

Table S1. Sacbrood virus sequence alignment by Basic Local Alignment Search Tool (BLAST - NCBI), to confirm SBV, extracted from 3 sampled infected larvae of each *A. mellifera* and *A. cerana*.

Sample	Query Length	Matching	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
SBV_AC1	348	Sacbrood virus isolate MD1, complete genome	532	532	98%	3.00E-147	95.06%	MG545286.1
SBV_AC2	349	Sacbrood virus isolate MD1, complete genome	540	540	98%	2.00E-149	95.36%	MG545286.1
SBV_AC3	347	Sacbrood virus isolate MD1, complete genome	553	553	93%	3.00E-153	97.54%	MG545286.1
SBV_AM1	346	Sacbrood virus isolate MD1, complete genome	564	564	98%	1.00E-156	96.77%	MG545286.1
SBV_AM2	350	Sacbrood virus isolate MD1, complete genome	534	534	98%	9.00E-148	95.09%	MG545286.1
SBV_AM3	348	Sacbrood virus isolate MD1, complete genome	538	538	98%	7.00E-149	95.35%	MG545286.1

AC is *A. cerana*.

AM is *A. mellifera*.

Table S2. Beta actin sequence alignment by Basic Local Alignment Search Tool (BLAST - NCBI), to confirm the beta actin gene of *A. cerana*.

Sample	Query Length	Matching	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
AC1	125	Apis cerana mRNA for actin, partial cds	193	193	99%	2.00E-45	95.16%	AB072495.1
AC2	123	Apis cerana mRNA for actin, partial cds	213	213	99%	1.00E-51	98.36%	AB072495.1
AC3	127	Apis cerana mRNA for actin, partial cds	183	183	99%	1.00E-42	93.65%	AB072495.1
SBV_AC1	124	Apis cerana mRNA for actin, partial cds	204	204	99%	9.00E-49	96.75%	AB072495.1
SBV_AC2	127	Apis cerana mRNA for actin, partial cds	189	189	99%	2.00E-44	94.44%	AB072495.1
SBV_AC3	143	Apis cerana mRNA for actin, partial cds	198	198	86%	5.00E-47	95.97%	AB072495.1

AC is *A. cerana*.

SBV_AC is infected *A. cerana*.

Table S3. Beta actin sequence alignment by Basic Local Alignment Search Tool (BLAST - NCBI), to confirm the beta actin gene of *A. mellifera*.

Sample	Query Length	Matching	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
AM1	124	Apis mellifera mRNA for actin, partial cds	209	209	99%	2.00E-50	97.56%	AB023025.1
AM2	126	Apis mellifera mRNA for actin, partial cds	206	206	99%	2.00E-49	96.80%	AB023025.1
AM3	125	Apis mellifera mRNA for actin, partial cds	204	204	99%	9.00E-49	96.77%	AB023025.1
SBV_AM1	123	Apis mellifera mRNA for actin, partial cds	213	213	99%	1.00E-51	98.36%	AB023025.1
SBV_AM2	126	Apis mellifera mRNA for actin, partial cds	200	200	99%	1.00E-47	96.00%	AB023025.1
SBV_AM3	125	Apis mellifera mRNA for actin, partial cds	209	209	99%	2.00E-50	97.58%	AB023025.1

AM is *A. mellifera*.

SBV_AM is infected *A. mellifera*.

Table S4. Ribosomal Protein S5 sequence alignment by Basic Local Alignment Search Tool (BLAST - NCBI), to confirm the ribosomal protein S5 gene of *A. cerana*.

Sample	Accession	Query Length	Matching	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
AC1		123	PREDICTED: Apis cerana 40S ribosomal protein S5 (LOC107998344), transcript variant X2, mRNA	189	189	96%	2.00E-44	95.80%	XM_017057561.2
AC2		119	PREDICTED: Apis cerana 40S ribosomal protein S5 (LOC107998344), transcript variant X2, mRNA	202	202	96%	3.00E-48	98.26%	XM_017057561.2
AC3		119	PREDICTED: Apis cerana 40S ribosomal protein S5 (LOC107998344), transcript variant X2, mRNA	196	196	96%	1.00E-46	97.39%	XM_017057561.2
SBV_AC1		121	PREDICTED: Apis cerana 40S ribosomal protein S5 (LOC107998344), transcript variant X2, mRNA	193	193	96%	2.00E-45	96.58%	XM_017057561.2
SBV_AC2		120	PREDICTED: Apis cerana 40S ribosomal protein S5 (LOC107998344), transcript variant X2, mRNA	187	187	98%	8.00E-44	95.76%	XM_017057561.2

AC is *A. cerana*.

