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Abstract

This document contains abstracts and papers of the oral and poster presentations offered at the 33rd USDA Interagency Research Forum on Invasive Species held in Annapolis, MD, in February 2025. The forum, sponsored by the Forest Service, Animal and Plant Health Inspection Service, National Institute of Food and Agriculture, and Agricultural Research Service, illustrates the depth and breadth of studies supported by the agencies and their cooperators.

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Annapolis, MD

Compiled by:
Katherine A. McManus
Therese Poland
Nathan Havill

Sponsored by:



U.S. Forest Service Research & Development



Agricultural Research Service



Animal and Plant Health Inspection Service



U.S. Department of Agriculture

FOREWORD

This meeting was the 33rd in a series of annual USDA Interagency Research Forums that are sponsored by the Forest Service, Animal and Plant Health Inspection Service, National Institute of Food and Agriculture, and Agricultural Research Service. The Group's original goal of fostering communication and providing a forum for the overview of ongoing research among the Agencies and their cooperators continues to be realized and facilitated through this meeting. This proceedings documents the efforts of many individuals: those who organized and sponsored the meeting, those who provided oral and poster presentations, and those who compiled and edited the contributions. The proceedings illustrates the depth and breadth of studies being supported by the agencies and their many cooperators and demonstrates the benefits and accomplishments that can result through the spirit of collaboration.

Acknowledgments

The program committee would like to thank the four USDA agencies for their continued support of this meeting, and the Management and Staff of the Graduate Annapolis. Thanks to Bella D'Amico for creating the cover artwork, Vince D'Amico for poster coordination, and Kristine LaVigna for facilitating registration.

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Proceedings

Katherine McManus, Therese Poland, Nathan Havill

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KEYNOTE

Presentation

ECOLOGY OF *SIREX NOCTILIO*: TOWARD A BETTER UNDERSTANDING OF A GLOBAL FOREST INSECT INVASION

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ABSTRACT

The woodwasp *Sirex noctilio* F. (Hymenoptera: Siricidae) is native to Europe and North Africa but has spread globally over the last century. In many invaded regions, it has formed new associations with pine trees, which are often sourced from North America for commercial plantations. Notably, severe population outbreaks occur in these invaded areas, a phenomenon not observed in the native range. This discrepancy, closely tied to damage levels, highlights the need to understand the drivers behind these outbreaks.

Sirex noctilio population outbreaks are described as displaying textbook eruptive pulse-like patterns, initiated at irregular intervals that rapidly increase local population densities, and spreading from focal epicenters to cover large areas (Berryman 1986). The occurrence of severe *S. noctilio* population outbreaks has resulted in extensive tree mortality. In South America, for example, tree mortality has reached local damage levels close to 75 percent in Southern Argentina, 70 percent in Uruguay, 50 percent in Chile, and 60 percent in Brazil and necessitated unprecedented management actions (Corley et al. 2019).

My research focuses on population outbreaks in Argentina, where *Sirex* woodwasps were first reported in the early 1980s and are now found throughout pine plantations of the country. We sampled pine plantations covering most of NW Patagonia and found 29 outbreak sites. We dated these outbreaks and by conducting experiments and simple modeling, we determined that resource availability plays a critical role at the onset of outbreaks. Prolonged droughts have been identified at the onset of outbreaks, which is of increasing concern given the expected effects of climate change on sites currently selected for pine plantation forestry (Lantschner and Corley 2015, Lantschner et al. 2019). Additionally, we observed strong spatial aggregation, likely driven by volatiles from a fungal symbiont carried by female wasps (Masague et al. 2024). This, in turn, suggests a positive density-dependent feedback loop that boosts insect performance. We also measured dispersal capacity in both laboratory and field conditions that helped explain spatial connectivity among plantations (Corley et al. 2019).

Our results demonstrate that both density-independent and density-dependent effects modulate key mechanisms in different ways and can be central in triggering population outbreaks that lead to significant tree mortality in the invaded range. Density-independent factors act as primary drivers of host-tree location by females, while density-dependent mechanisms were found to have substantial impacts on the quantity and size of offspring (Stazione et al. 2025).

There is a critical need to enhance our understanding of forest insect population ecology in both native and simplified human-induced forest landscapes to improve management actions and mitigate their impacts. In a global context marked by increased environmental stress to trees, our results emphasize the importance of promoting more comprehensive and context-dependent management strategies based on in-depth ecological knowledge of the species. While implementing preventive measures against forest insect outbreaks is challenging and often costly, especially in invaded areas, the potential benefits in avoiding and reducing massive tree mortality are significant.

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The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

ORAL

Presentations

OPTIMIZING MASS REARING OF *SPATHIUS GALINAE*, A PARASITOID OF EMERALD ASH BORER

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ABSTRACT

Emerald ash borer (*Agrilus planipennis*) is a non-native wood boring beetle that is devastating ash trees in North America. To control this pest, many federal, state and private entities have collaborated to implement a biological control program that includes four parasitoids, including the larval parasitoid *Spathius galinae*. Here we will explore six studies that were conducted to improve the efficiency of mass rearing *S. galinae* at the EAB Biocontrol Rearing Facility in Brighton, Michigan.

Decreasing *S. Galinae* Brood Mortality During Cold Storage

Typically, immature, *diapausing S. galinae* are stockpiled in cold storage under the bark of ash bolts infested with EAB larvae. The ash bolts are placed in trays of reverse osmosis (RO) water, where broods of *S. galinae* located in the lower part of the bolt, near or below the water line, would drown and die due to excess moisture.

Study 1: Our first study focused on minimizing parasitoid drowning while still allowing water uptake in the ash bolt. Each week for 26 weeks, 50 percent of the ash bolts destined for cold storage on a single day were placed in a standard tray of RO water and 50 percent were placed in a tray lined with floral foam saturated with RO water. Cold storage periods ranged from 13–23 weeks at 4° C. All bolts were peeled one week after removing from cold storage and the number of drowned broods was recorded.

We sampled 172 bolts for each treatment and found that bolts in trays of water averaged 1.25 ± 0.101 drowned *S. galinae* broods, while bolts on trays of foam averaged 0.05 ± 0.019 drowned broods. In general, lab reared ash bolts average 6.6 *S. galinae* broods per bolt, indicating that preventing the loss of an average of 1.2 broods per bolt would yield an 18 percent increase in production by lining the storage trays with floral foam. This method has been fully incorporated into *S. galinae* production methods.

The effects of waxing ash bolts to increase emergence rates of *S. galinae*

During the cold storage stage of *S. galinae*, ash bolts dry out causing the bark to contract, compressing the *S. galinae* underneath, making it difficult or impossible for the adults to chew out. Therefore, it has been necessary to peel the bark off the bolts for optimal emergence. Using sharp tools to peel the bark off can be tedious, time consuming and hazardous.

Study 2: In this study, we examined the effects of dipping the bolts in melted soy wax to help maintain bark moisture and improve *S. galinae* emergence rates without peeling. Each week for 12 weeks, 50 percent of the ash bolts exposed to *S. galinae* on a given day were dipped in soy wax 14 days after parasitization. Bolts were then placed in a 10° C chamber for two weeks then moved to a 4° C chamber for a minimum of 10 weeks. Cold storage ranged from 15–20 weeks. Upon removal from storage, bolts were allowed to emerge for 6 weeks; adults were collected and recorded, then the logs were peeled to check for unemerged *S. galinae*. Emergence data from standard, peeled rearing bolts throughout the season were also collected to compare to the waxed and unpeeled treatment bolts.

We sampled 47 waxed, 43 unpeeled and 101 peeled ash bolts. Waxed bolts had higher emergence rates than peeled and unpeeled bolts, averaging 83.3 ± 2.41 percent (Fig. 1). There appeared to be little to no negative impact of the hot wax to the development of *S. galinae* under the bark.

Study 3: A follow-up experiment was conducted to determine if other wax types might further increase *S. galinae* emergence rates over soy wax. Beeswax, along with paraffin wax were tested after being mixed at a 5:1 ratio of wax to canola oil (to decrease wax melting point and brittleness). A sample size of 30 bolts per treatment type was taken over a five-week period. Treatments included soy wax, beeswax plus oil, paraffin plus oil, and peeled and unpeeled bark. Using methods similar to Study 2, bolts were dipped in their assigned wax treatment 14 days after parasitization by *S. galinae*, just before being placed into cold storage for 15-17 weeks. Adults were allowed to emerge for six weeks after removal from storage and data were collected.

All three wax types appeared to perform equally well compared to each other and the peeled treatments (Fig. 2). Based on price and availability, the paraffin wax mixed with canola oil was selected as the preferred wax type and has been fully incorporated into *S. galinae* production methods at the rearing facility.

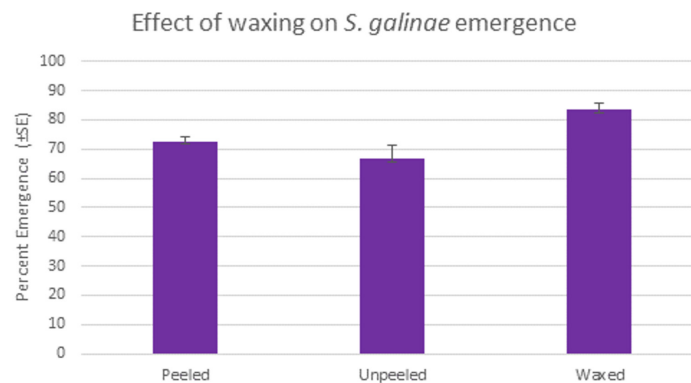


Figure 1.—Study 2: Effect of waxing on emergence of *Spathius galinae*, compared to bark peeling and no peeling.

