# Supplementary Material

# Accumulation and Competition Amongst Deformed Wing Virus Genotypes in Naïve Australian Honeybees Provides Insight Into the Increasing Global Prevalence of Genotype B

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This file contains

- Supplementary Figure S1-S4
- Supplementary Tables S1-S9
- Supplementary Text S1-S2
- Supplementary References

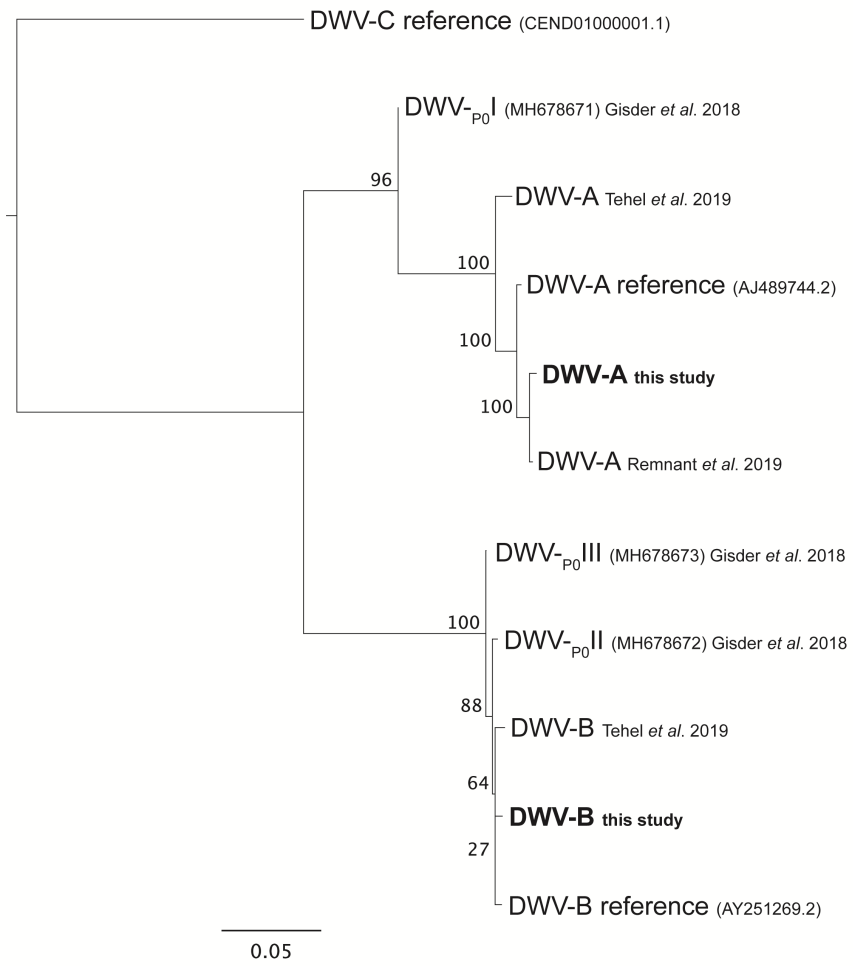
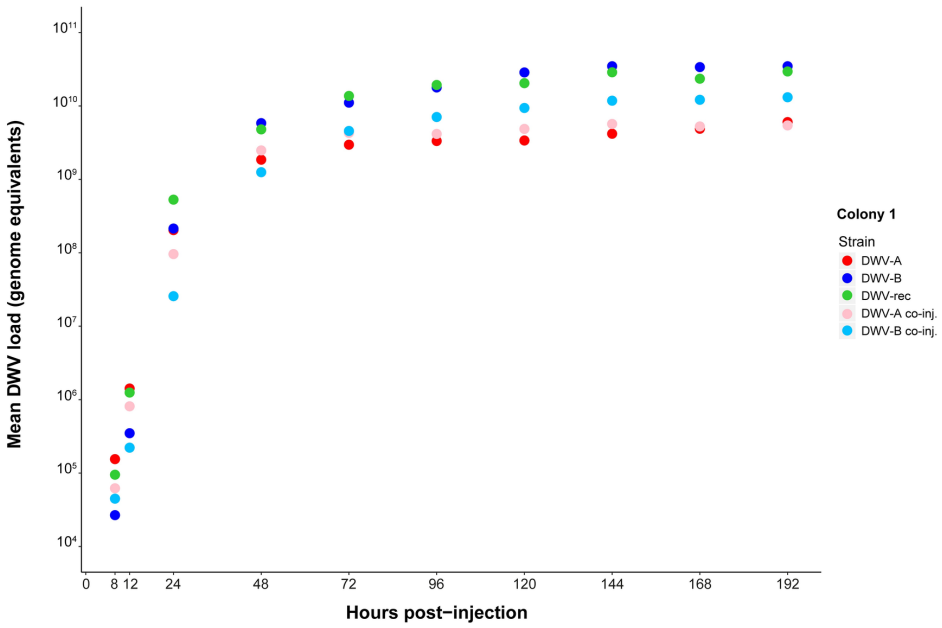
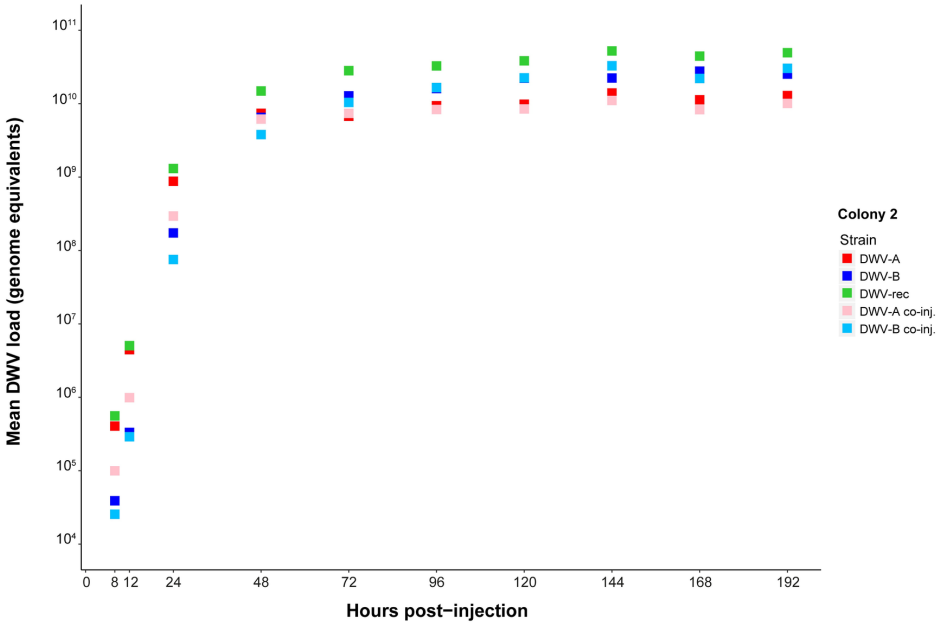



