Final Abstract

Final Report Approved on October 29, 2026

M.L. 2024 Project Abstract

For the Period Ending June 30, 2026

Project Title: Early Detection of Invasive Viruses in Native Pollinators

Project Manager: Declan Schroeder

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Funding Source:

Fiscal Year:

Legal Citation: M.L. 2024, Chp. 83, Sec. 2, Subd. 06d

Appropriation Amount: $200,000

Amount Spent: $198,000

Amount Remaining: $2,000

Sound bite of Project Outcomes and Results

We discovered three new bee viruses in wild bees that are related to the known honey bee killing deformed wing and sacbrood viruses. This sheds new light into the evolutionary history of viruses in bees; a likely major player in bee population health status in both Minnesota and indeed worldwide.

Summary of Project and Outcomes

Iflaviruses are known killers of honey bees worldwide. This family of viruses are currently composed of a single expanding group of positive-sense single-stranded RNA viruses associated with insects. Deformed wing virus (DWV) is the most well-known iflavirus and intensively studied honey bee pathogen. It exists as a virus species complex, made up of four variants, namely DWV A, B, C & D. While DWV spillover from honey bees to other insects has been observed, ancestral species of DWV (aladeformis) and DWV-like variants have only been reported to cause disease in honey bee colonies. The discovery and genomic characterization of a new DWV-like Iflavirus associated with Agapostemon virescens, a sweat bee, named Verdyl virus (VV), provides clear evidence of the broader natural host range for DWV-like viruses. Consequently, VV was assigned to a new Iflavirus species named verdylis. Finally, we describe two viruses, Grandis virus 1 (GV1) and Grandis virus 2 (GV2), found in wild Bombus impatiens and Bombus terricola, respectively.

Both are iflaviruses that fall into a unique subgroups and therefore species, gigas, within the genus Iflavirus. Virus genome organization and family inference trees with 3D predictive modeling of the replicase viral protein confirm the evolutionary origin these iflaviruses in ancient lineages of bees. Bees have been battling with iflaviriuses for a very very long time. Are the viruses winning and the bee losing the fight? More research is required to answer this question.

Project Results Use and Dissemination

We submitted this discovery in the form of a manuscript to a high impact scientific journal. It is currently under review. Once accepted and published, we will continue to present our results to the scientific community through presentations and invited lectures. We will also attend honey bee beekeeper focused and general pollinator meetings.

Environment and Natural Resources Trust Fund

M.L. 2024 Approved Final Report

General Information

Date: November 2, 2026

ID Number: 2024-198

Staff Lead: Michael Varien

Project Title: Early Detection of Invasive Viruses in Native Pollinators

Project Budget: $200,000

Project Manager Information

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Project Reporting

Final Report Approved: October 29, 2026

Reporting Status: Project Completed

Date of Last Action: October 29, 2026

Project Completion: June 30, 2026

Legal Information

Legal Citation: M.L. 2024, Chp. 83, Sec. 2, Subd. 06d

Appropriation Language: $200,000 the second year is from the trust fund to the Board of Regents of the University of Minnesota to create a baseline inventory of the quantity and diversity of viruses in, and determine the threat of these viruses to, Minnesota native bees.

Appropriation End Date: June 30, 2027

Narrative

Project Summary: Forewarned is Forearmed: Our goal is to protect the newly described MN DNR native bees from invasive virus-derived diseases and population declines.

Describe the opportunity or problem your proposal seeks to address. Include any relevant background information.

There are thousands of insect pollinator species in Minnesota, including over 500 species of native bees. Bees are the most efficient pollinators because their bodies are designed to collect and store pollen to feed to their young. Pollinators are integral parts of functioning environments. The plants they pollinate provide food and habitat for animals, buffer waterways, and store carbon. Without pollinators, we would not have many nutritious fruits and vegetables. Pollinator conservation provides economic benefits through improved crop pollination, and intrinsic value in beautiful, flowering landscapes. Numerous pollinators are in decline with disease being a potential leading cause. However, we have little to no information on the viruses present in our native bees. Through an ongoing ENRTF 2021-309 grant entitled Bee Minnesota – Protect our Native Bumblebees, we were the first to uncover at least two new invasive viruses not previously known to infect bumblebees, mainly Bombus impatiens. How many other invasive bee viruses are we missing? Without knowing the viral landscape, we cannot be prepared to mitigate their impact on our bees and thus pollination services.