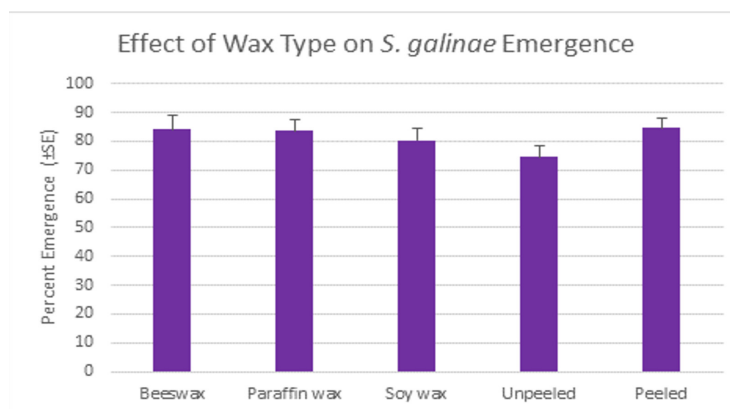


Figure 2.—Study 3: Effect of 3 wax types on emergence of *Spathius galinae*, compared to bark peeling and no peeling.

Harvesting Dormant Ash Trees and Storing for Use During Summer Production

Ash trees are only suitable for growing EAB larvae in the laboratory if they are harvested while the trees are dormant during the winter months, therefore, larval parasitoid production was historically limited to late September through March. Previous preliminary studies suggested that ash trees could be harvested in the winter, stored at 4° C until the summer, and then used to grow EAB larvae and *S. galinae* after a period of cold storage.

Study 4: To test whether the length of cold storage affected parasitoid emergence, we harvested ash trees in March 2022, then stored them at 4° C for 5 to 8.5 months. Each week from August to December 2022, 20–30 bolts were removed from cold storage and infested with EAB eggs (N = 234 bolts). Eggs hatched and EAB larvae were allowed to develop for 24–26 d at 30° C to reach 4th instar, then were exposed to *S. galinae* for one week. Ash bolts were peeled three weeks after exposure, then *S. galinae* adults were allowed to emerge for another three weeks and data were collected.

Overall, the average percentage emergence of *S. galinae* from the bolts was 86.5 ± 0.58 percent across all storage lengths (Fig. 3). Parasitoids appeared to emerge equally well regardless of cold storage length. Prolonged storage does not appear to substantially impact EAB or *S. galinae* development. When sorted by diameter, percentage emergence does not vary greatly either, with large diameter bolts having similar emergence rates as small diameter bolts (Fig. 4). Emergence rates appear to be driven more by the quality of the trees at a harvest site, with the lowest emergence rates coming from the Fowlerville site, where trees were heavily stressed by flooding and EAB infestation (Fig. 5).

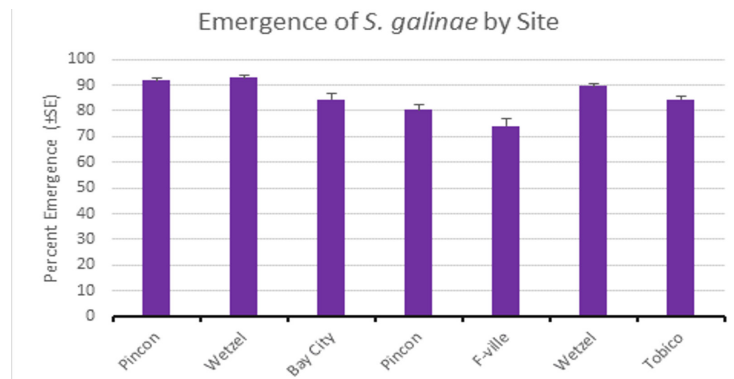


Figure 3.—Study 4: Effect of cold storage length on percent emergence of *Spathius galinae*.

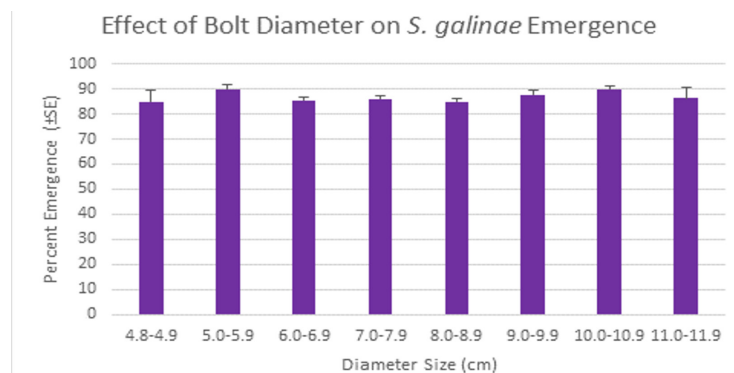


Figure 4.—Study 4: Effect of bolt diameter on percent emergence of *Spathius galinae*.

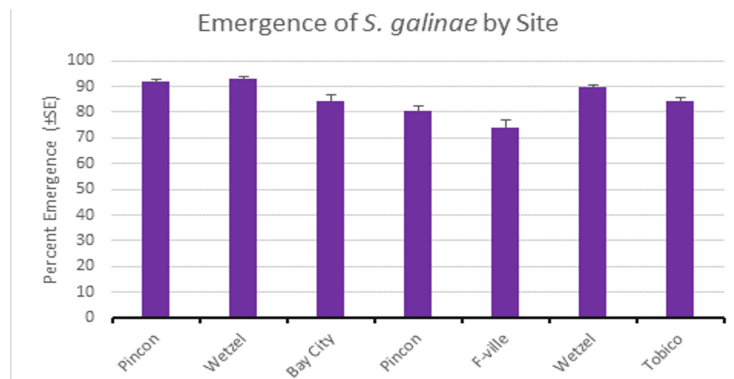


Figure 5.—Study 4: Percent emergence of *Spathius galinae*, from bolts harvested from seven different sites in March 2022.

Study 5: The objective of this experiment was to determine the optimal time for harvesting dormant ash trees during the winter months, prior to storing until use in the summer months. Trees were harvested over nine collection dates in 2022: early January (control), early and late February (control), early and late March, early and late April, early November and early December. All trees were stored at 4° C, for 28 weeks, prior to infesting with EAB and exposing to *S. galinae* (35–40 bolts per harvest date; N = 335 bolts total).

All harvest dates appear to have equally high *S. galinae* emergence rates (over 75 percent) except for the early March harvest date (Fig. 6). This may be due to the lower quality of the site from which trees were harvested in early March, more than the date of the harvest itself. On this date, trees were harvested from a site with moderate flooding and EAB infestation levels. If possible, future studies examining harvest date should attempt to control for site quality. The rearing facility now incorporates winter ash tree harvesting and cold storage to allow for parasitoid production during the summer months.

Study 6: This study was conducted to examine *S. galinae* emergence rates if ash bolt material that was harvested in the winter and stored prior to *S. galinae* infestation could be stored again after infestation by the parasitoid. All ash trees were harvested in late February and early March 2023, stored at 4° C for 23–30 weeks, then infested with EAB larvae and exposed to *S. galinae* for 1 week. After exposure, bolts were assigned to one of five treatments before being moved back into 4° C for 12 weeks: 1) bark removed prior to second storage, 2) bark removed after second storage, 3) waxing the bark, 4) no bark removal, and 5) no second storage (quality control). This was repeated for 10 weeks from August to October 2023, with 80 bolts per treatment, plus 40 bolts for the quality control (N = 360 bolts total).

Bolts that had their bark removed prior to the second cold storage period had similar *S. galinae* emergence rates as bolts that were not cold-stored for a second time after exposure (Fig. 7). There appeared to be little to no impact on the *S. galinae* cocoons being stored in the open air in the growth chambers. The other three treatments that underwent a second cold storage period had emergence rates at or below 60 percent (Fig. 7). These bolts were very difficult to peel after a second cold storage period and were more prone to wood rot. Though rare, if ash bolts infested with *S. galinae* required a second cold storage period, then it is recommended to remove the bark prior to the second storage period to allow for optimal emergence.

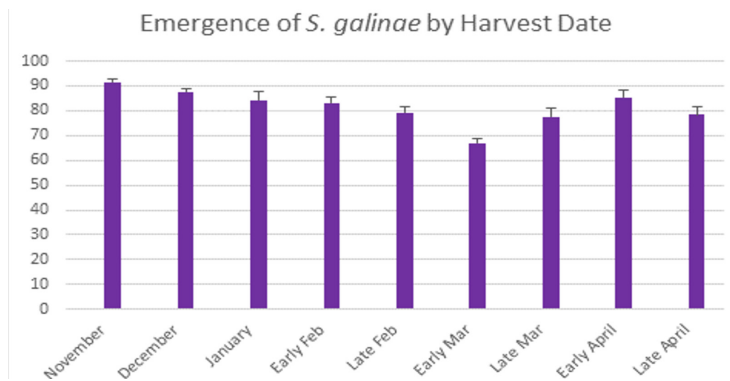


Figure 6.—Study 5: The effect of harvest date on the percent emergence of *Spathius galinae* during 2023.

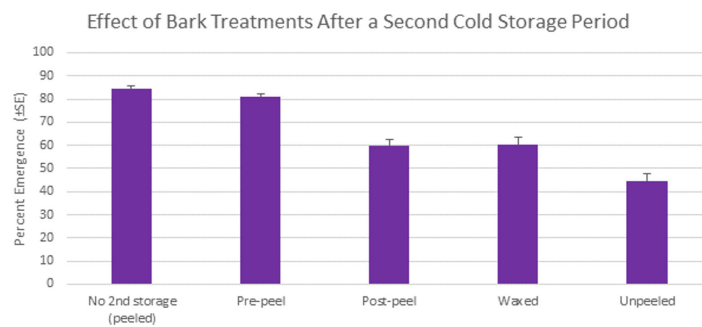


Figure 7.—Study 6: Percent emergence of *Spathius galinae* on four treatments after a second cold storage period and a control.