**Figure S1.** Phylogenetic tree comparing whole genome sequences of the DWV-A (accession number MN538208) and DWV-B (MN538209) inocula obtained in this study to isolates experimentally injected by Remnant et al. (2019), Tehel et al. (2019) and Gisder et al. (2018) (MH678671-73). DWV-A (AJ489744.2; Lanzi et al. (2006)), DWV-B (AY251269.2; Ongus et al. (2004)) and DWV-C (CEND01000001; (Mordecai et al., 2016)) were used as reference sequences, with DWV-C as the outgroup. The DWV-A and DWV-B whole genome sequences from this study were obtained from transcriptome sequencing (see Materials and Methods) and are highlighted in bold. Sequences were aligned in Geneious using Muscle and trimmed where required. Maximum likelihood trees were produced using PhyML HKY85 model after 100 bootstrap replicates.


Mean DWV load (genome equivalents)
$10^{11}$
$10^{10}$
$10^{9}$
$10^{8}$
$10^{7}$
$10^{6}$
$10^{5}$
$10^{4}$
0 8 12 24 48 72 96 120 144 168 192
Hours post−injection
Colony 1
Strain
DWV-A
DWV-B
DWV-rec
DWV-A co-inj.
DWV-B co-inj.


Mean DWV load (genome equivalents)
$10^{11}$
$10^{10}$
$10^{9}$
$10^{8}$
$10^{7}$
$10^{6}$
$10^{5}$
$10^{4}$
0 8 12 24 48 72 96 120 144 168 192
Hours post−injection
Colony 2
Strain
DWV-A
DWV-B
DWV-rec
DWV-A co-inj.
DWV-B co-inj.

