

**DECODING THE ANTIMICROBIAL POTENTIAL OF *BACILLUS SUBTILIS* ONU 1125 FROM
DEEP BLACK SEA SEDIMENTS: AN INTEGRATED GENOMIC AND METABOLOMIC
APPROACH**

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Supplement Table 1: Genomic characteristics of *B. subtilis* ONU 1125 and its closely related strains (sourced from the NCBI Genome Assembly and Annotation report)

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Table S1: Genomic characteristics of *B. subtilis* ONU 1125 and its closely related strains (sourced from the NCBI Genome Assembly and Annotation report)

RefSeq	Strain	Final Assembly Type	Size (bp)	G+C (%)	Isolation Source	Geographic Location
NZ_JBZVEQ000000000	<i>B. subtilis</i> ONU 1125	Whole-genome shotgun	4,259,067	43.4	Deep-sea bottom sediments	Black Sea open waters
NZ_CP034484.1	<i>B. subtilis</i> ATCC 6051 ^T	Complete genome	4,215,610	43.51	Not recorded	Unknown
NZ_CP096889	<i>B. cabrialesii</i> TE3	Complete genome	4,125,766	44.01	<i>Triticum turgidum</i> rhizosphere	Mexico
NC_016047.1	<i>B. spizizenii</i> TU-B-10	Complete genome	4,207,222	43.82	Mojave Desert soil	USA
NZ_JAHBMK020000000	<i>B. cabrialesii</i> subsp. <i>tritici</i> TSO2	Whole-genome shotgun	4,297,452	44.01	<i>Triticum turgidum</i> rhizosphere	Mexico
NZ_AMXN01000006.1	<i>B. inaquosorum</i> KCTC 13429	Whole-genome shotgun	4,342,448	43.69	Soil	South Korea
NZ_JHCA01000008.1	<i>B. stercoris</i> D7XPN1	Whole-genome shotgun	4,079,419	43.82	Food waste bioreactor	Australia

Table S2: Comparative analysis of BGCs and signaling loci in *B. subtilis* ONU 1125 and reference strains

Programs used								
antiSMASH 8.04			PRISM 4		BAGEL4		GECCO	
Region	Cluster type	Cluster range	Cluster type	Cluster range	Cluster type	Cluster range	Cluster type	Cluster range
1.1	Terpene	197,762-218,559	–	–	–	–	Terpene_probability	205,813-209,964
1.2	transAT-PKS, PKS-like, T3PKS, NRPS	806,854-921,622	PKS-like, NRPS	824,995-901,622	–	–	PKS-like, NRPS	824,996-905,812
1.3	NRPS, Betalactone	990,025-1,067,773	NRPS	1,004,401-1,065,496	–	–	NRPS	996,579-1,053,760
1.4	Terpene	1,146,838-1,168,736	–	–	–	–	–	–
1.5	Glycocin	1,315,946-1,336,116	Glycocin	1,321,649-1,326,116	Glycocin, Sublancin_168	1,311,107-1,336,114	RiPP	1,322,093-1,328,082
1.6	T3PKS	1,353,382-1,394,479	–	–	–	–	–	–
1.7	Terpene-precursor	1,572,469-1,593,359	–	–	–	–	–	–
2.1	NRP-metallophore NRPS	67,292-133,551	ComX	77,115-78,236	ComX	67,159-87,276	NRPS	99,579-114,613
			NRPS	101,773-	–	–	–	–

				111,515				
2.2	CDPS, Pulcherriminic acid	413,429- 434,175	Cyclodipeptide (NYH family)	422,195- 426,341	–	–	Saccharide_ probability	416,907- 426,729
2.3	Sactipeptide	693,380- 714,991	Sactipeptide	703,379- 709,619	Subtilosin_A (SboX)	693,380- 714,016	–	–
3.1	Epipeptide	114,231- 135,929	–	–	–	–	–	–
3.2	Other, Bacilysin	357,044- 392,454	Bacilysin	358,230- 392,116	–	–	–	–
4	–	–	–	–	Sactipeptides	63,806- 83,806	–	–
5.1	NRPS	200,406- 225,580	NRPS	208,186- 224,465	–	–	NRPS	216,757- 225,580
6.1	Sactipeptide, Ranthipeptide	31,364- 54,317	Sactipeptide	41,363- 62,755	Sporulation killing factor (SkfA)	31,364- 51,934	Alkaloid_ probability	37,638- 60,394
6.2	NRPS	183,456- 211,202	NRPS	203,455- 211,201	–	–	–	–
10.1	NRPS	1-9,068	NRPS	2-9,068	–	–	–	–

