Endoparasitoids at Odds: Not All Rely on Viral Domestication

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Of all the threats an insect's immune system encounters, an endoparasitoid is definitely among the worst. Endoparasitoidism is a life-history strategy in which eggs stealthily develop inside a host, which is then consumed as the parasitoid larvae hatch and grow; contrary to traditional parasitism, endoparasitoids steal nutrients and benefit from protection until the host eventually dies. To successfully develop, endoparasitoids have evolved remarkable strategies to counteract, evade, or suppress their hosts' immune systems.

Endoparasitoid wasps (Hymenoptera), the most well-characterized endoparasitoids, inject host immune-suppressing factors alongside the eggs, such as venom or cells that diminish the host's ability to recognize the endoparasitoid's offspring; some clades of Hymenoptera evolved a particularly unique innovation: viral domestication.

Viral domestication occurs when viral genomes, or portions of viral genomes, are integrated into the hymenopteran wasp genome and eventually expressed in ways that assist parasitism in useful ways (Fig. 1). Some wasp–virus partnerships produce viral particles in the wasp ovaries that hold either domesticated viral DNA or virulence proteins; when injected into the unlucky host, they suppress the immune system. "These viral systems are key to parasitic success in Hymenoptera," says Dr. Sara Oukkal (Fig. 2), an evolutionary genomicist from the Université Claude Bernard Lyon 1. "They likely offer advantages over venom alone, notably by enabling intracellular delivery of effectors and for some, a prolonged expression through integration of viral DNA circles into host genomes." Comparative genomics has found that endoparasitoid lifestyles in Hymenoptera are associated with increased presence of co-opted viral sequences (Guinet et al. 2023), indicating that endoparasitoid lifestyles may result in a higher frequency of viral sequence integration.

However, endoparasitoidism has evolved in other insect groups outside of Hymenoptera, but whether they also rely on viral domestication is less clear. Tachinid flies (Tachinidae), for example, are endoparasitoids that rely on host immune evasion instead of immune suppression by laying their eggs in under-monitored host tissues. "The difference in endoparasitoid strategy between Hymenoptera and Tachinidae may have important implications for the evolutionary trajectories available to these 2 groups," Oukkal shared.

In a new *Genome Biology & Evolution* article (Oukkal et al. 2026), Oukkal and her team of researchers tested whether co-option of viral sequences is a common evolutionary strategy associated with the endoparasitoid lifestyle by investigating tachinid flies (Diptera). Oukkal et al. (2026) leveraged a large dataset featuring 52 tachinid genomes: in addition to 15 genomes generated by the Darwin Tree of Life project (Darwin Tree of Life Project Consortium 2022), the authors contributed 37 new genomes to a decades-long DNA barcoding project focused on the biodiversity of a protected area in Costa Rica (Área de Conservación Guanacaste; Janzen and Hallwachs 2016). Oukkal considers biodiversity barcoding initiatives such as these paramount to her study and to others.

Using this dataset, Oukkal et al. (2026) identified endogenous viral sequences in nearly all included lineages of Tachinidae. Whereas over 90% of viruses known to infect insects are RNA viruses, almost half of the identified viral sequences originated instead from double-stranded DNA (dsDNA) viruses; this is also true for hymenopteran