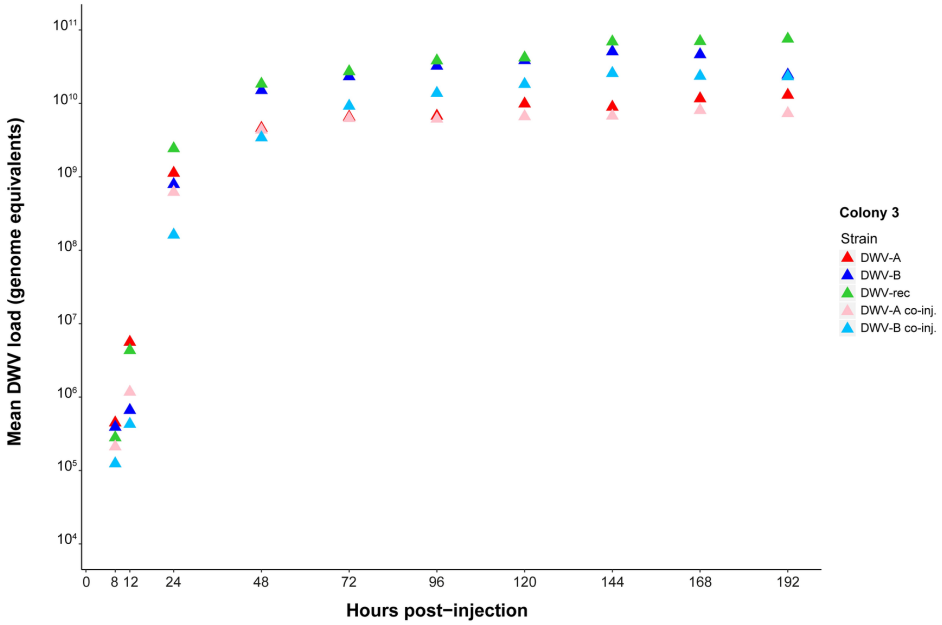

Mean DWV load (genome equivalents)
$10^{11}$
$10^{10}$
$10^{9}$
$10^{8}$
$10^{7}$
$10^{6}$
$10^{5}$
$10^{4}$
0 8 12 24 48 72 96 120 144 168 192
Hours post−injection
Colony 3
Strain
DWV-A
DWV-B
DWV-rec
DWV-A co-inj.
DWV-B co-inj.

**Figure S2.** Mean DWV viral loads (genome equivalents) of individually infected pupae from 8 to 192 hours post-injection ($n$ = 120 per treatment), as calculated by standard curve in cDNA synthesized from 0.8 µg RNA. White-eyed pupae from colonies one to three were singly injected with $1 \times 10^7$ genome equivalents of DWV-A, DWV-B or recombinant strain ('DWV-rec'), or co-injected with $5 \times 10^6$ genome equivalents of DWV-A and DWV-B. Each figure displays the mean viral load by colony to illustrate colony differences.

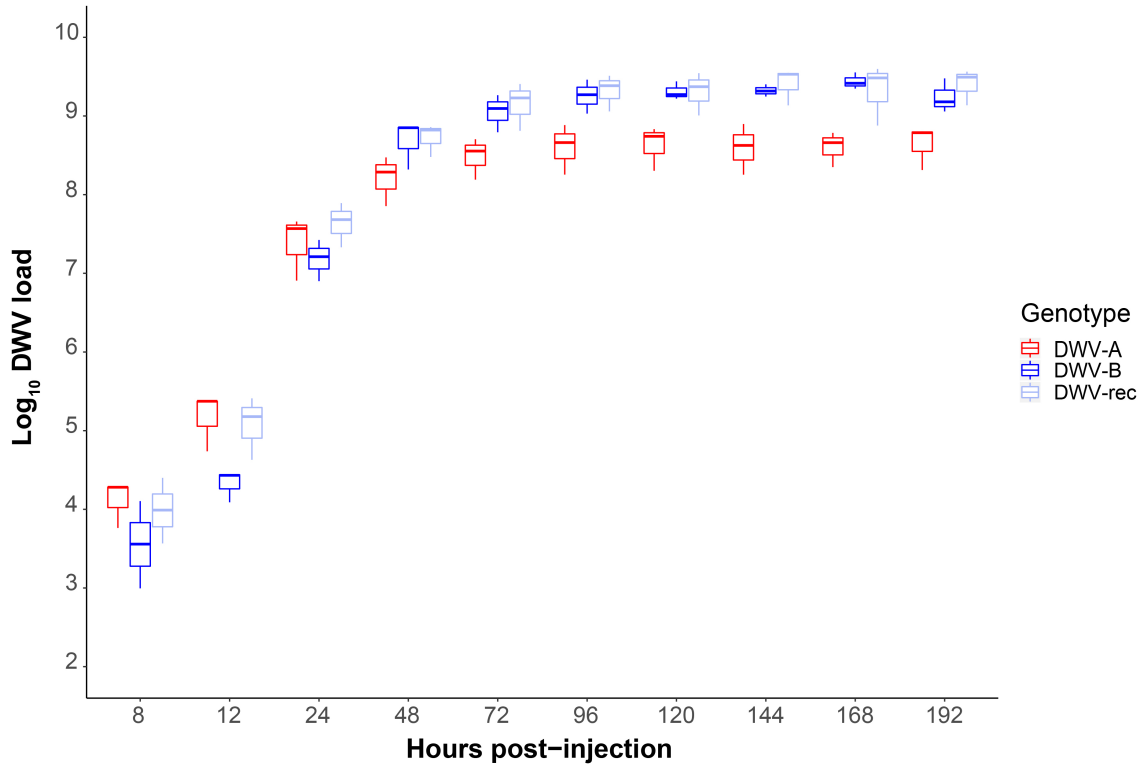



**Figure S3.** $Log_{10}$ DWV viral loads of singly infected pupae from 8 to 192 hours post-injection, relative to housekeeping gene *Actin*. Colonies 1-3 have been combined (per treatment) to illustrate the distribution of viral accumulation per genotype.