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DISPERSAL OF PIONEERING MOUNTAIN PINE BEETLES FROM ACTIVE INFESTATIONS: IMPLICATIONS TO RANGE EXPANSION FOR THIS DOMESTIC INVASIVE

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ABSTRACT

The mountain pine beetle *Dendroctonus ponderosae* (Hopkins) has killed tens of millions of acres of mature pines in the western U.S. and Canada. Range expansion into northwestern Alberta from British Columbia during the recent hyperepidemic in western Canada precipitated concern of further eastward range expansion and access to species of pine of North America with which the insect has no coevolutionary relationship. There are two routes by which the insect might someday reach pine forests of eastern North America. First, it could traverse pockets of jack pine within the Canadian boreal forest to the Great Lakes region. Second, it could move eastward from ponderosa pine forests of the Black Hills of South Dakota.

In this presentation, we described how voluntary surveys of small sawmills and log home and furniture builders in Minnesota by the Minnesota Department of Agriculture in 2012 revealed that western species of pine were occasionally imported into the state with bark attached. In one instance, a few dead mountain pine beetles were found in the bark. Education and regulations reduced further introductions but led to questions about whether mountain pine beetle could move 400 miles entrained on air currents from the Black Hills to Great Lakes forests during epidemics.

In the summer of 2020, we conducted an experiment in which pairs of traps were deployed from pine forests in western Montana in a transect running eastward to the Fort Shaw and Sun River area. One trap in each pair was baited with aggregation pheromones of mountain pine beetle while the other was baited with aggregation pheromones of *Ips grandicollis* (Eichhoff). The traps in each pair were separated by approximately 25 meters. The eastern-most region of the transect was devoid of pine forests and characterized by pasture and rangeland. Approximately 3,750 mountain pine beetles were captured. As expected, most were captured in forested areas. Two specimens, however, were captured more than 50 kilometers from the nearest pine forest. One of these was captured in a trap baited with ipsenol. Lipid contents of captured beetles declined with distance from outbreaking areas of mountain pine beetles.

It is difficult to infer patterns from rare events, which, by definition, characterize the tails of dispersal kernels. However, this instance of finding a far-flung mountain pine beetle in a trap for *Ips grandicollis* in an area 50 kilometers from any pine trees suggests that mountain pine beetles in poor physiological condition—such as those that may have moved long distances through passive or active flight—may respond to pheromones of heterospecifics when seeking host material not otherwise accessible in the absence of conspecifics and mass attacks. As such, competing species may become facilitators in some instances and may influence success in new environments (Smith et al. 2011).

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CHANGES IN TREE DEMOGRAPHIC STRUCTURE IN THE FACE OF INVASIVE FOREST PESTS

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ABSTRACT

The iconic forests of northeast North America have repeatedly been ravaged by introduced pests and pathogens over the past 140 years. The immediate and short-term effects of these invasions are high-mortality events and threats to upend forest demography and disrupt meaningful carbon sequestration. However, whether the addition of novel forest diseases changes forest demographic equilibria in consistent and predictable ways remains unknown. Here, we utilize remeasured plots from the U.S. Forest Inventory and Analysis program and county-level pest spread space-for-time gradient to elucidate differences in baseline relative mortality and estimated sapling abundance as defined by DeLiocourt's Law. We focused on both recent and established invasion–Beech Bark Disease (BBD, *Cryptococcus fagisuga* and *Neonectria* spp.), Hemlock Woolly Adelgid (HWA, *Adelges tsugae*), Emerald Ash Borer (EAB, *Agrilus planipennis*), Spongy Moth (SM, *Lymantria dispar*), Chestnut Blight (CB, *Cryphonectria parasitica*) and Butternut Canker (BNC, *Ophiognomonia clavignenti-juglandacearum*). Additionally, we used contemporaneous newspaper publications to recreate the historical spread of Dutch Elm Disease (DED, *Scolytus multistriatus* and *Ophiostoma ulmi*). Due to the biology of the host and etiology of the invasion, there have been variable effects on the focal species as a function of invasion duration. Ultimately, it is the regenerative capabilities of American beech and American elm, combined with the relatively slow spread and mortality caused by their respective agents, that results in a sustained demographic shift. Our findings allow for meaningful predictions about how American northeast forests change from anthropogenic invasive pests and connect the biology of affected trees to the fate of forests at a sub-continent scale.

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HEMLOCK WOOLLY ADELGID BIOLOGICAL CONTROL: SIGNS OF HOPE FOR EASTERN FORESTS

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ABSTRACT

The hemlock woolly adelgid (HWA, *Adelges tsugae*, Hemiptera: Adelgidae) is a non-native forest pest threatening eastern hemlock and Carolina hemlock forests in eastern North America. Multiple management strategies are being implemented throughout the introduced range, with chemical treatment and classical biological control receiving the most attention (Limbu et al. 2018). The classical biological control program for HWA has been ongoing since the 1990's. Currently, two species of predatory beetles; *Laricobius osakensis* from southern Japan and *La. nigrinus* from western North America, and two predatory flies; *Leucotaraxis argenticollis* and *Le. piniperda* from western North America, show the most promise (Mayfield et al. 2023).

The expansion of HWA's introduced range from the Richmond, Virginia epicenter has led to a spectrum of management approaches, from preserving hemlocks in aftermath forests of the south to early detection rapid response at the northern leading edge. The two *Laricobius* spp. have shown widespread establishment and dispersal in much of the introduced southern range, being successfully integrated with chemical treatments (Mayfield et al. 2020, 2023). Until recently, the success of these beetle predators was under-studied in the Northeastern U.S., with previous research indicating establishment is limited by cold winter temperatures (Mayfield et al. 2023). Crandall et al. (2023) found both *La. nigrinus* and *La. osakensis* successfully establishing at release sites across Pennsylvania, New York, and Maine, but found a link between low winter temperatures and establishment success. While winter can influence *Laricobius* establishment, it is unclear whether this is influenced by overwintering mortality of their prey or direct beetle mortality (Mayfield et al. 2023). New findings show *La. nigrinus* spreading, being detected at locations more than 40 km from known release sites in New York, offering evidence that beetles can remain on the landscape and spread to new locations in the northeastern U.S.¹

Documented success of *Laricobius* species in the eastern United States offers optimism for the HWA biological control program. Even with significant rates of predation on the overwintering (sistens) generation of HWA, minimal long-term efficacy has been observed due to the density-dependent rebound by the spring-summer (progredivens) generation, indicating the need for additional predators. The two species of *Leucotaraxis* show promise for complementing *Laricobius* predation (Mayfield et al. 2023). One species, *Le. argenticollis*, has demonstrated successful overwintering throughout the eastern hemlock range, in controlled experiments, showing suitability to eastern North America (Dietschler et al. 2023; Preston et al. 2023). A single larval *Le. argenticollis* was recovered in New York displaying successful reproduction from a wild release of adult flies (Crandall et al. 2023). Additionally in 2023, one adult *Le. argenticollis* and one adult *Le. piniperda* were collected two years post-release from a release site in Virginia, offering the first evidence of potential establishment (Phillips 2023).

¹ Crandall, R.S. [n.d.]. Unpublished data. On file with: USDA Forest Service, Northern Research Station, Morgantown, WV.

Ongoing field releases of *Laricobius* spp. and documentation of landscape scale dispersal continue to demonstrate these species utility in HWA management. The combination of these species offers significant hope for the development of a sustainable biological control program. Currently release and establishment surveys for *Leucotaraxis* continues, with ongoing research into their biology aiming to improve implementation for management.

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ECOLOGICAL TRAITS AND CURRENT STATUS OF INVASIVE INSECTS IN SOUTH KOREA

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ABSTRACT

The spread of invasive insects is increasing due to global trade and climate change, posing serious threats to forests and ecosystems. In Korea, several invasive species have become major concerns, including the Pine Needle Gall Midge (PNGM), Fall Webworm (FW), and Pine Wilt Disease (PWD), caused by the pine wood nematode. Among these, PWD is particularly devastating, rapidly killing pine trees and leading to significant forest loss. In addition, invasive hemipteran species such as the Spotted Lanternfly, Citrus Flatid Planthopper, and Brown Winged Cicada have continued to spread, affecting forests, crops, and urban landscapes. The recent establishment of subtropical species such as *Anoplophora horsfieldii* in Korea suggests that climate change is facilitating the new establishment of invasive pests. To assess the risk of future invasions, we analyzed 75 non-native insect species using Ecological Niche Modeling (ENM). By incorporating Classification Tree Analysis (CTA), Boosted Regression Tree (BRT), and Random Forest (RF) models, we found that species with higher bioclimatic suitability were more likely to establish and spread, particularly in warmer regions such as southern Korea and coastal areas. This correlation suggests that bioclimatic suitability is a valuable predictor of invasion risk and can enhance proactive management strategies. Our findings highlight the need for early detection, predictive modeling, and international collaboration to mitigate the long-term impacts of invasive insects. Strengthening risk assessment methodologies and improving monitoring techniques will be crucial in managing future invasions.

Keywords: Invasive species, forest pests, Pine Wilt Disease, bioclimatic suitability, ecological niche modeling, risk assessment, South Korea

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OPTIMIZING RELEASE DEVICE FOR A 10-COMPOUND BLEND: NOTES ON CHEMISTRY AND FIELD TRAPPING OF LONGHORN BEETLES IN BRITISH COLUMBIA, CANADA

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ABSTRACT

In different locations in Europe traps baited with a wick loaded with 10 compounds are used to monitor invasive beetle woodborers. Synergy Semiochemicals Corporation was asked to improve the device to have a life longer than three weeks without losing effectiveness in terms of the diversity of trapped insects. Synergy conducted a chemical analysis of the 10-compound mixture and found formation of secondary products, differences in release ratios of each compound, and device depletion after 14 days. As a first approach and based on each compound's boiling point, we tested three devices (bubble caps) containing 2, 3, and 3 of the original 10 compounds respectively and a fourth bubble cap containing all components. Chemical analysis of each device revealed a similar release rate of each component and a life span of 120 days for the four devices. Formation of impurities was confirmed when the 10 components were together that may impact the duration of the bait but not affect release rates of any specific components. As a next step, the all-in-one bubble cap was field tested to compare it to two different release devices with all the components, one pouch and the original wick. The wick had to be replaced every two weeks; the others lasted the entire trial.