SBV_AC is infected *A. cerana*.

Table S5. Ribosomal protein S5 sequence alignment by Basic Local Alignment Search Tool (BLAST - NCBI), to confirm the ribosomal protein S5 gene of *A. mellifera*.

Sample	Query Length	Matching	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
AM1	123	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	198	198	95%	4.00E-47	97.46%	XM_006570237.3
AM2	119	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	198	198	98%	4.00E-47	97.44%	XM_006570237.3
AM3	119	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	213	213	96%	1.00E-51	100.00%	XM_006570237.3
SBV_AM1	122	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	198	198	96%	4.00E-47	97.46%	XM_006570237.3
SBV_AM2	119	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	213	213	96%	1.00E-51	100.00%	XM_006570237.3
SBV_AM3	120	PREDICTED: Apis mellifera 40S ribosomal protein S5 (LOC409728), transcript variant X2, mRNA	206	206	98%	2.00E-49	98.31%	XM_006570237.3

AM is *A. mellifera*.

SBV_AM is infected *A. mellifera*.

Table S6: Proportion of bacterial genera found in control *A. mellifera*.

Genus	proportion (%)					
	healthy 1	healthy 2	healthy 3	healthy 4	healthy 5	healthy 6
<i>Gilliamella</i>	75.27	75.16	23.73	34.92	68.45	71.74
<i>Frischella</i>	0.00	0.16	19.48	22.86	9.23	6.52
Orbaceae unclassified	13.98	16.77	9.21	10.63	3.65	3.75
Clostridiales unclassified	1.38	1.11	7.91	8.57	3.00	3.95
<i>Snodgrassella</i>	0.15	0.16	8.85	11.11	0.86	0.99
<i>Lactobacillus</i>	0.46	0.32	1.42	1.43	4.08	4.35
Lactobacillales unclassified	0.15	0.16	1.30	0.79	2.15	1.98
Proteobacteria unclassified	0.31	0.32	2.13	2.22	0.43	0.00
<i>Bombella</i>	0.77	0.47	0.71	0.63	0.86	0.79
<i>Fructobacillus</i>	0.61	0.79	0.12	0.00	1.07	0.40
other	6.91	4.59	25.15	6.83	6.22	5.53

Table S7: Proportion of bacterial genera found in SBV infected *A. mellifera*.

Genus	proportion (%)					
	infected 1	infected 2	infected 3	infected 4	infected 5	infected 6
<i>Gilliamella</i>	42.31	43.32	82.38	83.51	84.54	83.66
<i>Frischella</i>	17.27	15.40	6.85	6.18	0.68	0.56
Orbaceae unclassified	33.28	33.81	0.10	0.10	1.18	1.01
Clostridiales unclassified	3.51	3.57	8.42	7.92	11.33	12.67
<i>Snodgrassella</i>	3.10	3.30	0.97	0.90	1.74	1.59
<i>Lactobacillus</i>	0.24	0.25	0.91	0.95	0.31	0.29
Lactobacillales unclassified	0.04	0.03	0.01	0.03	0.01	0.01
Proteobacteria unclassified	0.04	0.05	0.00	0.01	0.01	0.01
<i>Bombella</i>	0.05	0.07	0.20	0.20	0.13	0.09
<i>Fructobacillus</i>	0.07	0.08	0.00	0.00	0.00	0.01
other	0.10	0.11	0.16	0.19	0.08	0.12

Table S8: Proportion of bacterial genera found in control *A. cerana*.

Genus	proportion (%)					
	healthy 1	healthy 2	healthy 3	healthy 4	healthy 5	healthy 6
<i>Gilliamella</i>	36.17	34.93	54.30	58.13	55.43	50.83
<i>Frischella</i>	27.10	26.85	22.20	18.19	20.09	22.28
Orbaceae unclassified	12.28	14.11	5.61	3.27	4.22	7.14
Clostridiales unclassified	7.58	8.76	5.53	6.61	7.76	7.40
<i>Snodgrassella</i>	2.18	3.75	2.23	2.08	2.67	2.26
<i>Lactobacillus</i>	2.53	1.93	2.15	2.82	2.07	2.70
Lactobacillales unclassified	2.76	1.93	1.00	0.67	2.16	1.31
Proteobacteria unclassified	1.61	1.37	1.61	0.67	1.47	1.65
<i>Bombella</i>	0.57	0.80	0.84	0.59	0.78	1.04
<i>Fructobacillus</i>	0.00	0.00	0.92	1.78	0.00	0.00
other	7.23	5.57	3.61	5.20	3.36	3.39

Table S9: Proportion of bacterial genera found in SBV infected *A. cerana*.

