

1 Enrichment and isolation of *Flavobacterium* strains with tolerance to  
2 high concentrations of cesium ion

3

4 Authors:

5 Souichiro Kato<sup>1,2,3\*</sup>, Eri Goya<sup>1</sup>, Michiko Tanaka<sup>1</sup>, Wataru Kitagawa<sup>1,2</sup>, Yoshitomo Kikuchi<sup>1,2</sup>,  
6 Kozo Asano<sup>1</sup>, Yoichi Kamagata<sup>1,2</sup>

7

8 <sup>1</sup>*Division of Applied Bioscience, Graduate School of Agriculture, Hokkaido University, Kita-9*  
9 *Nishi-9, Kita-ku, Sapporo, Hokkaido 060-8589, Japan*

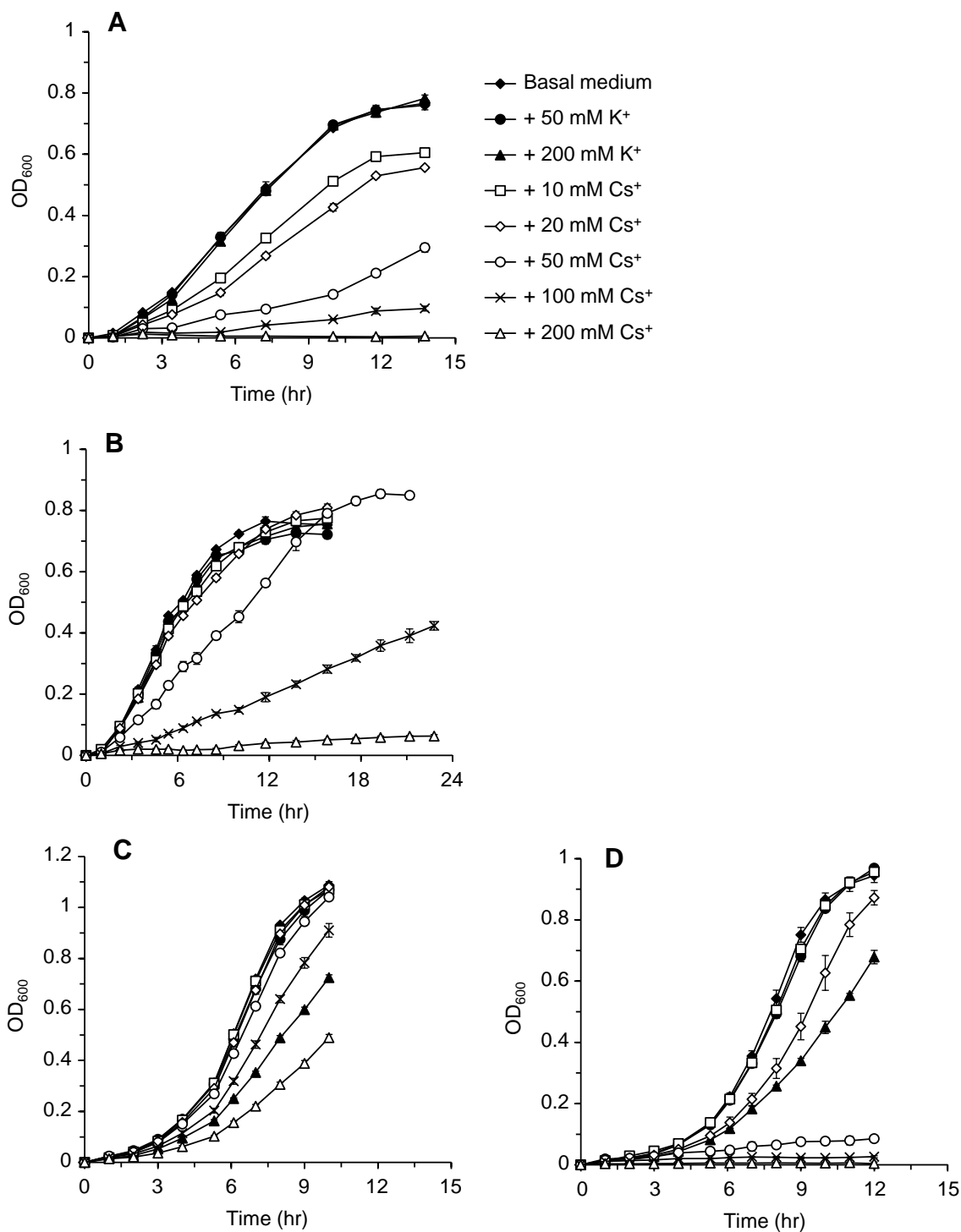
10 <sup>2</sup>*Bioproduction Research Institute, National Institute of Advanced Industrial Science and*  
11 *Technology (AIST), 2-17-2-1 Tsukisamu-Higashi, Toyohira-ku, Sapporo, Hokkaido 062-8517,*  
12 *Japan*

