

Sacbrood Virus

Comprehensive Findings Review

Synthesised from the abstracts and full texts of the most-cited and representative papers within a harvested corpus of 718 records (587 open access). A curated review of landmark findings, not an exhaustive catalogue. Generated 2026-06-12.

Executive Summary

Sacbrood virus (SBV) is a positive-sense, single-stranded RNA virus of the family **Iflaviridae** and one of the first honey bee viruses ever described. It is a disease of **larvae**: infected larvae fail to pupate and die, their bodies becoming fluid-filled sacs of ecdysial fluid under the unshed skin — the namesake 'sac'. In the Western honey bee SBV is highly prevalent but usually causes only sporadic, low-level brood loss; in the Asian honey bee *Apis cerana*, the related Chinese sacbrood virus can be devastating. SBV was among the first bee viruses to have its genome fully sequenced, exists as multiple genotypes, and spreads through food, vertical and mite-mediated routes. This document synthesises the findings by theme and catalogues the landmark studies.

Family	Iflaviridae; positive-sense ssRNA, 8,832 nt, single ORF → 2,858-aa polyprotein (Ghosh 1999)
Disease	Larval disease: infected larvae fail to pupate and die as a fluid-filled 'sac'
Relatives	Distantly related to infectious flacherie virus of the silkworm (Ghosh 1999)
Genotypes	At least three distinct SBV genotypes identified by RT-PCR phylogeny (Grabensteiner 2001)
Prevalence	Very common — 86% of French apiaries (adults), 80% (pupae) (Tentcheva 2004)
Transmission	Food/brood-food-borne, transovarial (queen→eggs), and via Varroa mites/saliva (Shen 2005)
Asian form	Chinese sacbrood virus (in <i>A. cerana</i>) causes severe, often colony-destroying outbreaks

Taxonomy, Genome and Disease

SBV is a member of the family **Iflaviridae**. Its genome was among the first bee-virus genomes fully sequenced: 8,832 nucleotides with a single large open reading frame encoding a 2,858-amino-acid polyprotein, with the structural (capsid) genes at the 5' end and the non-structural enzymes (helicase, protease, RNA-dependent RNA polymerase) at the 3' end — a picornavirus-like organization (Ghosh 1999). It is distantly related to infectious flacherie virus of the silkworm (Ghosh 1999). The disease is one of **larvae**: infection prevents pupation, and the larva dies with its body fluid trapped under the unshed cuticle, forming the characteristic fluid-filled 'sac' (Grabensteiner 2001). Because no honey bee cell lines exist, SBV cannot be cultured, so molecular (RT-PCR) detection superseded older microscopy/serology methods (Grabensteiner 2001).

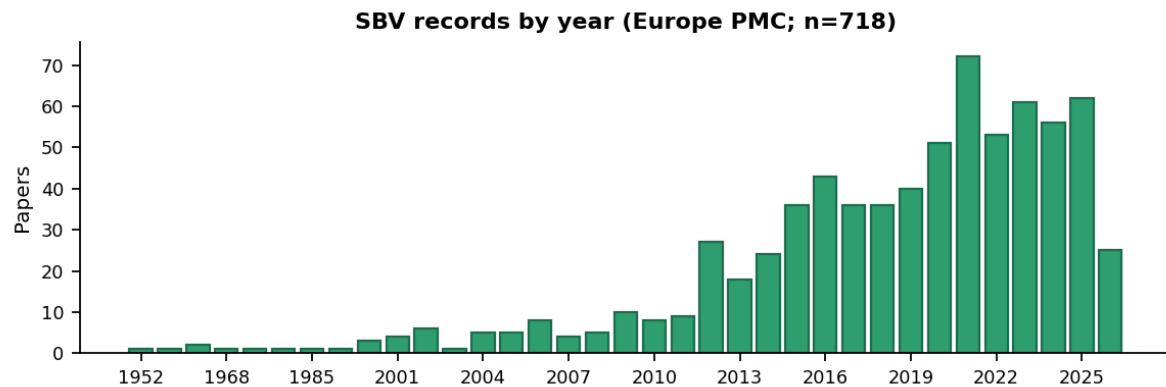
Genotypes and Distribution

SBV exists as multiple genotypes: phylogenetic analysis of isolates from geographically distinct regions revealed at least three distinct SBV genotypes (Grabensteiner 2001). In the Western honey bee SBV is one of the most prevalent and widely distributed viruses — found in 86% of French apiaries in adults and 80% in pupae, and in 45% of *Varroa* samples (Tentcheva 2004) — yet usually causes only sporadic, self-limiting brood loss. The picture differs sharply in the Asian honey bee *Apis cerana*, where the related Chinese sacbrood virus produces severe, frequently colony-destroying epidemics, making sacbrood one of the most economically damaging diseases of *A. cerana* beekeeping.

Transmission Routes

SBV uses several transmission routes, studied in detail alongside Kashmir bee virus (Shen 2005). **Food-borne/horizontal** transmission is prominent: SBV is present in brood food, honey, pollen and royal jelly, and is detected across all developmental stages — nurse bees infect larvae through contaminated food (Shen 2005; Singh 2010). **Vertical (transovarial)** transmission occurs, with SBV RNA detected in queens and eggs (Shen 2005; Chen 2006). The mite *Varroa destructor* provides an additional horizontal route — SBV was detected in mites and their saliva (Shen 2005) — although, unlike DWV, SBV is not strongly dependent on *Varroa* and its titres do not track mite infestation closely.

Research Activity



Landmark Study Catalogue

Selected by citation impact and thematic importance. Core studies:

Ghosh 1999 — The nucleotide sequence of sacbrood virus of the honey bee: an insect picorna-like virus (1999, *J. General Virology*; cited 123)

Sequenced and characterised the SBV genome.

