fermentation

Supplementary Material

1.Supplementary Figures and Tables

1.1. Supplementary Table

Table S1. RT-qPCR validation genes and their primers between MSC14 and 14P9.

GeneID	Gene-Name	Product	log2Fold Change	primer F	primer R
K7H94_RS06185	xylB	xylulokinase	3.989064441	GTTGTTTGAAGGCAAC-CAGATTACC	GTTGCGGATTGCTGAGA-TAGC
K7H94_RS04630	trxC	thioredoxin TrxC	2.101548039	GATGCGC-TATTTAGCGGTGAAG	CAGCATAATGGTTGG-GATGCTG
K7H94_RS09630	rhaD	rhamnulose-1-phosphate aldolase	-1.32488372	AGGTG-GATGACAAAGGGCTGTC	ATAAAGTGGGTGGCGTGACAGTG
K7H94_RS07385	phnE	phosphonate ABC transporter%2C permease protein PhnE	-2.061368699	AA-TATCGCTGCTGGTGCGC	CGTAACGGTGTTTTT-GCAGGCT

Table S2. RT-qPCR validation genes and their primers for culture medium with and without dried corn syrup powder.

GeneID	Gene Name	Product	log2Fold Change	primer F	primer R
K7H94_RS17195	aceA	isocitrate lyase	4.764881745	ACGCTGCCGATCTGAT-TACCT	TGAAAGCGG-TAGCCCATCTCG
K7H94_RS14005	adhP	alcohol dehydro-genase AdhP	4.338894934	GCAGAATGCCGGC-TATTCGGT	CACCGAGCCGTTTGG-CAAA
K7H94_RS19830	mqo	malate dehydro-genase (quinone)	-1.019716494	AGCTTT-GTCTGGGGCGACA	CGGTGACTTCAGAG-GAAGTTTCCAG
K7H94_RS03890	gcvH	glycine cleavage system protein GcvH	-2.91131273	TGAAGTACCGTGA-TAGCCACGAG	ACTCGTCGCTGGCTTT-GATG

Table S3. Carbohydrate metabolism-related gene variant locus.

Type	Ref	Obs	Gene ID
SNV	G	C	K7H94_RS07005
SNV	T	C	K7H94_RS07005
SNV	T	C	K7H94_RS07005
SNV	G	A	K7H94_RS07005
SNV	C	T	K7H94_RS07005
SNV	G	A	K7H94_RS07005
SNV	G	C	K7H94_RS07005
SNV	A	G	K7H94_RS00790
SNV	C	T	K7H94_RS00790
SNV	T	C	K7H94_RS00790
INDEL	-	T	K7H94_RS18140
INDEL	-	A	K7H94_RS18140
INDEL	-	C	K7H94_RS18140

INDEL	AC	-	K7H94_RS18140
SNV	A	T	K7H94_RS13050
SNV	T	C	K7H94_RS13050
INDEL	AAC	-	K7H94_RS03415
INDEL	-	T	K7H94_RS03415
INDEL	-	CCCATCC	K7H94_RS03415
INDEL	GATCAGACCG	-	K7H94_RS03415
INDEL	-	GGCA	K7H94_RS03415
INDEL	-	TCTGCGACGTGCTTCTGTAGAGAGC-TATCTGC	K7H94_RS03415

Table S4. Genes Containing Significantly Increased MSC14 Expression in Corn Slurry Medium in Transcriptome Analysis.

GeneID	GeneName	log2FoldChange
K7H94_RS08630	gapA	0.693103344
K7H94_RS22230	eno	1.195040846
K7H94_RS05705	glk	1.534747738
K7H94_RS13010	sucD	-1.718672395
K7H94_RS13045	sdhC	-2.185568885
K7H94_RS13015	sucC	-1.453737799
K7H94_RS13040	sdhD	-1.99903365
K7H94_RS13025	sucA	-1.212120414
K7H94_RS19830	mqo	-1.019716494
K7H94_RS13035	sdhA	-0.987234158
K7H94_RS17415	fadB	2.85724892
K7H94_RS17420	fadA	1.968343597
K7H94_RS14600	fadE	2.442142193
K7H94_RS08520	fadD	0.811821945
K7H94_RS08650	ansA	1.295915112
K7H94_RS07455	LivK	2.16788301
K7H94_RS01715	HisJ	2.11518486
K7H94_RS01710	BatB	1.98226369
K7H94_RS14645	HisM	1.923826507
K7H94_RS00890	gorA	1.406038412
K7H94_RS16490	yghU	1.372914368
K7H94_RS06630	AdhC	0.950581084
K7H94_RS10480	BtuE	0.780487463

Table S5. Genes with significantly increased expression in strain 14P9 compared to strain MSC14.