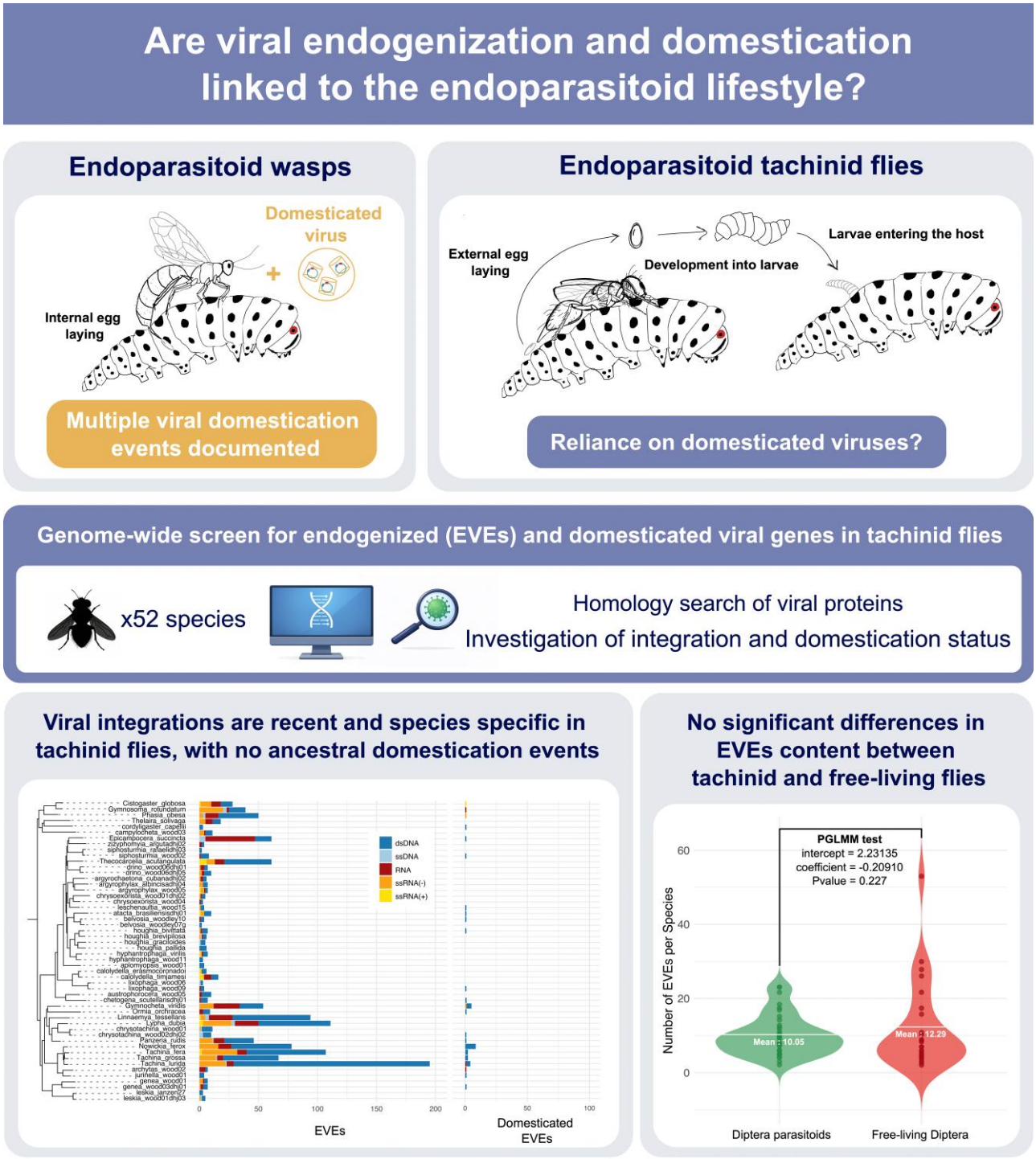

Fig. 1. Endoparasitoids, insects whose early development occurs within another insect host, exist within Hymenoptera and Tachinidae. These 2 different groups of endoparasitoids rely on different mechanisms to successfully counteract the host's immune system. In some hymenopteran wasps, immune suppression is accomplished through the co-option of viral genes. Tachinid flies, however, rely on immune evasion that does not appear to rely on integrated viral sequences, despite widespread viral endogenization in this clade. EVEs, endogenous viral elements. Figure provided by Sara Oukkal.

endoparasitoids. The disproportionate representation of dsDNA viruses may suggest a propensity of dsDNA viruses toward viral integration since their replication occurs in the nucleus, making them more likely to be picked up by transposable elements or genome repair mechanisms such as nonhomologous end-joining.

