

Table S1. methylation motifs detected for *X. axonopodis* pv. *glycines* strain 8ra

Motifs	No. of methylation detected	No. of motifs detected	% of methylation detected	Restriction enzyme	Origin
C_[A]_GNNNNNNNTCTY	1023	1272		80.42	
RAG_[A]_NNNNNNNNCTG	850	1272		66.82389937	
GAAAC_[A]_C	1663	3506		47.43297205	
G_[C]_GGC_[C]_G_[C]_	442	1860		23.76344086	Nocardia otitidis-caviarum
G_[C]_SSYABTG	496	3321		14.93526046	
_[C]_G_[C]_G	18048	162810		11.08531417	FnuDII
BN_[A]_KGVAVYA	134	1780		7.528089888	
G_[C]_NNNNNNNGC	13639	214192		6.367651453	MwoI
[C]_NSBVNYH	24611	459291		5.358476434	
CMG_[C]_KG	1651	36142		4.568092524	NspBII
ACG_[C]_GT	147	4016		3.660358566	MluI
CGW_[C]_G	1830	51540		3.550640279	Hpy99I
[C]_SNNNVV	42275	1439479		2.936826449	
C_[C]_GCTC	107	3739		2.861727735	BsrBI
AGCG_[C]_C	262	10643		2.461711923	M.MspCY2I
_[C]_YCGRG	190	7720		2.461139896	AvaI
ACGG_[C]_	545	22745		2.396131018	BceFI
A_[C]_GGC	535	22745		2.352165311	BceFI
C_[C]_TNNNNNAGG	64	2878		2.223766505	EcoNI
GAG_[A]_C	80	4180		1.913875598	BsmAI
CCGCT_[C]_C	70	3739		1.872158331	BsrBI
_[C]_MGCKG	655	36142		1.812295944	NspBII
CY_[C]_GRG	139	7720		1.800518135	AvaI
A_[C]_CGGT	71	4016		1.767928287	MluI
_[C]_CGCTC	61	3739		1.63145226	BsrBI
GGNC_[C]_	663	42414		1.563163107	AsuI
GAT_[C]_	1092	73194		1.491925568	MboI
AG_[A]_CC	133	9268		1.435045317	M.EcoPI
GGC_[C]_	1457	111646		1.305017645	HaeIII
_[C]_TAG	62	4788		1.294903926	MaeI
C_[C]_NNNNNNNGG	804	62566		1.285042995	BsiYI
GC_[C]_HR	1667	136492		1.221317	M.NgoDCXV
A_[C]_RYGT	77	7362		1.045911437	AflIII
T_[C]_GA	631	61494		1.026116369	TaqI
_[C]_CNNNNNNNGG	631	62566		1.008534987	BsiYI
G_[C]_CGT	221	22745		0.971642119	BceFI
GTA_[C]_	206	22616		0.910859568	RsaI
RGAT_[C]_Y	79	8972		0.880517165	XhoII
GG_[C]_C	976	111646		0.874191641	HaeIII
CAG_[C]_TG	52	8376		0.620821394	PvuII
C_[C]_WGG	291	49172		0.591800212	M.EcoNDM5DcmP
GCCC_[A]_G	53	9112		0.581650571	HbaII
G_[C]_CNNNNNGC	98	17016		0.575928538	BglI
_[C]_CNNNGG	352	62184		0.56606201	SecI
G_[A]_GG	148	26362		0.561414157	MnlI
A_[C]_TGG	61	11267		0.5414041	BsrI
CAGC_[A]_G	56	12286		0.455803353	EcoP15I
GCGC_[A]_G	74	18837		0.392843871	Cdi11397I
CTSS_[A]_G	65	19476		0.333744095	M.PhiMx8I
G_[A]_TC	216	73194		0.295106156	MboI
G_[A]_TGC	60	29243		0.205177307	SfaNI
_[C]_CWGG	90	49172		0.183030993	M.EcoNDM5DcmP
TGC_[A]_	93	65698		0.141556821	CviRI
					Chlorella virus XZ-6E

Table S2. methylation motifs detected for *X. campestris* pv. *vesicatoria* strain 85-10