GeneID	GeneName	log2FoldChange
K7H94_RS06180	dalD	4.377700203
K7H94_RS06185	xylB	3.989064441
K7H94_RS00210	BaeS	2.945729734
K7H94_RS02630	FrwB	2.11180154
K7H94_RS04630	trxC	2.101548039
K7H94_RS17950	TauC	1.908167226
K7H94_RS09260	UgpE	1.902171044
K7H94_RS07365	phnN	1.90164988
K7H94_RS01185	PilN	1.858383315
K7H94_RS19775	argE	1.84925138
K7H94_RS05280	PurR	1.82391641
K7H94_RS03455	urtB	1.807438266
K7H94_RS16520	FabG	1.730868519
K7H94_RS19505	AraJ	1.599651321
K7H94_RS12995	cydX	1.221426812

K7H94_RS16990	ugpE	1.174888966
K7H94_RS07660	fliQ	1.148697202
K7H94_RS05440	alsE	1.136550839
K7H94_RS01855	yhcN	1.054887989
K7H94_RS00075	ibpA	1.049190045
K7H94_RS01845	yhcN	1.043153821
K7H94_RS01695	rrf	1.010651451
K7H94_RS06180	dalD	4.377700203
K7H94_RS12630	idi	0.02241129
K7H94_RS14910	ispC	0.248985408
K7H94_RS04350	ispF	0.23129869
K7H94_RS04345	ispD	0.129355683

Table S6. The sequences of gene or primer.

The name of gene or primer	sequences
trxC	ATGAATACTGTATGTGCCTCCTGTCAGGCAACTAACCGCGTTCCCGAGGAAC-GTCTGGCCGACGGAGCCAAATGCGGTCGCTGCGGCGATGCGCTATTTAGCGGTG AAGTGGTGAATGCCACGGCGGCCACGCTGGATAAATACCTGCAGGAC-GATCTGCCGGTCGTGGTCGACTTCTGGGCGCCATGGTGCGGCCCGTGCGTGAAC TTCGCGCCGGTGTTTAAAGACGTCGCTGACGAGCGGCGCGG-CAAAGTGCGCTTCGTGAAAGTGAACACTGAGGCGGAACCTGCGCTGAGCACGC GTTTTCGCATCCGCAGCATCCCAACCATTATGCTGTTCAAAAACGGTGA-GATGGTG-GACATGCTGAACGGTGCGATGCCGAAAGCGCCATTCAACGAATGGCTCGACGA ATCACTCTAA
trxCF	CCCAAGCTTTATGAATACTGTATGTGCCTCCT
trxCR	TGCTCTAGAAAtTTAGAGTGATTCGTCGAGCC
trxCF(for RT-qPCR)	GATGCGCTATTTAGCGGTGAAG
trxCR(for RT-qPCR)	CAGCATAATGGTTGGGATGCTG

1.2. Supplementary Figures

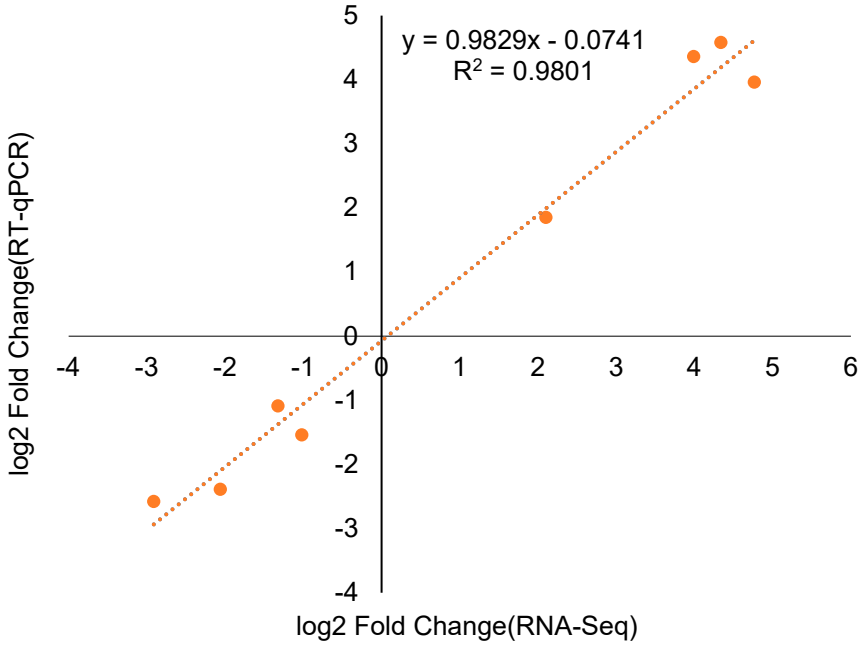


Figure S1. Correlation analysis of RT-qPCR with differential gene log2 Fold Change.