- SBV genome is 8,832 nt with a single large ORF encoding a 2,858-aa polyprotein.
- Structural genes at the 5' end; helicase, protease and RdRp at the 3' end (picornavirus-like order).
- Distantly related to infectious flacherie virus of the silkworm.
- Established SBV as a picorna-like insect virus (now family Iflaviridae).

None · doi:10.1099/0022-1317-80-6-1541

Grabensteiner 2001 — Sacbrood virus of the honeybee: rapid identification and phylogenetic analysis using RT-PCR (2001, *Clin. Diagnostic Lab. Immunology*; cited 99)

Developed an RT-PCR assay and analysed SBV phylogeny.

- SBV infects larvae, causing failure to pupate and death.
- Developed a rapid, specific, sensitive RT-PCR test detecting SBV regardless of geographic origin.
- Phylogenetic analysis suggested at least three distinct SBV genotypes.
- Noted SBV cannot be cultured (no honey bee cell lines), motivating molecular diagnostics.

PMC96016 · doi:10.1128/cdli.8.1.93-104.2001

Shen 2005 — Intricate transmission routes of KBV and SBV with the honeybee host and the Varroa mite (2005, *J. General Virology*; cited 117)

Systematically studied SBV/KBV transmission across stages, castes and mites.

- SBV detected in all developmental stages and in food sources (brood food, honey, pollen, royal jelly).
- SBV RNA found in queens and eggs — evidence of transovarial (vertical) transmission.
- SBV detected in Varroa mites and their saliva — a route of mite-mediated horizontal transmission.
- First detection of co-occurrence of viruses in Varroa, underlining the mite's role in vectoring.

None · doi:10.1099/vir.0.80824-0

Tentcheva 2004 — Prevalence and seasonal variations of six bee viruses in France (2004, *Applied & Environmental Microbiology*; cited 285)

Large-scale PCR survey of six viruses across 36 French apiaries.

- SBV found in 86% of apiaries (adults) and 80% (pupae) — among the most prevalent viruses.
- SBV detected in 45% of Varroa samples.
- Infections persisted without clinical signs in seemingly healthy colonies.

PMC535170 · doi:10.1128/aem.70.12.7185-7191.2004

Supporting studies:

Chen 2006 — Prevalence and transmission of honeybee viruses (2006, *Applied & Environmental Microbiology*; cited 165)

Examined queen tissues and offspring for six viruses including SBV.

- SBV present in queens was detected in their offspring (eggs, larvae, workers) — vertical transmission.

PMC1352288 · doi:10.1128/aem.72.1.606-611.2006

Singh 2010 — RNA viruses in hymenopteran pollinators: inter-taxa transmission via pollen (2010, PLoS ONE; cited 283)

Surveyed viruses in bees, pollen and non-Apis pollinators.

- First detection of SBV (with DWV, BQCV) in pollen pellets; contaminated food was infective.
- SBV detected across multiple non-Apis hymenopteran species.

PMC3008715 · doi:10.1371/journal.pone.0014357

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

Synthesised global diversity and distribution of A. mellifera viruses.

- SBV is among the most prevalent and most widely distributed bee viruses.
- Often multi-host; global trade contributes to dissemination.

PMC7240362 · doi:10.3390/insects11040239

Chen 2004 — Multiple virus infections in the honey bee and genome divergence of honey bee viruses (2004, J. Invertebrate Pathology; cited 118)

Screened colonies for mixed infections and analysed viral phylogeny.

- Phylogenetically, SBV groups with DWV in the iflavirus clade (distinct from KBV/BQCV).
- Individual bees can carry SBV alongside three other viruses simultaneously.

None · doi:10.1016/j.jip.2004.07.005

Scope note: studies excluded as off-topic

- **Vanengelsdorp 2009 / Cornman 2012 / Bromenshenk 2010 / Hristov 2020:** CCD/colony-loss studies — SBV is one of many factors, not the focus.
- **Park 2015 / Raymann 2018:** Honey bee gut-microbiome / antibiotic studies — not SBV-specific.
- **Lanzi 2006 / Highfield 2009 / Di Prisco 2013:** DWV-specific papers surfaced via shared surveys.

References

Ghosh 1999. *The nucleotide sequence of sacbrood virus of the honey bee: an insect picorna-like virus*. J. General Virology (1999). doi:10.1099/0022-1317-80-6-1541

Grabensteiner 2001. *Sacbrood virus of the honeybee: rapid identification and phylogenetic analysis using RT-PCR*. Clin. Diagnostic Lab. Immunology (2001). doi:10.1128/cdli.8.1.93-104.2001 · PMC96016

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Shen 2005. *Intricate transmission routes of KBV and SBV with the honeybee host and the Varroa mite*. J. General Virology (2005). doi:10.1099/vir.0.80824-0

Chen 2006. *Prevalence and transmission of honeybee viruses*. Applied & Environmental Microbiology (2006). doi:10.1128/aem.72.1.606-611.2006 · PMC1352288

Singh 2010. *RNA viruses in hymenopteran pollinators: inter-taxa transmission via pollen*. PLoS ONE (2010). doi:10.1371/journal.pone.0014357 · PMC3008715

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

Provenance & caveat. Curated synthesis of landmark SBV studies from a corpus of 718 records (587 open access); not exhaustive. Findings are from the cited papers' abstracts and full texts; values are as reported by the original authors. Not peer-reviewed — verify against the cited DOIs. The Asian honey bee form (Chinese sacbrood virus, CSBV/AcSBV) is closely related but epidemiologically distinct.