

## Supplementary Information

### **Bacterial chemotaxis towards polysaccharide pectin by pectin-binding protein**

Hidenori Konishi<sup>1</sup>, Mamoru Hio<sup>2</sup>, Masahiro Kobayashi<sup>1</sup>, Ryuichi Takase<sup>1,2</sup>, & Wataru Hashimoto<sup>1,2</sup>

<sup>1</sup>Laboratory of Basic and Applied Molecular Biotechnology, Division of Food Science and Biotechnology, Graduate School of Agriculture, Kyoto University, Uji, Kyoto 611-0011, Japan;

<sup>2</sup>Laboratory of Basic and Applied Molecular Biotechnology, Department of Food Science and Biotechnology, Faculty of Agriculture, Kyoto University, Uji, Kyoto 611-0011, Japan;

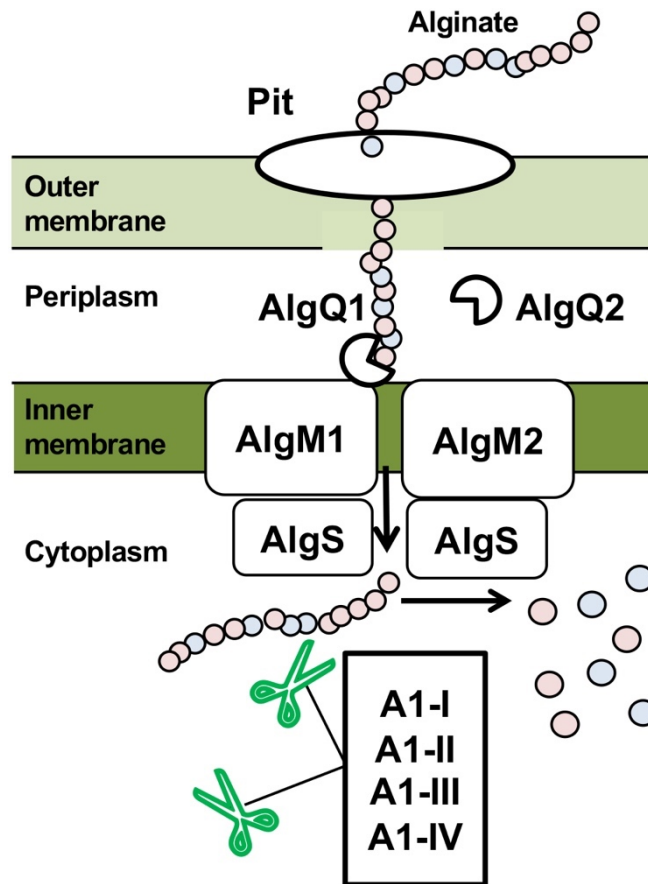
Correspondence and requests for materials should be addressed to W. H. (email: [whasimot@kais.kyoto-u.ac.jp](mailto:whasimot@kais.kyoto-u.ac.jp))

**Table S1.** Mutations in the genome of strain A1-M5.

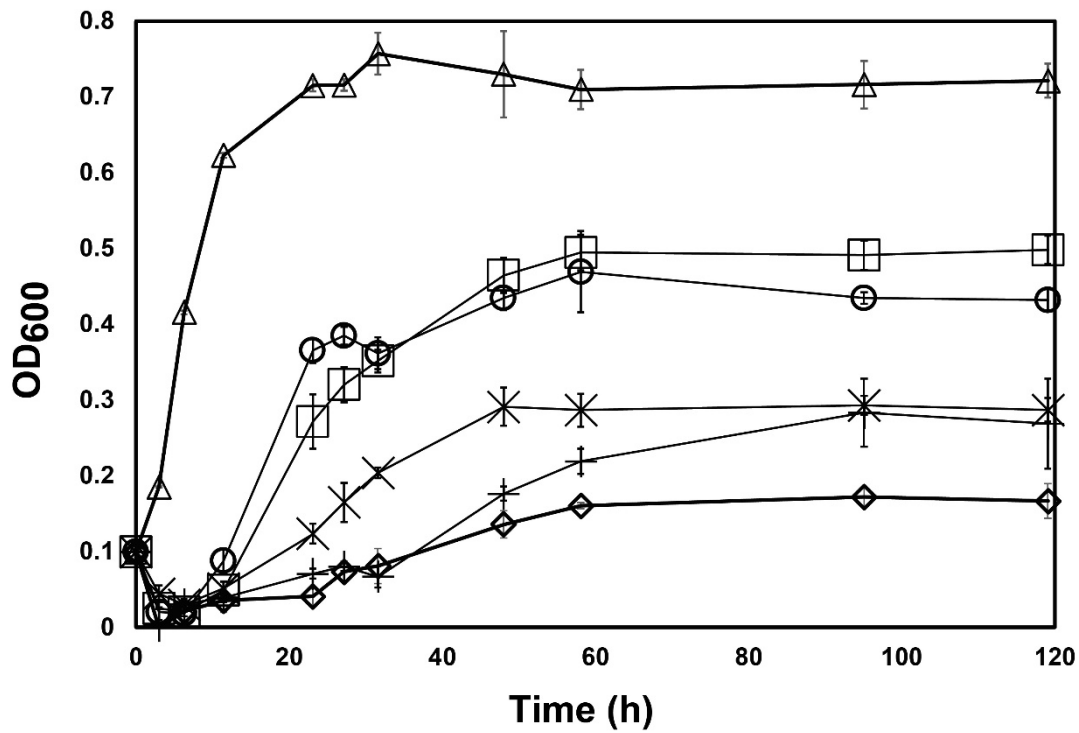
An excel file for Table S1 was separately uploaded.