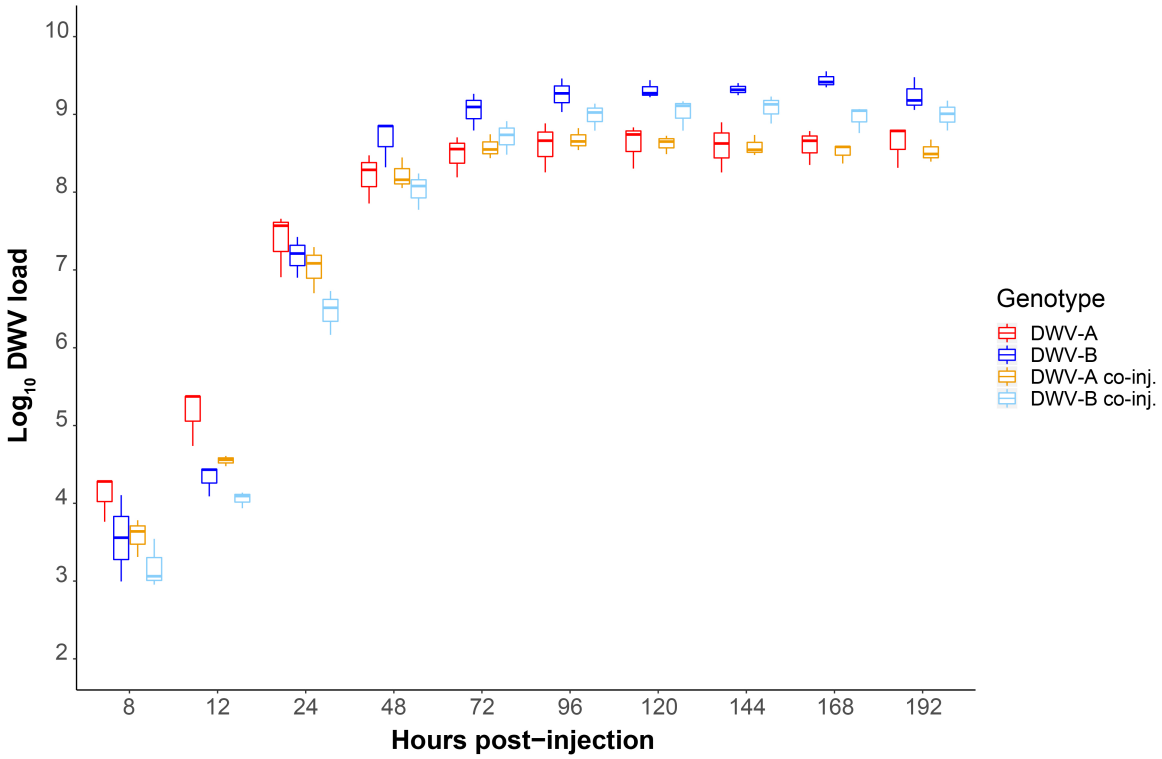



**Figure S4.** Comparison of $\log_{10}$ DWV viral loads of pupae singly infected with DWV-A or DWV-B versus pupae co-injected with DWV-A and DWV-B, relative to housekeeping gene *Actin*. Colonies 1-3 have been combined (per treatment) to illustrate the distribution of viral accumulation per genotype.

**Table S1.** Comparison of pairwise identity values, generated from pairwise Muscle alignments of whole genome sequences in Geneious. DWV-A (MN538208) and DWV-B (MN538209) inocula sequences obtained in this study were compared to DWV-A (AJ489744.2) and DWV-B (AY251269.2) reference sequences, in addition to the DWV-A isolate we previously injected in Remnant et al. (Remnant et al., 2019) and those experimentally injected by Tehel et al. (2019) and Gisder et al. (2018).

| | DWV-A (this study) MN538208 | DWV-A (AJ489744.2) (Lanzi et al., 2006) | DWV-A Remnant et al. (2019) | DWV-A Tehel et al. (2019) | DWV-$_{P0}$ I Gisder et al. (2018) | DWV-$_{P0}$ II Gisder et al. (2018) |
|---|---|---|---|---|---|---|
| DWV-A (AJ489744.2) | 98.50% | | | | | |
| DWV-A Remnant et al. (2019) | 99.50% | 98.72% | | | | |
| DWV-A Tehel et al. (2019) | 97.30% | 97.70% | 97.46% | | | |
| DWV-$_{P0}$ I Gisder et al. (2018) | 91.20% | 91.50% | 91.29% | 91.80% | | |
| DWV-$_{P0}$ II Gisder et al. (2018) | 84.70% | 85.00% | 84.87% | 84.90% | 90.70% | |
| DWV-$_{P0}$ III Gisder et al. (2018) | 85.80% | 85.90% | 85.85% | 86.00% | 91.60% | 94.50% |

| | DWV-B (this study) MN538209 | DWV-B (AY251269.2) (Ongus et al., 2004) | DWV-B Tehel et al. (2019) | DWV-$_{P0}$ I Gisder et al. (2018) | DWV-$_{P0}$ II Gisder et al. (2018) |
|---|---|---|---|---|---|
| DWV- B (AY251269.2) | 99.30% | | | | |
| DWV-B Tehel et al. (2019) | 99.20% | 98.90% | | | |
| DWV-$_{P0}$ I Gisder et al. (2018) | 91.40% | 91.40% | 91.40% | | |
| DWV-$_{P0}$ II Gisder et al. (2018) | 95.00% | 94.90% | 94.90% | 90.70% | |
| DWV-$_{P0}$ III Gisder et al. (2018) | 96.90% | 96.80% | 96.80% | 91.60% | 94.50% |