The experiment was conducted in British Columbia from June to August 2024 and the main woodborer species were taxonomically identified and counted. The 5,374 insects trapped represented a total of 60 species belonging to 25 families. Simple Tukey Test comparison tests were run for nine species with more than 10 individuals at each 15-day collection period, finding that as a whole, there were no statistical differences in the number of insects collected, but depending on the species, some preferences were suggested. Release rates of field used bubble caps were practically the same as those calculated in the laboratory. Synergy has thus created an operational and economical bait, comparable to the original wick, with a field life of 120 days.

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POPULATION GENOMIC EVIDENCE FOR A SINGLE POINT ORIGIN AND LOCAL CLIMATE ADAPTATION OF THE DOMINANT BEECH BARK DISEASE PATHOGEN

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ABSTRACT

Beech bark disease (BBD), a cankering disease of American beech (*Fagus grandifolia* Ehrh.), is widespread throughout the U.S. and Canada resulting in significant ecological, aesthetic, and economic impacts on beech forests. The disease is caused by an invasive scale insect (*Cryptococcus fagisuga* Lind.) and two presumptively native fungal pathogens, *Neonectria faginata* and *N. ditissima*. Attack by *C. fagisuga* is believed to initiate fungal infection. The scale insect has spread through the range of American beech in a relatively consistent spatiotemporal pattern, with fungal infection typically occurring within a few years of initial attack of trees by the scale. Interestingly, *N. faginata* is apparently isolated to the disease complex, suggesting it may have dispersed in a pattern consistent with the spread of BBD, though the geographic origins and dispersal patterns of *N. faginata* are currently unknown. By contrast, *N. ditissima* can infect a wide range of hosts and is therefore presumed to have a historically broad distribution. A third *Neonectria* species, *N. coccinea*, is the sister species to *N. faginata* and causes beech bark disease of *Fagus sylvatica* L. in Europe. Here we use population genetics approaches to address two primary hypotheses (1) *N. faginata* is historically widely distributed in North America despite lack of detection prior to the emergence of beech bark disease; (2) *N. faginata* emerged after invasion and attack of American beech by *C. fagisuga* resulting in robust population growth and spatiotemporal spread in conjunction with the beech scale. Evidence for the first hypothesis includes a signal of genetically divergent populations (i.e., population structure) in *N. faginata* and/or similar signals of population structure to *N. ditissima*. Further, given H1 we expect similar levels of genetic diversity to *N. ditissima* and the European sister species *N. coccinea*. Evidence for the second hypothesis includes a signal of genetic isolation by distance, implicating dispersal coinciding with the slow, steady spread of the beech scale, and restricted genetic diversity compared to *N. ditissima* and *N. coccinea*. We address these hypotheses by performing low-depth genome resequencing of 115 *N. faginata* isolates across 27 sites and 30 *N. ditissima* isolates across 18 sites spanning the range of BBD as well as five *N. coccinea* isolates originating from three sites in Europe. We further present evidence of local adaptation to abiotic conditions, using a latent factor mixed modeling (LFMM) approach to identify SNPs associated with heat accumulation in the nongrowing season (i.e., when trees are dormant, but the infecting fungus may remain active), number of freeze-thaw cycles, and mean annual precipitation (MAP).

We found strong support for the second hypothesis. *Neonectria faginata* did not display a signal of population structure across its range, with individuals from only three of the 27 total sites differentiating based on PCA and ADMIXTURE analysis. Instead, *N. faginata* displayed a signal of genetic isolation by distance (IBD Mantel $r = 0.25$, $P = 0.001$) indicating a continuum of diversity across the range. By contrast, PCA and ADMIXTURE indicated five genetically differentiated populations in *N. ditissima*, whereas there was no correlation between geographic distance and genetic distance between individuals (IBD Mantel $r = -0.09$, $P = 0.79$). Further, *N. faginata* displayed lower genetic diversity (4.01–4.03 SNPs Kb⁻¹ bootstrap 95 percent confidence interval) than either *N. ditissima* (9.17–9.32 SNPs Kb⁻¹) or *N. coccinea* (12.64–13.88 SNPs Kb⁻¹)

when considering individuals originating from different sites. When considering individuals originating from the same site, *N. faginata* displayed lower genetic diversity than *N. ditissima* (Nf 3.47–3.64 SNPs Kb⁻¹; Nd 9.06–9.43 SNPs Kb⁻¹) but not *N. coccinea* (0.77–0.80 SNPs Kb⁻¹), though *N. coccinea* sampling was likely not dense enough for a robust estimate (three total pairwise comparisons all derived from a single site). Preliminary results from LFMM analysis identified 62 SNPs uniquely associated with nongrowing season heat accumulation, 65 SNPs uniquely associated with the number of freeze-thaw events, and 358 SNPs uniquely associated with MAP (all abiotic variables represent means of the 10 years prior to sampling). Another 116 SNPs were associated with both heat accumulation and MAP, but no SNPs were shared between freeze-thaw cycles and the other variables.

Our results suggest that the predominant *N. faginata* population infecting American beech is derived from a single primary colonization event. This does not preclude the possibility that *N. faginata* was geographically widespread (e.g., as an endophyte) prior to the arrival of the beech scale and subsequent advancement of BBD through the landscape. However, it does suggest that any endemic diversity is quickly outcompeted by the dominant population. This pattern may suggest that the genomic potential for transition to pathogenicity is widespread but is typically a relatively minor component of any extant diversity, given that this transition apparently occurred rapidly at the point of invasion of the beech scale and the high competitiveness of a single, virulent population. Our data further suggest potential for rapid adaptation to new environmental conditions. Beech scale spread across the landscape over the course of ~130 years (from initial invasion to the time of our sampling) and our data suggest that *N. faginata* dispersal coincided with that of the beech scale. Accumulation of adaptive SNPs has therefore likely occurred over that period. The majority of SNPs were associated with MAP, potentially suggesting adaptation of *N. faginata* to precipitation-dependent tree responses or traits. Several additional SNPs were uniquely associated with the number of annual freeze-thaw cycles, highlighting this potential stressor as an important control on fitness. Together our data support high potential for emergence of novel pathogens from existing fungal diversity. Surveys of leaf and stem endophytes of tree species unaffected by major diseases may help to identify potential facultative pathogens, especially in cases where congeners are affected by disease in other regions.

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INSIGHTS FROM AN INTERNATIONAL SENTINEL GARDEN PROJECT FOR FUNGAL PATHOGEN SURVEILLANCE: ARE WE DOING EVERYTHING WRONG?

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ABSTRACT

Invasive species contribute significantly to biodiversity loss and economic damage, with global costs estimated at \$423 million U.S. dollars annually. *Ex patria* sentinel plantings have been proposed as an early warning strategy to identify harmful organisms before they are exported to new regions. This study establishes a proof of concept for an international, fully reciprocal, *ex patria* sentinel garden system aimed at detecting potential fungal pathogens of trees in naïve areas.

Six sentinel gardens were established: two in North America (Ohio, New Hampshire) to monitor potential pathogens of Asian and European trees, two in China (Baima, Lukou) to monitor potential pathogens of European and North American trees, and two in Europe (Italy, Sweden) to monitor potential pathogens of Asian and North American trees. A total of 32 tree species were tested, with 10 species overlapping in at least two locations. Fungal pathogens were detected and identified using both traditional isolation techniques, followed by molecular phylogenetic placement, and metabarcoding using the ITS1 region. The classification of pathogenic species was performed using the USDA fungal database.

Several novel host-fungal associations were identified, including *Coleosporium vernoniae* on *Pinus nigra* and a canker caused by *Fusarium californicum* on *Acer truncatum* and *Albizia julibrissin*, respectively. Metabarcoding analysis revealed 63,977 Amplicon Sequence Variants (ASVs), of which 12,629 were classified as pathogens. Of these, 18 percent were found in both symptomatic and asymptomatic plants, 28 percent exclusively in symptomatic plants, and 54 percent exclusively in asymptomatic plants. Pathogenic ASVs were more abundant in asymptomatic plants regardless of season. Alpha diversity indices (Observed, Chao1, ACE, and Shannon) were significantly higher ($p < 0.05$) in asymptomatic trees, suggesting that symptom presence does not correlate with higher pathogen abundance or diversity. Season significantly influenced alpha diversity, with higher values in the late season ($p < 0.05$). Geographic location had the strongest effect on fungal community composition, followed by tree species, season, and health status. Interestingly, in general, health status had a low or nonsignificant impact on both the overall fungal community and the fungal pathogenic community composition.

Pathogen detection varied between methods; certain pathogens were more abundant in symptomatic plants and correlated with those identified via traditional microbiological techniques (e.g. *Tubakia* sp.). However, some symptomatic cases had no significant increase in pathogenic genera or ASVs, and identification relied solely on classical methods (e.g. *Colletotrichum* sp., *Alternaria* sp., *Diaporthe* sp. and *Neopestalotiopsis* sp.). Conversely, sequencing revealed potential pathogens in symptomatic and asymptomatic plants that were not detected by culturing, e.g. *Rosellinia* spp., *Sarocladium* spp., *Diaporthe* spp., *Lachnum* spp., *Talaromyces* spp., *Botrytis* spp., *Selenophoma* spp., *Symmetrospora* spp., *Zasmidium* spp., *Pseudopithomyces* spp.,

and *Pseudocercospora* spp. Additionally, obligate, fastidious biotrophs such as *Taphrina* spp., were detected, representing an advantage over traditional diagnostic methods. Furthermore, the metabarcoding analysis revealed that some pathogenic genera were more abundant in asymptomatic plants, indicating that asymptomatic hosts may serve as reservoirs for pathogens capable of affecting other plant species. Core pathogenic mycobiomes were identified in specific tree species across different locations, suggesting a potential phylogenetic signature in fungal community composition.

