

Supplementary Material I

Table S1. Isolates from human microbiota samples and 16S RNA partial gene homology description.

Microbiota Isolates	Best hit	bp position 16S RNA gene	Query cover (%)	Identity (%)	Accession Number
C1	<i>Bacillus siamensis</i> [LRM10-3D]	430 - 1150	100	100	MT645306.1
	<i>Bacillus velezensis</i> [XC1]		100	100	MT649755.1
C2	<i>Bacillus siamensis</i> [LRM10-3D]	430 - 1150	100	100	MT645306.1
	<i>Bacillus velezensis</i> [XC1]		100	100	MT649755.1
C3	<i>Bacillus amyloliquefaciens</i> [SRCM 112835]	430 - 1150	100	100	MT626036.1
	<i>Bacillus velezensis</i> [XC1]		100	100	MT649755.1
C4	<i>Bacillus</i> sp. [hb97]	430 - 1150	100	100	KF863885.1
	<i>Bacillus siamensis</i> [Van19-4]		100	99.86	JX065213.1
	<i>Bacillus amyloliquefaciens</i> [AD8]		100	99.86	MW325953.1
C5	<i>Bacillus amyloliquefaciens</i> [SRCM 112835]	430 - 1150	100	100	MT626036.1
	<i>Bacillus siamensis</i> [LRM10-3D]		100	100	MT645306.1
	<i>Bacillus velezensis</i> [XC1]		100	100	MT649755.1
C6	Uncultured organism	430 - 1150	100	100	HQ745049.1
	<i>Enterococcus faecalis</i> [2675]		100	99.87	MT611694.1
	<i>Enterococcus faecalis</i> [2674]		100	99.87	MT611693.1
B1	<i>Bacillus subtilis</i> [J-5]	430 - 1150	100	99.80	CP018295.1
	<i>Bacillus amyloliquefaciens</i> [UMAF6614]		100	99.87	CP006960.1
	<i>Bacillus velezensis</i>		100	99.87	MK092976.1
B2	<i>Bacillus amyloliquefaciens</i> [SRCM 112835]	430 - 1150	100	100	MT626036.1
	<i>Bacillus velezensis</i> [XC1]		100	100	MT649755.1
	<i>Bacillus siamensis</i> [LRM10-3D]		100	100	MT645306.1
B3	<i>Bacillus amyloliquefaciens</i> [SRCM 112835]	430 - 1150	100	99.86	MT626036.1
	<i>Bacillus velezensis</i> [XC1]		100	99.86	MT649755.1
	<i>Bacillus siamensis</i> [LRM10-3D]		100	99.86	MT645306.1
B4	<i>Bacillus amyloliquefaciens</i> [SRCM 112835]	430 - 1150	100	99.86	MT626036.1
	<i>Bacillus velezensis</i> [XC1]		100	99.86	MT649755.1
	<i>Bacillus siamensis</i> [LRM10-3D]		100	99.86	MT645306.1
B5	<i>Bacillus amyloliquefaciens</i> [MG3047]	430 - 1150	100	99.72	MW433897.1
	<i>Bacillus velezensis</i> [XC1]		99	100	MT649755.1
	<i>Bacillus siamensis</i> [IA1]		99	100	MW361063.1
B6	<i>Streptococcus salivarius</i> [2789]	430 - 1150	100	100	MT611793.1
	<i>Streptococcus salivarius</i> [2658]		100	100	MT611678.1
	<i>Streptococcus salivarius</i> [2619]		100	100	MT611641.1
B7	<i>Staphylococcus pasteurii</i> [RPS6]	430 - 1150	100	100	MT539733.1
	<i>Staphylococcus pasteurii</i> [IsprtNis008]		100	100	MT500567.1
	<i>Staphylococcus pasteurii</i> [CT1]		100	100	MT072161.1

Table S2. Gene-encoding and corresponding enzymes involved in EPS biosynthesis.

Gene	Enzyme	Enzyme description	EC number	Gene locus CDS Protein ID	Reactions
<i>epsO</i>	EpsO	Pyruvyl transferase	EC: 2.-.-.-	3526057..3527022 QHJ04937.1	Transferase activity
<i>epsN</i>	EpsN	Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	EC: 2.6.1.-	3527001..3528173 QHJ04938.1	Transaminase activity
<i>epsM</i>	EpsM	Acetyltransferase	EC: 2.3.1.-	3528178..3528825 QHJ04939.1	Transferase activity
<i>epsL</i>	EpsL	Sugar transferase	EC: 2.-.-.-	3528822..3529430 QHJ04940.1	Transferase activity
<i>epsK</i>	EpsK	MATE family efflux transporter	-	1130278..1131645 QHJ02774.1	Integral membrane component
<i>epsJ</i>	EpsJ	Glycosyltransferase	EC: 2.4.-.-	3530941..3531975 QHJ04942.1	Transferase activity
<i>epsI</i>	EpsI	Pyruvyl transferase	EC: 2.-.-.-	3531972..3533048 QHJ04943.1	Transferase activity
<i>epsH</i>	EpsH	Glycosyltransferase family 2 protein	EC: 2.4.-.-	3533053..3534090 QHJ04944.1	Transferase activity
<i>epsG</i>	EpsG	EpsG family protein	-	3534109..3535212 QHJ04945.1	Integral membrane component O4 family O-antigen polymerase
<i>epsF</i>	EpsF	Glycosyltransferase family 1 protein	EC: 2.4.-.-	3535216..3536352 QHJ04946.1	Transferase activity
<i>epsE</i>	EpsE	Glycosyltransferase	EC: 2.4.-.-	3536345..3537187 QHJ04947.1	Transferase activity
<i>epsD</i>	EpsD	Glycosyltransferase family 4 protein	EC: 2.4.-.-	3537184..3538323 QHJ04948.1	Transferase activity

Table S3. Proposed gene-encoding and corresponding enzymes involved in PHA biosynthesis.

