

In vitro* and *ex vivo* antibiofilm activity of a lipopeptide biosurfactant produced by the entomopathogenic- *Beauveria bassiana* strain against *Microsporum canis



Figure S1: fungal free- *Vespa orientalis* wasp

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident
✓	Beauveria bassiana isolate Bb1 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	699	699	97%	0.0	99.74%
✓	Cordyceps bassiana strain Bb126 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	699	699	97%	0.0	99.74%
✓	Beauveria bassiana strain C1CR-RSS-0006 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	697	697	97%	0.0	99.74%
✓	Beauveria bassiana strain SJ-1 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	697	697	97%	0.0	99.74%
✓	Beauveria bassiana isolate endophytic fungi small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	697	697	97%	0.0	99.74%
✓	Beauveria bassiana strain YNSK1106 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	697	697	97%	0.0	99.74%
✓	Beauveria bassiana isolate B4 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	697	697	97%	0.0	99.74%
✓	Beauveria bassiana clone F19-N small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	695	695	97%	0.0	99.74%

Beauveria bassiana isolate Bb1 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: **MH355649.1** Length: 543 Number of Matches: 1

Range 1: 1 to 381 [GenBank](#) [Graphics](#)

▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
699 bits(378)	0.0	380/381(99%)	0/381(0%)	Plus/Minus
Query 7	CCGACCTCCCCAAGGGGAGGT	CGAGGGTTGAAATGACGCTCGAACAGGCATGCCCGCCAG	66	
Sbjct 381	CCGACCTCCCCAAGGGGAGGT	CGAGGGTTGAAATGACGCTCGAACAGGCATGCCCGCCAG	322	
Query 67	AATGCTGGCGGGCGCAATGTGCGTTCAAAGATTCGATGATTCAGTGGATTCTGCAATTCA	126		
Sbjct 321	AATGCTGGCGGGCGCAATGTGCGTTCAAAGATTCGATGATTCAGTGGATTCTGCAATTCA	262		
Query 127	CATTACTTATCGCGTTTCGCTGCGTTCTTCATCGATGCCAGAGCCAAGAGATCCGTTGTT	186		
Sbjct 261	CATTACTTATCGCGTTTCGCTGCGTTCTTCATCGATGCCAGAGCCAAGAGATCCGTTGTT	202		
Query 187	GAAAGTTTTGATTCAATTTGTTTGCCTTGCGGCGTATTAGAAGATGCTGGAATACAAGA	246		
Sbjct 201	GAAAGTTTTGATTCAATTTGTTTGCCTTGCGGCGTATTAGAAGATGCTGGAATACAAGA	142		
Query 247	GTTTGAGGTCCCGGGCGGGCCGCTGGTCCAGTCCGCGTCCGGGCTGGGGCGAGTCCGCCG	306		
Sbjct 141	GTTTGAGGTCCCGGGCGGGCCGCTGGTCCAGTCCGCGTCCGGGCTGGGGCGAGTCCGCCG	82		
Query 307	AAGCAACGATAGGTAGGTTACAGAAAGGTTAGGGAGTTGAAAACCGGTAAATGATCCCT	366		
Sbjct 24	AAGCAACGATAGGTAGGTTACAGAAAGGTTAGGGAGTTGAAAACCGGTAAATGATCCCT	22		