Motifs	No. of methylation d	No. of motifs detected	% of methlation detected	Restriction enzyme	Origin
A_[A]_GNNNNNCTC	1153	1156		99.74048443 Hpy99XVII	Helicobacter pylori J99
[A]_CCNNNNNGTCY	1117	1126		99.20071048	
G_[A]_GNNNNNCTT	1143	1156		98.87543253 Hpy99XVII	Helicobacter pylori J99
TACG_[A]_G	971	983		98.7792472	
RG_[A]_CNNNNNGGT	1113	1127		98.75776398	
C_[C]_CGGG	2241	2722		82.32916973 SmaI	Citrobacter freundii
C_[C]_NNGG	2241	63872		3.508579659 BsaJI	Bacillus stearothermophilus J695
CGAAG_[A]_C	53	1573		3.369357915 SstE37I	Sagittula stellata E-37
GAAG_[A]_C	92	3276		2.808302808 BbvII	Bacillus species IS4
G_[A]_GTC	65	3093		2.10151956 PfiI	Micrococcus lysae
GGG_[A]_C	82	4334		1.892016613 FlnI	Bacillus pumilus
CTTG_[A]_G	51	2884		1.768377254 Bce83I	Bacillus pumilus 2187a
G_[A]_GG	472	27072		1.743498818 MnlI	Moraxella nonliquefaciens
CA_[A]_GNAC	59	3489		1.691028948 DraRI	Deinococcus radiophilus R1
AG_[A]_CC	155	9438		1.642297097 M.EcoPI	Escherichia coli (PI)
CAG_[A]_G	64	4123		1.552267766 M.StyLTI	Salmonella typhimurium LT7
GAG_[A]_C	63	4100		1.536585366 BsmAI	Acinetobacter lwoffii RFL26
TG_[A]_G	357	23744		1.503537736 M.MmyCI	Mycoplasma mycoides subsp. capri str. GM12
CA_[A]_RCA	69	5288		1.304841115 Tth111II	Thermus thermophilus strain 111
TCG_[A]_G	129	10827		1.19146578 SpnRII	Streptococcus pneumoniae R6
G_[A]_CCAC	55	4648		1.183304647 EsaSSI	Environmental sample Sargasso Sea
GAA_[A]_G	56	5311		1.054415364 HpyUM032XIV	Helicobacter pylori UM032
GCCR_[A]_G	139	14265		0.974412899 Awo1030IV	Acetobacterium woodii DSM 1030
GCCG_[A]_G	73	8069		0.904696988 NmeAIII	Neisseria meningitidis Z2491
AGC_[A]_CC	54	6154		0.877478063 Lsp48III	Leeuwenhoekella sp. Hel_L_48
GCA_[A]_GG	58	6629		0.87494343 CjeFIII	Campylobacter jejuni strain 81-176
ACC_[A]_CC	57	6515		0.874904068 M.EcoGVIII	Escherichia coli O104
GC_[C]_HR	1158	138295		0.837340468 M.NgoDCXV	Neisseria gonorrhoeae MS11 DC
GA_[A]_GG	92	12334		0.745905627 Hin4II	Helicobacter pylori 26695
CTS_[A]_G	81	11576		0.699723566 BseMII	Ruminococcus gnavus AGR2154
CC_[A]_CC	186	26672		0.697360528 M.NgoAX	Neisseria gonorrhoeae FA 1090
GCCGN_[A]_C	58	9081		0.638696179 AqulI	Agmenellum quadruplicatum PR-6
CRTCN_[A]_G	61	9760		0.625 LiaGI	Lactococcus lactis
CGA_[A]_G	121	19760		0.612348178 M.BceSI	Bacillus cereus ATCC 10987
GTNN_[A]_C	169	29100		0.580756014 MjaIV	Helicobacter pylori A 8-5
[C]_CNNGG	313	63872		0.490042585 SseI	Bacillus stearothermophilus J695
TCNG_[A]_	84	19454		0.431787807 Hpy188I	Helicobacter pylori J188
GGTG_[A]_	70	16629		0.42095135 HphI	Haemophilus parahaemolyticus
GTS_[A]_C	69	17128		0.402849136 Tsp45I	Helicobacter pylori J99
G_[A]_NTC	81	20782		0.38976037 Hinfl	Agrobacterium tumefaciens str. C58
C_[C]_NNNNNNGG	221	64330		0.343541116 BsiYI	Bacillus schlegelii 4
GN[C]_[C]_	149	43510		0.342450011 AsuI	Arthrobacter species S9
[C]_CNNNNNNGG	213	64330		0.331105239 BsiYI	Bacillus schlegelii 4
TCG_[A]_	177	61464		0.287973448 TaqI	Chlorella virus NC-1A
CTSS_[A]_G	54	19384		0.278580272 M.PhiMx8I	Myxococcus xanthus phage Mx8
CRTCN_[A]_	88	32359		0.271949071 HpyAXVI-mut2	Helicobacter pylori 26695
GGC_[C]_	282	114958		0.245306982 HaeIII	Bacillus cereus ATCC 10987
GGWCN_[A]_	52	21278		0.244383871 Hpy99XIV-mut1	Helicobacter pylori J99
[C]_NSBVNYH	623	462121		0.134813177	
[C]_SNNVVV	1433	1445206		0.099155415	

Table S3. Comparison of putative methyltransferases from *X. axonopodis* pv. *glycines* strain 8ra and *X. campestris* pv. *vesicatoria* strain 85-10

	XCV1110 ^a (299) ^b	XCV2165 (926)	XCV2267 (369)	XCV2286 (512)	XCV2345 (333)	XCV2405 (538)	XCV2710 (207)	XCVd0131 (272)	XCVd0133 (407)	XCVd0145 (501)
XAR_0064 (499)	-	-	-	491/512 (96%) ^c	-	428/538 (80%)	-	-	-	-
XAR_0578 (452)	-	-	-	204/512 (40%)	-	206/518 (38%)	-	-	-	-
XAR_0579 (638)	-	-	-	-	-	-	-	-	-	-
XAR_0638 (280)	-	-	-	-	-	-	-	-	-	-
XAR_1331 (278)	-	-	-	-	-	-	-	-	-	-
XAR_1938 (393)	-	-	-	-	-	-	-	-	-	-
XAR_2050 (361)	-	-	-	-	-	-	-	-	-	-
XAR_2149 (352)	-	-	-	-	-	-	-	-	-	-
XAR_2182 (260)	-	-	-	-	-	-	-	-	-	-
XAR_2195 (275)	-	-	-	-	-	-	-	-	-	-
XAR_2472 (233)	72/299 (24%)	-	-	-	-	-	-	-	-	-
XAR_3374 (284)	-	-	-	-	-	-	-	-	-	-
XAR_3653 (289)	-	-	-	-	-	-	-	-	-	-
XAR_3868 (449)	-	-	-	-	-	-	-	-	-	-
XAR_4420 (231)	75/299 (25%)	-	-	-	-	-	-	-	-	-

^a locus tag

^b length (numbers of amino acids)

^c identity at amino acid levels

-, no homology