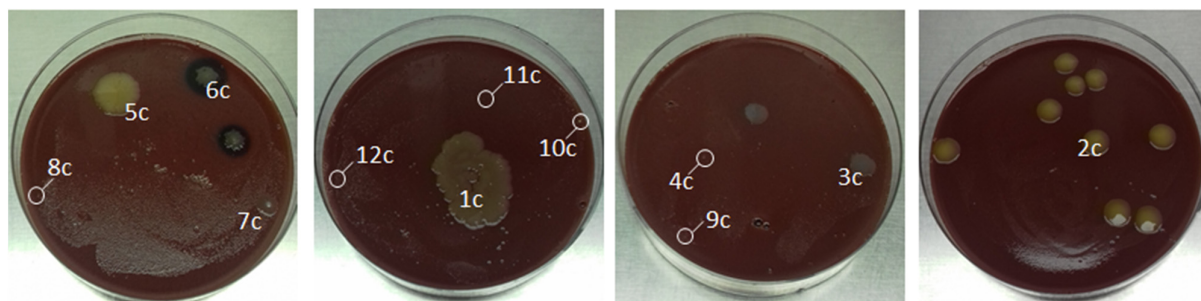


Supplementary Materials



(a)

Colony name	Day of appearance	Colony aspect	Positive for EVP-1
1C	1-3	pale yellow, irregular, flat, undulate margin	
2C	1-3	bright yellow, circular, raised, smooth margin	
3C	1-3	white, irregular, flat, undulate margin	
4C	7-10	white transparent, circular, tiny	x
5C	1-3	bright yellow, circular, raised, irregular margin	
6C	1-3	white, irregular, flat, lobate margin, black halo	
7C	1-3	white, irregular, umbonate, lobate margin,	
8C	7-10	white transparent, circular, tiny	x
9C	7-10	white transparent, circular, tiny	x
10C	7-10	yellow, circular, tiny	
11C	7-10	white transparent, circular, tiny	
12C	7-10	white transparent, circular, tiny	x
13C	7-10	white transparent, circular, tiny	x
14C	7-10	white transparent, circular, tiny	x
15C	7-10	white transparent, circular, tiny	x
1P	1-3	orange, circular, raised, lobate margin	
2P	1-3	pale yellow, irregular, flat, smooth margin	
3P	7-10	white transparent, circular, tiny	x
4P	7-10	white transparent, circular, tiny	x
5P	7-10	white transparent, circular, tiny	x

(b)

Figure S1. (a) Examples of chocolate agar plates with colonies grown after plating hemolymph extracted from *Euscelidius variegatus* Torino population. **(b)** List and characteristics of all the isolated colonies from chocolate (C) and purple (P) agar plates; positivity to EVP-1 was determined by PCR with EVP-1 primers.

Z14096.1	-----CATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGC	50
16S_colony	AGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGC	60

Z14096.1	GGTAGCACAAAGGAGCTTGCTCCCCGGGTGACGAGCGGCGGACGGGTGAGTAGTGTCTGG	110
16S_colony	GGTAGCACAAAGGAGCTTGCTCCCCGGGTGACGAGCGGCGGACGGGTGAGTAGTGTCTGG	120

Z14096.1	GAAACTGCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCG	170
16S_colony	GAAACTGCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCG	180

Z14096.1	CAAGACCAAAGTGGGGGACCTTCGGGCCTCACGCCATCAGATGTGCCAGATGGGATTAG	230
16S_colony	CAAGACCAAAGTGGGGGACCTTCGGGCCTCACGCCATCAGATGTGCCAGATGGGATTAG	240

Z14096.1	CTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGAC	290
16S_colony	CTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGAC	300

Z14096.1	CAGCCACACTGGAAGTGAACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATAT	350
16S_colony	CAGCCACACTGGAAGTGAACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATAT	360

Z14096.1	TGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTT	410
16S_colony	TGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTT	420

Z14096.1	GTAAAGCACTTTCAGCGAGGAGGAAGGCAGTAAGGTTAATAACCTTGCTGATTGACGTTA	470
16S_colony	GTAAAGCACTTTCAGCGAGGAGGAAGGCAGTAAGGTTAATAACCTTGCTGATTGACGTTA	480

Z14096.1	CTCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAA	530
16S_colony	CTCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAA	540

Z14096.1	GCGTTAATCGGAATGACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTTGGATGTGA	590
16S_colony	GCGTTAATCGGAATGACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTTGGATGTGA	600