Genus	proportion (%)				
	infected 1	infected 2	infected 3	infected 4	infected 5
<i>Gilliamella</i>	1.45	6.44	6.64	2.58	2.39
<i>Frischella</i>	3.38	1.87	2.36	1.15	1.30
Orbaceae unclassified	48.39	29.73	24.63	30.37	42.83
Clostridiales unclassified	10.45	1.87	2.78	8.60	6.30
<i>Snodgrassella</i>	10.29	26.40	26.34	15.47	16.52
<i>Lactobacillus</i>	7.56	16.22	16.49	13.75	10.87
Lactobacillales unclassified	0.32	0.00	0.00	0.00	0.22
Proteobacteria unclassified	2.89	1.04	1.93	2.58	2.17
<i>Bombella</i>	3.05	4.78	3.64	4.87	2.17
<i>Fructobacillus</i>	2.09	0.00	0.00	0.00	0.00
other	10.13	11.64	15.20	20.63	15.22

Table S10. LDA score of Functional gene prediction based on KEGG database.

Functional gene	LDA score	increase/decrease
Lipopolysaccharide biosynthesis	2.22141423784	decrease
Ascorbate and aldarate metabolism	2.11809931208	decrease
Ubiquinone and other terpenoid-quinone biosynthesis	1.7923916895	decrease
Pentose and glucuronate interconversions	2.0960405543	decrease
Lipoic acid metabolism	2.21484384805	decrease
Glutathione metabolism	2.12139568071	decrease
Bacterial secretion system	2.17609125906	decrease
C5-Branched dibasic acid metabolism	2.33994806169	decrease
D-Arginine and D-ornithine metabolism	1.98000337158	increase
Biosynthesis of vancomycin group antibiotics	2.51121470114	increase
beta-Lactam resistance	1.81624129999	increase
Secondary bile acid biosynthesis	2.09342168516	increase
Biosynthesis of ansamycins	2.73359846096*	increase
Synthesis and degradation of ketone bodies	2.07371835035	increase
Bacterial chemotaxis	2.63748972951*	increase

* These are the most affected functions in SBV infected *A. cerana*

Table S11. LDA score of bacteria affected in *A. cerana*.

Bacteria taxa	LDA score
<i>Gilliamella</i>	2.70520346596**
<i>Lactobacillus</i>	2.11316664674
<i>Bombella</i>	1.85797792939
<i>Snodgrassella</i>	0.73293969148
Firmicutes_unclassified	1.32688027974
Bacilli_unclassified	1.56870843394
Clostridiales_unclassified	2.54640904842*
Proteobacteria_unclassified	1.14991384179
Lactobacillales_unclassified	2.27887045036
Orbaceae_unclassified	2.34084185769**
other	2.16329390352

* This is the most affected function in SBV infected *A. cerana*

**These are the most affected functions in healthy *A. cerana*

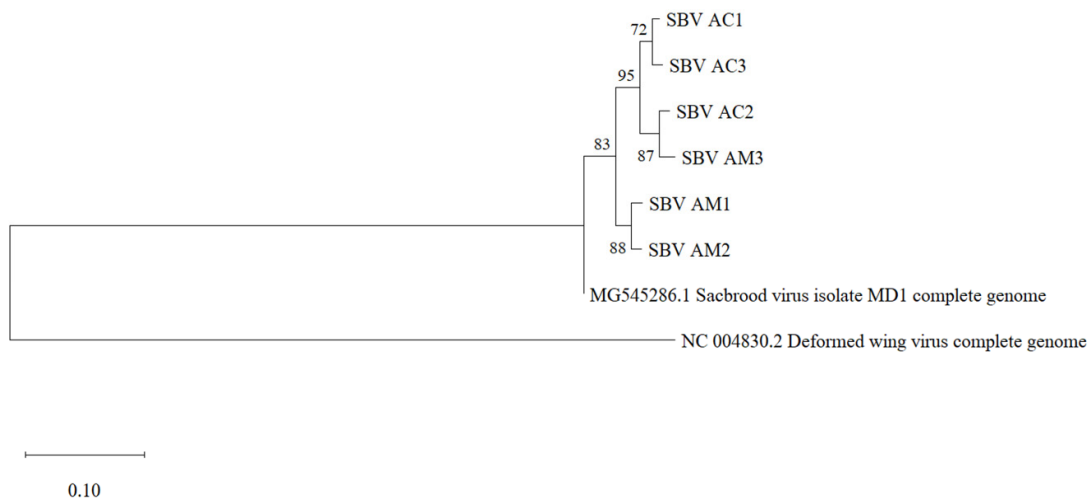


Figure S1: Phylogenetic tree of Sacbrood virus in infected honey bees.

