

Supplementary materials for the article:  
 Quach N.T. et al. Genome-guided investigation provides new insights into secondary metabolites of *Streptomyces parvulus* SX6 from *Aegiceras corniculatum*.  
 Pol J Microbiol. 2022, Vol. 71, No 3, 381–394

Table SI

Molecular identification of 27 bioactive strains recovered from *Aegiceras corniculatum*.

Endophyte code	Plant organ	Closest match	Accession number of closest matched reference species (GenBank)	Percentage identity (%)
SX2	Root	<i>Streptomyces cacaoi</i>	NR_041061	100
SX3	Leave	<i>Streptomyces coelicoflavus</i>	NR_041175	99.63
SX4	Leave	<i>Streptomyces cacaoi</i>	NR_041061	100
SX5	Stem	<i>Streptomyces canescens</i>	NR_119346	99.49
SX6	Stem	<i>Streptomyces parvulus</i>	NR_041119	100
SX7	Root	<i>Streptomyces cacaoi</i>	NR_041061	100
SX8	Root	<i>Streptomyces champavatii</i>	NR_115669	99.51
SX9	Stem	<i>Microbacterium resistens</i>	NR_026437	98.85
SX10	Stem	<i>Streptomyces tendae</i>	NR_025871	100
SX11	Leave	<i>Streptomyces geysiriensis</i>	NR_112459	100
SX12	Leave	<i>Streptomyces cavourensis</i>	NR_112345	98.76
SX14	Leave	<i>Streptomyces cacaoi</i>	NR_041061	100
SX15	Leave	<i>Streptomyces coelicoflavus</i>	NR_041175	99.34
SX24	Root	<i>Streptomyces cacaoi</i>	NR_041061	100
SX25	Leave	<i>Micromonospora aurantiaca</i>	NR_112459	98.44
SX26	Root	<i>Micromonospora peucetia</i>	NR_044882	97.63
SX27	Root	<i>Streptomyces cacaoi</i>	NR_041061	100
SX28	Root	<i>Streptomyces albus</i>	NR_118467	100
SX29	Root	<i>Streptomyces cacaoi</i>	NR_041061	100
SX30	Root	<i>Streptomyces tendae</i>	NR_025871	100
SX31	Leave	<i>Streptomyces cacaoi</i>	NR_041061	100
SX32	Stem	<i>Streptomyces sampsonii</i>	NR_025870	99.49
SX34	Root	<i>Streptomyces althioticus</i>	AY999791	99.87
SX35	Leave	<i>Streptomyces geysiriensis</i>	NR_112459	100
SX36	Leave	<i>Ochrobactrum intermedium</i>	U70978	98.79
SX37	Leave	<i>Nocardia jiangxiensis</i>	NR_043060	97.90
SX38	Leave	<i>Microbacterium resistens</i>	NR_026437	97.18

Table SII  
Physiological and biochemical characteristics of isolate SX6.

Characteristics	Result
Morphological characteristics	
Aerial mycelium	Greyish
Substrate mycelium	Pale yellow
Diffusible pigment	Yellow
Spore chain	Spiral
Spore surface	Warty
Spore shape	Oval-shaped
Physiological properties	
Temperature range	22–37°C
Optimum temperature	30°C
pH range	3–9
Optimum pH	7
NaCl range	1–5%
Optimum NaCl	1%
Enzymatic properties	
Amylase	-
Cellulase	+
Chitinase	+
Protease	+
Xylanase	+
Biochemical properties	
Glucose	+
Glucosamine	+
Fructose	+
Myo-inositol	-
Manitol	-
Mannose	+
Raffinose	-
Sorbitol	+
Trehalose	+
Asparagine	+
Histidine	-
Phenylalanine	+
Leucine	+
Tryptophane	+
Arginine	+
Isoleucine	+
Valin	+
Methionine	+
Lysin	+
Threonin	+

Table SIII  
Biosynthetic gene clusters predicted in the genome of *Streptomyces parvulus* SX6.

