Figure S1. Comparison of *B. subtilis* subsp. *spizizenii strain* MC6B-22 showing percentage of genes matching known gene clusters for secondary metabolite biosynthesis. BLAST analysis and diagram was produced with antiSMASH 6.0 (https://antismash.secondarymetabolites.org).

Table S1. Primer and cycles for PCR amplification and lipopeptides biosynthesis genes in MC6B-22.

Family Lipopeptide	Temperature cycling used °C/seg	Primer name	Sequence 5'-3'	Product length[a]	Reference
Surfactins	94/60 48/30 72/45	As1-F	CGCGGMTACCGVATYGAGC	0.42	[58]
		Ts2-R	ATBCCTTTBTWDGAATGTCCGCC		
Mycosubtilins	94/60 48/30 72/45	Am1-F	CAKCARGTSAAAATYCGMGG	0.42	
		Tm1-R	CCDASATCAAARAADTTATC		
Fengycins	94/30 48/30 72/30	Af2-F	GAATAYMTCGGMCGTMTKGA	0.45	
		Tf1-R	GCTTTWADKGAATSBCCGCC		
Plipastatins	94 30 50/30 72/90	Ap1-F	AGMCAGCKSGCMASATCMCC	0.90	
		Tp1-R	GCKATWWTGAARRCCGGCGG		
Iturin	94/30 55/30 72/150	ITUP1-F	AGCTTAGGGAACAATTGTCATCGG GGCTTC	2.0	[86]
		ITUP2-R	TCAGATAGGCCGCCATATCGGAAT GATTCG		
Bacillomycin D	Various conditions were tested	BACC1F	GAAGGACACGGCAGAGAGTC	0.87	[87]
		BACC1R	CGCTGATGACTGTTCATGCT		
Kurstakins	94/60 40/30 72/45	Aks-F	TCHACWGGRAATCCAAAGGG	1.2	[88]
		Tks-R	CCACCDKTCAAAKAARKWATC		
		Tks-R	CCACCDKTCAAAKAARKWATC		
16s rDNA	95/30 53/30 72/60	fD1	AGAGTTTGATCCTGGCTCAG	1.5	[89]
		rD1	AAGGAGGTGATCCAGCC		
*gyr*B	94/30 60/30 72/120	gyrBBAUP2	GCGGAAGCGGCCNGSNATGTA	~1.5	[90]
		gyrBBNDN1	CCGTCCACGTCGGCRTCNGYCAT		

[a] Kilo base pairs expected as reported at literature.

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