Evolutionary analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method and Tamura 3-parameter model [1]. The tree with the highest log likelihood (-1250.85) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 8 nucleotide sequences. There were a total of 371 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

1. Tamura K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9:678-687.
2. Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.
3. Felsenstein J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.

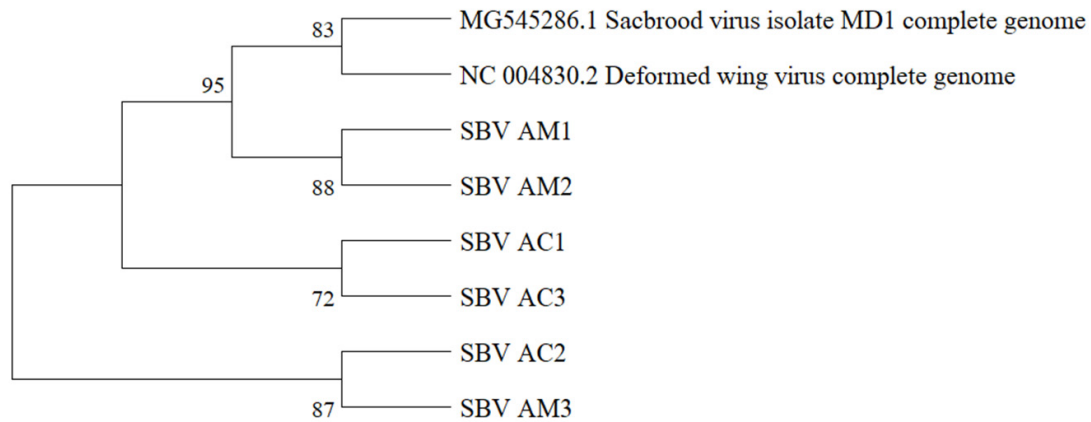


Figure S2: Bootstrap consensus tree of Sacbrood virus in infected honey bees.

Evolutionary analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method and Tamura 3-parameter model [1]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. This analysis involved 8 nucleotide sequences. There were a total of 371 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

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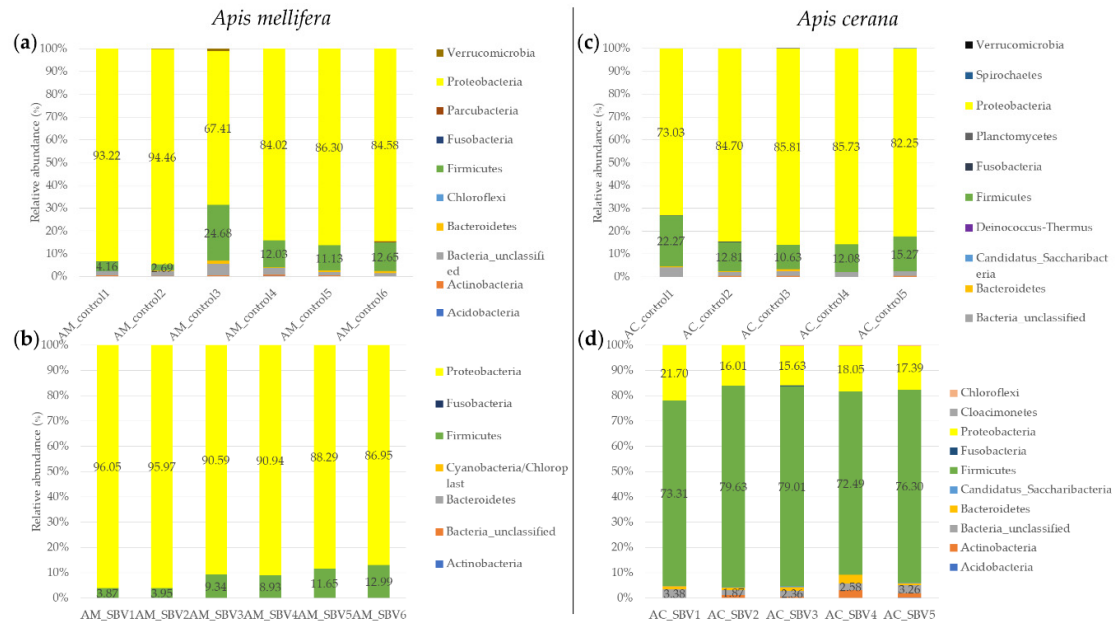


Figure S3: Proportion of gut bacterial community (phylum) found in healthy and infected honeybees.