What is your proposed solution to the problem or opportunity discussed above? Introduce us to the work you are seeking funding to do. You will be asked to expand on this proposed solution in Activities & Milestones.

We propose to collect baseline data of virus in Minnesota bee populations, conduct a threat analysis, and develop a pathogen list to determine whether neutralizing protocols should be in acted against invasive virus bee pathogens. Our first objective is to target five main native bee pollinator families, namely Andrenidae, Apidae, Colletidae, Halictidae and Megachilidae. These were selected because 1) these bees are on the MN DNR native species list, 2) they are relatively common and we are confident that we can collect the 20-25 species within these families from the funded study locations. Our second objective is to use the NGS Oxford Nanopore Technologies metagenome sequencing platform to describe the RNA virus diversity in native populations in Minnesota. We will create virus distribution lists as it relates to species & family, ecological province, abundance of pollinator and their life history traits Finally, we will carry out a threat analysis (hazard vs risk) on the potential and therefore invasive threat these native bee viruses pose. This will provide new data for a hazard vs risk threat analysis on whether viruses pose a real and present danger to the health and longevity of bee pollinators in Minnesota

What are the specific project outcomes as they relate to the public purpose of protection, conservation, preservation, and enhancement of the state's natural resources?

This project complements the ongoing research currently funded by ENRTF. The importance of identifying and profiling the true viral landscape in our bee pollinators cannot be overstated. A project outcome is a pathogen list. The data generated in this project will create a new body of work that lists the potential viral pathogens damaging native bee pollinator communities in Minnesota. This will provide natural resource managers the information needed to develop and implement solutions to better protect Minnesota's native bee populations from invasive virus-derived diseases and population declines. Project outcomes and updates will be posted on the Bee Minnesota website.

Project Location

What is the best scale for describing where your work will take place?

Statewide

What is the best scale to describe the area impacted by your work?

Statewide

When will the work impact occur?

During the Project

Activities and Milestones

Activity 1: Sampling, cataloging and extraction of viruses from sentinel native MN bees

Activity Budget: $71,700

Activity Description:
Dr Cariveau has secured funding from USDA and US Fish and Wildlife Service, to collect native bees across Minnesota from new study sites. We will target five main families, namely Andrenidae, Apidae, Colletidae, Halictidae and Megachilidae. These were selected because 1) these bees are on the MN DNR native species list, 2) they are relatively common and we are confident that we can collect the 20-25 species within these families from the funded study locations, 3) spans five of the six bee families in Minnesota (the sixth family is too rare, there are only a total of seven bee families globally and one is relegated to Australia), 4) includes a mix of important life-history traits such as social vs. solitary and ground nesting vs. stem nesting and 5) we can reliably identify them quickly. Funding from ENRTF will be used to transfer samples into the correct containers and to transfer them to the Schroeder Virology Lab, where we will use a new virus extraction workflow, first developed in the ENRTF 2021-309 Bee Minnesota grant, to extract any resident virus from the bees.

Activity Milestones:

Description	Approximate Completion Date
Collection of MN native bees for only this project	April 30, 2025
Taxonomic identification of native bees collected	May 31, 2025
Synthesize an agency report of samples collected	June 30, 2025
Extraction of viruses from the native bee samples	September 30, 2025

Activity 2: Screening for viruses in native bees by applying genomic sequencing technologies

Activity Budget: $128,300

Activity Description:
High through-put DNA/RNA extraction on bee pools per location will be achieved using a commercially available Viral DNA/RNA Isolation Kit. Quantity and quality of nucleic acids extracted will be assessed using a fluorometer. We will apply a custom designed sequencing pipeline to describe the viral metagenomic diversity. Briefly, gDNA/cDNA will be sequenced on the GridION device (Oxford Nanopore Technologies), which allows multiple library preparations to be run simultaneously. The sequence reads will be assembled into contigs using a Minimap2 de novo assembler, which was designed to assemble highly heterogeneous virus populations and is well suited to the computational challenge that the virus quasispecies present. The virus genomes will be visualized in Anvi'o. Outputs include read count tables by sample, virus load and diversity per sample, whole-recombinant and partial viral genomes, and identification of quasispecies. A threat analysis will be undertaken to assess which invasive viruses to target for mitigation or eradication.

