Apis Rhabdovirus

Comprehensive Findings Review

Synthesised from the full text of 37 open-access papers harvested via Europe PMC. This comprehensive edition presents detailed findings for all core and survey studies, with remaining detections tabulated. Generated 2026-06-12.

Executive Summary

Apis rhabdovirus (ARV) is a negative-sense, single-stranded, enveloped RNA virus (family **Rhabdoviridae**) of honey bees, wild bees and *Varroa destructor* mites, first described in 2017. Two principal genotypes (ARV-1, ARV-2) are recognised, with further members (ARV-3 to ARV-5) since described. It is globally distributed and reaches high titres, yet **no disease has been attributed to it**: the evidence base is descriptive. A key, still-unresolved question is whether the bee or the mite is its primary host. The sections below synthesise the published findings by theme, then catalogue the individual studies.

Discovery and Naming

Apis rhabdovirus was first described in 2017. Two genotypes, ARV-1 and ARV-2, were identified in Australian honey bee surveys (Remnant et al. 2017), and in the same year Levin et al. independently confirmed and extended the finding, detecting ARV-1 in honey bees (*Apis mellifera*), bumble bees (*Bombus impatiens*) and *Varroa destructor* mites from the United States and Israel (Levin 2017). Before this, the bee viruses shown to be shared across species and vectored by *Varroa* were all positive-sense RNA viruses; ARV was the first negative-sense, enveloped virus shown to circulate this way (Levin 2017).

The naming is unsettled. Because the abbreviation “ARV” was already assigned to Adelaide River virus, and because the virus occurs in non-*Apis* hosts, Levin et al. proposed the alternative “bee rhabdovirus” (BRV-1, BRV-2) (Levin 2017); Galbraith et al. independently reached the same conclusion after detecting it in both *A. mellifera* and *Bombus impatiens* (Galbraith 2018). Both names (ARV-1/ARV-2 and BRV-1/BRV-2) remain in active use across the literature, which can complicate data searches.

Virology and Genome Organization

ARV belongs to the family **Rhabdoviridae** (order *Mononegavirales*; phylum *Negarnaviricota*) — the same family as rabies and vesicular stomatitis virus. Virions are enveloped and bullet-shaped, reported at 100–430 nm long and 45–100 nm in diameter (Levin 2017). The genome is a single, negative-sense RNA strand carrying the five genes typical of rhabdoviruses in the canonical N–P–M–G–L organization: nucleoprotein (N), phosphoprotein (P), matrix (M), glycoprotein (G) and the large polymerase (L) (Galbraith 2018). Because the genome is negative-sense, it cannot act directly as mRNA — it must first be transcribed by a virion-packaged RNA-dependent RNA polymerase, unlike the positive-sense iflaviruses and dicistroviruses that dominate the bee-virus literature.

Phylogenetically, ARV-1 and ARV-2 form a monophyletic group with Farmington virus, a rhabdovirus of birds: their L proteins share roughly 30% (ARV-1) and 23% (ARV-2) amino-acid identity with Farmington virus (Levin 2017). The L protein is large (~2,143 aa), and across honey bee, bumble bee and *Varroa* isolates the ARV-1 proteins were essentially identical (99.9–100% identity) (Levin 2017). The genus has since expanded beyond the original two genotypes: nationwide sequencing in China described additional members provisionally named Apis rhabdovirus 3, 4 and 5 (Li 2023), and ARV-5 was subsequently recorded in Korea (Kwon 2023).

Host Range and the Varroa Question

ARV has been detected in managed honey bees (*A. mellifera*), the eastern honey bee (*A. cerana*), bumble bees (*Bombus impatiens*), several wild/solitary bees, and consistently in *Varroa destructor* mites (Levin 2017; Galbraith 2018; Schoonvaere 2018; Li 2023). Which host it primarily replicates in is the central open question. Levin et al. presented evidence that ARV-1 actively replicates in *both* bees and mites, detecting the positive-sense (replicative) RNA strand in both (Levin 2017).