These findings emphasize the need to expand pathogen surveillance beyond symptomatic plants, as relying solely on visible symptoms may overlook significant threats. The combination of traditional isolation techniques and metabarcoding produced a more complete picture of tree host's fungal microbiome. Using diverse tree hosts in a common garden setting yielded an astounding number of potentially new fungal-host associations. We conclude that sentinel gardens, integrated with both classical microbiology and metabarcoding methods, are invaluable for early fungal pathogen detection for enhanced pathogen surveillance. Additionally, this study highlights the importance of collaborative approaches for the prevention of invasive fungal species, ultimately contributing to global biosecurity efforts.

The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.

THE IMPACTS OF PRESCRIBED FIRE ON THE SPREAD OF LAUREL WILT IN THE SOUTHEASTERN UNITED STATES

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ABSTRACT

The recently introduced forest disease, laurel wilt (LW), is an ambrosia beetle vectored fungal disease caused by the fungus *Harringtonia lauricola* and is primarily vectored by *Xyleborus glabratus*. This disease affects all native Lauraceae species in the U.S. including many species important to the economy, ecosystems, and conservation. Since its discovery in Georgia in 2002, LW has been confirmed in twelve states across the southeastern U.S. This spread is mainly attributed to the contiguous flights of ambrosia beetle vectors and is predicted to continue to spread throughout the U.S., if not managed. However, management of LW is currently only effective at the local level through fungicide macro-injections and chipping of infected woody material. A better understanding of the population dynamics of ambrosia beetle vectors and novel management methods to control LW need to be examined to better understand how LW spreads and to manage disease. One understudied method for managing LW is prescribed burns. These low intensity, controlled burns could potentially control non-native pests and pathogens by promoting healthy forests and reducing inoculum loads.

To better understand how prescribed burns affect the spread of LW, our project will determine the rates of colonization, population, and emergence of ambrosia beetle vectors, and the presence of *H. lauricola* within redbay (*Persea borbonia*) tissue and ambrosia beetle vectors pre- and post-prescribed burns. This will be accomplished using various types of insect traps and molecular diagnostic methods. Though this project is ongoing, once completed it will serve as a novel study investigating how prescribed burns may influence insect-vectored forest diseases and will be the first to explore the incidence of LW and the population dynamics of ambrosia beetle vectors post LW endemic. Additionally, this study will potentially lead to new research questions exploring how changes in host volatile profiles post-prescribed burn may affect host detection in ambrosia beetle vectors.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

DISCOVERY AND FINE-TUNING THE USE OF FLUOPYRAM AND THIABENDAZOLE AS POTENT NEMATICIDES TO INCLUDE IN BEECH LEAF DISEASE IPM PROGRAMS

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ABSTRACT

Since its initial discovery in 2012, beech leaf disease (BLD) has spread rapidly from a single county in Ohio to at least 15 states and a significant portion of Ontario, Canada. The pace and impact of the spread have drawn comparisons to infamous 20th century tree epidemics such as chestnut blight and Dutch elm disease. Like those diseases, BLD threatens both forest and ornamental trees, affecting stakeholders across forestry and natural lands management, nursery production, and urban tree care. But unlike chestnut blight and Dutch elm disease, which irreversibly damage vascular function, BLD directly affects leaves and buds, causing a progressive damage through severe canopy disfunction over time.

As we have learned more about the causal agent *Litylenchus crenatae mccannii* (Lcm), BLD increasingly resembles chronic stressors like hemlock woolly adelgid which has caused widespread decline in hemlock, another native, shade-tolerant tree species sharing much of the same geographic range as American beech and cultivated European beech. Rather than purely semantic, such differentiation shapes our approach to management strategies. A zero-tolerance threshold for BLD may be unrealistic. Instead, accepting some low level of Lcm infestation is likely to have minimal consequences for beech health if sufficient canopy function is restored and maintained. This premise is key to designing integrated pest management strategies that address the priorities of each stakeholder community and need for informed decision-making.

We continue to observe the discouraging effects of declining populations of American elm, ash, and Eastern hemlock in forests as well as urban or cultivated settings. The loss of beech in close human interface brings similar concerns for nursery, homeowner, and industry stakeholders. These include loss of ecological associates, threats to public safety due to declining trees, increased management costs, tree removal costs, loss of shade and cooling, reduced property value, and irreplaceable loss of specimen beech with historical significance. Initial efforts to protect individual beech trees will likely serve as important first additions to the Integrated Pest Management (IPM) toolbox as BLD becomes more widespread across eastern North America.

To meet this challenge, we have led an extensive research program since 2018 to discover and develop novel management options for BLD partnering with several collaborators from the arboriculture industry, arboreta, and government agencies. We have explored many compounds, including abamectin, emamectin benzoate, azadirachtin, chitosan, fluopyram, thiabendazole, oxamyl, acephate, potassium phosphite, spirotetramat, thiophanate-methyl, paraffin barrier, tebuconazole, and paclobutrazol. Some of these showing potential have been used in field trials where application methods have included foliar, drench, paint, soil injection, and root flare injection. To date, two compounds have demonstrated success in multi-state trials to directly target Lcm thereby reducing bud damage—fluopyram and thiabendazole. Both have been integrated into management programs for the tree care industry by working with product manufacturers and affected states to obtain appropriate labeling. Each has limitations and is appropriate for specific beech-growing situations. Ongoing research aims to fine-tune application variables such as timing, dosage, and treatment intervals appropriate for this novel threat.

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OAK WILT DETECTION ACROSS SCALES FROM LEAVES TO LANDSCAPES

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ABSTRACT

The oak genus (*Quercus*) is among the most abundant tree lineages in the northern hemisphere and a major component of forests in the Upper Midwest. Oak wilt, caused by the fungus *Bretziella fagacearum*, is considered one of the most destructive threats to oak trees in the U.S.. Optical remote sensing from satellite, aircraft, and ground-based spectrometry at leaf and crown levels, used together, provide opportunities to develop tools to detect oak wilt and to distinguish it from other diseases and stress factors for accurate detection and delineation of oak wilt at multiple scales. Early detection of oak wilt infection enables rapid response. Removing infected trees and eliminating their physical contact with neighboring trees has been successful in preventing further local spread of the disease.

Differentiating oak wilt from other maladies that cause symptoms of wilt and stress helps managers refine their management efforts and refine their approach. Some of the confounding stressors include two-lined chestnut borer, bur oak blight, and drought stress. The oak wilt pathogen spreads most rapidly belowground through grafts between neighboring trees via vascular connections. Once in the vascular system of a tree, it can spread through the xylem. The tree responds by forming tyloses, which block water transport, resulting in wilting. The fungus can spread overland long-distances by beetle vectors that carry the spores from an infected tree to a tree that is susceptible due to wounds or exposed cambium. The oak wilt pathogen presents differently in different oak lineages and is lethal in red oaks (*Quercus* subgenus *Lobatae*), at least those common in the Midwest, including *Quercus rubra* and *Quercus ellipsoidalis*. Detecting and differentiating oak wilt from drought and other diseases under experimental conditions at the leaf and canopy level has been successful using spectrometers and multispectral sensors on drones. At landscape scales airborne hyperspectral imagery is used, and at regional scales land surface phenology metrics are used.

Understanding the physiological progression of the disease at the whole plant scale is critical to using optical methods across scales to detect disease using remote sensing. The pathogenic effects cause declines in photosynthesis, stomatal conductance and transpiration, and loss of chlorophyll pigments. These symptoms are readily detectable using spectroscopy at leaf and canopy scales. The spatial patterning by which an oak tree blocks the xylem conduits directly influences which branches and leaves become cut off from water and nutrient supply. Some parts of the canopy remain functional and asymptomatic for much longer than other parts, which wilt and turn brown, leading to patchy symptom expression and heterogeneous canopies. The heterogeneous pattern of symptoms aids detection at the canopy scale. The characteristic spatial structure of oak wilt pockets, formed by belowground pathogen spread, makes it possible to find oak wilt at the landscape scale using aerial imagery. Aerial imagery can be used to train models that use satellite imagery to track changes in photosynthetic function across the season and through time using land surface phenology metrics. By developing detection approaches across scales, there is increased flexibility for disease detection.

This work is important for informing forest managers working across scales. Advances in optical methods for oak wilt detection contribute to monitoring to aid local park managers, private landowners, and state, provincial, and federal forest managers in the U.S. and Canada working to stop the spread of oak wilt and protect North American forests.

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MODELING DISEASE RISK: CASE STUDIES IN LOBLOLLY PINE

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ABSTRACT

Managing disease is a critical component for forest health and meeting operational objectives. Modeling and forecasting disease distribution and spread can help with strategic planting and planning, especially with high-impact pathogens. Here, we discuss two diseases that afflict loblolly pine: fusiform rust (caused by *Cronatium quercuum* f. sp. *fusiforme*) and brown spot needle blight (caused by *Lecanosticta acicola*). The former is considered the most important forest disease in southern timber operations and is well-documented, allowing us to create high-quality predictive models that illustrate local disease risk given a specific genotype. The latter is considered an emerging pathogen, and documentation and research on its interaction with loblolly pine are sparse. We use the methods and results of the fusiform rust hazard maps to make a case for surveying and surveilling brown spot needle blight in a multi-tiered and scalable manner. Overall, the goal is to highlight the power of data and modeling in the field of forest health and pathology.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

THE IMPACTS OF BEECH LEAF DISEASE ON TREE CARBON BALANCE

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ABSTRACT

Beech leaf disease (BLD) is a growing concern for American beech (*Fagus grandifolia*) forests across North America, attributable to the plant-parasitic nematode *Litylenchus crenatae* ssp. *mccannii* (Lcm). This research investigates the physiological impacts of BLD on beech trees, including carbon allocation, growth, and bud retention. We assessed the storage of non-structural carbohydrates (NSC) in root, bole, and twig tissues, and used tree rings to estimate growth declines associated with the onset of BLD infection. Our data from three stands across a gradient of disease severity show that BLD negatively impacts NSC storage, with diminished starch content preceding growth reductions. Significant growth reductions in high-severity stands were observed alongside low NSC content, though no mature tree mortality was recorded. We also studied bud retention and leaf production in two forest stands with different disease pressures, and found that trees with two or more years of infection exhibited 52.3 percent fewer buds and 67.8 percent fewer leaves per branch compared to a control stand. Diseased trees showed a decoupling from expected foliage production, with increased casting of symptomatic leaves and second flush leaf production in late summer. Nematode abundance varied significantly between spring and late summer. These findings highlight the complex interplay between nematode infestation and physiological declines, emphasizing the potential long-term consequences of BLD for beech forests and their resilience to future stressors.

