Viruses in astrobiology: origins, ecosystems, and life detection

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Abstract. Viruses constitute the most abundant biological entities on Earth, yet they remain markedly underrepresented in astrobiological research frameworks. This mini-review examines three interrelated dimensions of their relevance: their potential roles in the origin and early evolution of life, the constraints on their existence independent of complex ecosystems, and the challenges and opportunities they present for extraterrestrial life detection. Competing hypotheses - including viruses-first, viroids-first, and models situating viral emergence during the transition from the First Universal Common Ancestor to the Last Universal Common Ancestor - highlight viruses and virus-like entities as candidate participants in precellular evolution and as powerful drivers of subsequent cellular diversification. Although obligately dependent on host cellular machinery for replication, viruses display exceptional resilience in extreme terrestrial environments and under simulated interstellar conditions, suggesting that virions may persist where cellular life cannot. Detection of extraterrestrial viruses is currently hindered by the absence of validated biosignatures, instrument biases favoring cellular definitions of life, and limitations in metagenomic identification tools. Future missions targeting Mars or the subsurface oceans of icy moons offer unique opportunities to test viral origin hypotheses and to incorporate virus-aware detection strategies. Integrating virology into astrobiological thinking is therefore essential for a more complete understanding of life's possible distribution and evolutionary trajectories beyond Earth.

Keywords: astrovirology, extraterrestrial life detection, extreme environments, Mars sample return, panspermia, viral biosignatures, viroids, viruses-first hypothesis.

Introduction. Viruses are the most abundant biological entities on Earth, with an estimated 10^{31} virions in the oceans alone, yet they remain largely neglected in astrobiological frameworks (Jalasvuori et al., 2009; Griffin, 2013; Berliner et al., 2018; Moelling & Broecker, 2019a; Jamal et al., 2021; De La Higuera & Lázaro, 2022; Trubl et al., 2023). The NASA Astrobiology Strategy mentions viruses only six times in over 250 pages, and the European AstRoMap includes only nine parenthetical mentions of viral elements (Berliner et al., 2018).

This review synthesizes current evidence across three interconnected dimensions: the role of viruses in life's origin and evolution, the possibility of viruses existing without complex ecosystems, and the implications for detecting extraterrestrial life.

Role of Viruses in the Origin and Evolution of Life. Viruses are the only biological entities on modern Earth that use RNA or DNA in both single- and double-stranded forms for their genetic material, making them potential models for the putative RNA-protein world and suggesting deep antiquity (Berliner et al., 2018; Trubl et al., 2023). The "viruses-first" hypothesis (VFH) proposes that viruses represent the oldest domain of life and are direct descendants of precellular life-forms predating the Last Universal Common Ancestor (LUCA), originating in an "ancient virus world". This view is compatible with replication-first models of prebiotic evolution, suggesting that molecular replicators rather than metabolic systems-initiated life (Janjic, 2018).

Viroids, non-coding circular RNA molecules that function as ribozymes, can cleave, join, replicate, and undergo Darwinian evolution, fulfilling multiple criteria of life without protein-coding information. As ribozymes are essential elements for protein synthesis as parts of ribosomes, they must have preceded DNA and proteins during evolution, supporting a "viroids-first" specification of the viruses-first scenario (Moelling & Broecker, 2019b; Moelling & Broecker, 2021). These simplest biological entities may serve as more universal models for early life than highly complex cellular organisms (Moelling & Broecker, 2019b).

An alternative framework proposes that viruses originated during the transition from the First Universal Common Ancestor (FUCA) to LUCA, with transitional entities (T-LUCA) remaining as undifferentiated subsystems with virus-like structures that shared protein synthesis apparatuses with emerging cellular life (De Farias et al., 2019; Haja & Nmeribe, 2026). Under this model, viruses represent a survival strategy of life reached through two paths: T-LUCA-like entities and genomic reduction of cellular life forms (De Farias et al., 2019; Bora & Kovacs, 2023). Giant viruses, with capsids as large as some bacteria and megabase-range genomes, further blur the boundary between living and non-living entities, suggesting an evolutionary continuum rather than a sharp border (Janjic, 2018; Moelling & Broecker, 2019a; Petrescu-Mag & Proorocu, 2022; Schulz et al., 2022) (Table 1).

