

Supplementary Data

Heterologous Biosynthesis of Hyaluronic Acid Using a New Hyaluronic Acid Synthase Derived from the Probiotic *Streptococcus thermophilus*

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Table S1 Primers used in this study

Primers	Oligonucleotides (forward, 5' to 3')
CghasB-F	agataaaaaggagcgatttacatatgcggatgacagtgattgggtacgggttaccttggcg
CghasB-R	gcttgagctcgactctagaggatcctaaagggtgcggccgagcgct
amhasC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgaaaaaagtacgcaaagc
amhasC-R	gcttgagctcgactctagaggatcttataattcatcttttctta
cghasC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgagtttgccaatagctca
cghasC-R	gcttgagctcgactctagaggatcttaagattcaaaactcagcgagta
bshasC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgagaaaaaagtgagaaa
bshasC-R	gcttgagctcgactctagaggatcttaccgcagcatttcttctgt
sphasC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgacgatcaagccgctgcgc
sphasC-R	gcttgagctcgactctagaggatcttaaccgagcgcacgctcgg
pahasC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgtctgcctataagtcaaaa
pahasC-R	gcttgagctcgactctagaggatcttactttttattttcaactgt
ccpA-F	cgctcggccgcaaccttagaaaggagcgatttacatatgagcaacattacgatatac
ccpA-R	agctagcttgagctcgactctagaggatttatgacttgggtgattgtct
cody-F	cgctcggccgcaaccttagaaaggagcgatttacatatggctttactacaaaaaca
cody-R	agctagcttgagctcgactctagaggatttaattgtgatttaagatttc
thrA-F	cgctcggccgcaaccttagaaaggagcgatttacatatgacgacagacgaacaatctt
thrA-R	gcttgagctcgactctagaggatctcagcggtttttatatttaa
comK-F	cgctcggccgcaaccttagaaaggagcgatttacatatgtgccagaaaacacacg
comK-R	gcttgagctcgactctagaggatc ctaatatctctccccagctc
spo0A-F	cgctcggccgcaaccttagaaaggagcgatttacatatggagaaaattaaagtt
spo0A-R	gcttgagctcgactctagaggatc ttatgaagctttatgctcaa
abrB-F	cgctcggccgcaaccttagaaaggagcgatttacatatgaaatctactggtatcg
abrB-R	gcttgagctcgactctagaggatc ttatttttggtttgaagctg
rex-F	cgctcggccgcaaccttagaaaggagcgatttacatatgaacaaggatcaatc
rex-R	gcttgagctcgactctagaggatc ttattcaatttcttccaaaac
fruR-F	cgctcggccgcaaccttagaaaggagcgatttacatatgctcactcctgaaaggat
fruR-R	gcttgagctcgactctagaggatctcatggtttactacctttac
bkdR-F	cgctcggccgcaaccttagaaaggagcgatttacatatgcagaaggtgctgattatagg
bkdR-R	gcttgagctcgactctagaggatcttattgcatgccgtcatttgcaa
ctsR-F	cgctcggccgcaaccttagaaaggagcgatttacatatgggacataatatttctgacat
ctsR-R	gcttgagctcgactctagaggatcttacttttagtttaaatgtga
gltC-F	cgctcggccgcaaccttagaaaggagcgatttacatatgggtgtggacgcaatggaatt
gltC-R	gcttgagctcgactctagaggatcttattgatattgtcaagtttgg
sigK-F	cgctcggccgcaaccttagaaaggagcgatttacatatggctgataaacaacccacga
sigK-R	gcttgagctcgactctagaggatcttattcgagaaaatccttcagac

Table S2 Amino acid sequence homology analysis

HAS	Homology (%)							
SthasA	100.00	19.48	29.95	30.00	30.03	33.59	36.62	36.36
PmhasA	19.48	100.00	17.52	18.00	18.82	13.97	17.98	20.11
HshasA1	29.95	17.52	100.00	53.93	56.23	29.49	26.25	26.12
HshasA2	30.00	18.00	53.93	100.00	70.02	29.73	27.07	26.93
HshasA3	18.82	30.03	56.23	70.02	100.00	29.49	27.07	26.93
CvhasA	13.97	33.59	29.49	29.73	29.49	100.00	26.12	25.00
SehasA	17.98	36.62	26.25	28.28	27.07	26.12	100.00	71.39
SphasA	20.11	36.36	26.12	27.64	26.93	25.00	71.39	100.00