More recent small-RNA work shifts the emphasis toward the mite. Damayo et al. found ARV-1 and ARV-2 in almost all *Varroa* samples but at low prevalence in honey bees, and showed an abundant antiviral small-interfering-RNA response (a 24-nt antisense peak) against both genotypes inside mites — a signature of active replication — leading them to argue that *V. destructor* may be the primary host rather than the bee (Damayo 2023). A bee-virus review similarly judged the mite a "genuine host" because the viral small-RNA profiles differ between mites and bees (Yañez 2020). Crucially, ARV-1 also occurs in *Bombus impatiens*, which is not parasitized by *Varroa* — so the virus does not strictly require the mite and is likely also shared directly among co-foraging bees (Levin 2017).

Geographic Distribution and Prevalence

ARV has a near-global footprint, reported from North America, the Middle East, Europe, Asia, South America, Africa and the South Pacific (Thaduri 2018; Li 2023). Reported prevalence varies widely with host, region, method and season. In the discovery work, 21 of 104 Israeli colonies (~20%) were ARV-1-positive, with per-apiary rates of 28.1%, 26.5% and 7.9%; within positive colonies the virus was found in only 4.8% of individual bees but 76.2% of mites, and titres reached 10^7–10^8 genomic copies per individual bee or mite (Levin 2017).

Subsequent surveys reinforce the wide distribution: ARV-1 and ARV-2 were detected in all seven sampled regions of China (Li 2023); across 15 European countries ARV-1 was found in 26% (n=24) and ARV-2 in 9% (n=8) of samples (Sircoulomb 2025); ARV-1 appeared in 25 of the New Zealand samples, occasionally exceeding a third of the total viral load (Lester 2022); and first-record detections were reported for Korea (as ARV-5; Kwon 2023), southern Brazil (da Silva 2023) and western Canada (Lee 2023). The prevailing pattern is high prevalence in *Varroa* mites and lower, patchier prevalence in bees.

Replication, Seasonality and Co-occurrence

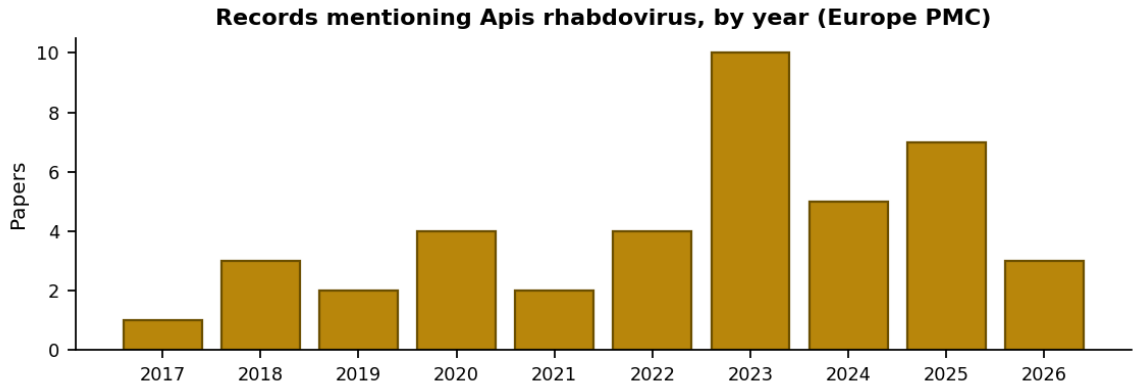
Active replication has been inferred by two complementary methods: detection of the positive-sense replicative RNA strand (Levin 2017) and the presence of a characteristic 24-nt antisense small-RNA (vsiRNA) peak generated by the host RNAi response (Damayo 2023). ARV shows clear seasonal dynamics. In Swedish colonies ARV-1 titres rose from summer into autumn and peaked the following spring, increasing by roughly an order of magnitude over the season (Thaduri 2018; Thaduri 2021). A Belgian nanopore study detected ARV-1 and ARV-2 specifically in autumn (October) and only in nurse bees, not foragers — suggesting infection before adult emergence (Van Herzele 2024).

