RNAseq analysis reveals virus diversity within Hawaiian apiary insect communities

Brettell, LE, Schroeder, DC and Martin, SJ

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<table>
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<tr>
<th>Title</th>
<th>RNAseq analysis reveals virus diversity within Hawaiian apiary insect communities</th>
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</thead>
<tbody>
<tr>
<td>Authors</td>
<td>Brettell, LE, Schroeder, DC and Martin, SJ</td>
</tr>
<tr>
<td>Type</td>
<td>Article</td>
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<td>URL</td>
<td>This version is available at: <a href="http://usir.salford.ac.uk/id/eprint/51169/">http://usir.salford.ac.uk/id/eprint/51169/</a></td>
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<td>Published Date</td>
<td>2019</td>
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Supplementary Materials: The following are available online at www.mdpi.com/1999-4915/11/5/397/s1, Figure S1: DWV genome coverage plots for individual samples created using Geneious. Read depths are shown on a log-10 scale and represent DWV-A (red), -B (blue), and -C (yellow) along the ~10.1 kb genomes. Table S1: DWV-A RdRp sequences originally from [4] and used in this study in the construction of the DWV-A phylogeny in Figure 5. Table S2: Viruses commonly found in bees used for BLAST analysis along with accession numbers. Table S3: Numbers of reads mapping to DWV types A, B, and C using BLAST top hit analysis for each sample, along with location and total numbers of reads passing QC (read1.fasta).

Figure S1: DWV genome coverage plots for individual samples created using Geneious. Read depths are shown on a log-10 scale and represent DWV-A (red), -B (blue), and -C (green) along the ~10.1 kb genomes.
Figure S2: DWV alignments (MUSCLE) created using Geneious showing de novo assembled contigs from samples A_tum-5 and V_pen-8, which contain recombination breakpoints. (a) Contig A_tum-5-a aligned with DWV-A (NC_004830.2) and DWV-C (CEND01000001.1) reference genomes, (b) contig V_pen_8-b aligned with DWV-A (NC_004830.2) and DWV-B (AY251269.2), and (c) a second contig from sample V_pen_8; V_pen_8-t also aligned with DWV-A (NC_004830.2) and DWV-B (AY251269.2). All alignments show disagreements with the consensus sequences highlighted in black and recombinant contigs are shaded red where they map most closely to DWV-A, blue to DWV-B, and green to DWV-C.
Table S1: Samples used in this study. Sample names are given along with the site from which they were sampled, species name, and the symbol used to denote them in Figures 1 and 5.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Site</th>
<th>Species</th>
<th>Symbol</th>
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<tbody>
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<td><em>A. mellifera</em></td>
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<td><em>V. destructor</em></td>
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Table S2: DWV-A RdRp sequences originally from [4] and used in this study in the construction of the DWV-A phylogeny in Figure 5.

<table>
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<th>Accession no</th>
<th>host</th>
<th>country</th>
<th>year</th>
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<td>KP734616</td>
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<td>KP734692</td>
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Table S3: Viruses commonly found in bees used for BLAST analysis along with accession numbers.

<table>
<thead>
<tr>
<th>Virus</th>
<th>Accession number</th>
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<td>Deformed wing virus – type A</td>
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<td>Deformed wing virus – type A, Kakugo virus</td>
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<td>Deformed wing virus – type B, Varroa destructor virus 1</td>
<td>AY251269.2</td>
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<td>Deformed wing virus – type C</td>
<td>ER567949</td>
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<td>Milolii virus</td>
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<td>Moku virus</td>
<td>NC_031338.1</td>
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<td>Acute bee paralysis virus (ABPV)</td>
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<td>Israeli acute paralysis virus (IAPV)</td>
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<td>Kashmir bee virus (KBV)</td>
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<td>Slow bee paralysis virus (SBPV)</td>
<td>NC_014137.1</td>
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Table S4: Numbers of reads mapping to DWV types A, B, and C using BLAST top hit analysis for each sample, along with the total numbers of reads passing QC (read1.fasta).

<table>
<thead>
<tr>
<th>Sample</th>
<th>DWV A</th>
<th>DWV B</th>
<th>DWV C</th>
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<th>Total reads</th>
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