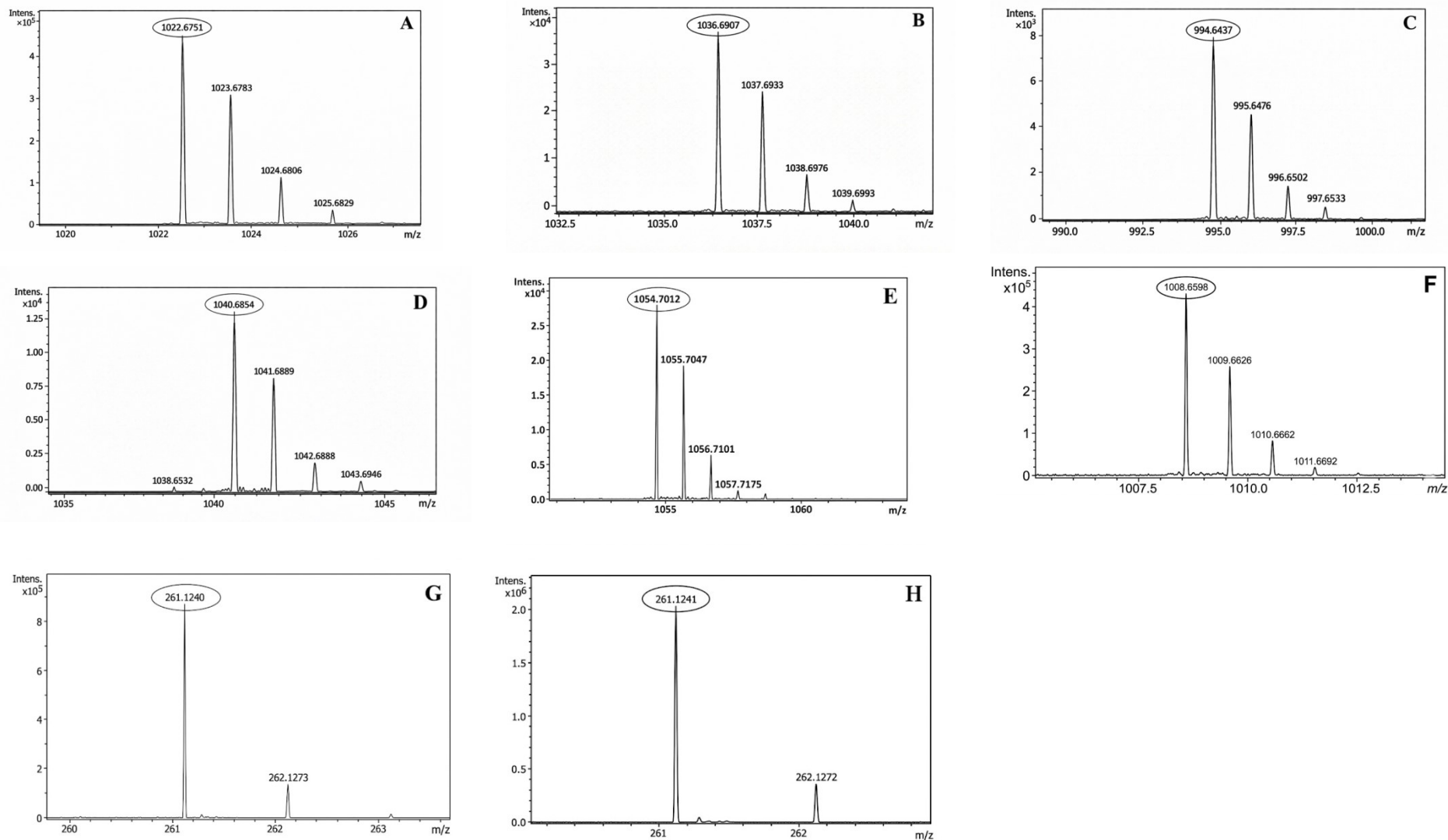


Figure S1: Mass spectra (ESI-MS) of secondary metabolites identified in *B. subtilis* ONU 1125 extracts: A – Surfactin B1/B2; B – Surfactin C1; C – [4-L-Alanine]-surfactin B2/B1; D – Gageostatin A; E – Gageostatin B; F – Gageostatin C; G – Cyclo(L-prolyltyrosyl) (L,L-diketopiperazine); H – Cyclo(D-prolyltyrosyl) (D,L-diketopiperazine).