Gene	Enzyme	Enzyme description	EC number	Gene locus CDS Protein ID	Reactions
<i>phaA</i>	PhaA	Acetyl-CoA C- acetyltransferase	EC:2.3.1.9	3374301..3375476 QHJ04794.1	2 Acetyl-CoA <=> CoA + Acetoacetyl-CoA
<i>phaB</i>	PhaB	3-oxoacyl-[acyl-carrier- protein] reductase	EC:1.1.1.100 EC:1.1.1.36	1662062..1662802 QHJ03260.1	Acetoacetyl-CoA reduction =>R-3-hydroxybutyryl-CoA
<i>phaC</i>	PhaC*	Polymerase	EC:2.3.1.-	-	Polymerization
<i>phaR</i>	PhaR	enoyl-CoA hydratase/isomerase family protein / 3-hydroxyacyl- CoA dehydrogenase	EC:4.2.1.17	3375487..3377856 QHJ04795.1	3-hydroxybutyryl-CoA dehydrogenase Fatty acid metabolism
<i>phaJ</i>	PhaJ	enoyl-CoA hydratase	EC:4.2.1.17	2914743..2915522 QHJ04362.1	Crosspathway with Fatty acid metabolism/B-oxidation

Table S4. WGS *Bacillus* sp. AM1 comparisons (Genbank Accession no:CP0476444.1)

Microorganism Species	Accession no	OrthoANI (%)	isDDH (%)	G+C content (%)	Total length (pb)
<i>Bacillus amyloliquefaciens</i> HM618	NZ_CP029466.1	98.36	83	46.28	4,021,851
<i>Bacillus velezensis</i> AGVL-005	CP024922.1	98.07	79.8	45.98	4,146,154
<i>Bacillus siamensis</i> SCSIO 05746	NZ_CP025001.1	94.32	54.5	45.99	4,268,316
<i>Bacillus subtilis</i> subtilis168	NZ_CP053102.1	77.59	18.7	43.25	4,316,079
<i>Bacillus licheniformis</i> DSM 13	NC_006270.3	72.73	17.3	46.19	4,222,645
<i>Bacillus pumilus</i> ASM299836V1	NZ_PVQT01000001.1	70.65	17.2	41.57	3,787,586
<i>Bacillus coagulans</i> DSM2314	NZ_CP033687.1	68.72	34.3	44.24	3,628,651
<i>Bacillus clausii</i> KSM-K16	NC_006582.1	67.47	28.2	44.75	4,303,871

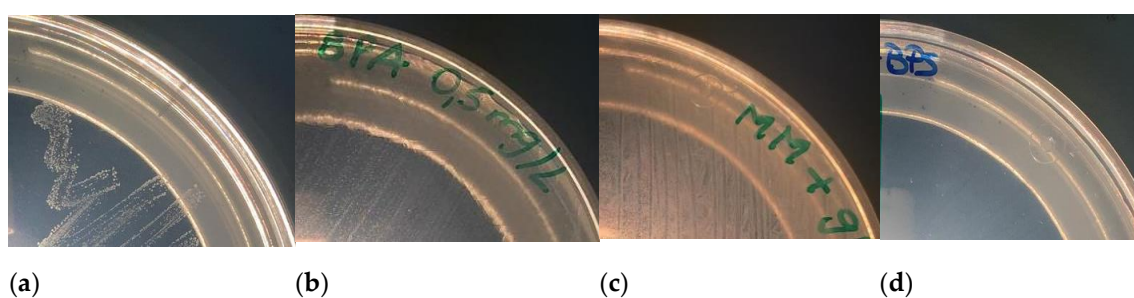


Figure S1. Image of the growth of *Bacillus* sp. AM1 in diferent medias; (a) control bacteria growth in M9 without exposure to BPA; (b) bacteria growth in M9+BPA (0.5 ppm); (c) bacteria growth in M9+glucose (0.5 ppm); (d) bacteria growth in M9+BPS (0.5 ppm).

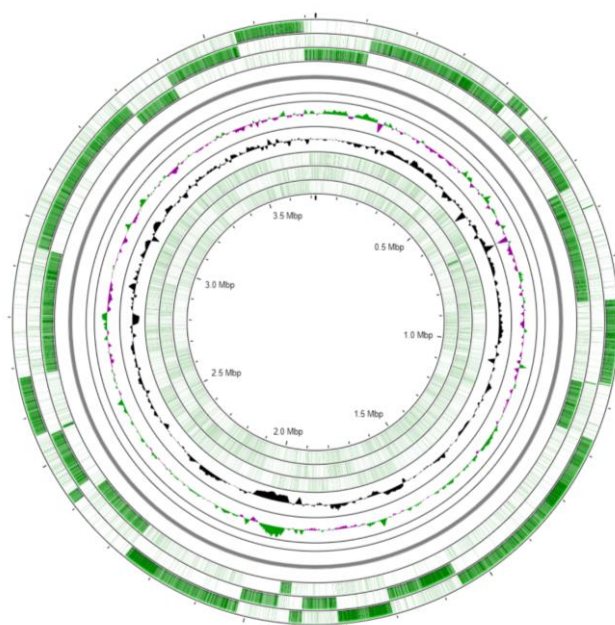


Figure S2. Circular whole genome sequence map of strain *Bacillus* sp AM1. Genome-map was drawn using Circos v0.64(<http://circos.ca/>).