Fig. 2. Sara Oukkal is an evolutionary genomics researcher, exploring interactions between viruses and eukaryotic genomes. She conducted her PhD at the Laboratory of Biometry and Evolutionary Biology, Université Claude Bernard Lyon 1 (France). There, she studied endogenous viral elements and viral domestication in host–parasitoid systems, leveraging large-scale comparative genomics. Her research combines evolutionary biology with bioinformatic approaches to understand how viral sequences are acquired, maintained, and co-opted across evolutionary timescales. Dr. Oukkal is now continuing her work on host–microbe interactions at the Institute of Clinical Molecular Biology (Germany), shifting toward metagenomic analyses of the human gut microbiome in the context of chronic inflammation. Keep up with Sara's research at www.linkedin.com/in/sara-oukkal.

Despite viral integrations being common in endoparasitoid flies, they did not resemble the viral domestication events documented in hymenopteran wasps. In the wasps, viral domestication events occurred independently in a common ancestor and persisted during the diversification of multiple wasp clades (Guinet et al. 2023). Oukkal et al., however, found that endogenized viral sequences were not shared between closely related tachinid species (Fig. 2). When Oukkal queried the genomes of non-endoparasitoid flies from the same taxonomic group as endoparasitoid flies, she found no difference in the number of integration events. Further, a phylogenetic generalized mixed linear model, a method that tests for relationships between variables while accounting for evolutionary relatedness, did not suggest an effect of the endoparasitoid lifestyle on viral sequence abundance. Because these findings contradict those in Hymenoptera, it is unlikely that endoparasitism alone increases the likelihood of viral gene co-option; instead, these opposing findings suggest that the evolutionary pressures experienced by these 2 groups may differentially affect the outcome of viral integration.

Viral domestication has proven advantageous to hymenopteran endoparasitoids, but why this strategy is not observed in endoparasitoid flies may be due to differences in their approach to endoparasitoidism. "Tachinids have evolved predominantly passive strategies that minimize immune detection rather than actively suppressing host defenses," Oukkal shared. "In this context, viral co-option may simply integrate less naturally into the parasitic strategy than it does in hymenopteran wasps." If and when viral sequences were integrated into tachinid genomes and became functional, an already rare event, they may not have provided a clear fitness advantage. Further work across insects, vertebrates, and other eukaryotes is required to clarify what evolutionary pressures affect the outcome of viral integration. Oukkal specified that these comparisons could "reveal whether the integration patterns observed in some insect groups are exceptional or reflect a more general tendency."

Want to learn more? Check out these other articles on endoparasitoids and their hosts recently published in *Genome Biology and Evolution*:

- Burke GD, Hines HM, Sharanowski BJ (2021). The Presence of Ancient Core Genes Reveals Endogenization from Diverse Viral Ancestors in Parasitoid Wasps, *Genome Biol Evol.*; 13(7): evab105, https://doi.org/10.1093/gbe/evab105.
- Yang X, Fors L, Slotte T, Theopold U, Binzer-Panchal M, Wheat CW, Hambäck PA. (2020). Differential Expression of Immune Genes between Two Closely Related Beetle Species with Different Immunocompetence following Attack by Asecodes parviclava, *Genome Biol Evol.*; 12(5):522 to 534, https://doi.org/10.1093/gbe/evaa075.
- Leobold M, Bézier A, Pichon A, Herniou EA, Volkoff A, Drezen J. (2018). The Domestication of a Large DNA Virus by the Wasp *Venturia canescens* Involves Targeted Genome Reduction through Pseudogenization, *Genome Biol Evol.*; 10(7):1745-1764, https://doi.org/10.1093/gbe/evy127.

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Janzen DH, Hallwachs W. DNA barcoding the Lepidoptera inventory of a large complex tropical conserved wildland, Area de Conservacion Guanacaste, northwestern Costa Rica. Genome. 2016:59:641–660. https://doi.org/10.1139/gen-2016-0005.

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