Activity Milestones:

Description	Approximate Completion Date
Assembled virus genomes that includes a list of invasive native bee viruses	June 30, 2026
Quantification of virus load and diversity per sample and location.	June 30, 2026
Threat analysis of invasive viruses found	June 30, 2026
Submit draft manuscript to free and open access online preprint server such as bioRxiv	June 30, 2026

Dissemination

Describe your plans for dissemination, presentation, documentation, or sharing of data, results, samples, physical collections, and other products and how they will follow ENRTF Acknowledgement Requirements and Guidelines.
CVM and the Bee Lab manage several active social media channels as well as a website and an electronic newsletter. In addition to using these communication tools to disseminate project data, D. Schroeder and D. Cariveau frequently present to both the public and beekeepers throughout Minnesota and the US. We will also disseminate information using well developed communication channels within the Minnesota Extension system. Where appropriate, communications will acknowledge ENRTF as per ENTRF Acknowledgment guidelines.

Long-Term Implementation and Funding

Describe how the results will be implemented and how any ongoing effort will be funded. If not already addressed as part of the project, how will findings, results, and products developed be implemented after project completion? If additional work is needed, how will this work be funded?
The data generated in this project will create a new body of work that lists the potential viral pathogens damaging native bee pollinator communities in Minnesota. The College of Veterinary Medicine, University of Minnesota, has an active Extension and Outreach program that who will continue to disseminate results after project completion. Drs. Schroeder and Cariveau will publish research findings and present to scientific communities. Funds from this project will build on federal resources being used to pursue these goals, greatly expanding the scope of our efforts

Other ENRTF Appropriations Awarded in the Last Six Years

Name	Appropriation	Amount Awarded
Bee Minnesota – Protect Our Native Bumblebees	M.L. 2021, First Special Session, Chp. 6, Art. 5, Sec. 2, Subd. 03h	$650,000

Budget Summary

Category / Name	Subcategory or Type	Description	Purpose	Gen. Ineligible	% Benefits	# FTE	Classified Staff?	$ Amount	$ Amount Spent	$ Amount Remaining
Personnel										
Project Manager		Dr Schroeder will project manage and to oversee and implement the molecular screening protocol previously developed in his lab. In addition, he will be directly responsible for all communication for the team			36.8%	0.32		$71,000	-	-
Postdoc or Research Assistant		Responsible for running the sequencing assays for cataloging invasive viruses in native bees			25.7%	1.5		$102,600	-	-
							Sub Total	**$173,600**	**$173,600**	**-**
Contracts and Services										
Contribution to the annual maintenance contract (for 2 years) on the ONT GridION sequencer	Service Contract	Servicing and maintenance of GridION sequencing machine				-		$8,000	$8,000	-
							Sub Total	**$8,000**	**$8,000**	**-**
Equipment, Tools, and Supplies										
	Tools and Supplies	Supplies to setup and collection of field samples	For the purchasing of nets, collection tubes and preservation material.					$1,500	$1,500	-
	Tools and Supplies	Virus screening molecular consumables (Virus extraction, Nucleic acid extraction, molecular grade chemicals, NGS sequencing etc.) for bee samples	Surveying the viral pathogens in bee material collected					$14,900	$14,900	-
							Sub Total	**$16,400**	**$16,400**	**-**

Capital Equipment										
							Sub Total	**-**	**-**	**-**
Acquisitions and Stewardship										
							Sub Total	**-**	**-**	**-**
Travel In Minnesota										
							Sub Total	**-**	**-**	**-**
Travel Outside Minnesota										
							Sub Total	**-**	**-**	**-**
Printing and Publication										
	Publication	Scientific publication in open access journal	Outreach and publication of results					$2,000	-	$2,000
							Sub Total	**$2,000**	**-**	**$2,000**
Other Expenses										
							Sub Total	**-**	**-**	**-**
							Grand Total	**$200,000**	**$198,000**	**$2,000**

Classified Staff or Generally Ineligible Expenses

Category/Name	Subcategory or Type	Description	Justification Ineligible Expense or Classified Staff Request