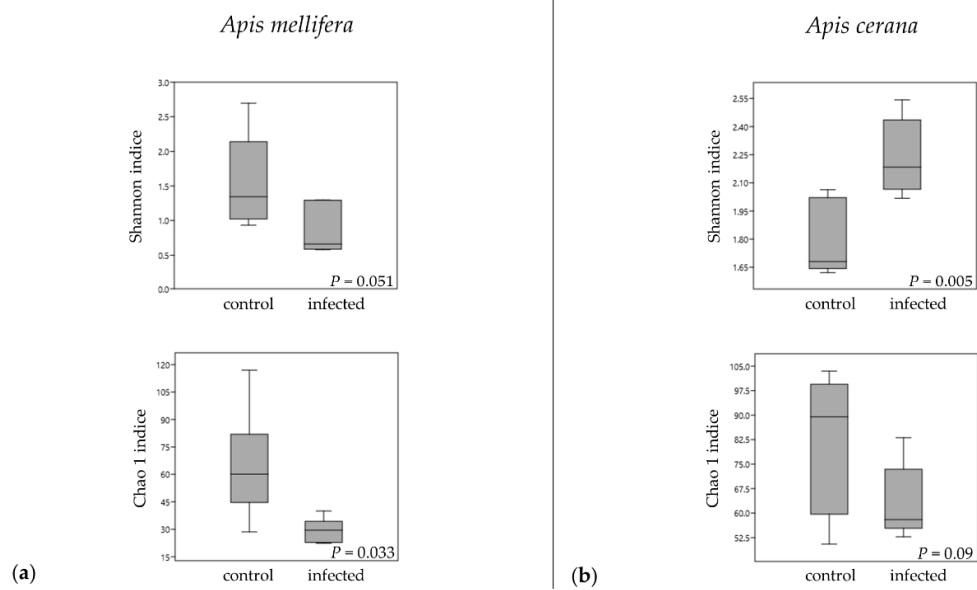


Figure S4: Alpha diversity boxplots compare the gut microbiota between the control and infected worker larvae of *A. mellifera* (a) and *A. cerana* (b) designated by Shannon and Chao 1 index.

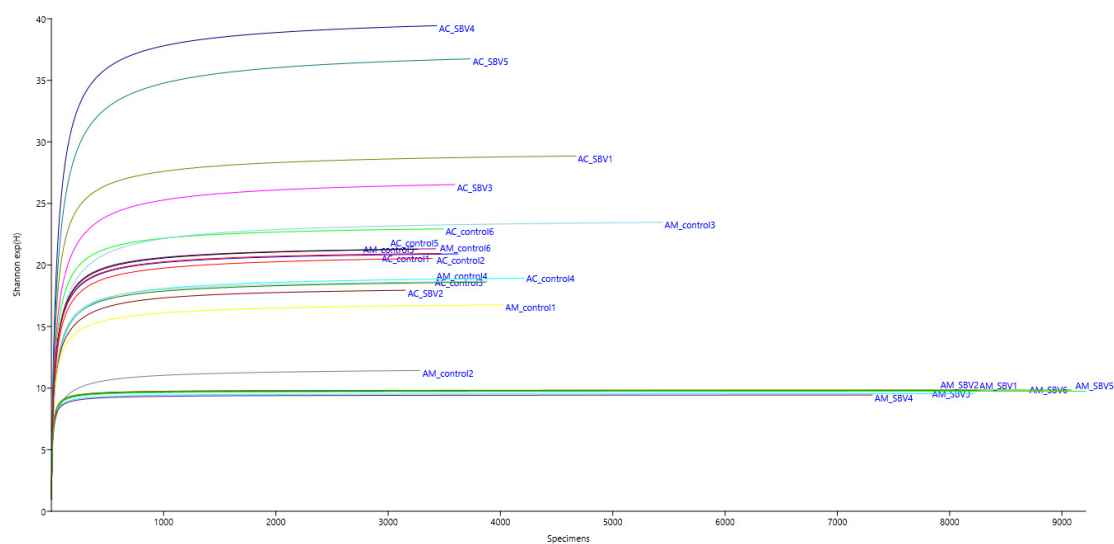


Figure S5: Rarefaction curves of bacterial OTUs and Shannon index constructed by PAST software version 3.14.