A recurrent observation is that ARV-1 and ARV-2 tend to travel together: a Czech virome study reported that bee rhabdovirus 1 and 2 were always present simultaneously, with BRV-1 more abundant than BRV-2, and present in only one of three replicate samples per hive — the first description of this paired-occurrence relationship (Kadlečková 2022). ARV is typically found as one member of a multi-virus community alongside the negative-sense Varroa orthomyxovirus-1 and the mite-associated VDV-2/VDV-3/VDV-5 viruses (Levin 2019; Li 2023; Damayo 2023).

Pathology: What ARV Does to Bees

There is, as yet, **no demonstrated disease caused by ARV**. It has been detected in honey bees with deformed wings in the United States, but no causal link has been shown, and the discovering authors explicitly stated that whether ARV-1 causes symptoms “remains to be determined” and that controlled studies are needed (Levin 2017). It is routinely found in apparently healthy colonies (Kadlečková 2022). The only suggestive signals are indirect: a honey bee line bred for low *Varroa* population growth carried significantly lower ARV-1/ARV-2 levels than a high-growth line, prompting the authors to call for investigation of ARV-2’s potential pathogenicity and effects on the bee central nervous system (Morfin 2023). On current evidence ARV is best described as a widespread, actively circulating, but biologically uncharacterized virus.

Research Activity and Prevalence



Reported prevalence and viral-load findings across key studies:

Study	Region	Host	Key prevalence / load finding
Levin 2017	Israel	Honey bees / mites	21/104 colonies (~20%); 4.8% of bees vs 76.2% of mites; 10^7–10^8 copies/individual
Li 2023	China	Bees & mites	ARV-1/ARV-2 in all 7 regions; ARV-1 in >75% of mite libraries
Sircoulomb 2025	15 EU countries	Honey bees	ARV-1 26% (n=24); ARV-2 9% (n=8)
Lester 2022	New Zealand	Bees & mites	ARV-1 in 25 samples (>1/3 of viral load in 4); ARV-2 in 9 (≤0.02%)
Damayo 2023	(mite panel)	Varroa destructor	ARV-1/ARV-2 in all but 1 mite sample; active vsiRNA (24-nt) response
Van Herzele 2024	Belgium	Honey bees (haemolymph)	ARV-1/ARV-2 in autumn, nurses only
Thaduri 2018	Sweden (Gotland)	Honey bees	Higher in susceptible than resistant; peak spring; near-global note

Study Findings Catalogue

Core studies — substantial ARV-specific findings:

Levin 2017 — Presence of Apis Rhabdovirus-1 in Populations of Pollinators and Their Parasites from Two Continents (2017, Frontiers in Microbiology; cited 25)

First characterization of ARV-1 distribution, prevalence, replication and infectivity across pollinators and Varroa, using metagenomics + RT-PCR/RT-qPCR.

- Detected ARV-1 in *A. mellifera*, *Bombus impatiens* and *Varroa destructor* from the US and Israel — first report of ARV-1 in a bumble bee and of rhabdovirus replication in honey bees.
- Confirmed active replication in both bees and mites by detecting the positive-sense (replicative) RNA strand.
- Titres reached 10^7–10^8 viral genomic copies per individual bee or mite.
- Screened 104 Israeli colonies: 21 (~20%) ARV-1-positive; per-apiary 28.1% / 26.5% / 7.9%.
- Within positive colonies: virus in 4.8% of individual bees vs 76.2% of mites; amplified in 7/10 honey bees and 1/10 bumble bees.
- Genome/virology: enveloped bullet-shaped virion (100–430 x 45–100 nm); ARV-1/ARV-2 L proteins ~30%/23% identity to Farmington virus of birds, forming a monophyletic group; ARV-1 isolates 99.9–100% identical across hosts.
- Because *Bombus* is not parasitized by *Varroa*, argued ARV does not require the mite and is shared among co-foraging bees; proposed the name bee rhabdovirus (BRV-1).
- Stated plainly that whether ARV causes symptoms remains undetermined and controlled studies are needed.