Non ENRTF Funds

Category	Specific Source	Use	Status	$ Amount	$ Amount Spent	$ Amount Remaining
State						
			State Sub Total	**-**	**-**	**-**
Non-State						
In-Kind	United States Department of Agriculture (USDA)	Dr Cariveau (Co-PI, 0.1 FTE total) will advise on the sampling design and collecting of native bees (Activity 1) and will assist with data analysis and publication, and with all dissemination of results and outreach.	Secured	$25,000	$25,000	-
In-Kind	United States Department of Agriculture (USDA)	Postdoc time (0.1 FTE total) in Co-PI lab. Collect native bees and species identification	Secured	$7,300	$7,300	-
			Non State Sub Total	**$32,300**	**$32,300**	**-**
			Funds Total	**$32,300**	**$32,300**	**-**

Attachments

Required Attachments

Visual Component

File: bd5b401d-f1f.docx

Alternate Text for Visual Component

The five families of native bees targeted in our proposal is shown. We provide the results from our active project that found a new invasive virus in bumblebees. We the go on to outline the aim and outcome of the project....

Supplemental Attachments

Capital Project Questionnaire, Budget Supplements, Support Letter, Photos, Media, Other

Title	File
Audit	52bf597b-dbb.pdf
SPA Letter	cd1de974-a51.pdf
Research Addendum revised 2024-198	28360e57-d78.pdf
Updated Budget Research Addendum	ca4bed3f-311.docx
Research Addendum revised 2024-198 accepted	9677b952-8bc.pdf
Data Table	1d5b2ee3-d4d.pdf
IMV symposium	1167afe8-ca6.pdf
Bee_images	366305f6-20e.pdf
Poster_IMV_2025	00f1b663-65c.pdf
International Pollinators Conference talk	08155425-efc.pptx
Poster for International Pollinator Conference	24406e5a-d89.pdf

Media Links

Title	Link
MHPA annual meeting_2025	https://minnesotahoneyproducers.com/mhpa-annual-meeting-and-2024-convention/

Difference between Proposal and Work Plan

Describe changes from Proposal to Work Plan Stage

I made the following changes as per Comment ID:
1) I added the submission of an agency report (new milestone) to Activity one and similarly, added a 4th milestone to Activity two for the submission of a preprint to an open access journal server.
2) in the Narrative section (project outcomes) we rephrased the final sentence "It is essential that we collect baseline data." to read "A project outcome is a pathogen list."
4) in the Narrative section, we removed the reference in the text that mentions almonds.
5) the USDA grant will fund the person hours to collect the bees for this study. The bees themselves are unique to this study so its NOT part of the USDA study. As this collection is not part of the USDA study, it's not appropriate to specify the USDA grant in the narrative. We rephrased the Activity two, milestone one heading to read as follows "Collection of MN native bees for only this project"
6) The USDA grant is not "contributing" to this award. What it does allow is for Dr Cariveau and his postdoc to advise and provide bees without charge to this grant. The budget has "$0" amount assigned to their time effort.
8) Agreed, we moved the expense to the correct section.
9 & 10) In the Narrative, we do state the "problem" that our "proposal seeks to address" in the last sentence: "How many other invasive bee viruses are we missing? Without knowing the viral landscape, we cannot be prepared to mitigate their impact on our bees and thus pollination services." Therefore the ENTRF funds are being using to... Activity

One "Sampling, cataloging and extraction of viruses from sentinel native MN bees" and Activity Two "Screening for viruses in native bees by applying genomic sequencing technologies". We respectfully disagree with the statements that suggest that our proposed solution or outcomes to the problem is unclear. The confusion might lie with the assumption that we are going to find a solution to the pathogens discovered. This is a small project that first seeks to identity the players involved in bee declines. Future projects will be proposed to identify solutions. This is a low risk high reward strategy. It's too high risk to request a larger amount of funding to proposed mitigation strategies before parametrizing the true problem.
11) Agreed, as per Comment ID one, we now added an agency report plus preprint that will be made publicly available upon submission.
12) Budget has been updated
14 & 15) No changes required to be made.
16) Agreed, moved Co-PI and Co-PI's postdoc to Non-ENRTF section.
17 & 20). Agreed. I used the suggested text in the updated Narrative.
17 & 21). Agreed, the outcomes text has now been updated.
19) I uploaded a revised Research Addendum, because of the suggested changes (comment ID 12) to the Suppl. Attachment link. I could not replace the current version as upload.

