTGCAAACCTTCTTATCTGTGGAGAAAGGAG TAGTCATGATTACAGAACGTCAAAGACAAATTTTAAATTTGATTGTTTTCTTTATGCCAAAGAGCATACGCC AATCGGTTCAAAGTCGCTCCTTGATAGTATTC
<i>hrcA-grpE</i>	<i>grpE</i>	-3.1	
	<i>dnaK</i>	-2.77	ATTAAAAAATAAATTGACCGCAAAGTCTTTAAACTATTCATAAGTAATAAGAAATAAAGGAGATTTAAAATAT GTCTAAAATTATCGGTATTGACCTTGGTACAACAACTCAGCAGTAGCAGTTCTTGAAGGAAGTGAATCAAAA AATTATTCAAATCCAGAAGGAAATC
	<i>gapA</i>	-7.86	TAGGGTAAAAAAGTAGTATCATTATATTAGAGATAAGAGATATCTCTAATAGCTATAATTATTTATTTCTATTAT AGCAAAAAAAGAGAAGAATCTCATCATCTAAATAAAAAAACGGAGGACTACATCATGGTAGTTAAAGTTGG TATTAACGGTTTTGGTCGTATTGGACGTTTGGCATTACGTCGAATTCGAAGGAGTTGAAGTTGC GCATATCAACG

\*represents fold change in log<sub>2</sub>-scale