

**Horizontal Transfer of a Novel Soil Agarase Gene from Marine Bacteria to Soil
Bacteria via Human Microbiota**

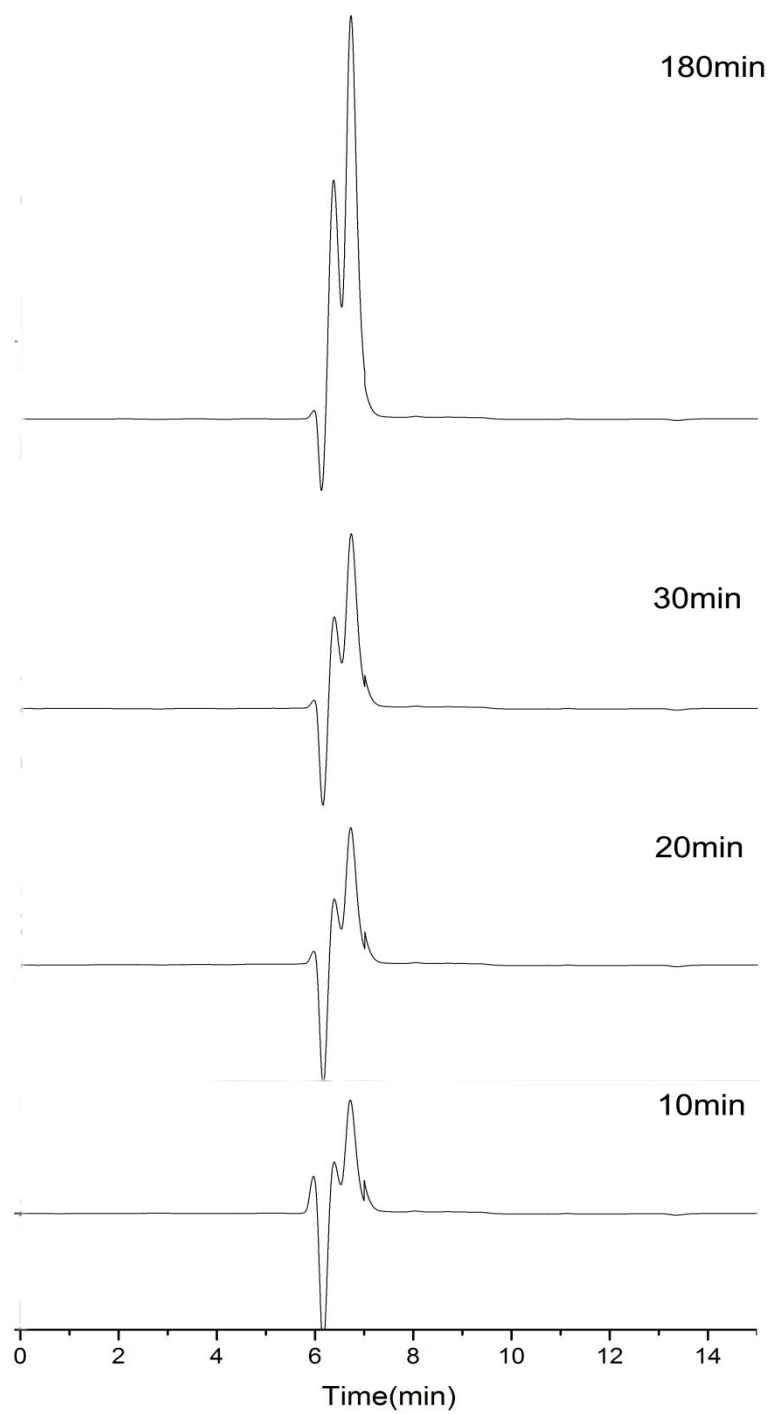
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Supplemental Figure S1: HPLC analysis of the hydrolysis product at different time.

Supplemental Table S1: Mascot search result using tandem mass data as query. If Pep_scores of matched peptides were more than 50, the results were confident.

Matched protein	Pep_score	Sequences of matched peptides
Aga 1	130.61	AEVVAQDALATDSEINTALEDLTK
Aga 1	163.32	YHVNSGPIGVEQADGEITVLDEAYHK
Aga 1	155.79	FYVFSPTTEPITNAALAFDR
Aga 1	56.37	ISFEDGEAVDYTYNVDTVTTTTDSQGATDGSK
Aga 1	74.51	MGFQESNPTEGITHPWLIKDENGDVIYDGYK
Aga 1	92.28	WMWENPNSGQSEHFGTPSYSNFDAAADAAAQLIK

Supplemental Table S2: Effects of various reagents on the activity of Aga 1. Data are mean \pm SD of three independent experiments.