Additional Acknowledgements and Conditions:

The following are acknowledgements and conditions beyond those already included in the above workplan:

Do you understand and acknowledge the ENRTF repayment requirements if the use of capital equipment changes?

N/A

Do you understand that travel expenses are only approved if they follow the "Commissioner's Plan" promulgated by the Commissioner of Management of Budget or, for University of Minnesota projects, the University of Minnesota plan?

N/A

Does your project have potential for royalties, copyrights, patents, sale of products and assets, or revenue generation?

No

Do you understand and acknowledge IP and revenue-return and sharing requirements in 116P.10?

N/A

Do you wish to request reinvestment of any revenues into your project instead of returning revenue to the ENRTF?

N/A

Does your project include original, hypothesis-driven research?

Yes

Does the organization have a fiscal agent for this project?

Yes, Sponsored Projects Administration

Does your project include the pre-design, design, construction, or renovation of a building, trail, campground, or other fixed capital asset costing $10,000 or more or large-scale stream or wetland restoration?

No

Do you propose using an appropriation from the Environment and Natural Resources Trust Fund to conduct a project that provides children's services (as defined in Minnesota Statutes section 299C.61 Subd.7 as "the provision of care, treatment, education, training, instruction, or recreation to children")?

No

Do you understand that a named service contract does not constitute a funder-designated subrecipient or approval of a sole-source contract? In other words, a service contract entity is only approved if it has been selected according to the contracting rules identified in state law and policy for organizations that receive ENRTF funds through direct appropriations, or in the DNR's reimbursement manual for non-state organizations. These rules may include competitive bidding and prevailing wage requirements

Not acknowledged

Work Plan Amendments

No Amendments Entered

Status Update Reporting

Final Status Update August 14, 2026

Date Submitted: August 13, 2026

Date Approved: September 28, 2026

Overall Update

We set out to target five main native bee pollinator families, namely Andrenidae, Apidae, Colletidae, Halictidae and Megachilidae, to screen for viruses that could cause harm to MN bee species. We achieved this objective for 4/5 families, we could only find bees belonging to Tiphiidae and not Andrenidae. We processed and sequenced 100 individual bee samples, and reanalyzed the LCCMR 2020-003 project sequences collected from honeybee and bumblebees (both belong to Apidae) to find host-specific viruses. We found three new viruses in bumblebees (Apidae) and sweat bees (Halictidae). All three belong to a family of viruses known to kill honeybees. The Verdyl virus (VV), provides clear evidence of the broader natural host range for honeybee killing DWV-like viruses. Grandis virus 1 (GV1) and Grandis virus 2 (GV2) was found in two wild species of bumblebees. One of these bumblebee species has undergone substantial declines in North America. Importantly, our recovery of GV 1 & 2 confirms that this virus can cause disease, which can contributes to population declines in bumblebees. Urgent research is needed to better describe these three new viruses (VV, GV1 & GV2) and how we can stop the declining wild bumblebee populations in MN and the US.

Activity 1

This activity was previously marked complete.
(This activity marked as complete as of this status update)

Activity 2

Here we used metagenomic RNA sequencing using the Oxford Nanopore technologies genomics sequencing platform. We applied a new comparative genomic analyses pipeline to characterize the RNA viral communities associated with bee species within the families Tiphiidae, Apidae, Colletidae, Halictidae and Megachilidae. We also used our new bioinformatics pipeline to reanalyze the LCCMR 2020-003 project sequences previously collected from honeybee and bumblebees (both belong to Apidae). Notably we found new viruses in Agapostemon virescens Fabricius, Bombus impatiens Cresson, Bombus ternarius Say, and B. terricola. The discovery and genomic characterization of a novel DWV-like Iflavirus associated with Agapostemon virescens, a sweat bee, named Verdyl virus (VV), provides clear evidence of the broader natural host range for DWV-like viruses. Consequently, VV was assigned to a new Iflavirus species named verdylis. Finally, we describe two viruses, Grandis virus 1 (GV1) and Grandis virus 2 (GV2), found in wild Bombus impatiens and Bombus terricola, respectively. Both are iflaviruses that fall into a unique clade and therefore species, gigas, within the genus Iflavirus. Genome organization, conserved motifs, phylogenetic inference and 3D predictive modeling of the RdRp protein confirm the evolutionary divergence and congruence of these iflaviruses with divergent hosts. The paper is currently under peer review.
(This activity marked as complete as of this status update)