**Table S2.** Primers used in this study.

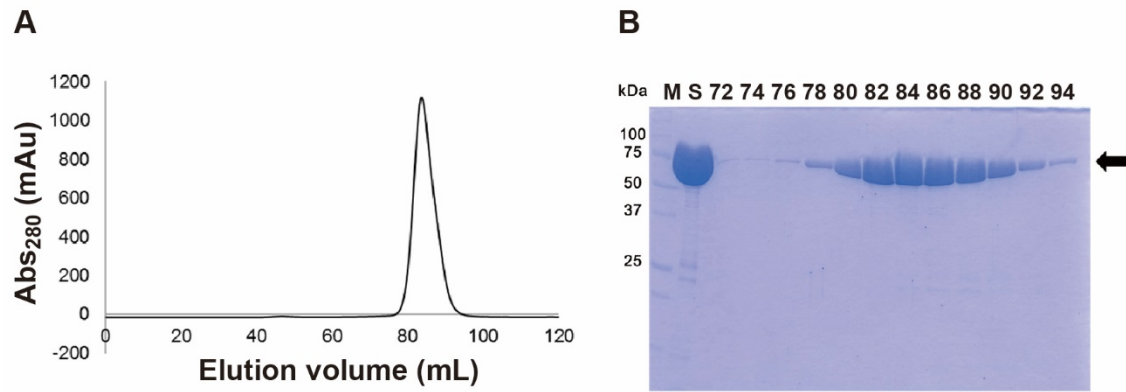
<b>Primer</b>	<b>Sequence (5'-3')</b>
pKS_F1	AAAAATGGCAGCGCTGGCAGTCCTT
pKS_R2	GGCGGTGCTACAGAGTTCTTGAAGT
r-3kbp→6kbp f	TGATCGACCTGCAAGAGCGCATCCA
r-3kbp→6kbp r	TGTTCAAGCGCTCGACGCGAGTGCT
f→3.2kbp	GGGTTCGTCGTCAAAGCGTCCTGTCA
r-6kbp→9kbp f	ACACACCCAAAGCGCCGCTTGACTG
r-6kbp→9kbp r	GCTCAGGTCAACATGAGCAACCTGC
f-3.2kbp→6.2kbp f	TGCTCAAGCCACGTTTGGCCGCGTT
f-3.2kbp→6.2kbp r	CACGACGCGCCCAATGTTACCTCA
r-9kbp→12kbp f	GGTTCGTAGCTGTTCGTCAGTCATT
r-9kbp→12kbp r	TTTCACGCAAGCGCCGATGCTGGAA
f-6.2kbp→9.2kbp f	ATGAGGTGAACATTGGGCGCGTTCGT
f-6.2kbp→9.2kbp r	ATGGCGATGTCCAGCCCCACGGTAT
r-12kbp→f	TTGCGTGAAAGCAGCAGCGATCGCC
f-9.2kbp→12kbp f	ATACCGTGGGGCTGGACATCGCCAT
f-9.2kbp→12kbp r	GACCAACCACGTGACGGTGGCGATA
f-12kbp→f	TATCGCACCGTACGCTGGTTGGTC
r-1289838~	TAGACCAGCGTCTGCAATTCCAGGC
f-3135268~	TACGCTGTGGGAGACCGACGAGGTT
sph2942 BamHI infusion f	TCGCGCGACCGGATCAATGCAAGGCCGTTCAACGC
sph2942 BamHI infusion r	AACGTTGCCCCGGATCCGACAAGGGCAGATACACGT
sph1119 BamHI infusion f	TCGCGCGACCGGATCGCGGGAACATTTCTTGTTC
sph1119 BamHI infusion r	AACGTTGCCCCGGATCGTTCGATTACGCAACCAGCCG
sph1117 BamHI infusion f	TCGCGCGACCGGATCCCGTTCGTACCACCGTTAACC
sph1117 BamHI infusion r	AACGTTGCCCCGGATCGTATCGGAGAAGTTCGCCCCG
sph1118 BamHI infusion f	TCGCGCGACCGGATCACGAACTTGCCGATCGACCA
sph1118 BamHI infusion r	AACGTTGCCCCGGATCATTGGCGCCCATACCTCCAG
sph2733 BamHI infusion f	TCGCGCGACCGGATCTTCAAGCTGGGCTACCTCGC
sph2733 BamHI infusion r	AACGTTGCCCCGGATCGGACGTACGGATGATGTCGA
sph1118 BamHI infusion f new	TCGCGCGACCGGATCTGATGATCACGGGGATCACC
sph1118 BamHI infusion r new	AACGTTGCCCCGGATCTTAAAACGGCCGCGCAACCA
sph1117 f	AAGCGATACCACATCAGCGTCCACT
sph1117 r	AGAAGCGTATGGCGCTGTACGACCA
sph1118 f	TACGTTCTTCATGCTTTTCGTTTCGG
sph1118 r	TCGTAGTTCATCCCTAGGAGGACAA
sph1119 f	ATGAGTCGACCCCTTCATTTTCTGC
sph1119 r	TCAGGCGTTTGAACCTACCTGATGTC
sph1117 f inverse	AAGTCATCGGCACGGTTCGTCCGGC
sph1117 r inverse	TGAGTCTTGGCGGCGACGAACTGGT
sph1118 f inverse	GACGGTGTAAATCGTCAACCTTCGAA
sph1118 r inverse	TGGCTATGGACCGTGACGAGATCAA
sph1119 f inverse	GGGCGACCTCCAGTGCCTCGGTATT
sph1119 r inverse	AATGACCGCGCACGCCATGCACGGA
SPH1118 NdeI(S)	GGCATATGGCTGCTTTCACGCAAGCGCCGA
SPH1118 NdeI(L)	GGCATATGATGAGGTTTTACTCTCGCAAGTTTGGC
Km-F	GGGGGCGCTGAGGTCTGCCTCGTGAAG
Km-R	GGGGGAAAGCCACGTTGTGTCTCAAAA
sph1118-NdeI in fusion	AAGGAGATATACATATGGCTGCTTTCACGCAAGCGCCGA
sph1118-XhoI in fusion	GGTGGTGGTGTCTCGAGCTTGGAGAAGTACCACTGCT