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CASCADING IMPACTS FROM EMERALD ASH BORER-CAUSED BLACK ASH MORTALITY

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ABSTRACT

Invasive species significantly threaten ecosystem function by altering ecological processes and reducing biodiversity. The emerald ash borer (EAB) (*Agrilus planipennis*) has devastated ash (*Fraxinus*) populations across North America, with black ash (*Fraxinus nigra*) forests among the most vulnerable. These forests cover approximately 1.2 million hectares in the western Great Lakes region, providing essential habitat for a range of wildlife and supporting traditional cultural practices of Indigenous communities. The loss of black ash trees due to EAB infestations leads to pronounced changes in forest structure, soil composition, and water dynamics, with cascading effects on associated flora and fauna, nutrient cycling, and carbon storage.

To assess the impacts of EAB-induced tree mortality on wildlife communities, researchers conducted a dual approach study. Seasonal bird, mammal, and amphibian diversity were documented across 27 mature black ash wetlands in northern Minnesota, U.S. Additionally, experimental manipulations of black ash forests simulated EAB-related mortality and management strategies. A total of 85 wildlife species were recorded, including 57 bird species, 5 amphibian species, and 23 mammal species. Results indicated that hydrologic regime, ash canopy cover, and understory cover were key habitat characteristics influencing bird and amphibian populations; long-term EAB-induced mortality is expected to drive significant shifts in community composition. To mitigate these large-scale impacts, management strategies that prioritize the establishment of alternative tree species to maintain forest cover and structural complexity will be critical for conserving wildlife diversity. Comprehensive, multidisciplinary research integrating ecological, hydrological, and socio-cultural perspectives remains essential to inform adaptive management and ensure the resilience of black ash wetlands in the face of EAB threats.

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NATIVE PERENNIALS' GERMINATION AND GROWTH RESPONSE TO DECOMPOSING *AILANTHUS ALTISSIMA* STEMS

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ABSTRACT

Ailanthus altissima (Mill.) Swingle or tree of heaven has documented allelopathic compounds (Heisey 1990). These compounds may be released from its leaves, stems, and roots and may impact the germination and growth of plants growing nearby. Longer exposure time may decrease severity of impact from the allelopathic compounds (Lawrence et al. 1991). Tree of heaven stems left behind after herbicide treatments and tree falls due to tree mortality caused by Verticillium wilt (*Verticillium nonalfalfae* Inderb., H.W. Platt, Bostock, R.M. Davis and Subbarao) may also result in legacy effects that could negatively impact native plant restoration efforts. Legacy effects vary with soil conditions. The allelopathic compounds found in tree of heaven, aianthone and quassin, tend to break down in alkaline, fertile soils but not in acidic, sterile soils, suggesting a possible microbial mechanism (Sasnow 2012).

Tree of heaven was grown in a common garden for four years as part of a competition experiment; these trees were removed by basally cutting the stem and applying glyphosate to the stump. The stems were then cut into 1-m sections and placed in stacks three stems high with stems varying in diameter from 3–10 centimeters. These stacks were left to decompose for 18 months both on grass and on garden fabric. After this time, the wood stacks were mulched in a chipper, and the mulch was stored in bags outside for eight months. Four soil cores 10 centimeters deep were taken from directly under each stack as well as 2 meters above and below the stacks. Soil was sieved and stored in a freezer for eight months. Fifty grams of this soil were added as 0.5 centimeters layer over potting soil in 1-gallon pots in which 20 seeds each of three native perennial species were planted. These species were purple coneflower (*Echinacea purpurea* (L.) Moench; open areas species), dogbane (*Apocynum cannabinum* L.; roadside species), and false nettle (*Boehmeria cylindrica* (L.) Sw.; woodland species). A 1 centimeter layer of potting soil was placed on top of the seed for half the pots. The other half the pots had tree of heaven mulch added (1 centimeter layer). These were grown in a high light ($\sim 400 \mu\text{mol m}^{-2} \text{s}^{-1}$) room and a low light ($\sim 200 \mu\text{mol m}^{-2} \text{s}^{-1}$) room in a greenhouse with daytime and nighttime temperatures between 24° and 29° C and 16° and 21° C, respectively, as well as ample nutrients and water for three months. Germinations were tallied each month, and dry shoot biomass was determined at the end of the third month.

Pots with soil collected directly under the decomposing tree of heaven wood had significantly lower germinations and biomass production for purple cone flower and dogbane, but mulch reduced the negative impact. False nettle only germinated under low light conditions and only in pots with mulch. Plants growing in soil collected from under the garden fabric tended to have germination values similar to plants growing in soil from below the wood piles, suggesting some negative impacts on soil microorganism due to the fabric. Productivity values were higher with mulch for both soil from decomposing tree of heaven wood and the controls, but those without mulch growing in soil from decomposing tree of heaven wood, remained lower than the controls. The potting soil only treatment showed some negative impacts on germination due to the mulch, but only under high light conditions, suggesting some possible leaching of allelopathic compounds from the mulch that would normally be broken down by soil microbes or a lack of nutrients from the mulch that mycorrhizae would help provide. This study has implications for restoration of sites with tree of heaven that includes seeding or transplanting with native perennials. There may be value in mulched stems that have already leached out allelopathic compounds, but soil under decomposing tree of heaven wood is likely to negatively impact both germination and growth of newly seeded or planted species if planted within 18 months.

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IMPACTS OF EMERALD ASH BORER BIOLOGICAL CONTROL ON ASH GROWTH AND MORTALITY IN RIPARIAN FORESTS IN MASSACHUSETTS

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ABSTRACT

The emerald ash borer (*Agrilus planipennis*, EAB) is a devastating invasive beetle that has killed hundreds of millions of native ash trees (*Fraxinus* spp.) (Herms and McCullough 2014). Green ash (*F. pennsylvanica*), which is commonly found in riparian ecosystems and floodplain forests, is highly susceptible and may be functionally extirpated by EAB invasion (Siebert et al. 2021). Floodplain forests represent transition zones between the upland and riparian ecosystems and provide ecosystem services such as flood regulation (Ewel et al. 2001, Risser 1995). Nutrient inputs from riparian trees also help support diverse aquatic ecosystems (Richardson et al. 2010, Wallace et al. 1997). Ash leaf litter also has a high C:N ratio and is preferred by consumers (Ferreira et al. 2012, Kreutzweiser et al. 2019, Vesterdal et al. 2008). Loss of ash due to EAB therefore has widespread implications for the provisioning of ecosystem services and the communities that floodplain forests support.

Biological control of EAB, involving the introduction of hymenopteran parasitoids from its native range in East Asia, is a potential long-term management solution (Duan et al. 2018). The larval parasitoids *Spathius galinae* and *Tetrastichus planipennisi* have been shown to establish and contribute to a reduction in EAB population growth rate (Duan et al. 2019, 2023). The egg parasitoid *Oobius agrili* has also established in sites where it is released, but its impacts are more challenging to quantify (Duan et al. 2023). Despite successful establishment of parasitoids, the focus of the EAB biological control program is on protecting the regenerating ash cohort. This is because larger, mature ash often succumbed to the initial wave of EAB invasion.

In this study, we sought to assess the ash growth and survival responses to EAB invasion at six floodplain forests in Massachusetts and the impacts of early releases of biological control agents. We released the parasitoids *O. agrili*, *S. galinae*, and *T. planipennisi* at three of the sites from 2017 to 2022. We were interested in whether early releases of parasitoids (i.e., prior to significant overstory ash mortality) would be able to keep ash mortality below the 90–95 percent mortality that has been observed in other areas of the country (Klooster et al. 2014, Knight et al. 2013). We also sought to examine ash growth at these sites to determine how ash growth is impacted by both EAB and biological control.

We tagged approximately 100 trees (d.b.h. range from 6.7 to 113.5 centimeters) at each of our six sites in 2018 and evaluated their d.b.h. and canopy condition annually over six years. To determine if trees were growing significantly over this period, we first fit a linear regression to the DBH of each tree over time. We then classified trees as either growing or not growing, based on whether the slope coefficient for the regression line was positive and significant, creating a binary variable. To determine the probability that trees were significantly growing over the course of the study period, we conducted binomial logistic regression with our binary response variable as a function of initial canopy condition (2018) and site. To examine the probability of mortality of trees across our sites, we fit another binomial logistic regression model with mortality by 2024 as our binary response variable and initial canopy condition and site as our response variables. We also deployed sentinel logs infested with developing third and fourth instar EAB larvae across all our sites in 2024 to assess parasitoid establishment and impacts.

We found significant effects of site and initial crown dieback on ash tree growth. The probability of tree growth was highest at two sites that had significantly smaller trees (d.b.h. range 6.7–54.7) than other sites. Mortality was also highest at a single site with no recovery of introduced parasitoids. We also found that the ash mortality rate was negatively correlated to the level of parasitism of EAB larvae in sentinel ash bolts deployed across the six study sites in 2024. Finally, our sites had relatively low levels of mortality over six years compared to other published studies, with only one site recording mortality of over 50 percent of tagged trees.