No.	Length (bp)	Type	Most similar known BGCs	MIBiG accession	Biological activity
1	6,745	NRPS	-	-	-
2	31,732	NRPS other	Actinomycin D (67%)	BGC0000296	Anticancer, antimicrobes
3	50,467	NRPS	Arylomycin (22%)	BGC0000306	Antimicrobes
4	13,180	Siderophore	Grincamycin (5%)	BGC0000229	Anticancer
5	50,467	NRPS	Fijimycin A (5%)	BGC0000459	Antibacteria
6	22,199	Terpene	Geosmin (100%)	BGC0001181	Earthy smelling substance
7	11,335	RiPP-like	-	-	-
8	21,014	Terpene	Albaflavenone (100%)	BGC0000660	Antibacteria
9	72,549	T2PKS	Spore pigment (66%)	BGC0000271	Unknown
10	21,128	Indole	Spore pigment (23%)	BGC0001483	Unknown
11	54,129	Terpene	Isorenieratene (100%)	BGC0001456	Antioxidant
12	11,770	Siderophore	Desferrioxamin (83%)	BGC0000940	Anticancer, antioxidant
13	10,507	Melanin	Melanin (60%)	BGC0000909	Antioxidant
14	10,216	Bacteriocin	Informatipeptin (42%)	BGC0000518	Unknown
15	50,920	NRPS	Coelichelin (90%)	BGC0000325	Iron chelator
16	41,110	Other	Ulleungmycin (16%)	BGC0001814	Antibacteria
17	29561	RiPP	Citrulassin D (60%)	BGC0001550	Unknown
18	11,917	Siderophore	-	-	-
19	1,927,275	NRPS T1PKS T2PKS	Streptovaricin (48%)	BGC0001785	Anticancer, antibacteria
20	24,076	NRPS	Actinomycin D (28%)	BGC0000296	Anticancer, antimicrobes
21	10,399	Ectoine	Ectoine (100%)	BGC0000853	Natural cell protectant
22	23,879	Terpene	Hopene (100%)	BGC0000663	Unknown
23	22,688	Lantipeptide	SapB (100%)	BGC0000551	Biosurfactant
24	21,059	Terpene	Ebelactone (5%)	BGC0001580	Enzyme inhibitor
25	103,851	NRPS T1PKS other	Polyoxypeptin (48%)	BGC0001036	Anticancer
26	41,332	T3PKS	Kanamycin (1%)	BGC0000703	Antibacteria
27	69,093	NRPS	Vazabotide A (34%)	BGC0001818	Immunosuppressant
28	5,386	NRPS	-	-	-
29	5,160	NRPS	-	-	-

Biosynthetic gene clusters (BGCs) predicted by the antiSMASH database (% indicates the proportion of genes with similarities).

T1PKS – type I polyketide synthase, T2PKS – type II polyketide synthase, T3PKS – type III polyketide synthase, NRPS – non-ribosomal peptide synthase, RiPP – ribosomally synthesized and post-translationally modified peptide, - – not determined