Z14096.1	AATCCCCGGGCTTAACCTGGGAAACTGCATTCAAACTGGCAAGCTAGAGTCTCGTAGAG	650

16S_colony	AATCCCCGGGCTTAACCTGGG-AACTGCATTCAAACTGGCAAGCTAGAGTCTCGTAGAG	659

Z14096.1	GGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGC	710
16S_colony	GGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGC	719

Z14096.1	GAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGG	770
16S_colony	GAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGG	779

Z14096.1	ATTAGATACCCTGGTAGTCCACTCTGTAAACGATGTCGATTTGGAGGTTGTGCCCTTGAG	830
16S_colony	ATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGAGGTTGTGCCCTTGAG	839

Z14096.1	GCGTGGCTTCCGGACGTAACGCGTTAAATCGACCGCTGGGGAGTACGGCCGCAAGGTT	890
16S_colony	GCGTGGCTTCCGGAGCTAACGCGTTAAATCGACCGCTGGGG-AGTACGGCCGCAAGGTT	898

Z14096.1	AAAAGTGAAATGAATTGACGGGG-CCGCTACAAGCGGTGGAGCATGTGGTTTAATTCGAT	949
16S_colony	AAAACTCAAATGAATTGACGGGGGCCGCAAGCGGTGGAGCATGTGGTTTAATTCGAT	958
	**** * ***** ** *****	
Z14096.1	GCAACGCGAAG-ACCTTACCTACTCTTGACATCCAGAGAATTTAGCAGAGATGCTTTAGT	1008
16S_colony	GCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAATTTAGCAGAGATGCTTTAGT	1018

Z14096.1	GC-TTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGAAATGT	1067
16S_colony	GCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGAAATGT	1078
	** *****	
Z14096.1	TGGGTTAAGTCCCGCAACGAGCGCAACCCTTATGCTTTGTTGCCAGCGATTTCGGTCGGGA	1127
16S_colony	TGGGTTAAGTCCCGCAACGAGCGCAACCCTTATGCTTTGTTGCCAGCGATTTCGGTCGGGA	1138

Z14096.1	ACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCAT	1187
16S_colony	ACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCAT	1198

Z14096.1	GGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGTATACAAAGAGAAGCGACCGC	1247
16S_colony	GGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGTATACAAAGAGAAGCGACCTC	1258

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Z14096.1      GCGAGAGCAAGCGGACCTCATAAAGTACGTCGTAGTCCG-ATTGGAGTGTGCAACTCGAC      1306
16S_colony    GCGAGAGCAAGCGGACCTCATAAAGTACGTCGTAGTCCGGATTGGAGTCTGCAACTCGAC      1318
*****

Z14096.1      TCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCG      1366
16S_colony    TCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCG      1378
*****

Z14096.1      GGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTT      1426
16S_colony    GGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTT      1438
*****

Z14096.1      AACCTTCGGGAGGGCGCTTACCACCTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGG      1486
16S_colony    AACCTTCGGGAGGGCGCTTACCACCTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGG      1498
*****

Z14096.1      TAACCGTAGGG----- 1498
16S_colony    TAACCGTAGGGGAACCTGCGGTTGGATCACCTCCTTACCTAATGATACTGATTCTGTGAA      1558
*****

Z14096.1      ----- 1498
16S_colony    GTGTT 1563

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Figure S2. Alignment of the 16S ribosomal sequence of the three colonies with the one from the “Bacterial parasite of *Euscelidius variegatus*” (BEV) GenBank accession number: Z14096; (Campbell and Purcell, 1993)

Table S1. Blastn analysis of the 12 selected phage sequences against the BEV sequences submitted to the GenBank Trace Archive

Trasncript IDs	Length (nt)	hit accession number	hit length	E- value	identities %	query coverage %
MW965288	768	gnl ti 2292004869	1322	0	98	94
MW965287	1419	gnl ti 2292004924	1177	0	100	63
MW965291	6115	gnl ti 2292005037	1289	0	99	17
MW965289	1777	gnl ti 2292005093	1272	0	100	38
MW965290	5544	gnl ti 2292005198	1211	6E-176	100	6
MW965282	770	gnl ti 2292005213	1160	2E-157	97	42
MW965292	1852	gnl ti 2292005268	1315	0	88	42
MW965284	345	gnl ti 2292005461	1125	2E-31	95	23
MW965286	251	gnl ti 2292005461	1125	5E-50	98	43
MW965283	3268	gnl ti 2292005498	1266	0	99	32
MW965281	2188	gnl ti 2292005561	1072	0	98	46
MW965285	299	No hits found				