Table 1

Comparison of major hypotheses on viral origins and their supporting evidence

Hypothesis	*Central proposition*	*Key evidence*
Viruses-First (VFH)	Viruses are precursors of cellular life, predating LUCA	Viruses span all nucleic acid types; compatible with RNA world (Janjic, 2018)
Viroids-First	Non-coding RNA ribozymes are the simplest model for earliest life	Viroids replicate and evolve without proteins; ribozymes predate DNA (Moelling & Broecker, 2021)
FUCA-to-LUCA Transition	Viruses originated during transition between ancestral states	T-LUCA entities had virus-like structures sharing protein synthesis (De Farias et al., 2019)
Virus Reduction (VRH)	Viruses evolved from greatly reduced microorganisms	Parasitic bacteria lacking metabolism represent intermediates (Janjic, 2018).

Regardless of their exact origin, viruses have profoundly shaped cellular evolution. Retroviruses contributed approximately half of mammalian genomic sequences and drove the evolution of the mammalian placenta (Moelling & Broecker, 2019a). Viruses serve as one of the most powerful selective pressures in nature, accelerating the evolution of cellular defense mechanisms and exchanging genetic material with hosts during infection, thereby providing organisms with capacities for colonizing new ecological niches (Berliner et al., 2018; De La Higuera & Lázaro, 2022). The structure of the tree of life itself is largely the result of intertwined interactions between cellular and viral worlds throughout evolutionary history (De La Higuera & Lázaro, 2022).

Can Viruses Exist Without Complex Ecosystems? The question of whether viruses can exist independently of complex ecosystems is fundamentally constrained by their obligate dependence on host cellular machinery for replication (Moelling & Broecker, 2019a; Shapshak, 2019; De La Higuera & Lázaro, 2022; Mcminn et al., 2026). Viruses always require cellular resources to multiply, establishing intimate interactions with their hosts (De La Higuera & Lázaro, 2022). This dependency means that detection of extraterrestrial viruses necessitates the prior existence of cellular life, since viruses cannot replicate without it (Shapshak, 2019).

Viruses thrive in Earth's most extreme environments, including sea ice, hydrothermal vents, and ocean trenches, surviving temperatures from -30 to 122°C and pressures exceeding 100 MPa (De La Higuera & Lázaro, 2022; Mcminn et al., 2026). Their distribution in these extreme environments correlates closely with that of their extremophile hosts, which are predominantly bacteria, archaea, and microeukaryotes (Mcminn et al., 2026). Viruses in virion form can withstand more extreme conditions than most cellular life, and some have demonstrated prolonged survival in cold-temperature settings (Griffin, 2013; De La Higuera & Lázaro, 2022). Viruses have even been shown capable of long-term survival under conditions simulating interstellar environments (Mcminn et al., 2026).

The question of whether biospheres without viruses are possible remains open. If a biosphere lacking viruses existed, it would almost certainly be less rich and diverse than the one we know (De La Higuera & Lázaro, 2022). Interestingly, ecosystems of panspermial origin - life transferred between planetary bodies via bacterial endospores - might yield biospheres in which viruses are absent, because viruses seem less likely to survive interplanetary transfer than microbial cells (Jalasvuori et al., 2009; Janjic, 2018). The evolutionary trajectory of life in such virus-free systems would likely differ significantly from the path observed on Earth (Jalasvuori et al., 2009). All hypothetical extraterrestrial living systems composed of cells, however, would be expected to harbor their own viruses given the overwhelming abundance and evolutionary significance of these entities on Earth (Bamford & Jalasvuori, 2014).

Implications for the Detection of Life. The lack of validated virus biosignatures makes detection of extraterrestrial or ancient viruses exceptionally challenging (Berliner et al., 2018). Current life-detection instruments follow a biased definition of life that could miss important viral biosignatures (Janjic, 2018). Most viral signals remain "hidden" in metagenomic and metatranscriptomic datasets due to the absence of universal gene markers, limited database representatives, and insufficiently advanced identification tools (Guo et al., 2021). The virosphere's diversity, defined by numbers of species, genetic information types, individuals, and unique non-homologous genes, far exceeds what current detection frameworks account for (Trubl et al., 2023) (Table 2).