Figure S2 Alignment and DNA sequence of *Beauveria bassiana*

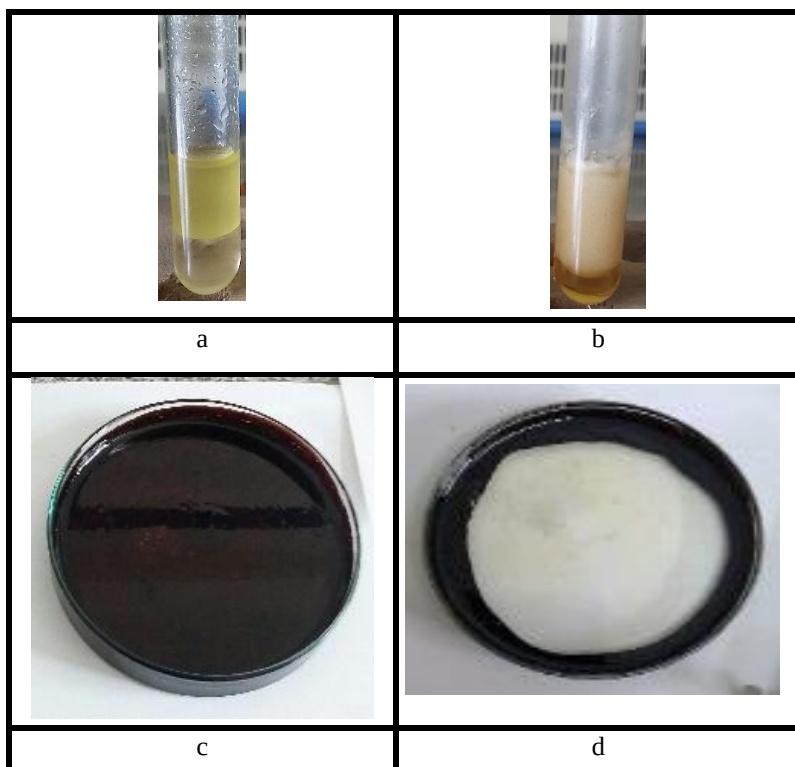


Figure S3. Emulsification index test (EI24) (a) control, (b) with BBLP; oil displacement test (c) control, (d) with BBLP.

Statistical analysis tables:

Table (S1) Comparison of Mycelial growth inhibitory percentages (%) of *M. canis* as affected by BBLP (ANOVA test)

BBLP conc (µg/ml)	Mean	Std. Dev	Std. Error	95% Confidence Interval for Mean		Min	Max	F	P
				Lower Bound	Upper Bound				
0.00	0.00 ^f	0.00	0.00	0.00	0.00	0.00	0.00	28589.4	<0.0001*
0.12	13.14 ^e	0.86	0.50	11.00	15.29	12.38	14.08		
0.24	28.96 ^d	0.54	0.31	27.62	30.30	28.35	29.37		
0.49	53.03 ^c	0.24	0.14	52.42	53.63	52.76	53.24		
0.98	80.69 ^b	0.59	0.34	79.22	82.15	80.22	81.35		
1.95	100 ^a	0.00	0.00	100.00	100.00	100.00	100.00		
3.90	100 ^a	0.00	0.00	100.00	100.00	100.00	100.00		
7.81	100 ^a	0.00	0.00	100.00	100.00	100.00	100.00		

Significance level $p < 0.05$, *significant

Tukey's post test: Means sharing the same superscript letter are not significantly different

Table (2) In vitro Biofilm eradication percentages (%) of *M. canis* as affected by BBLP (ANOVA test)

BBLP conc (µg/ml)	Mean	Std. Dev	Std. Error	95% Confidence Interval for Mean		Min	Max	F	P
				Lower Bound	Upper Bound				
0	0.00 ^e	0.00	0.00	0.00	0.00	0.00	0.00	13963.03	<0.0001*
MIC	25.76 ^d	.77	0.44	23.85	27.67	24.89	26.35		
2×MIC	63.01 ^c	.63	0.37	61.44	64.59	62.58	63.74		
4×MIC	88.22 ^b	1.12	0.65	85.44	91.01	87.25	89.45		
6×MIC	100 ^a	0.00	0.00	100.00	100.00	100.00	100.00		
8×MIC	100 ^a	0.00	0.00	100.00	100.00	100.00	100.00		

Significance level $p < 0.05$, *significant

Tukey's post test: Means sharing the same superscript letter are not significantly different

Table (S3) Descriptive statistics of log 10 (CFU/ml) and comparison of different BBLP MBE-based concentrations (ANOVA test)

	Mean	Std. Dev	Std. Error	95% Confidence Interval for Mean		Min	Max	F	P
				Lower Bound	Upper Bound				
Control	6.94 ^a	0.04	0.03	6.83	7.05	6.91	6.99	29258.3	0.05*
At MBEC	5.58 ^b	0.01	0.01	5.56	5.60	5.57	5.59		
At 2XMBEC	2.77 ^c	0.04	0.03	2.66	2.88	2.72	2.80		
At 4XMBEC	0.00 ^d	0.00	0.00	0.00	0.00	0.00	0.00		

Significance level $p \leq 0.05$, * significant

Tukey's Post hoc test: means with different superscript letters are significantly different