**Table S2.** List of the primers used for viral detection by endpoint PCR and quantitative PCR. (ARV: *Apis* rhabdovirus, BQCV: black queen cell virus, DWV: deformed wing virus, LSV: Lake Sinai virus, SBV: sacbrood virus).

| Virus | Primer name | Sequence | Product size (bp) | Primer efficiency | Reference |
|---|---|---|---|---|---|
| **LSV** | LSV_2108_F | TCATCCMAAGAGAACCA | 400 | - | This study |
| | LSV_uni_R | GTCAAAGGTGTCGTATCC | | | |
| **qPCR primers** | | | | | |
| **DWV** | DWV_F | TACTAGTGCTGGTTTTCCTTT | 155 | 1.91 | Kevill et al. (2017) |
| | DWV-A_R | CTCATTAACTGTGTCGTTGAT | | | |
| | DWV-B_R | CTCATTAACTGAGTTGTTGTC | 155 | 1.92 | |
| **BQCV** | BQCV_qPCR_F | AGGTTTACGCTCCAAGATCG | 112 | 1.73 | Remnant et al. (2019) |
| | BQCV_qPCR_R | TTTGTTCAGCAGGTAAATTGTTC | | | |
| **SBV** | SBV_ qPCR_F | CGAGGAGGGAAAAACTACGC | 115 | - | Remnant et al. (2019) |
| | SBV_ qPCR_R | GTGGCTTAACTGGATCATAGCC | | | |
| **ARV-1** | ARV-1_F | ATGAGGCTTGGAGACACAGC | 100 | - | This study |
| | ARV-1_R | GGAGCTTTCCTGAGGACACG | | | |
| **ARV-2** | ARV-2_F | CTAAACCCCACCTGTCTGCC | 150 | - | This study |
| | ARV-2_R | ATTGAGCACTGGAGCGTTGG | | | |
| ***Actin*** | Actin_F | TGCCAACACTGTCCTTTCTG | 155 | 1.70 | Scharlaken et al. (2008) |
| | Actin_R | AGAATTGACCCACCAATCCA | | | |

**Table S3.** Two-way ANOVA comparing mean DWV loads relative to housekeeping gene *Actin* in pupae singly injected with DWV-A, DWV-B, DWV-rec, or co-injected with DWV-A and DWV-B, from 48 to 192 hours post injection ($n$ = 401). Comparison of DWV loads between genotype and colonies (1-3) over time. Data plotted in Figure 2 and Figure 3, where we have presented the mean relative viral loads as single injection by colony (DWV-A, DWV-B and DWV-rec), and single injection versus co-injection (DWV-A and DWV-B), respectively.

| **Summary** | ***df*** | **Sum sq** | **Mean sq** | **F value** | ***p*** |
|---|---|---|---|---|---|
| DWV genotype | 4 | 344421 | 86105 | 248.642 | <0.0001 |
| hour post injection (HPI) | 1 | 76077 | 76077 | 219.685 | <0.0001 |
| colony | 2 | 102420 | 51210 | 147.876 | <0.0001 |
| DWV genotype:HPI | 4 | 21228 | 5307 | 15.325 | <0.0001 |
| DWV genotype:colony | 8 | 13400 | 1675 | 4.837 | <0.0001 |
| residuals | 381 | 131941 | 346 | | |

**Table S4.** Tukey HSD post-hoc analysis of two-way ANOVA (S3 Table), showing pairwise comparisons of mean relative viral loads by genotype and colony. Lettering denotes genotype followed by numbering 1-3, which indicates colony (A: DWV-A single injection, B: DWV-B single injection, R: DWV-rec single injection, CA: DWV-A co-injection, and CB: DWV-B co-injection). Significant comparisons ($p < 0.05$) denoted as letters on Figure 2 and Figure 3.