Table 2

Key challenges and proposed directions for extraterrestrial virus detection

Detection challenge	*Current limitation*	*Proposed direction*
Biosignature validation	No validated virus biosignatures exist for extraterrestrial or ancient samples (Berliner et al., 2018)	Develop virus-specific biosignature frameworks (Berliner et al., 2018)
Instrument bias	Mission instruments follow biased cellular definition of life (Janjic, 2018)	Include virology hypotheses in Mars sample return design (Janjic, 2018)
Sequence identification	Most viral signals hidden due to lack of universal gene markers (Guo et al., 2021)	Deploy multi-classifier tools like VirSorter2 for broad viral diversity (Guo et al., 2021)
Microscopy	Viruses too small for standard life-detection approaches	Portable electron and atomic force microscopes for virion imaging (Shapshak, 2019).

Future Mars missions represent a unique opportunity to test competing hypotheses about viral origins. If only viruses or virus-like entities are found in Martian regolith without evidence of microbial cells, this would be the only way to exclude the virus escape and virus reduction hypotheses and confirm the virus-first hypothesis through evidence-based science. Finding viruses on Mars could also indicate they are descendants of Martian microbes, supporting reduction or escape hypotheses. The discovery of viruses carrying metabolic genes could further support the reduction hypothesis, or indicate genes acquired during host infiltration (Janjic, 2018).

The most likely candidates for extraterrestrial habitability in our solar system are the sea ice moons of Jupiter and Saturn — Europa and Enceladus — which are thought to contain subsurface oceans of liquid water with potentially accessible elements for microbial growth. If microorganisms were detected in these environments, viruses might also be found coexisting with their host cells (Mcminn et al., 2026). Viroids and virus-like entities, as the simplest replicating biological molecules, may serve as more universal biosignatures than complex cellular organisms, since highly complex cellular life forms are unlikely to have evolved independently on other planets (Moelling & Broecker, 2019b).

Viruses should be explicitly considered in organism-level astrobiological investigations, and the ability to detect virus-like entities must be a point of assessment for instruments and missions targeting direct detection of extraterrestrial organisms for planetary protection, human spaceflight safety, and sample return (Trubl et al., 2023). The possibility that extraterrestrial viruses could infect humans, while uncertain, warrants precautionary treatment of any prospective contact (Griffin, 2013; Shapshak, 2019; Shapshak et al., 2024). As viruses have coexisted with cellular life since the earliest stages of life on Earth and have profoundly influenced cellular evolution, their integration into astrobiological frameworks is essential for a comprehensive search for life beyond Earth (Berliner et al., 2018; Janjic, 2018; De La Higuera & Lázaro, 2022).

Conclusions. Viruses occupy a uniquely informative position at the interface of prebiotic chemistry, cellular evolution, and planetary habitability, yet their systematic exclusion from most astrobiological strategies leaves a significant conceptual and methodological gap. The diversity of nucleic-acid chemistries they employ, the evolutionary antiquity suggested by viroids and the viruses-first hypothesis, and their documented capacity to shape host genomes and ecological niches collectively argue that viral entities must be considered both as potential relics of early life and as active participants in any biosphere that harbors cellular organisms.

Their obligate dependence on hosts implies that the presence of viruses would normally indicate the prior or concurrent existence of cellular life; conversely, the discovery of virus-like particles in the absence of detectable cells—should such a finding ever occur—would provide decisive empirical support for viruses-first scenarios. At the same time, the remarkable environmental resilience of virions, including survival under conditions approximating interstellar space, raises the possibility that viruses could outlast or travel farther than their cellular hosts, with implications for panspermia and for the interpretation of putative biosignatures on Mars or icy moons.

Current life-detection architectures remain poorly equipped to recognize viral signals. Progress will require the development of validated virus-specific biosignatures, the incorporation of multi-classifier metagenomic tools, and the explicit inclusion of virological hypotheses in the design of sample-return and in situ instruments. Only by treating viruses as integral components of life’s evolutionary continuum, rather than as peripheral parasites, can astrobiology achieve a more comprehensive and biologically realistic framework for searching for life beyond Earth.

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References

Bamford, J. K. H., & Jalasvuori, M. (2014). Evolutionary approach to viruses in astrobiology. In V. M. Kolb (Ed.), *Astrobiology: an evolutionary approach* (pp. 413-420). CRC Press. https://doi.org/10.1201/b17348-25

Berliner, A., Mochizuki, T., & Stedman, K. M. (2018). Astrovirology: viruses at large in the universe. *Astrobiology*, *18*(3), 207-223. https://doi.org/10.1089/ast.2017.1649

Bora, F. D., & Kovacs, E. (2023). Prions: Involution and adaptation or just proteins? *ELBA Bioflux*, *15*(1), 24-27.