Reagents(1mM)	Relativity activity (% \pm S.D.)
Na ⁺	107.57 \pm 4.14
K ⁺	104.93 \pm 2.13
Mn ²⁺	93.54 \pm 16.89
Cu ²⁺	37.87 \pm 1.94
Zn ²⁺	83.51 \pm 5.71
Ba ²⁺	113.57 \pm 8.62
Ca ²⁺	99.24 \pm 9.70
Fe ³⁺	104.31 \pm 3.10
Ni ⁺	102.86 \pm 1.43
Mg ²⁺	111.51 \pm 2.33
Pb ²⁺	96.58 \pm 6.93
Co ²⁺	95.69 \pm 3.80
β -Me	122.33 \pm 7.18
DTT	133.44 \pm 11.59
SDS	118.84 \pm 10.08
EDTA	104.02 \pm 7.02
Urea	97.74 \pm 11.24
Control	100.00 \pm 12.95

Supplemental Table S3: GC content variety and GC3 content variety between Aga 1 and corresponding genome

ID	GC content variety	GC3s content variety
Aga 1	8.72	19.60

Supplemental Table S4: Analysis of the RSCU difference between Aga 1 and the

genome, RSCU represents relative synonymous codon usage

	Code	Aga 1 RSCU	Genome RSCU		Code	Aga 1 RSCU	Genome RSCU
Ala	GCA	1.3037	0.606	Cys	UGC	0	1.538
	GCC	0.7111	1.4822		UGU	2	0.462
	GCG	1.1556	1.3331	Asp	GAC	0.6281	1.02
	GCU	0.8296	0.5787		GAU	1.3719	0.981
Gly	GGA	1.1171	0.8914	Glu	GAA	1.0323	1.003
	GGC	1.5856	1.7346		GAG	0.9677	0.997
	GGG	0.3243	0.8198	Phe	UUC	1.2239	1.016
	GGU	0.973	0.5541		UUU	0.7761	0.984
Leu	CUA	0.3652	0.1564	His	CAC	0.8148	0.739
	CUC	0.3652	0.9367		CAU	1.1852	1.261
	CUG	1.6696	2.9811	Ile	AUA	0.4369	0.198
	CUU	1.4609	0.7406		AUC	0.7282	1.721
	UUA	0.8348	0.3268	AUU	1.835	1.082	
	UUG	1.3043	0.8585	Met	AUG	1	1
Lys	AAA	0.8837	0.9163	Pro	CCA	1.3731	0.369
	AAG	1.1163	1.0837		CCC	0.1791	0.677
Asn	AAC	0.6733	1.2099	Ser	CCG	1.1343	2.318
	AAU	1.3267	0.7901		CCU	1.3134	0.636
Arg	AGA	2.2642	0.5212		AGC	1.6034	1.805
	AGG	0.1132	0.5075		AGU	0.931	0.385
	CGA	0.6792	0.3655	UCA	0.6724	0.393	
	CGC	1.2453	1.78	UCC	1.2414	1.587	
	CGG	0.4528	2.0344	UCG	0.9828	1.385	
	CGU	1.2453	0.7913	UCU	0.569	0.445	
SeCys	ACA	1.4444	0.5055	Val	GUA	0.8254	0.569
	ACC	0.4444	1.344		GUC	0.6349	1.323
	ACG	1.3056	1.8481		GUG	1.1429	1.423
	ACU	0.8056	0.3024		GUU	1.3968	0.685
Gly	CAA	0.7347	0.5766	Tyr	UAC	0.6111	0.988
	CAG	1.2653	1.4234		UAU	1.3889	1.012
Trp	UGG	1	1	Ter	UAG	3	0.589

Supplemental Table S5: The primers used for Aga 1. The restrict enzyme sites were red colored.

Name	Sequence of oligosaccharide primer
Aga(F)	ATTT GCGGCCG CGTTGAGGCAAGCGA
Aga(R)	CCG CTCGAG AATGACGGCGTAAGTGC

Supplemental Table S6: Accession number and origin of the query protein

Gene function	Accession Number	Origin
α -neoagarobiose hydrolase	WP_013995985.1	<i>Zobellia galactanivorans</i>
galactosidase	WP_014232195.1	<i>Vibrio sp.</i> EJY3
3,6-anhydro-L-galactonate cycloisomerase	WP_014232231.1	<i>Vibrio sp.</i> EJY3
2,5-diketo-3-deoxy-L-galactonate 5-reductase	WP_011575334.1	<i>Pseudoalteromonas atlantica</i>
3,6-anhydro-L-galactose dehydrogenase	WP_014232205.1	<i>Vibrio sp.</i> EJY3
2-keto-3-deoxy-L-galactonate 5-dehydrogenase	WP_011575334.1	<i>Pseudoalteromonas atlantica</i>

Supplemental Table S6: Accession numbers of Aga's surrounding proteins

Gene locus	Gene function	Accession number
7137	transposase	LC164143
7138	transposase	LC164144
7142	α -neoagarobiose hydrolase	LC164136
7144	3,6-anhydro-L-galactonate cycloisomerase	LC164138
7145	2,5-diketo-3-deoxy-L-galactonate 5-reductase	LC164141
7146	3,6-anhydro-L-galactose dehydrogenase	LC164140
7155	3,6-anhydro-L-galactose dehydrogenase	LC164137
7156	galactosidase	LC164139
7158	sulfatase	LC164142