PMC5732965 · doi:10.3389/fmicb.2017.02482

Galbraith 2018 — Investigating the viral ecology of global bee communities with high-throughput metagenomics (2018, Scientific Reports; cited 58)

Screened A. mellifera and 11 other bee species across 9 countries / 4 continents with a novel virus-discovery pipeline.

- Identified ARV-1 (family Rhabdoviridae) as one of the first negative-sense ssRNA viruses in bees, detecting it in two species (*A. mellifera* and *Bombus impatiens*) from the US (Pennsylvania) at >99% identity.
- Recovered the five canonical rhabdovirus genes — L, G, N, P and M — from assembled contigs.
- Given occurrence in two bee species, recommended the name Bee Rhabdovirus (BRV).

PMC5995813 · doi:10.1038/s41598-018-27164-z

Thaduri 2018 — Temporal changes in the viromes of Swedish Varroa-resistant and Varroa-susceptible honeybee populations (2018, PLoS ONE; cited 25)

RNA-seq + RT-qPCR comparison of the mite-resistant Gotland population vs susceptible colonies across the 2009–2010 season.

- Identified ARV-1 and obtained a near-complete genome — first record of ARV-1 in Swedish bees; all known ARV-1 sequences were >99% identical.
- ARV-1 titres were consistently higher in mite-susceptible than mite-resistant colonies, rising from summer to autumn 2009 and peaking in spring 2010 (differences significant in Aug and Oct 2009).
- Strand-distribution evidence (uneven +/− read coverage) supported replication of ARV-1 in bees.
- Confirmed near-global distribution: noted ARV-1 detections across North America, Europe, Middle East, Africa and the South Pacific.

PMC6283545 · doi:10.1371/journal.pone.0206938

Levin 2019 — New Viruses from the Ectoparasite Mite Varroa destructor Infesting Apis mellifera and Apis cerana (2019, Viruses; cited 39)

RNA metagenomics of Western/Eastern honey bee subspecies and their Varroa mites; discovery of Varroa orthomyxovirus-1 (VOV-1).

- ARV-1/BRV-1 was present in all *Varroa* libraries, showing the mite as a consistent reservoir; distribution differed across bee vs mite libraries.
- In one *A. cerana* sample the dominant viral component was ARV-2, illustrating genotype-specific abundance differences.
- Placed ARV within an emerging group of negative-sense bee/mite viruses (with VOV-1, VDV-2, VDV-3), raising the question of how these co-infecting viruses interact with major pathogens (DWV, ABPV, IAPV, CBPV).

PMC6409542 · doi:10.3390/v11020094

Damayo 2023 — Virus replication in the honey bee parasite, Varroa destructor (2023, Journal of Virology; cited 26)

Used small-RNA (vsiRNA) sequencing of individual mites to define which viruses actually replicate in V. destructor vs the bee.

- ARV-1 and ARV-2 were present in all but one *Varroa* sample (the exception from South Africa), among the most prevalent mite-associated viruses.
- Both genotypes elicited an abundant antiviral vsiRNA response in mites with a 24-nt antisense peak — a signature of active replication within *V. destructor*.
- Negative-sense viruses (ARV-1/-2, VDV-2/-3/-5) showed a strong antisense read bias (60–99%).
- Concluded that, given high mite prevalence and low bee prevalence, *V. destructor* is likely the primary host for these −ssRNA rhabdoviruses rather than *A. mellifera*.
- Noted additional rhabdovirus diversity in *Varroa jacobsoni* and in *A. mellifera*/*A. cerana* in China.