| Comparison | *df* | t.ratio | *p* | Comparison | *df* | t.ratio | *p* |
|---|---|---|---|---|---|---|---|
| A,1 - B,1 | 381 | -13.138 | <.0001 | R,1 - A,2 | 381 | 3.061 | 0.1358 |
| A,1 - CA,1 | 381 | -2.643 | 0.3451 | R,1 - B,2 | 381 | -9.501 | <.0001 |
| A,1 - CB,1 | 381 | -6.152 | <0.0001 | R,1 - CA,2 | 381 | 4.412 | 0.0013 |
| A,1 - R,1 | 381 | -11.214 | <.0001 | R,1 - CB,2 | 381 | -1.563 | 0.9654 |
| A,1 - A,2 | 381 | -8.205 | <0.0001 | R,1 - R,2 | 381 | -9.900 | <.0001 |
| A,1 - B,2 | 381 | -21.109 | <.0001 | R,1 - A,3 | 381 | 5.429 | <.0001 |
| A,1 - CA,2 | 381 | -6.931 | <.0001 | R,1 - B,3 | 381 | -5.388 | <.0001 |
| A,1 - CB,2 | 381 | -13.02 | <.0001 | R,1 - CA,3 | 381 | 6.912 | <.0001 |
| A,1 - R,2 | 381 | -22.646 | <.0001 | R,1 - CB,3 | 381 | 0.546 | 1.0000 |
| A,1 - A,3 | 381 | -5.679 | <.0001 | R,1 - R,3 | 381 | -9.075 | <.0001 |
| A,1 - CA,3 | 381 | -16.008 | <.0001 | R,2 - A,3 | 381 | 16.592 | <.0001 |
| A,1 - CA,3 | 381 | -4.175 | 0.0033 | R,2 - B,3 | 381 | 5.018 | <.0001 |
| A,1 - CB,3 | 381 | -10.871 | <.0001 | R,2 - CA,3 | 381 | 18.093 | <.0001 |
| A,1 - R,3 | 381 | -20.457 | <.0001 | R,2 - CB,3 | 381 | 11.874 | <.0001 |
| A,2 - B,2 | 381 | -12.71 | <.0001 | R,2 - R,3 | 381 | 1.955 | 0.0631 |
| A,2 - CA,2 | 381 | 1.337 | 0.9916 | CA,1 - CB,1 | 381 | -3.509 | 0.0371 |
| A,2 - CB,2 | 381 | -4.696 | <.0004 | CA,1 - R,1 | 381 | -8.62 | <.0001 |
| A,2 - R,2 | 381 | -14.311 | <.0001 | CA,1 - A,2 | 381 | -5.585 | <.0001 |
| A,2 - A,3 | 381 | 2.418 | 0.5027 | CA,1 - B,2 | 381 | -18.467 | <.0001 |
| A,2 - B,3 | 381 | -8.31 | <.0001 | CA,1 - CA,2 | 381 | -4.289 | 0.0021 |
| A,2 - CA,3 | 381 | 3.915 | 0.0091 | CA,1 - CB,2 | 381 | -10.377 | <.0001 |
| A,2 - CB,3 | 381 | -2.567 | 0.3956 | CA,1 - R,2 | 381 | -20.028 | <.0001 |
| A,2 - R,3 | 381 | -12.221 | <.0001 | CA,1 - A,3 | 381 | -3.089 | 0.1263 |
| A,3 - B,3 | 381 | -10.497 | <.0001 | CA,1 - B,3 | 381 | -13.572 | <.0001 |
| A,3 - CA,3 | 381 | 1.481 | 0.9783 | CA,1 - CA,3 | 381 | -1.582 | 0.9617 |
| A,3 - CB,3 | 381 | -4.983 | <.0001 | CA,1 - CB,3 | 381 | -8.229 | <.0001 |
| A,3 - R,3 | 381 | -14.502 | <.0001 | CA,1 - R,3 | 381 | -17.863 | <.0001 |
| B,1 - CA,1 | 381 | 10.545 | <.0001 | CA,2 - CB,2 | 381 | -6.089 | <.0001 |
| B,1 - CB,1 | 381 | 7.102 | <.0001 | CA,2 - R,2 | 381 | -15.779 | <.0001 |
| B,1 - R,1 | 381 | 1.891 | 0.8565 | CA,2 - A,3 | 381 | 1.118 | 0.9987 |
| B,1 - A,2 | 381 | 4.969 | <.0001 | CA,2 - B,3 | 381 | -9.62 | <.0001 |
| B,1 - B,2 | 381 | -7.576 | <.0001 | CA,2 - CA,3 | 381 | 2.626 | 0.3557 |
| B,1 - CA,2 | 381 | 6.337 | <.0001 | CA,2 - CB,3 | 381 | -3.94 | <.0083 |
| B,1 - CB,2 | 381 | 0.363 | 1.000 | CA,2 - R,3 | 381 | -13.655 | <.0001 |
| B,1 - R,2 | 381 | -9.206 | <.0001 | CA,3 - CB,3 | 381 | -6.493 | <.0001 |
| B,1 - A,3 | 381 | 7.319 | <.0001 | CA,3 - R,3 | 381 | -15.989 | <.0001 |
| B,1 - B,3 | 381 | -3.602 | <.0001 | CB,1 - R,1 | 381 | -5.177 | <.0001 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| B,1 - CA,3 | 381 | 8.802 | <.0001 | CB,1 - A,2 | 381 | -2.109 | 0.7284 |
| B,1 - CB,3 | 381 | 2.471 | 0.4639 | CB,1 - B,2 | 381 | -14.958 | <.0001 |
| B,1 - R,3 | 381 | -7.184 | <.0001 | CB,1 - CA,2 | 381 | -0.779 | 1.000 |
| B,2 - CA,2 | 381 | 14.178 | <.0001 | CB,1 - CB,2 | 381 | -6.869 | <.0001 |
| B,2 - CB,2 | 381 | 8.089 | <.0001 | CB,1 - R,2 | 381 | -16.551 | <.0001 |
| B,2 - R,2 | 381 | -1.730 | 0.9227 | CB,1 - A,3 | 381 | 0.353 | 1.000 |
| B,2 - A,3 | 381 | 15.026 | <.0001 | CB,1 - B,3 | 381 | -10.338 | <.0001 |
| B,2 - B,3 | 381 | 3.445 | 0.0454 | CB,1 - CA,3 | 381 | 1.862 | 0.8704 |
| B,2 - CA,3 | 381 | 16.54 | <.0001 | CB,1 - CB,3 | 381 | -4.720 | <.0003 |
| B,2 - CB,3 | 381 | 10.238 | <.0001 | CB,1 - R,3 | 381 | -14.42 | <.0001 |
| B,2 - R,3 | 381 | 0.259 | 1.000 | CB,2 - R,2 | 381 | -9.745 | <.0001 |
| B,3 - A,1 | 381 | -16.008 | <.0001 | CB,2 - A,3 | 381 | 7.091 | <.0001 |
| B,3 - CA,3 | 381 | 11.894 | <.0001 | CB,2 - B,3 | 381 | -4.008 | <.0064 |
| B,3 - CB,3 | 381 | 5.988 | <.0001 | CB,2 - CA,3 | 381 | 8.602 | <.0001 |
| B,3 - R,3 | 381 | -3.154 | 0.1062 | CB,2 - CB,3 | 381 | 2.149 | 0.7009 |
| | | | | CB,2 - R,3 | 381 | -7.680 | <.0001 |
| | | | | CB,3 - R,3 | 381 | -9.788 | <.0001 |