To our knowledge, this finding of a significant negative correlation between ash mortality and percent parasitism is the first such finding in the literature. Whether these findings extend to other areas of the country and habitat types is important to examine as EAB continues to spread across the country.

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HARNESSING AUTOTOXICITY FOR COGONGRASS MANAGEMENT: EARLY RESULTS AND FUTURE DIRECTIONS

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ABSTRACT

Cogongrass (*Imperata cylindrica*) is one of the most harmful invasive plants and threatens the health of many important ecosystems in the southeastern United States. Current cogongrass control methods, including repeated applications of glyphosate and/or imazapyr, are ineffective and can unintentionally harm native plants, necessitating the development of alternative methods. This research seeks to determine the potential to harness autotoxicity, or toxicity from compounds produced by cogongrass itself, for cogongrass management. To extract chemicals from cogongrass, we soaked cogongrass leaves and rhizomes (underground stems) separately in water for 72 hours. These extracts, or a water-only control, were applied to the leaves or soil of cogongrass and two native plants, longleaf pine (*Pinus palustris*) and blackberry (*Rubus fruticosus* 'Sweetie Pie'), to determine impacts on plant growth. Treatments were applied twice: at the beginning of the experiment and one week into the experiment. We determined the growth of each plant using daily measurements of plant length and the number of leaves. We took pictures of each plant every other day to document any visual changes or plant damage. Twenty-one days after the first treatment, we measured the wet and dry aboveground and belowground biomass of each plant. There was no statistically significant difference in plant growth or final biomass for any of the three plant species, and no visible plant damage was observed. However, data trends show that cogongrass rhizome extract applied to the soil slightly reduced cogongrass growth compared to the control and leaf extract treatments. This suggests that chemicals derived from the rhizome could reduce cogongrass growth without harming native plants. Future studies will explore the effect of different concentrations of rhizome extracts on cogongrass to determine if higher concentrations could provide more effective management.

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DEFINING THE INVASIVE FRONT OF *OPLISMENUS UNDULATIFOLIUS* (WAVEYLEAF BASKET GRASS; INVASIVE NONNATIVE) AND REGIONAL EXPANSION OF *OPLISMENUS*

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ABSTRACT

Wavyleaf basketgrass (*Oplismenus undulatifolius* (Ard.) P. Beauv. or WLBG) is an emerging invasive grass that was first introduced in 1996 in the Patapsco Valley State Park, MD. It is a perennial, shade tolerant grass with a seedbank of at least seven years, that is invading disturbed and undisturbed closed canopy forests (Beauchamp and Koontz 2013). WLBG can now be found as far south as North Carolina, as far north as Pennsylvania, and as far west as West Virginia. Its native range is relatively broad and includes southern Europe and southern Asia. As part of our goal of producing a risk map for wavyleaf basketgrass based on known pathways of spread, we evaluated existing distribution data from (1) expert-based databases, (2) regional flora, (3) digitized herbarium specimens, and (4) citizen scientist-based databases. Closely related natives, including *O. hirtellus* (L.) P. Beauv., and *O. hirtellus* ssp *setarius* (Lam.) Mez ex Ekman were evaluated due to potentially overlapping ranges with WLBG. Anecdotal observations and some plant distribution databases suggest that either WLBG is as far south as Florida or that the native *Oplismenus* species may be expanding further north.

We first used several expert-driven databases to better define the taxonomy of the native *Oplismenus* P. Beauv. species. The expert-driven databases included:

Kew Plants of the World Online (POWO), which uses herbarium records World Checklist of Vascular Plants (WCVP) and the International Plant Name Index (IPNI) to finalize species names and distributions

- The Integrated Taxonomic Information System (ITIS, developed by USGS) which uses experts in a Taxonomic Workbench Network USDA PLANTS which uses data originally from the Biota of North America Program (Kartesz 1994) and the IPNI.
- State and regional floras and plant atlases (e.g., the Flora of North America (Wipff 2021), Flora of Southeastern U.S. (Weakley et al. 2025), Atlas of Florida Plants (Wunderland et al. 2025), Alabama Plant Atlas (Keener et al. 2025), and Flora of North Central Texas (Diggs et al. 1999) which are organized by taxonomists and botanists who provide detailed trait-focused drawings, keys, and descriptions for morphological identification for plants and regions of their expertise
- Equally or more important are the digital herbaria databases (consortia of herbaria with photographs of voucher specimens), which also include older, historic samples and often provide a more complete picture of the traits of the individual plant.

The citizen scientist-based databases that we used were iNaturalist and EDDMapS, both of which have proven to be useful when attempting to define the distribution of WLBG. The photographs in iNaturalist provided another layer of confirmation and observation dates were used to look at the data temporally. Finally, we also evaluated each species in the Global Biodiversity Information Facility (GBIF) database, which combines expert and non-expert databases worldwide, including Kew and iNaturalist listed above. GBIF provides temporal and spatial data where available.

An evaluation of the expert databases revealed inconsistencies with the accepted names of the species used.

- Kew accepted the names *O. hirtellus* and *O. compositus*, with both located in the continental U.S. Flora of North America recognizes two subspecies of *O. hirtellus*, *O. hirtellus* ssp. *setarius* and *O. hirtellus* ssp. *fasciculatus* (which, based on morphological features, equals *O. hirtellus*) but maps them together.
- ITIS and USDA PLANTS recognize *O. hirtellus* ssp. *setarius*, and *O. compositus* (L.) P. Beauv., but the only U.S. location for *O. compositus* is in Hawaii, where it is introduced but not native.
- Flora of Southeastern U.S. and Plant Atlas of Florida recognize *Oplismenus hirtellus* and *Oplismenus setarius* (the distribution of which looks much like Kew's *O. compositus* distribution in the U.S.). This flora also questions the nativity of *O. hirtellus*, showing it as only in southern Florida, whereas it is much more widespread in the other databases.
- The Alabama Plant Atlas only recognizes *O. setarius*. The North Central Texas Flora combines *O. hirtellus* with *O. hirtellus* ssp. *setarius*, calling it *O. hirtellus*.
- Digitized images from the consortia of U.S. herbaria support the fact that the Kew information on *O. compositus* for the U.S. is inaccurate and most likely to be *O. hirtellus* ssp. *setarius*. Because GBIF utilizes Kew records, there exist similar questionable distributions of *O. compositus* in its database.
- Morphologically, WLBG has several traits that distinguish it from all the native *Oplismenus* species in the U.S., including the presence of pubescent sheaths, stems, and leaves with hairs 1–5 mm long depending on the key, whereas the natives are generally glabrous or with shorter hairs. The inflorescence of WLBG contains very short panicles with very few flowers, which have light blue stigmas. In contrast, the natives have longer panicles with more flowers in each grouping and bright pink to magenta stigmas. Notably, the inflorescences further differentiate the native species from each other. The lowest panicle branches in *Oplismenus hirtellus* are 13–70 mm long compared to those in *O. hirtellus* ssp. *setarius*, which are generally shorter than 11 mm.

Unfortunately, different expert keys show overlapping trait measures, adding to the complexity of understanding the distribution of the native species. Some experts argue for grouping the two under *O. hirtellus* based on some traits or traits varying even within the same individual (Davey and Clayton 1978). While it is somewhat certain *O. compositus* is unlikely to be currently present in the continental U.S., there is another nonnative (*Oplismenus burmannii* (Retz.) P. Beauv. recognized in Florida that shares similar characteristics to *O. hirtellus* in terms of panicle length, except that the awn is not viscid but scabrous. The latter characteristic is not easily discerned with digital images.

Using available collection dates for herbarium voucher images of *O. hirtellus* and *O. hirtellus* ssp. *setarius*, we determined that the oldest collections of either were from 1945 in North Carolina, whereas older collections existed in the early 1900s for Florida and Texas. There were older collections of *O. hirtellus* and *O. hirtellus* ssp. *setarius* in Washington, D.C., South Carolina, and Alabama, but label descriptions seem to indicate these specimens were planted in gardens. GBIF timelines show an increase and northward movement of both *O. hirtellus* and *O. hirtellus* ssp. *setarius* after about the year 2000, which may be an artifact of an increase in volume of data associated with the iNaturalist database.

Evaluating the images in the iNaturalist citizen scientist databases (using only the records classified as ‘research grade’), we confirmed with some certainty that all the occurrences identified as WLBG farther south than North Carolina in the continental U.S. were native *Oplismenus* species because of their glabrous stems, sheaths and leaves. However, there were several occurrences in Cuba, Mexico, and South America of specimens with evident hairs that could either be WLBG or possibly one of the other *Oplismenus* species with the shorter, sparser hairs; there were no flowers on these samples to further differentiate the species. Research grade records also show an increase in *O. hirtellus* and *O. hirtellus* ssp. *setarius* over time in states bordering the current southern range of WLBG (e.g., North Carolina).

Our results show that the taxonomy of species closely related to WLBG is complicated and in need of further review, perhaps with additional morphological and genetic analyses. Standardizing key traits used to differentiate emerging invasive species like WLBG and any closely related species improves the accuracy of the botanical databases and better predicts range expansion of the invader and any potential for hybridization with closely related native species or other nonnatives. Our study reveals that the ranges of the native and nonnative species overlap in North Carolina, increasing the potential for hybridization. The relatively small number of populations indicate that the current degree of local overlap is likely minimal, but the rapid spread of WLBG in Maryland and Virginia is indicative of how fast the populations could soon locally overlap.

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GENETIC DIVERSITY IN THE GENUS *IMPERATA*: HORTICULTURAL CULTIVARS, CO-OCCURRING CONGENERICS, AND THE WILD-TYPE INVASIVE IN THE UNITED STATES

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ABSTRACT

Cogongrass (*Imperata cylindrica*) is one of the most impactful invasive grasses threatening natural and agricultural forest systems throughout the U.S. and globally. The genus *Imperata* is comprised of several globally cosmopolitan species, but *Imperata cylindrica* var. *major* is presumably the most predominant global species, and is the species considered to be the invasive “wild-type” in the U.S. From this dominant species, several horticultural lineages, known as *Rubra*, *Japanese Bloodgrass*, and *Red Baron*, among many other common trade names, have been developed in the U.S. and in Japan, and are actively sold throughout the U.S. Though said to be sterile, it has been experimentally demonstrated that the horticultural *Rubra* varieties can and will hybridize with the wild-type cogongrass, the well-known invasive grass throughout the southern U.S., resulting in measurable heterosis in experimental F1-hybrids.