PMC10746231 · doi:10.1128/jvi.01149-23

Li 2023 — Nationwide genomic surveillance reveals the prevalence and evolution of honeybee viruses in China (2023, Microbiome; cited 27)

Meta-transcriptomic sequencing of ~2,000 honey bee and mite samples across China (2016–2019).

- ARV-1 and ARV-2 detected in all seven sampled Chinese regions; first evidence of ARV-1/ARV-2 (with VOV-1, VDV-2, VDV-3/5, BMLV) in China.
- ARV-1 among viruses found in >75% of mite libraries, reinforcing the mite-reservoir pattern.
- Expanded the genomic record: complete ARV-1 genomes from 22→29 and ARV-2 from 2→6.
- Described three novel negative-sense rhabdoviruses — Apis rhabdovirus 3, 4 and 5 — extending the genus beyond ARV-1/ARV-2.
- Antisense-strand (replication-intermediate) detection suggested ARV-1/ARV-2 can replicate in both honey bees and mites, whereas VDV-2/VDV-3/5 were mite-restricted.

PMC9832778 · doi:10.1186/s40168-022-01446-1

Kadlečková 2022 — The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses (2022, mSystems; cited 16)

Replicated virome sampling of healthy, Varroa-controlled colonies in Czechia at season's end.

- Reported the first description of a close relationship between two bee rhabdoviruses: BRV-1 and BRV-2 were always present together.
- In every positive sample BRV-1 was more abundant than BRV-2.
- The rhabdovirus pair appeared in only one of three replicate nine-bee samples per hive — highlighting strongly uneven within-hive distribution.
- Found ARV in apparently healthy colonies with no disease signs, underscoring the absence of an obvious pathology.

PMC9239248 · doi:10.1128/msystems.00072-22

Van Herzele 2024 — New insights into honey bee viral and bacterial seasonal infection patterns using nanopore sequencing on haemolymph (2024, Veterinary Research; cited 3)

Year-long third-generation nanopore monitoring of honey bee haemolymph for pathogens not in standard screens.

- Detected ARV-1 and ARV-2 (plus AmFV and BMLV) — viruses usually missed by routine screening.
- ARV-1/ARV-2 appeared specifically in autumn (October) and only in nurse bees, not foragers, implying infection before adult emergence.
- Interpreted nurse-only detection as either pre-foraging mortality or successful clearance of the virus before foraging age.
- Emphasized how little is known about ARV given its very recent identification.

PMC11430211 · doi:10.1186/s13567-024-01382-y

Survey studies — ARV among broader virome findings:

Lester 2022 — Viral communities in the parasite Varroa destructor and in colonies of their honey bee host in New Zealand (2022, Scientific Reports; cited 19)

Characterized the viral community of bees and mites in New Zealand (single introduced Varroa haplotype).

- ARV-1 detected in 25 samples — usually as few transcripts, but exceeding one-third of total viral load in four samples.
- ARV-2 found in nine samples but only at very low levels (≤0.02% of total viral load).

PMC9133037 · doi:10.1038/s41598-022-12888-w

Thaduri 2021 — Global similarity, and some key differences, in the metagenomes of Swedish varroa-surviving and varroa-susceptible honeybees (2021, Scientific Reports; cited 6)

Seasonal metagenome comparison of varroa-surviving vs susceptible Swedish colonies (2015).

- ARV-1 abundance increased through the season by ~1 order of magnitude in both colony types, peaking in September.
- ARV-1 was among the least genetically variable viruses studied; no significant difference between surviving and susceptible colonies at any sampling point.

PMC8636477 · doi:10.1038/s41598-021-02652-x

Morfin 2023 — Breeding honey bees for low and high Varroa destructor population growth: gene expression of grooming bees (2023, Frontiers in Insect Science; cited 4)

Compared virus loads and brain gene expression between bee lines bred for low vs high Varroa population growth.