De Farias, S. T., Jheeta, S., & Prosdocimi, F. (2019). Viruses as a survival strategy in the armory of life. *History and Philosophy of the Life Sciences*, *41*(4), 45. https://doi.org/10.1007/s40656-019-0287-5

De La Higuera, I., & Lázaro, E. (2022). Viruses in astrobiology. *Frontiers in Microbiology*, *13*, 1032918. https://doi.org/10.3389/fmicb.2022.1032918

Griffin, D. W. (2013). The quest for extraterrestrial life: What about the viruses? *Astrobiology*, *13*(8), 774-783. https://doi.org/10.1089/ast.2012.0959

Guo, J., Bolduc, B., Zayed, A. A., Varsani, A., Dominguez-Huerta, G., Delmont, T. O., Pratama, A. A., Gazitúa, M. C., Vik, D., Sullivan, M. B., & Roux, S. (2021). VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. *Microbiome*, *9*, 37. https://doi.org/10.1186/s40168-020-00990-y

Haja, R., & Nmeribe, O. D. (2026). Bridging prebiotic chemistry and protocellular systems: A critical perspective on RNA-centered and alternative models. *ELBA Bioflux*, *18*(1), 1-11.

Jalasvuori, M., Örmälä, A.-M., & Bamford, J. K. H. (2009). On the astrobiological relevance of viruses in extraterrestrial ecosystems. *International Journal of Astrobiology*, *8*(2), 95-100. https://doi.org/10.1017/S1473550409004479

Jamal, E. S., Ambalavanan, L., Iehata, S., & Zainathan, S. C. (2021). A review on marine viruses in sponges and seawater. *AACL Bioflux*, *14*(3), 1828-1854.

Janjic, A. (2018). The need for including virus detection methods in future Mars missions. *Astrobiology*, *18*(12), 1611-1614. https://doi.org/10.1089/ast.2018.1851

McMinn, A., Liang, Y., Wang, Z., & Wang, M. (2026). Viruses in extreme marine environments and their potential existence in extraterrestrial environments. *Viruses*, *18*(4), 457. https://doi.org/10.3390/v18040457

Moelling, K., & Broecker, F. (2019a). Viruses and evolution—Viruses first? A personal perspective. *Frontiers in Microbiology*, *10*, 523. https://doi.org/10.3389/fmicb.2019.00523

Moelling, K., & Broecker, F. (2019b). Viroids-first—A model for life on Earth, Mars and exoplanets. *Geosciences*, *9*(5), 241. https://doi.org/10.3390/geosciences9050241

Moelling, K., & Broecker, F. (2021). Viroids and the origin of life. *International Journal of Molecular Sciences*, *22*(7), 3476. https://doi.org/10.3390/ijms22073476

Petrescu-Mag, I. V., & Proorocu, M. (2022). Viruses—Existence on the border between living and non-living. *ELBA Bioflux*, *14*(1), 7-8.

Schulz, F., Abergel, C., & Woyke, T. (2022). Giant virus biology and diversity in the era of genome-resolved metagenomics. *Nature Reviews Microbiology*, *20*, 721-736. https://doi.org/10.1038/s41579-022-00754-5

Shapshak, P. (2019). Astrovirology, astrobiology, artificial intelligence: extra-solar system investigations. In P. Shapshak, S. Balaji, P. Kangueane, F. Chiappelli, C. Somboonwit, L. Menezes, & J. T. Sinnott (Eds.), *Global virology III: Virology in the 21st century* (pp. 541-573). Springer. https://doi.org/10.1007/978-3-030-29022-1_20

Shapshak, P., Zandi, M., Somboonwit, C., & Sinnott, J. T. (2024). Neutrinos to astrovirology: signatures. *Bioinformation*, *20*(1), 18-19. https://doi.org/10.6026/973206300200018

Trubl, G., Stedman, K. M., Bywaters, K. F., Matula, E. E., Sommers, P., Roux, S., Merino, N., Yin, J., Kaelber, J., Avila-Herrera, A., Johnson, P. A., Johnson, J., Borges, S. R., Weber, P., Pett-Ridge, J., & Boston, P. (2023). Astrovirology: how viruses enhance our understanding of life in the Universe. *International Journal of Astrobiology*, *22*(4), 247-271. https://doi.org/10.1017/S1473550423000058

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