Table S3 Top 3 most probable motifs in hyaluronic acid synthase

Motif	E-value	Sites	Width
1	6.2×10^{-21}	3	50
2	2.9×10^{-12}	3	37
4	7.2×10^{-2}	3	31

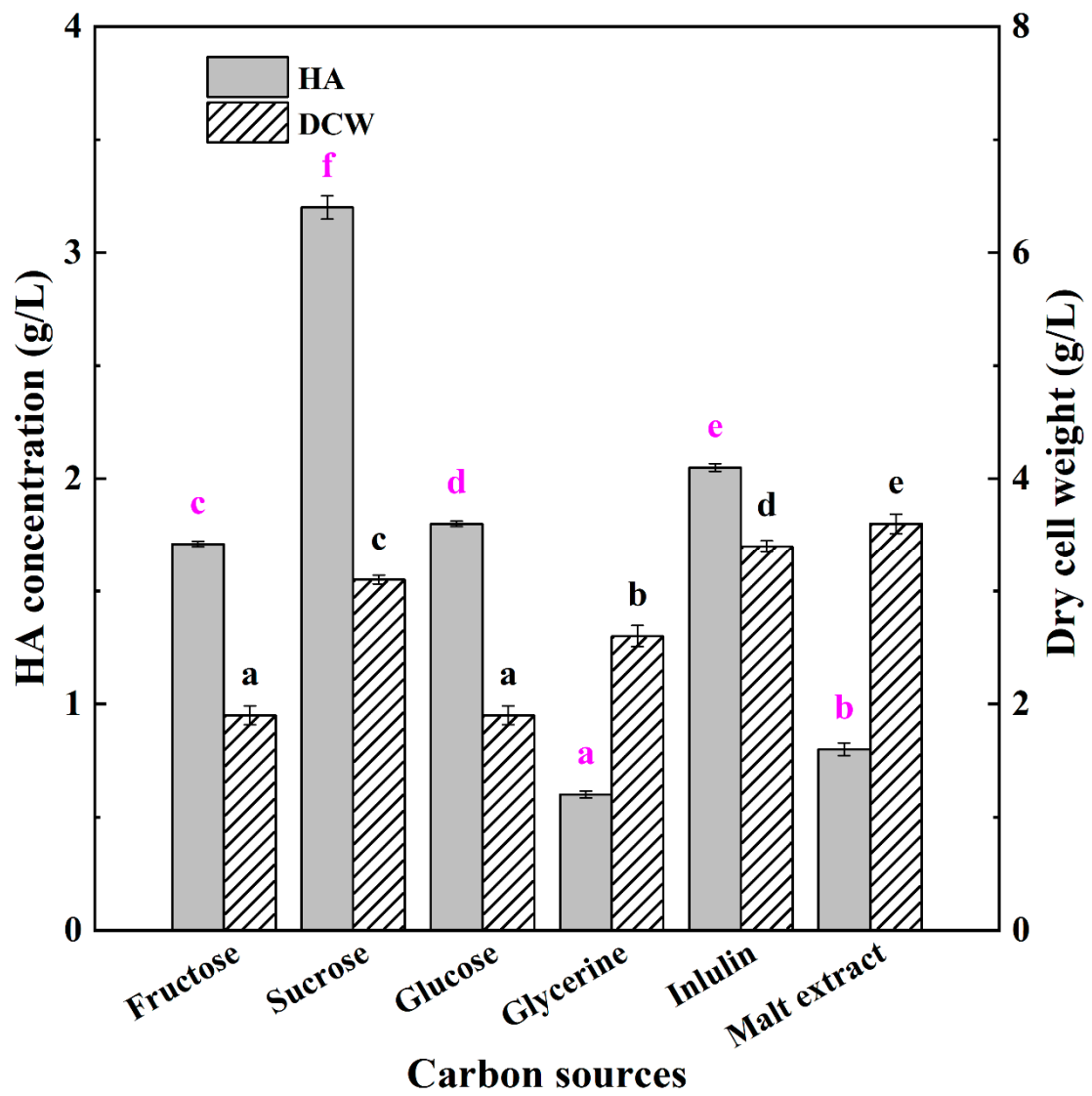


Figure S1. Effect of carbon source type on hyaluronic acid yield and bacterial volume.