- Low-Varroa-growth (LVG) bees had significantly lower ARV-1 and ARV-2 brain levels than high-growth (HVG) bees.
- ARV-1 and ARV-2 were among viruses present in ≥0.5 of samples (relatively high prevalence in the population).
- Higher ARV-2 in intense groomers prompted an explicit call to investigate ARV-2 pathogenicity and possible effects on the bee central nervous system and immunity.

PMC10926520 · doi:10.3389/finsc.2023.951447

Sircoulomb 2025 — Genotype B of deformed wing virus and related recombinants become dominant in European honey bee colonies (2025, Scientific Reports; cited 7)

Quantified DWV genotypes (and screened other viruses) across 15 European countries, 2010–2017.

- ARV-1 detected in 26% of samples (n=24) and ARV-2 in 9% (n=8), giving a broad European prevalence estimate.

PMC11807101 · doi:10.1038/s41598-025-86937-5

Yañez 2020 — Bee Viruses: Routes of Infection in Hymenoptera (review) (2020, Frontiers in Microbiology; cited 91)

Reviewed transmission routes of bee viruses across Apis and non-Apis hosts.

- Summarized that *V. destructor* was proposed as a biological vector for ARV-1/BRV-1.
- Argued the mite is a genuine host for ARV-1 and ARV-2, because the viral small-RNA profiles in mites differ from those in bees.
- Noted ARV-1/BRV-1 has been found in *Bombus* sp., and that vertical transmission of ARV remains unknown.

PMC7270585 · doi:10.3389/fmicb.2020.00943

Beaurepaire 2020 — Diversity and Global Distribution of Viruses of the Western Honey Bee (review) (2020, Insects; cited 132)

Synthesized the global diversity and distribution of A. mellifera viruses, including HTS-era discoveries.

- Catalogued ARV-1 and ARV-2 (Mononegavirales: Rhabdoviridae) among the negative-sense ssRNA viruses newly recognized in honey bees and noted they are harder to propagate in vivo.

PMC7240362 · doi:10.3390/insects11040239

Schoonvaere 2018 — Metatranscriptome of Eight Social and Solitary Wild Bee Species Reveals Novel Viruses (2018, Frontiers in Microbiology; cited 62)

Metatranscriptomic survey of wild Andrena, Bombus and Osmia species in Belgium.

- Found rhabdovirus-related sequences in wild bees; an *Andrena cineraria* RdRp had 36–42% identity to rhabdoviruses including ARV-1 and ARV-2.
- Cited evidence that both bee rhabdoviruses elicit an antiviral immune response in honey bees — indirect support for genuine infection.

PMC5817871 · doi:10.3389/fmicb.2018.00177

Norton 2020 — Accumulation and Competition Amongst Deformed Wing Virus Genotypes in Naïve Australian Honeybees (2020, Frontiers in Microbiology; cited 38)

Experimental DWV-genotype infections in Varroa/DWV-naïve Australian pupae; incidentally screened co-present viruses.

- A DWV-B inoculum contained low amounts of ARV-1 and ARV-2 (and LSV).
- When pupae were injected, ARV-1 and ARV-2 were NOT transmitted/detected in recipients — evidence that injection alone did not establish ARV infection in naïve pupae.

PMC7160646 · doi:10.3389/fmicb.2020.00620

McKeown 2025 — Distinct virome compositions indicate viral spillover is a dead-end between honey bee and bumblebee (2025, Communications Biology; cited 3)

Sequenced viromes of sympatric A. mellifera (n=389) and B. impatiens (n=117) over three years to test spillover/host-expansion.

- ARV-1 (apis rhabdovirus 1) was part of the honey bee virome; shared viruses between the two bees were >98% identical with no bumblebee-specific strains.
- Supports the view that honey-bee-to-bumblebee transmission is largely a spillover dead-end rather than true host expansion — relevant context for ARV's cross-species detections.