Dissemination

The Schroeder lab presented our scientific findings at the International Pollinators meeting in Bozeman, Montana (https://plantsciences.montana.edu/pollinatorconference2026/index.html) in June 2026 (poster & 3min talk). We submitted our discovery paper to Scientific Reports (manuscript in review). Once our paper is accepted, we intend on submitting commentary articles to newsagents and online podcast platforms. We submitted a new proposal to LCCMR in the 2026 grant cycle, so that we can continue to carry out research on these unique viruses.

Status Update Reporting

Status Update June 1, 2026

Date Submitted: August 13, 2026

Date Approved: September 28, 2026

Overall Update
We processed and sequenced 100 individual bee samples, and reanalyzed the LCCMR 2020-003 project sequences collected from honeybee and bumblebees (both belong to Apidae) to find host-specific viruses. We found three new viruses in bumblebees (Apidae) and sweat bees (Halictidae). All three belong to a family of viruses known to kill honeybees. We are currently working on the final manuscript for scientific peer review.

Activity 1
This activity was previously marked complete.
(This activity marked as complete as of this status update)

Activity 2
We developed a new comparative genomic analyses pipeline to characterize the RNA viral communities associated with bee species within the families Tiphiidae, Apidae, Colletidae, Halictidae and Megachilidae. We also used our new bioinformatics pipeline to reanalyze the LCCMR 2020-003 project sequences previously collected from honeybee and bumblebees (both belong to Apidae). Notably we found new viruses in Agapostemon virescens Fabricius, Bombus impatiens Cresson, Bombus ternarius Say, and B. terricola. These new viruses in bumblebees (Apidae) and sweat bees (Halictidae) all belong to a family of viruses known to kill honeybees. We are writing a new manuscript with a submission date in July.
(This activity marked as complete as of this status update)

Dissemination
Planning on presenting our scientific findings at the International Pollinators meeting in Bozeman, Montana (https://plantsciences.montana.edu/pollinatorconference2026/index.html) in June 2026.

Status Update Reporting

Status Update December 1, 2025

Date Submitted: December 30, 2025

Date Approved: March 16, 2026

Overall Update

Our goal in this project is to protect the newly described MN DNR native bees from invasive virus-derived diseases and population declines. As reported previously, viral community structure varied by genus with Apis, Bombus, and Agapostemon showing the highest viral loads. Only Bombus, and Agapostemon showed significant levels of virus infection. Our results were consistent with prior findings from the Schroeder Lab that underscore the host-specificity of viral communities in native bees. Therefore, further surveillance for species specific viruses is required in future virus disease monitoring programs. We continue to carry out bioinformatic analysis on the virus genomes captured in our bee samples. Our initial analysis revealed that both Bombus (bumblebees) and Agapostemon (western hemisphere sweat bee) have unique viruses compared to known viruses in Apis (western honey bee). Additional effort is being made to fully describe these viral genomes using genomic and bioinformatics tools.

Activity 1

This activity was previously marked complete.
(This activity marked as complete as of this status update)

Activity 2

We completed the analysis as the previously attached poster and confirmed that honey bees were primarily associated with Cripavirus mortiferum (CM), Aparavirus apisacutum (AA), Iflavirus aladeformis (IA), and Varroa destructor virus 1 (VDV1), which affected strongly along the positive PC1 axis. In contrast, Bombus clustered along the negative PC1 and positive PC2 axes and were characterized by bombus-associated virus vir4 (BAVV4), Allermuir Hill virus 1 (AHV1), Mayfield virus 1 (MV1), hymenopteran phasma-related virus OKIAV233 (HPRVOKIAV233), and Agassiz rock virus (ARV). Several viral taxa — including Lake Sinai viruses (LSV, LSV2, LSV3), hubei partiti-like virus 34 (HP-LV34), Iflavirus sacbroodi (IS), Sinaivirus sp. (SS), Cripavirus sp. (CS), Apis rhabdovirus 1 (AR1), and Triatovirus nigereginacellulae (TN) — were detected predominantly in Apis, but also in a limited number of Bombus samples. This pattern likely reflects incidental environmental exposure rather than sustained host infection or spillover. Agapostemon formed a distinct cluster characterized by overall lower viral loads, though partially overlapping with some Bombus samples in ordination space. We are actively using genome assembly software and associated bioinformatics tools to assemble partial or complete genomes found in Bombus and Agapostemon. Future work should include longer sampling periods to collect native bees that are less common.