13 <sup>3</sup>*Research Center for Advanced Science and Technology, The University of Tokyo, 4-6-1*  
14 *Komaba, Meguro-ku, Tokyo 153-8904, Japan*

15

16 \*For correspondence. E-mail s.katou@aist.go.jp; Tel (+81) 11 857 8968; Fax (+81) 11 857  
17 8915

18



**FIG S1** Growth curves of (A) *E. coli*, (B) *B. subtilis*, (C) the Cs<sup>+</sup>-tolerant isolate (strain 200Cs-4) and (D) the closest relative of the isolate (*F. chungbukense* CS100) with different concentrations of KCl and CsCl as described in the figure. Data are presented as means of three independent cultures, and error bars represent standard deviations.

**Table S1** The phylotypes detected in the soil and the enrichment cultures.

Phylogenetic group	Phylotype	Closest relative (Similarity, %)	Number of clones					
			Soil	FB	50K	200K	50Cs	200Cs
<i>Alphaproteobacteria</i>	HS01	AB121773 <i>Bradyrhizobium</i> sp. Shinshu-th2 (94)	4					
	HS02	FI859687 <i>Ochrobactrum pseudogrignomense</i> BIHB 340 (99)						4
	HS03	AF395032 <i>Sphingomonas</i> sp. SIA181-1A1 (99)	2					
	HS04	GQ369056 <i>Azospirillum</i> sp. T2-YC6788 (96)	1					
	HS05	GU269549 <i>Pedomicrobium manganicum</i> ATCC 33121 (96)	1					
	HS06	AJ563927 <i>Methylocella palustris</i> H4 (91)	1					
	HS07	AM412118 <i>Chelatococcus</i> sp. P-117 (94)	1					
	HS08	JN674090 <i>Comamonas</i> sp. p19 (100)			3		2	
	HS09	HM044161 <i>Ferroplasma myxofaciens</i> P3G (90)	1					
	HS10	AB649026 <i>Variovorax ginsengisoli</i> S32319 (96)	1					
<i>Betaproteobacteria</i>	HS11	HQ005420 <i>Variovorax paradoxus</i> HB44 (98)	1					
	HS12	AJ551104 <i>Burkholderia</i> sp. wp26 (93)						1
	HS13	NR_028719 <i>Comamonas terrigena</i> IMI 359870 (99)				1		
	HS14	KC195874 <i>Pseudomonas putida</i> BF111 (99)	4		18	2		
	HS15	EU337121 <i>Acinetobacter johnsonii</i> 3B2 (99)	3				11	
	HS16	DQ133596 <i>Pantoea agglomerans</i> B1 (99)	5		5	2		
	HS17	HM854373 <i>Enterobacter cloacae</i> P04 (99)	5		1	5		
	HS18	HM231274 <i>Raoultella ornithinolytica</i> NB1 (99)	2		3	1		
	HS19	EF520801 <i>Erwinia</i> sp. AJEY28 (98)	2		1	1		
	HS20	AF506040 <i>Pseudomonas fluorescens</i> LCSA0TU1 (99)	2		1			
<i>Gammaproteobacteria</i>	HS21	X60411 <i>Aeromonas eucrenophila</i> NCIMB 74 (99)	1					2
	HS22	JQ267508 <i>Enterobacter aerogenes</i> ger-BHI10 (99)				3		
	HS23	FM164626 <i>Pseudomonas</i> sp. PC IW 25 (98)				2		

**Table S1.** Continued.

Phylogenetic group	Phylotype	Closest relative (Similarity, %)	Number of clones					
			Soil	FB	50K	200K	50Cs	200Cs
<i>Gammaproteobacteria</i>	HS24	GU586313 <i>Stenotrophomonas rhizophila</i> IR (99)			2			
	HS25	AY234531 <i>Bacterium</i> Ellin5114 (94)	1					
	HS26	FN554396 <i>Gamma proteobacterium</i> CH43 (91)	1					
	HS27	FI940849 <i>Aeromonas veronii</i> CYJ205 (97)			1			
	HS28	HQ132731 <i>Leclercia adecarboxylata</i> Ld1 (98)		1				
	HS29	JQ954967 <i>Serratia</i> sp. ZI-2 (96)		1				
	HS30	EU304285 <i>Pseudomonas</i> sp. 73 (92)		1				
	HS31	FR687005 <i>Aeromonas hydrophila</i> Pa031 (96)			1			
	HS32	JX899634 <i>Pseudomonas</i> sp. REP-amp_124 (95)				1		
	HS33	HQ407278 <i>Enterobacter cancerogenus</i> H103 (99)				1		
	HS43	KC213922 <i>Leucobacter komagatae</i> Z3_S (97)				1		
	HS34	HQ436039 <i>Aeromonas</i> sp. MDCC2473 (96)					1	
	<i>Deltaproteobacteria</i>	HS35	JQ346737 <i>Syntrophus gentianae</i> HOGGOe1 (86)	2				
HS36		AJ233940 <i>Chondromyces pediculatus</i> Cm p17 (85)	1					
HS37		GU249611 <i>Sorangineae bacterium</i> SBSr004 (82)	1					
HS38		CP002297 <i>Desulfovibrio vulgaris</i> RCH1 (81)	1					
HS39		HF543825 <i>Kofleria flava</i> DSM114620 (87)	1					

