

Apis Rhabdovirus

A Comprehensive Literature Summary

Synthesised from 41 indexed records harvested via Europe PMC (2017–2026). Generated 2026-06-12.

Executive Summary

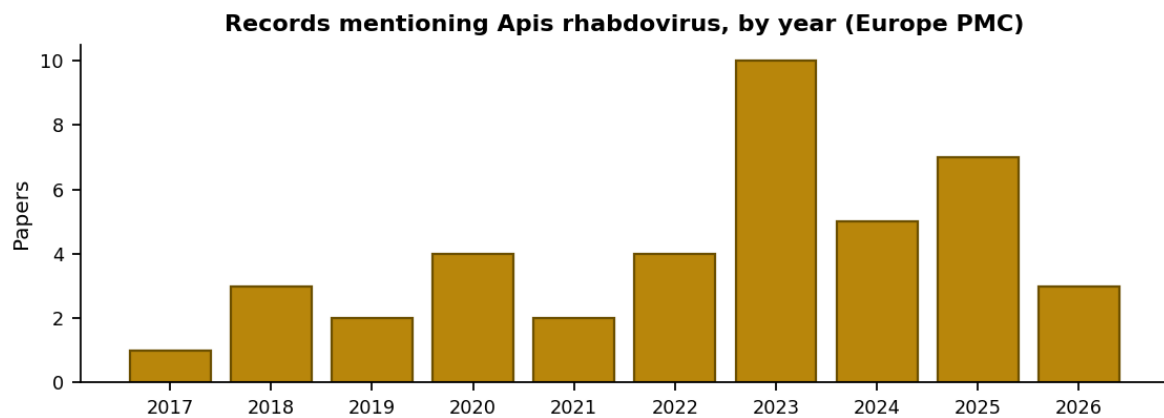
Apis rhabdovirus (ARV) is a negative-sense, single-stranded, enveloped RNA virus of honey bees and other pollinators, with two recognised genotypes, **ARV-1** and **ARV-2**. It is taxonomically distinctive among bee viruses: almost all the well-studied honey bee viruses (Deformed wing virus, Israeli acute paralysis virus, and the acute-paralysis complex) are *non-enveloped, positive-sense* RNA viruses, whereas ARV belongs to the family **Rhabdoviridae** — the same family as rabies and vesicular stomatitis virus. ARV was first described in 2017 from metagenomic sequencing and has since been detected across multiple continents in honey bees, wild bees, and *Varroa destructor* mites. Critically, **no disease or colony-level harm has yet been attributed to it**: the literature is descriptive (establishing that the virus exists and mapping where) rather than mechanistic. It remains one of the clearest examples of a 'metagenomic-era' bee virus — detected and tracked, but biologically uncharacterised.

Taxonomy & Virology

- **Family:** Rhabdoviridae (order Mononegavirales; realm Riboviria). Enveloped, characteristically bullet-shaped virions.
- **Genome:** negative-sense, single-stranded RNA — the genome must be transcribed by a virion-packaged RNA-dependent RNA polymerase before translation, unlike the positive-sense bee viruses whose genomes act directly as mRNA.
- **Genotypes:** ARV-1 and ARV-2, distinguished in early genomic surveys.
- **Why it stands out:** it was the first negative-sense, enveloped virus shown to be shared across bee species and present in *Varroa* mites — a contrast to the positive-sense, non-enveloped viruses that dominate the bee-virus literature.

Discovery & Research Timeline

- **2017 — Discovery & first host survey.** Levin *et al.* reported ARV-1 across multiple pollinator species and their *Varroa destructor* parasites on two continents (*Front. Microbiol.*), establishing broad host range and a mite association.
- **2018 — Wild & solitary bees.** Metatranscriptomic surveys of social and solitary wild bees (e.g. *Andrena*, *Bombus*) detected ARV among novel viruses, reinforcing cross-species circulation beyond managed honey bees.
- **2020–2024 — Global prevalence mapping.** ARV recurs in national/regional virome surveys: healthy Czech colonies (2022), nationwide surveillance in China (2023), post-collapse sampling in Korea (2023), southern Brazil (2023), Uzbekistan (2024), and Slovenia, where 22 complete honey-bee-virus genomes including rhabdovirus were sequenced (2024).
- **2025 — European honey bees.** First reported occurrence in European *Apis mellifera*, alongside La Jolla virus, via nanopore haemolymph sequencing.