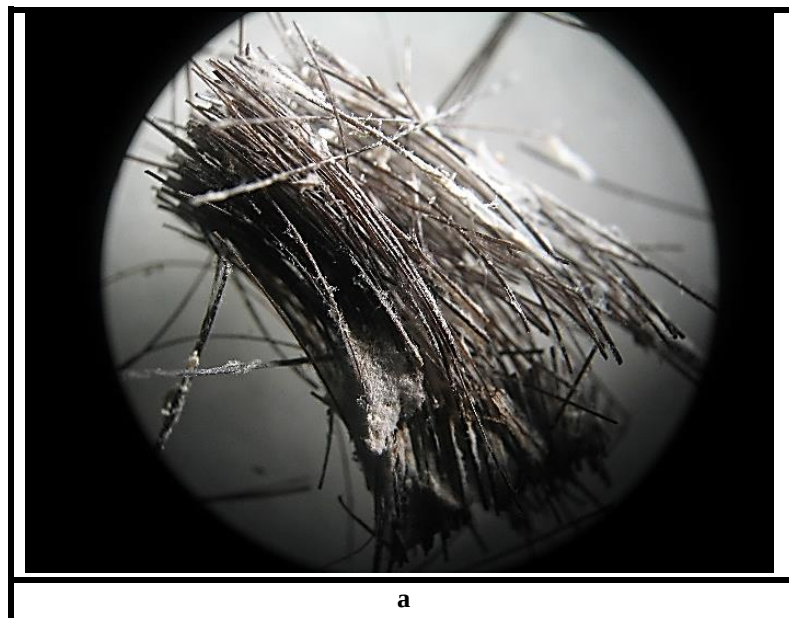


Figure S4. Close up view of *M. canis* ex- vivo biofilm

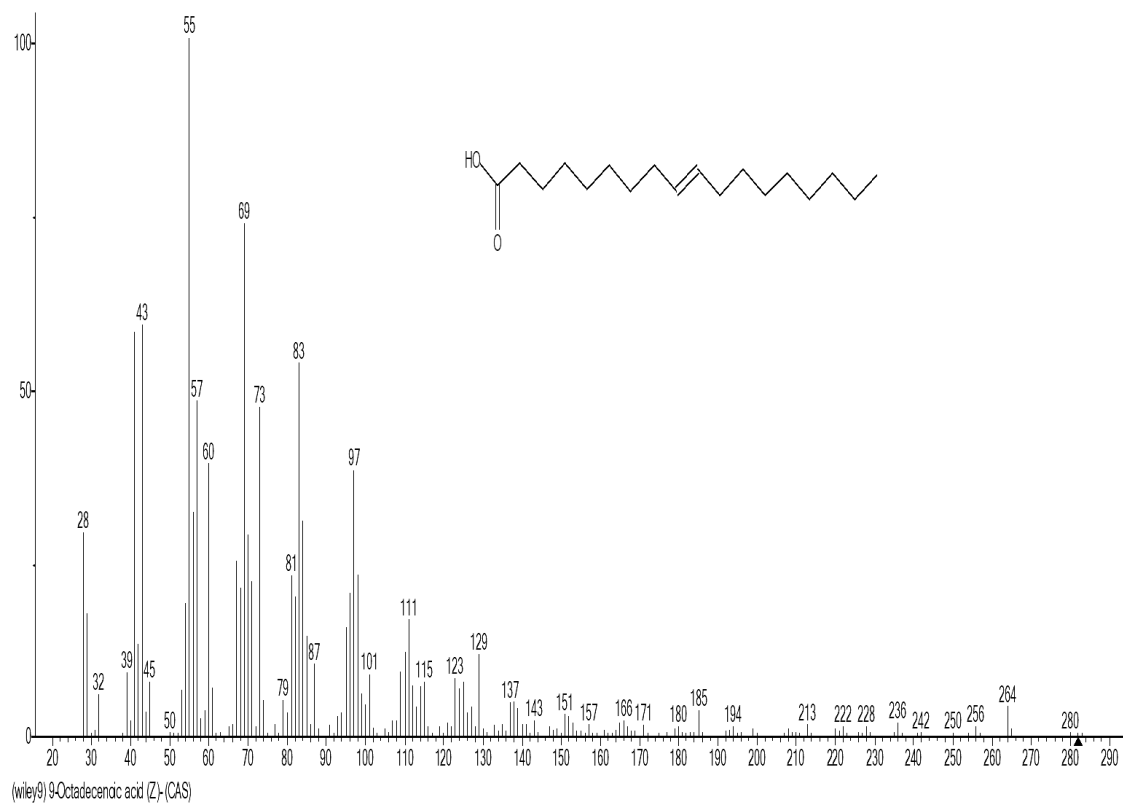


Figure S5. Mass fragmentation spectrum of oleic acid as obtained from the GC-MS analysis