**Table S5.** Two-way ANOVA repeated as above, with the inclusion of three pupae with low DWV loads for their time-point.

| **Summary** | ***df*** | **Sum sq** | **Mean sq** | **F value** | ***p*** |
|---|---|---|---|---|---|
| DWV strain | 4 | 351858 | 87965 | 167.09 | <0.0001 |
| hour post injection (HPI) | 1 | 65820 | 65820 | 125.03 | <0.0001 |
| colony | 2 | 94129 | 47064 | 89.40 | <0.0001 |
| DWV strain:HPI | 4 | 21683 | 5421 | 10.20 | <0.0001 |
| DWV strain:colony | 8 | 16258 | 2032 | 3.86 | <0.001 |
| residuals | 384 | 202685 | 526 | | |

**Table S6.** Tukey HSD post-hoc analysis of repeated two-way ANOVA (Table S5), showing the three pairwise comparisons that were significantly different in the repeated analysis.

| **Comparison** | ***df*** | **t.ratio** | ***p*** |
|---|---|---|---|
| B,1 - B,3 | 384 | -3.038 | 0.144 |
| B,2 - B,3 | 384 | 2.74 | 0.2848 |
| CA,2 - CA,3 | 384 | 3.592 | 0.0282 |

**Table S7.** Analysis of the mean proportion of survival of pupae subjected to five treatments (buffer control, DWV-A, DWV-B, DWV-rec and co-injection) at 192 hours post injection. We fit a generalized linear mixed effects model (glmer) with binomial distribution and logit link function, comparing mean proportion of survival per treatment. Colony had no effect on survival (using Akaike's information criterion during backward elimination; Table S9), thus was included in the model as a random factor. We then analysed the final model as a type II ANOVA. As treatment was a significant predictor of survival, we subsequently ran a Tukey pairwise comparison (Table S8).

| **Response: Proportion Survival** | **Chi sq** | ***df*** | ***p*** |
|---|---|---|---|
| (Intercept) | 92.583 | 1 | < 0.0001 |
| treatment | 44.472 | 4 | < 0.0001 |

**Table S8.** Tukey post-hoc analysis of ANOVA (Table S7); pairwise comparisons of mean proportion of survival between treatments.

| **Comparison** | **z. ratio** | ***p*** |
|---|---|---|
| Buffer Control - DWV-A | -4.384 | < 0.0001 |
| Buffer Control - DWV-B | 1.835 | 0.3532 |
| Buffer Control - DWV-rec | 0.280 | 0.9987 |
| Buffer Control - Co-injection | -2.586 | 0.0728 |
| DWV-A - DWV-B | 3.747 | 0.0017 |
| DWV-A - DWV-rec | 4.467 | < 0.0001 |
| DWV-A - Co-injection | 2.422 | 0.1095 |
| DWV-B - DWV-rec | -1.671 | 0.4522 |
| DWV-B - Co-injection | -3.036 | 0.0203 |
| DWV-rec - Co-injection | -2.778 | 0.0435 |

**Table S9.** Model testing of mean proportion of survival data per treatment (buffer control, DWV-A, DWV-B, DWV-rec and co-injection) and colony. Akaike's information criterion obtained during backward elimination showed that colony was not a significant predictor of survival. Colony was thus included as a random factor in survival analyses.

| | ***df*** | **Deviance** | **AIC** | **LRT** | ***p*** |
|---|---|---|---|---|---|
| | | 512.07 | 526.07 | | |
| treatment | 4 | 579.34 | 585.34 | 67.275 | < 0.0001 |
| colony | 2 | 514.71 | 524.71 | 2.641 | 0.267 |

**Text S1.** Partial contig sequence of the DWV-B isolate detected in low frequency in the DWV-rec inoculum, where Megahit average coverage per base was 408.0453.

