Supplementary Materials: The following are available online at www.mdpi.com/xxx/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 $\sim 10.1 \mathrm{~kb}$ genomes. Table S1: DWV-A $R d R p$ 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).
honeybees

varroa

big headed ants


ghost ants


small hive beetles




${ }^{20}$
yellowjacket wasps



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 $\sim 10.1 \mathrm{~kb}$ genomes.
a

b

c


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.

| Sample | Site | Species | Symbol |
| :--- | :--- | :---: | :---: |
| T_mel_1 | B2 | T. melanocephalum |  |
| T_mel_2 | B2 | T.melanocephalum |  |
| P_meg_1 | B3 | P.megacephala |  |
| P_meg_2 | O1 | P.megacephala |  |
| A_tum_1 | O2 | A.tumida |  |
| A_tum_2 | B1 | A.tumida |  |
| A_tum_3 | B1 | A.tumida |  |
| A_tum_4 | B1 | A.tumida |  |
| A_tum_5 | B1 | A.tumida |  |
| V_pen_1 | B4 | V.pensylvanica |  |
| V_pen_2 | B4 | V.pensylvanica |  |
| V_pen_3 | B4 | V.pensylvanica |  |
| V_pen_4 | B4 | V.pensylvanica |  |
| V_pen_5 | B4 | V.pensylvanica |  |
| V_pen_6 | B3 | V.pensylvanica |  |
| V_pen_7 | B3 | V.pensylvanica |  |
| V_pen_8 | B3 | V.pensylvanica |  |
| A_mel_1 | B3 | A. mellifera |  |
| A_mel_2 | O1 | A. mellifera |  |
| A_mel_3 | B1 | A. mellifera |  |
| A_mel_4 | B2 | A. mellifera |  |
| V_des_1 | B3 | V. destructor |  |
| V_des_2 | O1 | V. destructor |  |

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.

| Accession no | host | country | year |
| :---: | :---: | :---: | :---: |
| KP734679 | A. mellifera | France | 2009 |
| KP734616 | A. mellifera | Germany | 2009 |
| KP734641 | A. mellifera | Hawaii | 2009 |
| KP734623 | V. destructor | Hawaii | 2009 |
| KP734625 | V. destructor | Hawaii | 2009 |
| KP734687 | A. mellifera | Hawaii | 2009 |
| KP734692 | A. mellifera | Pakistan | 1998 |
| KP734713 | V. destructor | Poland | 2009 |
| KP734653 | A. mellifera | UK | 2009 |
| KP734694 | A. mellifera | USA | 2009 |

Table S3: Viruses commonly found in bees used for BLAST analysis along with accession numbers.

| Virus | Accession number |
| :--- | :---: |
| Deformed wing virus - type A | NC_004830.2 |
| Deformed wing virus - type A, Kakugo virus | NC_005876.1 |
| Deformed wing virus - type B, Varroa destructor virus 1 | AY251269.2 |
| Deformed wing virus - type C | ERS657949 |
| Milolii virus | MF155030.1 |
| Moku virus | NC_031338.1 |
| Acute bee paralysis virus (ABPV) | NC_002548.1 |
| Black queen cell virus (BQCV) | NC_003784.1 |
| Israeli acute paralysis virus (IAPV) | NC_009025.1 |
| Kashmir bee virus (KBV) | NC_004807.1 |
| Lake Sinai virus (LSV) | NC_032433.1 |
| Sacbrood virus (SBV) | NC_002066.1 |
| Slow bee paralysis virus (SBPV) | NC_014137.1 |

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).

| Sample | DWV A | DWV B | DWV C | Total DWV | Total reads |
| :---: | :---: | :---: | :---: | :---: | :---: |
| T_mel_1 | 92713 | 11747 | 461 | 104921 | 19669974 |
| T_mel_2 | 536208 | 183603 | 1009 | 720820 | 17461610 |
| P_meg_1 | 47074 | 3128 | 844 | 51046 | 18268406 |
| P_meg_2 | 8984109 | 691892 | 356 | 9676357 | 19795762 |
| A_tum_1 | 6636 | 808 | 15661 | 23105 | 18581324 |
| A_tum_2 | 6713 | 1031 | 9758 | 17502 | 16891197 |
| A_tum_3 | 9594 | 941 | 9493 | 20028 | 16609397 |
| A_tum_4 | 6612 | 898 | 14267 | 21777 | 17083341 |
| A_tum_5 | 7027 | 772 | 17290 | 25089 | 17683443 |
| V_pen_1 | 8757 | 9670 | 178 | 18605 | 11961813 |
| V_pen_2 | 10718 | 11858 | 82 | 22658 | 12807830 |
| V_pen_3 | 9709 | 11883 | 144 | 21736 | 14181324 |
| V_pen_4 | 9735 | 15421 | 48 | 25204 | 16089890 |
| V_pen_5 | 10981 | 13184 | 81 | 24246 | 17001465 |
| V_pen_6 | 956354 | 18679 | 717 | 975750 | 15504637 |
| V_pen_7 | 37106 | 371054 | 156 | 408316 | 14215385 |
| V_pen_8 | 687229 | 242371 | 586 | 930186 | 13394271 |
| A_mel_1 | 3839027 | 141563 | 239 | 3980829 | 17678449 |
| A_mel_2 | 4877249 | 269833 | 7187 | 5154269 | 13765791 |
| A_mel_3 | 24613 | 24797 | 241 | 49651 | 12183541 |
| A_mel_4 | 14705870 | 512418 | 131 | 15218419 | 23505172 |
| V_des_1 | 9653918 | 2452020 | 71 | 12106009 | 13498757 |
| V_des_2 | 28031169 | 2089009 | 1876468 | 31996646 | 35064635 |