PMC12170865 · doi:10.1038/s42003-025-08351-x

Detection records — ARV reported as a virome list-item:

Study	Yr	ARV detection finding
Tehel 2019	2019	ARV-1 (BRV-1) was present in both DWV inocula as near-full genomes but at low read counts (6,113 and 33,735 reads), i.e. a background co-infectant.
Daughenbaugh 2021	2021	Listed ARV-1 (also called BRV-1) and ARV-2 among the negative-sense ssRNA viruses newly recognized in honey bees (contextual mention).
Hasegawa 2023	2023	ARV (Apis rhabdovirus) included among the panel of honey bee viruses analysed (contextual mention).
Lannutti 2022	2022	Catalogued ARV-1 and ARV-2 as the first negative-sense ssRNA viruses (family Rhabdoviridae) identified in honey bees by HTS.
Lee 2023	2023	ARV-1 detected in British Columbia samples but absent from Ontario — a regional first-record-type detection.
Ryabov 2023	2023	ARV-1 and ARV-2 detected among reads in the surveyed US apiary viromes (contextual co-detection).
Kwon 2023	2023	Apis rhabdovirus 5 recorded for the first time in Korea (with BMLV, VOV-1, LSV-2/3/4 and others).
da Silva 2023	2023	ARV-1 among eight known viruses identified — a regional detection record for southern Brazil.
Norton 2025	2025	ARV-1 and ARV-2 included in the RT-qPCR screening panel (contextual mention).
Tauber 2020	2020	Apis rhabdovirus detected among colony viruses, consistent with bees harbouring more viruses than curated databases list.

Excluded as off-topic

- **Litov 2024** (Viruses): About tick-cell-line rhabdoviruses; only link to ARV is a 28% N-protein similarity to Apis rhabdovirus 4. Useful for genome organization (N–P–M–G–L) but not a bee study.
- **Kuhn 2023 / 2024** (J. General Virology): ICTV annual Negarnaviricota taxonomy updates; establish the rhabdovirus framework ARV sits within but contain no ARV-specific findings.

References

Levin 2017. *Presence of Apis Rhabdovirus-1 in Populations of Pollinators and Their Parasites from Two Continents.* Frontiers in Microbiology (2017). doi:10.3389/fmicb.2017.02482 · PMC5732965

Galbraith 2018. *Investigating the viral ecology of global bee communities with high-throughput metagenomics.* Scientific Reports (2018). doi:10.1038/s41598-018-27164-z · PMC5995813

Schoonvaere 2018. *Metatranscriptome of Eight Social and Solitary Wild Bee Species Reveals Novel Viruses.* Frontiers in Microbiology (2018). doi:10.3389/fmicb.2018.00177 · PMC5817871

Thaduri 2018. *Temporal changes in the viromes of Swedish Varroa-resistant and Varroa-susceptible honeybee populations.* PLoS ONE (2018). doi:10.1371/journal.pone.0206938 · PMC6283545

Levin 2019. *New Viruses from the Ectoparasite Mite Varroa destructor Infesting Apis mellifera and Apis cerana.* Viruses (2019). doi:10.3390/v11020094 · PMC6409542

Tehel 2019. *The Two Prevalent Genotypes of DWV Cause Equally Low Pupal Mortality and High Wing Deformities.* Viruses (2019). doi:10.3390/v11020114 · PMC6409761

Beaurepaire 2020. *Diversity and Global Distribution of Viruses of the Western Honey Bee (review).* Insects (2020). doi:10.3390/insects11040239 · PMC7240362

Norton 2020. *Accumulation and Competition Amongst Deformed Wing Virus Genotypes in Naïve Australian Honeybees.* Frontiers in Microbiology (2020). doi:10.3389/fmicb.2020.00620 · PMC7160646