>DWV-Rec_Netherlands_k141_295_multi=408.0453

AATCATATATTACTTTCTTAATTTTAAATAATAACATGGGCGATCGATTACAAACGGGCCTAACAACTTTCTCGCGCACAAAT
TTTGATGCCACCCGTTTCACTTTCTTACAAATCTTTGTATATTTGGGTTTCTTAAATACGAACTCACCCGCGTCTTTTCCTACCT
CAATCTTAAGGGATTCTAAAGGGGAATATCTATTACTGATTGAAATGGGGACATGTTCTTGAACAGGGCGGCGGGTACATCT
TTCAGCTATAGAATATATCGTGTATAAATTATTCAATTGTTCCGTAAGGAACTCATTATCACGCGCATCTTCTTGCTCCCACGT
TGTATGATCATACACAGTGACGTCAAGAACGTTTCGAATCCGTTCCTGTTCCAACGCCAAACGCTTAATAACGCGTCGACGC
CTAGCTTCATCAATCTCCCAACTACGGGGAGCATGAGCTACAGAGGGAGCTTGGGCAACAGCAGCATAAGAAAGAGTTCCA
CAACTAAATGCCATTTTTATATATATTTACCTTCAAAGTCAAAATCAAATTGAAAATATAAAATAAAAAGAATTGAATCTAA
TATATAAAGCAAAAATAGCAAAGAAATATATTTAGCAATAATGAAAATAGCAAAATATAATAGCAAATAAAAACAGCAAAA
TAAAACAGCAATAATCGTAGCATTAAAATATTAAATAATGTCTTTCCATTCGTCATCGTCTGGGCTATGTGACATTAACGGGT
GCCCTGCGAACGTAACGTACCGTGGCATAAATTATACTGTATTAAAAGGATTCTTGCCAAAGGAAATCCCAATACAGTCACT
TATGTATAGAGACATAAATTACTTTCACACTTTCGCCTCATACA

**Text S2.** Partial contig sequence of the secondary DWV-recombinant isolate detected at very low frequency in the DWV-rec inoculum, where Megahit average coverage per base was 26.3092.

>DWV-Rec_Netherlands_k141_7331_multi=26.3092

AAGAATGGATATACGTGTTTAAAAGGTATCACTAATTTTGCTTCATTACTCGCTGATGCGCTAATCAAAGCATGATCCATATG
CGAAAAACCATACACACTTCGCTTCGTCTGGATATTCAAATTTTCATGATCCGAATAATACCAAGTTGCCTGTAATTGACCAA
CTTGGAATTTATTTGAATTAATTTGAACTCTAACTTCCATATCGCCTCGCCAATATGCGTGCACCTTAAATGGGATAGTATTA
GGCACATCACATATAGCATCAGAATTAGCCTCTATACTAGATAACAAAGCACGAGGCAAAATTAAACGTGCTAACTCCTTAT
CAAATGGATCATCCTTCGACCAAACAAATTCAGCAATCTGATACCATCGAGATGTAATTGTGGCATAATCATCTACTACATC
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TACTATCCTTTTCTAATTCAACTTCACCCTCGCCATCAGGTCCTGGATTAGGGTTATCCATCTCTGGTTTTGCCTGCACCGGAT
TCGATAATTGTAACAGACTAGTGACACACTCTAACTCATAATCGCGCTGTTTTTGACGTCGCAACATCCTAATCTGTTTTCTTA
ATCTATATAAATGCAAATCATAAATTATCTTCTTAAGCTTAAATAATAGCATAGGGGATCTAGAACATATAGGACGAACAAC
TTTTTCACGAACGAAGCGAGTTGCAACGCGCTTCACTTTCTTGCAAACGCGCGTATATTTAGGTTTCTTAAATATACATTCGC
CTGCTTCTTGACCGACCTCGACCTTAAGGGATTCCAGTGGAGCAAACCTATTCGAAACTGATATAGGAGAGTACTCTTTGATA
GGCCGACGCGTACAACGTTCAGCGATCGAATAAATAGTATATAAGTTGTTTAATTGTTCCATTAGGAACTCATTATCGCGCGC
GTCCTCCTGTTCCCACGTTGCCTGGTCATAGACGTCAGCGTCAAGCACGTTACGAATACGTTCTTGCTCCAACGCCAAACGTT
TAATAACTCGGCGCCGCCTAGCTTCATCTACTTCCCATGTACGAGGTGCATGGGCGACAGATGGAGCTTGAGCGACGGCAGA
GTAAGAAAGAATTCCACAACTAAATGCCATTTTTATATATATTTACCTTGAAAATCAAAATCAAATTGAAAATATAAAATAA
AAAGAATTGAATCTAATATATAAAGCAAAAATAGCAAAGAAATATATTTAGCAATAATGAAAATAGCAAAATATAATAGCA
AATAAAAACAGCAAAATAAAACAGCAATAA

## References


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