Dissemination

The lecture given by Dr Schroeder, as an invited as a guest speaker at the Minnesota Honey Producers Annual Meeting and Convention on July 10-12th 2025 in St Cloud (https://minnesotahoneyproducers.com/mhpa-annual-meeting-and-2024-convention/) was well received. We are seeking to present at the upcoming International Conference on Pollinator Biology, Health, and Policy which will be held from June 25-26, 2026 at Montana State University in Bozeman, Montana.

Status Update Reporting

Status Update June 1, 2025

Date Submitted: June 2, 2025

Date Approved: June 25, 2025

Overall Update

Our goal in this project is to protect the newly described MN DNR native bees from invasive virus-derived diseases and population declines. We reanalyzed raw reads from the Project 2021-309 "Bee Minnesota – Protect our Native Bumblebees" project that focused mainly on Apis mellifera and Bombus impatiens, but on this occasion integrated new 2025 samples (this study) from additional genera that now includes Ceratina, Hylaeus, Lasioglossum, Melissodes, Halictus, Anthidium, Augochlorella, and newly collected Bombus. Viral community structure varied by genus, with Apis, Bombus, and Agapostemon showing the highest viral loads. Only Bombus, and Agapostemon showed significant levels of virus infection. Our results were consistent with prior findings from the Schroeder Lab that underscore the host-specificity of viral communities in native bees. Therefore, further surveillance for species specific viruses is required in future virus disease monitoring programs.

Activity 1

We collected 100 bees off flowers in Minnesota (see attached table). These fall into 10 genera. The two dominant native species collected fell within Bombus, and Agapostemon. A photo collection (see attached picture) was created of representative species found. Viral RNA was successfully extracted for sequencing as described in Activity 2.
(This activity marked as complete as of this status update)

Activity 2

Initial analysis on the primary sequence read data (see attached poster) revealed that honey bees were primarily associated with Cripavirus mortiferum (CM), Aparavirus apisacutum (AA), Iflavirus aladeformis (IA), and Varroa destructor virus 1 (VDV1), which loaded strongly along the positive PC1 axis. In contrast, Bombus clustered along the negative PC1 and positive PC2 axes and were characterized by bombus-associated virus vir4 (BAVV4), Allermuir Hill virus 1 (AHV1), Mayfield virus 1 (MV1), hymenopteran phasma-related virus OKIAV233 (HPRVOKIAV233), and Agassiz rock virus (ARV). Several viral taxa — including Lake Sinai viruses (LSV, LSV2, LSV3), hubei partiti-like virus 34 (HP-LV34), Iflavirus sacbroodi (IS), Sinaivirus sp. (SS), Cripavirus sp. (CS), Apis rhabdovirus 1 (AR1), and Triatovirus nigereginacellulae (TN) — were detected predominantly in Apis, but also in a limited number of Bombus samples. This pattern likely reflects incidental environmental exposure rather than sustained host infection or spillover. Agapostemon formed a distinct cluster characterized by overall lower viral loads, though partially overlapping with some Bombus samples in ordination space. Future work will focus on fully describing teh unique viruses found in th Bombus and Agapostemon.

Dissemination

Dr Clarissa Pellegrini Ferrera presented our preliminary results (poster 39) at the University of Minnesota 21st Annual Institute for Molecular Virology Symposium on the May 8th, 2025 (see attached PDF). Dr Schroeder is invited as a guest speaker at the Minnesota Honey Producers Annual Meeting and Convention on July 10-12th 2025 in St Cloud (https://minnesotahoneyproducers.com/mhpa-annual-meeting-and-2024-convention/)