Tauber 2020. *Colony-Level Effects of Amygdalin on Honeybees and Their Microbes.* Insects (2020). doi:10.3390/insects11110783 · PMC7698215

Yañez 2020. *Bee Viruses: Routes of Infection in Hymenoptera (review).* Frontiers in Microbiology (2020). doi:10.3389/fmicb.2020.00943 · PMC7270585

Daughenbaugh 2021. *Metatranscriptome Analysis of Sympatric Bee Species Identifies a New Virus, Andrena-Associated Bee Virus-1.* Viruses (2021). doi:10.3390/v13020291 · PMC7917660

Thaduri 2021. *Global similarity, and some key differences, in the metagenomes of Swedish varroa-surviving and varroa-susceptible honeybees.* Scientific Reports (2021). doi:10.1038/s41598-021-02652-x · PMC8636477

Kadlečková 2022. *The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses.* mSystems (2022). doi:10.1128/msystems.00072-22 · PMC9239248

Lannutti 2022. *Molecular Detection and Differentiation of Arthropod, Fungal, Protozoan, Bacterial and Viral Pathogens of Honeybees (review).* Veterinary Sciences (2022). doi:10.3390/vetsci9050221 · PMC9145064

Lester 2022. *Viral communities in the parasite Varroa destructor and in colonies of their honey bee host in New Zealand.* Scientific Reports (2022). doi:10.1038/s41598-022-12888-w · PMC9133037

Damayo 2023. *Virus replication in the honey bee parasite, Varroa destructor.* Journal of Virology (2023). doi:10.1128/jvi.01149-23 · PMC10746231

Hasegawa 2023. *Evolutionarily diverse origins of deformed wing viruses in western honey bees.* PNAS (2023). doi:10.1073/pnas.2301258120 · PMC10293827

Kwon 2023. *Metagenomic analysis of viromes in honey bee colonies after mass disappearance in Korea.* Front. Cell. Infect. Microbiol. (2023). doi:10.3389/fcimb.2023.1124596 · PMC9905416

Lee 2023. *Area-Wide Monitoring of Plant and Honey Bee Viruses in Blueberry Agroecosystems.* Viruses (2023). doi:10.3390/v15051209 · PMC10220920

Li 2023. *Nationwide genomic surveillance reveals the prevalence and evolution of honeybee viruses in China.* Microbiome (2023). doi:10.1186/s40168-022-01446-1 · PMC9832778

Morfin 2023. *Breeding honey bees for low and high Varroa destructor population growth: gene expression of grooming bees.* Frontiers in Insect Science (2023). doi:10.3389/finsc.2023.951447 · PMC10926520

Ryabov 2023. *Apis mellifera Solinvivirus-1, a Novel Honey Bee Virus Widespread in the USA.* Viruses (2023). doi:10.3390/v15071597 · PMC10384192

da Silva 2023. *Exploring viral infections in honey bee colonies: a metagenomic study in southern Brazil.* Brazilian J. Microbiology (2023). doi:10.1007/s42770-023-01078-z · PMC10485192

Van Herzele 2024. *New insights into honey bee viral and bacterial seasonal infection patterns using nanopore sequencing on haemolymph.* Veterinary Research (2024). doi:10.1186/s13567-024-01382-y · PMC11430211

McKeown 2025. *Distinct virome compositions indicate viral spillover is a dead-end between honey bee and bumblebee.* Communications Biology (2025). doi:10.1038/s42003-025-08351-x · PMC12170865

Norton 2025. *DWV genotypes A and B do not elicit immunologically different responses in naïve honey bees.* Insect Molecular Biology (2025). doi:10.1111/imb.12948 · PMC11705515

Sircoulomb 2025. *Genotype B of deformed wing virus and related recombinants become dominant in European honey bee colonies.* Scientific Reports (2025). doi:10.1038/s41598-025-86937-5 · PMC11807101