**Table S1.** Continued.

Phylogenetic group	Phylotype	Closest relative (Similarity, %)	Number of clones					
			Soil	FB	50K	200K	50Cs	200Cs
<i>Bacteroidetes</i>	HS40	HM627539 <i>Flavobacterium chungbukense</i> CS100 (99)			2		10	36
	HS41	HQ882702 <i>Flavobacterium denitrificans</i> JS14-1 (99)	1	3	1	1	10	2
	HS42	NR_040953 <i>Sphingobacterium multivorum</i> IAMI4316 (99)			1	2	7	
	HS43	AY468484 <i>Chryseobacterium</i> sp. LDVH 3 (99)		5	1			
	HS44	AB308367 <i>Bacterium</i> TG141 (91)	2					
	HS45	AY436806 <i>Bacteroidetes</i> bacterium RD4.3 (99)			2			
	HS46	HQ154576 <i>Wautersiella falsenii</i> R9-5A (96)					2	
	HS47	EU917053 <i>Niastella</i> sp. RHYL-67 (96)	1					
	HS48	AM411962 <i>Sphingobacterium</i> sp. P-38 (95)	1					
	HS49	AB308369 <i>Bacterium</i> TG124 (95)	1					
	HS50	EF647593 <i>Adhaeribacter</i> sp. KS35 (99)	1					
	HS51	AB682234 <i>Flavobacterium glycyces</i> NBRC 105008 (99)		1				
	HS52	AY538269 <i>Bacteroidetes</i> bacterium M2 (97)				1		
	HS53	JN020634 <i>Bacillus thuringiensis</i> (99)				10		7
	HS54	FI970034 <i>Exiguobacterium acetylicum</i> QD-3 (99)		3	2			
	HS55	JQ943914 <i>Lysinibacillus fusiformis</i> H5 (99)		1		3		
	HS56	AB376084 <i>Paenibacillus</i> sp. YT0147 (83)	1					
	HS57	EF101552 <i>Bacillus psychrodurans</i> KOPR124934 (98)						1

**Table S1.** Continued.

Phylogenetic group	Phylotype	Closest relative (Similarity, %)	Number of clones					
			Soil	FB	50K	200K	50Cs	200Cs
<i>Actinobacteria</i>	HS58	AY211130 <i>Arthrobacter protophormiae</i> Mali 36 (98)					8	
	HS59	AB021325 <i>Bacterium</i> r17 (93)	1					
	HS60	AY673309 <i>Acidimicrobidae</i> bacterium Ellin7143 (91)	1					
	HS61	NR_041871 <i>Nocardia cummideiens</i> DSM 44490 (99)	1					
	HS62	JX949768 <i>Compostimonas</i> sp. MDB2-25 (97)	1					
	HS63	JF423906 <i>Gaiella occulta</i> F2-233 (90)	1					
	HS64	HM748674 <i>Bacterium</i> Ellin6526 (98)	1					
	HS65	JF707525 <i>Acidobacteria</i> bacterium UCL-085 (91)	2					
<i>Acidobacteria</i>	HS66	HM748653 <i>Bacterium</i> Ellin6505 (94)	1					
	HS67	HM748677 <i>Bacterium</i> Ellin6529 (94)	1					
	HS68	DQ075304 <i>Bacterium</i> Ellin640 (95)	1					
	HS69	HMI54525 <i>Gemmatimonadetes</i> bacterium KBS708 (85)	1					
<i>Gemmatimonadetes</i>	HS70	NR_074708 <i>Gemmatimonas aurantiaca</i> T-27 (84)	1					
	HS71	FJ405899 <i>Verrucomicrobia</i> bacterium WSF2-44 (90)	1					
<i>Verrucomicrobia</i>	HS72	AB245341 <i>Spartrobacteria</i> bacterium Gsoil 133 (93)	1					
	HS73	NR_074379 <i>Sphaerobacter thermophilus</i> DSM 20745 (83)	1					
<i>Planctomycetes</i>	HS74	FJ405890 <i>Planctomycetacia</i> bacterium WSF3-27 (86)	1					
Total			46	45	48	46	45	48