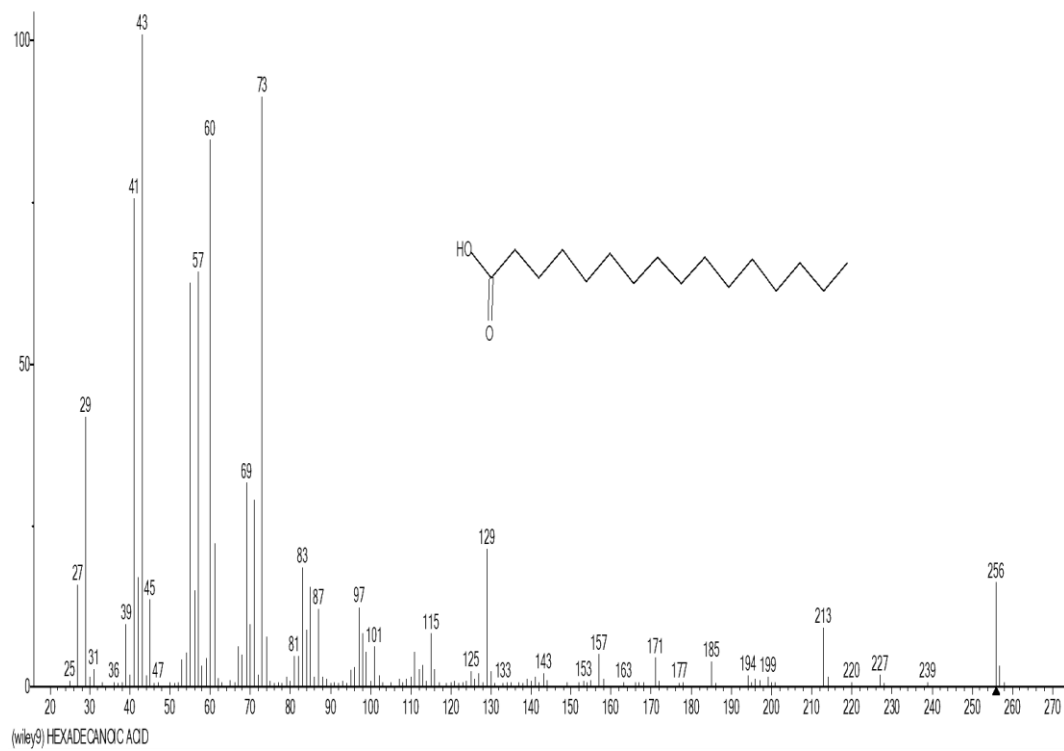


Figure S6. Mass fragmentation spectrum of palmitic acid as obtained from the GC-MS analysis

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T: {0,0} + c EI Full ms [40.00-1000.00]

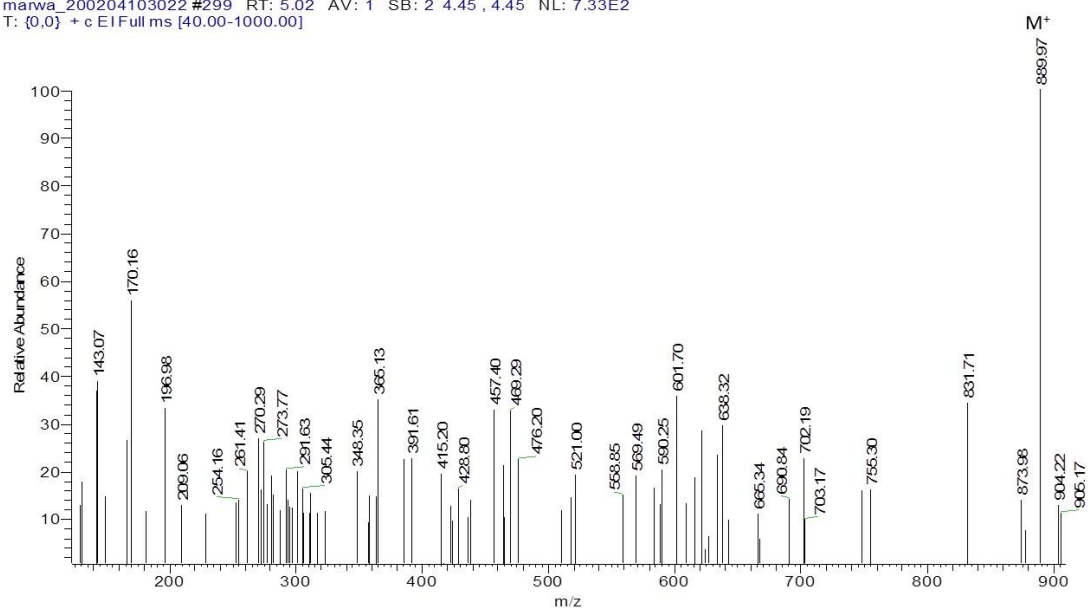


Figure S7. EI-MS of BBLP