**Figure S1.** Import and degradation of alginate polysaccharide by strain A1 cells. Extracellular alginate is incorporated to the periplasm through the cell-surface pit and bound to the periplasmic binding protein (AlgQ1 or AlgQ2). The binding protein delivers the polysaccharide to the ABC transporter (AlgM1-AlgM2/AlgS-AlgS), which imports alginate to the cytoplasm with an energy from ATP hydrolysis by AlgS-AlgS. Alginate is degraded to constituent monosaccharides by three endotype (A1-I, II, and III) and a exotype (A1-IV) alginate lyases.



**Figure S2.** Assimilation of pectin by strain A1 cells. Bacterial cells were cultured in test tubes ( $n = 3$ ). Values indicate the average optical density at 600 nm ( $OD_{600}$ ) as follows: triangle, non-motile wild-type strain A1 cells; circle, strain A1-MP cells; rhombus, strain A1-M5 cells ; square, *sph1118*-complemented strain  $\Delta$ *sph1118* cells derived from strain A1-MP; cross, strain  $\Delta$ *sph1118* cells derived from strain A1-MP; plus, *sph1117-sph1118*-complemented A1-M5 cells. Error bars indicate standard deviations.



**Figure S3.** Purification of SPH1118. **(A)** Elution profile of the recombinant SPH1118 from gel filtration column chromatography. **(B)** SDS-PAGE profile of the recombinant SPH1118. Lane S, proteins before subjected to the gel filtration column chromatography; lanes 72-94, fractions containing the eluted protein from the chromatography. This electrophoretic profile is not an image cropped from different parts of the same gel or from different gels.