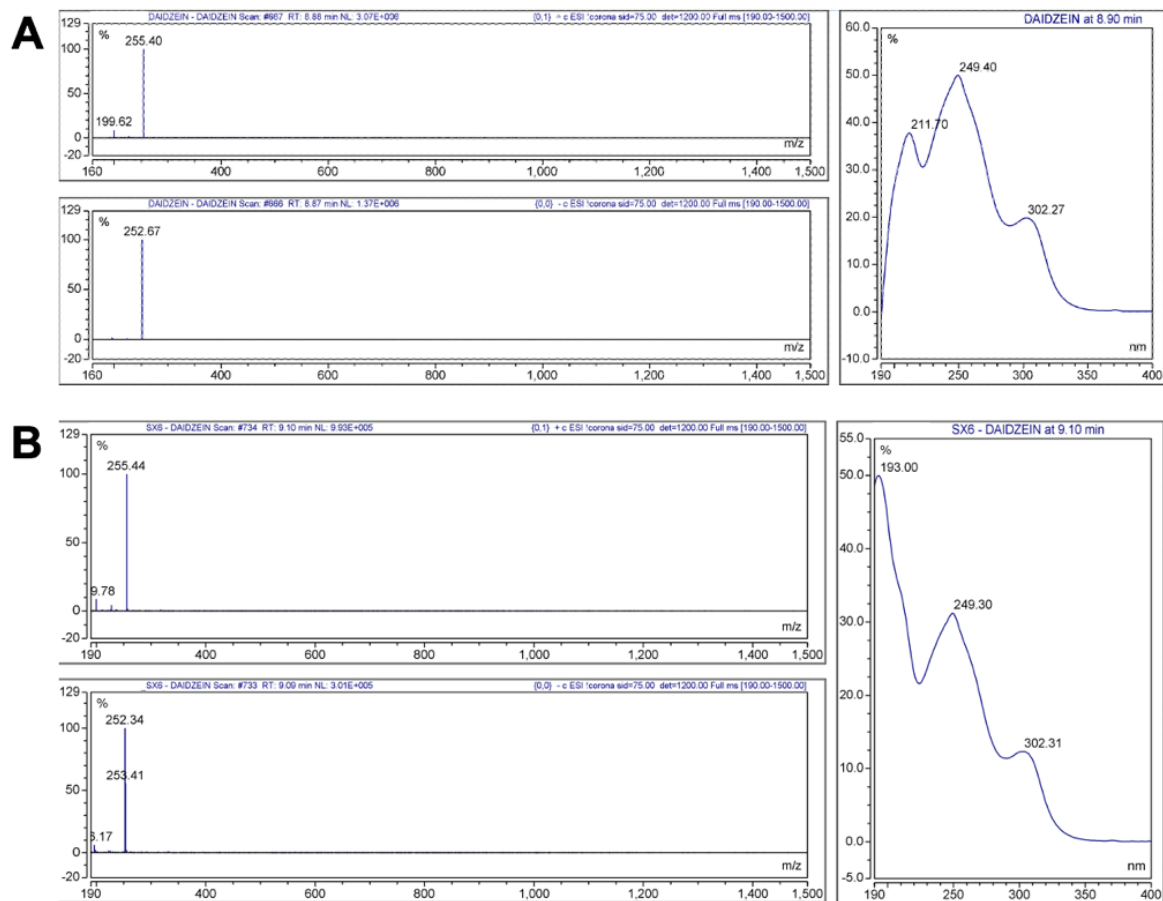


Fig. SI. MS and UV absorption spectra for A) the standard daidzein and B) SX6 extract.

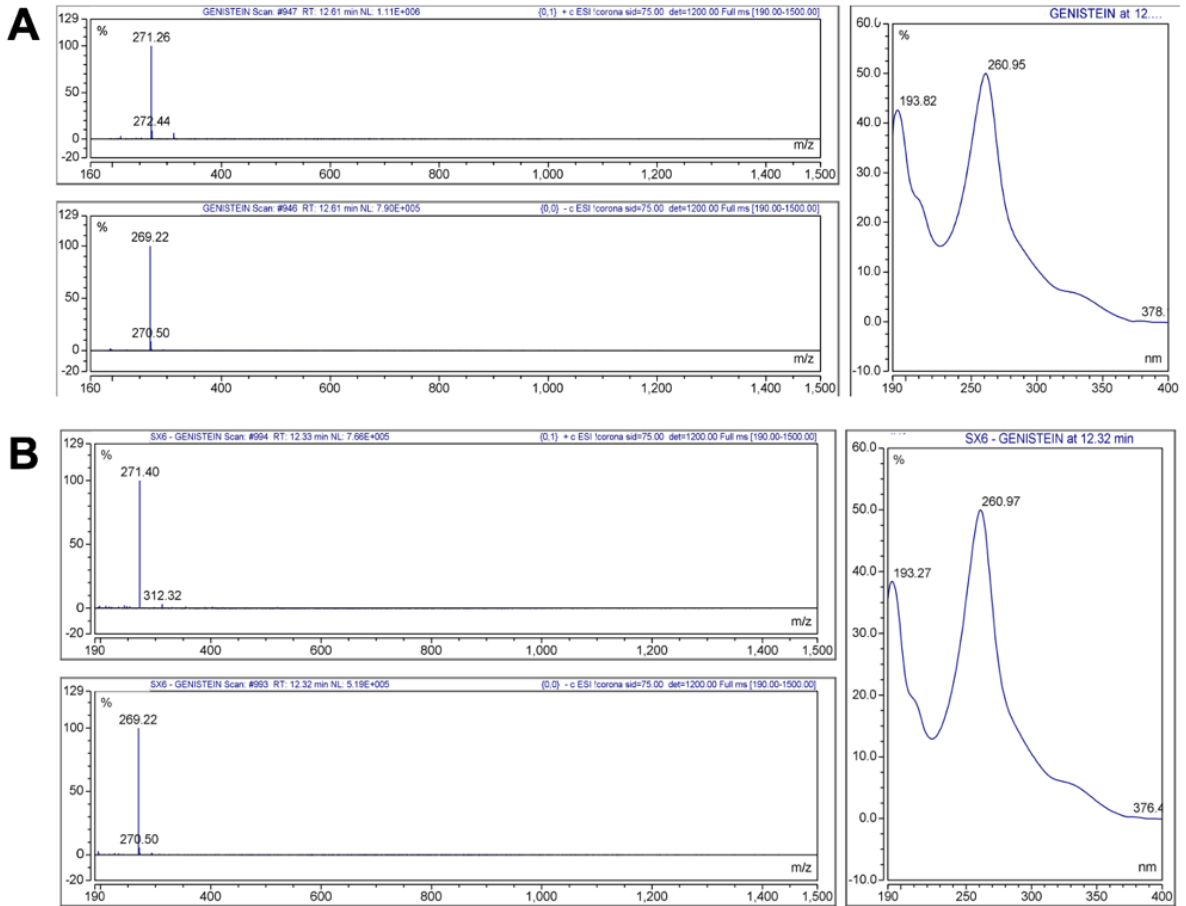


Fig. SII. MS and UV absorption spectra for A) the standard genistein and B) SX6 extract.