A diagnostic PCR-based method was published in 2012, by Cseke and Talley (2012), to detect *Rubra* and *Rubra* reversions, which is when the horticultural lineage reverts to green and appears identical to the wild-type. This research team has utilized this diagnostic method to assist state and local agencies regulate *Rubra* and wild-type cogongrass in the Intermountain Western U.S. However, it was found that the Cseke and Talley (2012) method is unreliable, resulting in non-reproducible results with the same gDNA. We are exploring alternative methods for rapid assays to continue to assist forest health cooperators with *Rubra*, *Rubra* hybrids, and *Rubra*-reverts.

Within the genus *Imperata*, two species are USDA-listed Federal Noxious Weeds: *I. cylindrica* (cogongrass) and *I. brasiliensis* (Brazilian satintail); both species co-occur at the southern-most extent of the State of Florida. Both species appear morphologically and phenologically identical, and the taxonomic separation between *I. cylindrica* from all other species within *Imperata* is the number of stamens within the flower: where *I. cylindrica* is reported to possess two stamens per flower, and all other *Imperata* spp., only possess one stamen per flower.

Utilizing Sanger sequencing methods of the Internal Transcribed Spacer (ITS) region designed for *I. cylindrica* by Nomura et al. (2022), we assessed 24 individuals, comprised of samples from the invasive wild-type inhabiting the southeastern U.S. for over a century since cogongrass introduction in 1912, into Grand Bay, Alabama, along with *Rubra* samples from Idaho, and emergent populations from the Carolinas. From this highly conserved gene region, we found 18.16 percent genetic diversity among all samples, with less than 0.20 genetic differentiation among all individuals. On an unrooted neighbor-joining (NJ) tree, we found that the invasive cogongrass common to the southeastern U.S. group together well and are indicative of separation from extant Japanese and putatively South American *I. brasiliensis*. From the NJ-tree, we also found equally different groupings of *Rubra* from Idaho, *I. brasiliensis*, and the samples from the Carolinas and a putatively “new” introduction into Dauphin Island, AL. From just the ITS region sequences, we suspect that ongoing propagule rain of *I. cylindrica* seeds are continuing to arrive near international maritime ports-of-entry and are establishing within a 100-mile radius of these entry points.

Immediate next steps are to continue genetic sequencing with the ITS as well as external transcribed spacers, along with new samples of *Imperata* from North and South Carolina, Tennessee, and Colorado. We intend to also compare our sequences with globally deposited GenBank sequences for a more thorough examination from the above preliminary data. We aim to test Isolation-by-distance (IBD) hypotheses and determine if next-generation sequencing technologies will fill in some of our knowledge gaps about the genus *Imperata*.

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DECODING GENOMIC DETERMINANTS OF INVASION IN SACCHARUM ACCHARUM SPONTANEUM L.

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ABSTRACT

The invasion success of *Saccharum spontaneum* L. (wild sugarcane) is driven by human-mediated dispersal, ecological adaptability, and genetic plasticity. Native to South Asia, this species has expanded globally, with documented presence in the U.S., particularly in Florida. Its dispersal is facilitated by germplasm exchange for breeding programs and global maritime trade. While seeds have been observed adhering to shipping containers in ports, direct evidence of successful establishment from these transported seeds remains unverified. Nevertheless, multiple introductions through shipping networks remain a plausible but yet-to-be confirmed pathway. Notably, *S. spontaneum* seeds have been identified as the most abundant taxon hitchhiking into the U.S. at the Port of Savannah, Georgia, on shipping containers that have transited the Panama Canal, a region heavily infested with this species. A key factor in its invasiveness is its remarkable polyploidy, ranging from diploid to highly polyploid forms, which enhances ecological plasticity and adaptive potential, allowing it to thrive in novel environments. Given these factors, we hypothesize that multiple introductions and genetic admixture have enhanced the adaptive potential of *S. spontaneum* in nonnative regions. This study aims to investigate the genomic differentiation, genetic structure, and ancestry of *S. spontaneum* to better understand the evolutionary and ecological mechanisms driving its invasion success.

This study leverages whole-genome sequencing and population genomics to unravel the genetic differentiation and ancestry in *S. spontaneum*. By analyzing 110 whole-genome resequenced samples, comprising 93 previously sequenced and 17 newly sequenced individuals, it reveals significant genetic structuring between native (n=93) and nonnative (n=17) samples. Principal component analysis (PCA) identifies two distinct genetic clusters within East Asian samples, differentiated by ploidy level (high vs. medium), while South and Southeast Asian populations form a broader genetic cluster that overlaps with many nonnative individuals. Despite the well-documented link between higher ploidy (12x–16x) and adaptive advantages, the role of polyploidy in nonnative populations remains uncertain due to the high proportion of individuals with unknown ploidy levels. Genomic differentiation between native and nonnative populations is low to moderate, as indicated by fixation index (F_{ST}) analysis, while haplotype diversity is highest in nonnative populations, highlighting the role of genetic admixture in the establishment of *S. spontaneum* in new environments. Inbreeding coefficients (F_{IS}) vary across populations, with most values indicating balanced inbreeding and outbreeding. However, negative F_{IS} values in certain individuals suggest recent hybridization or gene flow from genetically distinct populations. This aligns with concerns about hybridization potential with related species, including *S. officinarum*, which could further elevate invasion risk by increasing genetic variation and adaptability.

Environmental and functional genomics approaches are being applied to study gene-environment interactions in invasive populations, enabling predictions of the response of *S. spontaneum* to different ecological conditions. Predictive modeling integrating genomic, ecological, and climatic data is in development to anticipate potential invasion hotspots. Functional genomics is being used to identify key genes associated with stress tolerance, rapid growth, and reproductive flexibility, contributing to the species' invasion success.

This research provides valuable insights into the genomic mechanisms underlying the invasion dynamics of *S. spontaneum*. Future work will expand genomic sampling, refining predictive models, and further investigate the genetic ancestry of recently sampled individuals in Florida. Understanding the genetic basis of adaptability and invasiveness of *S. spontaneum* will aid in developing effective management strategies to mitigate its spread and ecological impact.

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POTENTIAL LEAF DAMAGE FROM EXTREME HEAT IN NATIVE AND INVASIVE TREES IN WEST VIRGINIA

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ABSTRACT

As global temperatures continue to rise, critical temperature thresholds may be crossed that cause elevated heat stress and long-term damage in plants. To date, the majority of work on heat tolerance in wild plants has focused on tropical, desert, or montane plants with fewer studies focusing on temperate forest trees. Further, it is unclear how heat stress may differentially impact native species relative to invasives. Invasive species are thought to have broad thermal niches, which assist them during the invasion process to establish in a wide range of climatic conditions. It is also thought that invasive species may possess higher heat tolerances, which may confer a competitive advantage during particularly hot years. Less is known about how heat tolerance shifts within and across years in response to growing season temperatures. In this ongoing study, the aim was to (1) quantify and compare heat tolerances in common, native eastern U.S. tree species relative to invasive trees, (2) determine if heat tolerance shifts throughout the year, and (3) assess if thermal safety margins (i.e., the temperature difference between heat tolerance and leaf temperatures) are sufficient to protect against heat stress from high temperatures.

Heat tolerance of photosystem II (PSII) was assessed with chlorophyll fluorescence and is defined as the temperature that causes the initial decrease (T_{crit}) in maximum quantum yield of F_v/F_m . Six individuals were sampled from each of 17 species occurring in Morgantown, West Virginia (12 broadleaf species: 8 native and 4 invasive) and the Monongahela National Forest near Parsons, West Virginia (5 conifer species: 3 native, 1 invasive, 1 hybrid). Each species was sampled twice, once during the early summer (late June/early July) and once during the late summer (late July/August) of 2024 with additional sampling planned for 2025 and 2026.

T_{crit} varied greatly from a low of 39.0 °C in the broadleaf native, *Liriodendron tulipifera* to a high of 48.3 °C in the broadleaf native, *Ulmus rubra*. There was no pattern of invasive species having higher T_{crit} than natives despite the prediction that invasive species would have broader thermal niches with higher heat tolerances. However, on average, broadleaf species did have higher T_{crit} than conifers, suggesting some heat tolerance variation based on leaf type. Additionally, there was no evidence that T_{crit} increased throughout the summer despite air temperatures increasing during the year. In fact, the majority of species showed lower T_{crit} later in the year, contrary to expectations.

Limited sampling of leaf temperatures for three broadleaf species (*Ailanthus altissima*, *Juglans nigra*, *Acer saccharum*) shows that air temperature is a poor proxy of realized leaf temperatures. The warmest air temperature recorded at our experimental site was 36.8 °C while leaf temperature extremes ranged up to 53 °C. These realized leaf temperatures were sufficient to surpass heat tolerances in *J. nigra* and *A. saccharum*, likely leading to heat induced damage in the leaves. The invasive *A. altissima* maintained T_{crit} above leaf temperatures suggesting that invasive trees may maintain lower leaf temperatures to increase thermal safety margins and avoid heat stress. These preliminary results suggest that current high temperature events may be enough to surpass critical temperature thresholds for some species. Continued data collection in 2025 and 2026 will provide better understanding of thermal safety margins and true heat stress in leaves.

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HORIZON SCANNING FOR RANGE SHIFTING FOREST PESTS IN A CHANGING CLIMATE

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ABSTRACT

Managing invasive species with prevention and early-detection strategies can avert severe ecological and economic impacts. