

Lake Sinai Virus

Comprehensive Findings Review

Synthesised from the abstracts and full texts of the most-cited and representative papers within a harvested corpus of 236 records (217 open access). A curated review of landmark findings, not an exhaustive catalogue. LSV is a recently discovered, metagenomic-era virus group. Generated 2026-06-12.

Executive Summary

Lake Sinai virus (LSV) is not a single virus but a rapidly expanding **group** of related, as-yet **unclassified** positive-sense RNA viruses (proposed genus *Sinaivirus*), first discovered by metagenomic sequencing of the honey bee microbiome around 2011. LSVs are now recognised as among the **most prevalent and abundant** viruses in honey bees, comprising many numbered lineages (LSV1, LSV2, LSV4, LSV6, LSV7 and beyond). Yet their biology and pathology remain poorly understood: for most LSVs there is no established disease, and they are a defining example of the 'detected-but-not-understood' viruses of the high-throughput-sequencing era. The clearest disease signal is for LSV2, which has been negatively associated with colony health. This document synthesises the findings by theme and catalogues the landmark studies.

Taxonomy	Unclassified positive-sense ssRNA virus group; proposed genus Sinaivirus
Discovery	Found via metagenomic sequencing of the honey bee microbiome, ~2011 (Runckel 2011)
Lineages	Many numbered members: LSV1, LSV2, LSV4, LSV6, LSV7... and counting (Daughenbaugh 2015)
Prevalence	Among the most prevalent and abundant honey bee viruses
Seasonality	LSV2 peaks in winter (Runckel 2011); abundance varies strongly with season
Disease signal	LSV2 negatively associated with colony health; otherwise pathology unclear (Faurot-Daniels 2020)
Transmission	Found in Varroa and in the gut → vector-, food- and faecal-oral routes proposed (Daughenbaugh 2015)

A Metagenomic-Era Virus Group

Lake Sinai virus was discovered not through disease investigation but through unbiased **metagenomic sequencing** of the honey bee microbiome. A temporal study of a large migratory beekeeping operation identified four novel RNA viruses, two of which (including LSV2) were the most abundant components of the honey bee microbiome — on the order of 10^{11} viral genome copies per bee (Runckel 2011). Crucially, 'Lake Sinai virus' refers to a **group**, not a single virus: it comprises many related but distinct lineages assigned sequential numbers, and it remains formally **unclassified** (a proposed genus *Sinaivirus*). Subsequent surveys steadily expanded the group — extending the LSV1 and LSV2 genomes, recording the first LSV4 in the US, and discovering LSV6 and LSV7 (Daughenbaugh 2015) — and added a fourth LSV strain in Belgium (Ravoet 2013).

Prevalence, Distribution and Seasonality

Despite their late discovery, LSVs are now recognised among the **most prevalent and abundant** viruses in honey bee populations. They show strong **seasonality**: in the founding study, LSV2 peaked in winter (January), in contrast to most other bee viruses that peak in summer (Runckel 2011), and longitudinal monitoring confirmed that LSV abundance varies markedly with sample date (Faurot-Daniels 2020). Initially reported from the United States, LSVs were soon detected in Europe — the first identification outside the US was in Spanish honey bees, alongside Aphid lethal paralysis virus and IAPV (Granberg 2013) — and they are now known to be globally distributed.

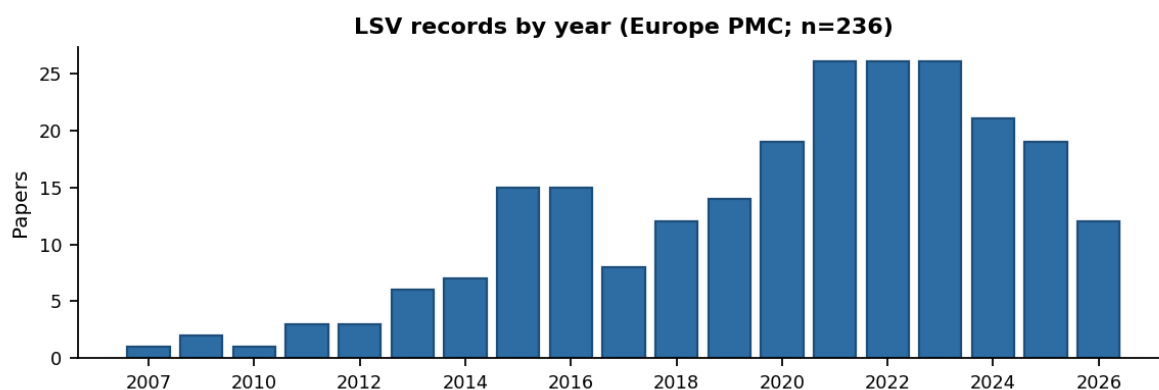
Pathology: Largely Unknown, with an LSV2 Signal

For most LSV lineages there is **no established disease** — they are detected ubiquitously, including in apparently healthy colonies, and their impact on bee health is uncertain. This makes LSV a textbook example of the metagenomic-era viruses whose detection has outpaced understanding of their biology. The clearest disease signal concerns **LSV2**: in a 50-colony year-long cohort tied to the California almond pollination event, LSV2 was associated with a negative impact on colony health, with its abundance declining from summer into fall (Faurot-Daniels 2020). LSV2, LSV1, black queen cell virus and *Nosema ceranae* were also found to be more abundant in weak colonies than strong ones (Daughenbaugh 2015) — correlative signals that motivate, but do not yet establish, a causal role.

Transmission and Host Associations

Evidence on LSV transmission comes largely from where the viruses are found. LSV1 and LSV2 have been detected in the *Varroa destructor* mite, and a large proportion of LSV2 localises to the honey bee **gut** — together suggesting that vector-mediated, food-associated and/or faecal-oral routes are important for LSV dissemination (Daughenbaugh 2015). LSVs also non-randomly co-occur with black queen cell virus (Ravoet 2013), and they appear within the shared pollinator virome rather than being strictly honey-bee-specific. Whether and where each LSV lineage actively replicates, and which are benign commensals versus genuine pathogens, are central open questions.

Research Activity



Landmark Study Catalogue

Selected by citation impact and thematic importance. Core studies:

Runckel 2011 — Temporal analysis of the honey bee microbiome reveals four novel viruses and seasonal prevalence (2011, PLoS ONE; cited 281)

High-frequency molecular + deep-sequencing survey of a migratory operation over time.

- Discovered four novel RNA viruses, including Lake Sinai virus — two were the most abundant components of the bee microbiome ($\sim 10^{11}$ viruses/bee).
- LSV2 peaked in winter (January), unlike most bee viruses that peak in summer.
- Established LSV as a newly recognised, highly abundant honey bee virus group.

PMC3110205 · doi:10.1371/journal.pone.0020656

Daughenbaugh 2015 — Honey Bee Infecting Lake Sinai Viruses (2015, Viruses; cited 76)

Sequenced and characterised circulating LSVs and quantified them across colonies.

- Extended the LSV1 and LSV2 genomes; first detection of LSV4 in the US; discovered LSV6 and LSV7.
- Detected LSV1 and LSV2 in Varroa destructor; a large proportion of LSV2 was in the bee gut.
- Proposed vector-mediated, food-associated and/or faecal-oral routes for LSV dissemination.
- LSV2, LSV1, BQCV and N. ceranae were more abundant in weak than strong colonies.

PMC4488739 · doi:10.3390/v7062772

Faurot-Daniels 2020 — Longitudinal monitoring reveals a negative impact of Lake Sinai virus 2 on colony health (2020, PLoS ONE; cited 45)

Year-long 50-colony cohort study tied to the 2016 California almond pollination event.

- BQCV, DWV, SBV and the Lake Sinai viruses were the most readily detected viruses through the year.
- LSV2 abundance decreased from summer to fall, while DWV increased over the same period.
- LSV2 was associated with a negative impact on colony health — the clearest LSV disease signal to date.
- Demonstrated the highly dynamic, season-dependent nature of LSV abundance.

PMC7478651 · doi:10.1371/journal.pone.0237544

Cornman 2012 — Pathogen webs in collapsing honey bee colonies (2012, PLoS ONE; cited 300)

Deep-sequencing survey of pathogens across CCD, weak and strong US colonies.

- Identified novel strains of the recently described Lake Sinai viruses via deep RNA sequencing.
- Greater incidence/abundance of pathogens (incl. LSVs) in CCD colonies; pathogen loads highly covariant.

PMC3424165 · doi:10.1371/journal.pone.0043562

Supporting studies:

Granberg 2013 — Metagenomic detection of viral pathogens in Spanish honeybees (ALPV, IAPV, LSV) (2013, PLoS ONE; cited 70)

Unbiased metagenomic survey of Spanish honey bees.

- First identification of Lake Sinai virus outside the United States.
- Co-detected with Aphid lethal paralysis virus and IAPV, plus a plant virus (Turnip ringspot virus).
- Confirmed LSV as an unclassified group of unclear impact on colony health.

PMC3583878 · doi:10.1371/journal.pone.0057459

Ravoet 2013 — Comprehensive bee pathogen screening in Belgium (2013, PLoS ONE; cited 167)

Screened 363 Belgian colonies for 18 pathogens vs winter mortality.

- Identified a new fourth strain of Lake Sinai virus (LSV).
- Viruses of the LSV complex and BQCV tended to non-randomly co-occur.
- Pathogen-species count correlated with colony losses.

PMC3753275 · doi:10.1371/journal.pone.0072443

Roberts 2017 — Honey bee viral landscape (incl. Lake Sinai viruses) surveys (2017, Scientific Reports; cited 66)

Surveyed honey bee viral communities including LSVs across populations.

- Documented LSVs as a prominent, prevalent component of the honey bee virome.
- Reinforced the wide distribution and diversity of the Lake Sinai virus group.

PMC5537221 · doi:10.1038/s41598-017-07290-w

Scope note: studies excluded as off-topic

- **Atkins 2016 / Adams 2009:** Ribosomal-frameshifting and plant-virology methods papers — general virology, not LSV-specific.
- **Vanengelsdorp 2009 / Hristov 2020:** CCD/colony-loss descriptive studies — LSV peripheral.
- **Bat/freshwater virome metagenomics:** Non-bee virome surveys matched via shared metagenomic methods.

References

Runckel 2011. *Temporal analysis of the honey bee microbiome reveals four novel viruses and seasonal prevalence*. PLoS ONE (2011). doi:10.1371/journal.pone.0020656 · PMC3110205

Cornman 2012. *Pathogen webs in collapsing honey bee colonies*. PLoS ONE (2012). doi:10.1371/journal.pone.0043562 · PMC3424165

Granberg 2013. *Metagenomic detection of viral pathogens in Spanish honeybees (ALPV, IAPV, LSV)*. PLoS ONE (2013). doi:10.1371/journal.pone.0057459 · PMC3583878

Ravoet 2013. *Comprehensive bee pathogen screening in Belgium*. PLoS ONE (2013). doi:10.1371/journal.pone.0072443 · PMC3753275

Daughenbaugh 2015. *Honey Bee Infecting Lake Sinai Viruses*. Viruses (2015). doi:10.3390/v7062772 · PMC4488739

Roberts 2017. *Honey bee viral landscape (incl. Lake Sinai viruses) surveys*. Scientific Reports (2017). doi:10.1038/s41598-017-07290-w · PMC5537221

Faurot-Daniels 2020. *Longitudinal monitoring reveals a negative impact of Lake Sinai virus 2 on colony health*. PLoS ONE (2020). doi:10.1371/journal.pone.0237544 · PMC7478651

Provenance & caveat. Curated synthesis of LSV studies from a corpus of 236 records (217 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. 'Lake Sinai virus' denotes a group of many numbered lineages (LSV1, LSV2, ...), not a single virus.