Publication activity is recent and survey-driven: the great majority of records appear from 2020 onward, reflecting the spread of high-throughput metagenomic sequencing rather than dedicated ARV research programmes.

Geographic Distribution

ARV has been reported across a wide geographic range, almost entirely through metagenomic detection rather than targeted study. Documented detections in the harvested literature span **North America, Europe (Sweden, Czechia, Slovenia, Belgium), Asia (China, South Korea, Uzbekistan), South America (Brazil), and Oceania**. This near-global footprint, combined with presence in both wild pollinators and *Varroa* mites, indicates an established and widely circulating virus rather than a localised or emerging one.

What Remains Unknown

- **Pathology.** No clinical disease, symptom set, or demonstrated colony-level harm has been attributed to ARV. Its effect on individual bees or colonies is essentially uncharacterised.
- **Transmission dynamics.** ARV is found in *Varroa destructor* and is shared among co-foraging pollinators, but whether the mite is an *active vector* (replicating and transmitting the virus) or merely a passive carrier is unresolved.
- **Replication host range.** Which hosts ARV actively replicates in — versus those where it is only passively present — has not been established.
- **Genotype significance.** Whether ARV-1 and ARV-2 differ in host range, prevalence, or (hypothetical) virulence is unexplored.

Research Landscape

The harvest returned **41 records** mentioning *Apis rhabdovirus*, of which only **~10 substantively discuss it**; most list it as one of many viruses detected in a virome survey, and a few keyword matches refer to unrelated rhabdoviruses (e.g. tick cell-line and lepidopteran viruses). For perspective, the same harvest returned **1,482 records for Deformed wing virus**. That roughly 150-fold gap is a fair measure of how thinly ARV is studied: it is real, distinctive, and globally distributed, yet sits firmly in the descriptive, pre-mechanistic phase of investigation.

Most-Cited Papers in the Harvest

Year	Cit.	Title	DOI
2020	132	Diversity and Global Distribution of Viruses of the Western Honey Bee, <i>Apis mellifera</i> .	10.3390/insects11040239
2020	91	Bee Viruses: Routes of Infection in Hymenoptera.	10.3389/fmicb.2020.00943

Year	Cit.	Title	DOI
2019	69	The Two Prevalent Genotypes of an Emerging Infectious Disease, Deformed Wing Virus, Cause Equally Low Pupal Mortality and Equally High Wing Deformities in Host Honey Bees.	10.3390/v11020114
2023	63	Annual (2023) taxonomic update of RNA-directed RNA polymerase-encoding negative-sense RNA viruses (realm Riboviria: kingdom Orthornavirae: phylum Negarnaviricota).	10.1099/jgv.0.001864
2018	62	Study of the Metatranscriptome of Eight Social and Solitary Wild Bee Species Reveals Novel Viruses and Bee Parasites.	10.3389/fmicb.2018.00177
2018	58	Investigating the viral ecology of global bee communities with high-throughput metagenomics.	10.1038/s41598-018-27164-z
2019	39	New Viruses from the Ectoparasite Mite Varroa destructor Infesting Apis mellifera and Apis cerana.	10.3390/v11020094
2020	38	Accumulation and Competition Amongst Deformed Wing Virus Genotypes in Naïve Australian Honeybees Provides Insight Into the Increasing Global Prevalence of Genotype B.	10.3389/fmicb.2020.00620
2023	27	Nationwide genomic surveillance reveals the prevalence and evolution of honeybee viruses in China.	10.1186/s40168-022-01446-1
2023	26	Virus replication in the honey bee parasite, Varroa destructor.	10.1128/jvi.01149-23

Data provenance. Records were harvested from Europe PMC (query: “Apis rhabdovirus” OR “bee rhabdovirus”); citation counts are Europe PMC values at harvest time. Of 41 records, 39 are open access; full-text PDFs and JATS XML for those are stored under pdf/10_ARV_apis_rhabdovirus/ and fulltext/10_ARV_apis_rhabdovirus/. This document summarises the literature corpus; it is not peer-reviewed and specific attributions should be verified against the cited DOIs.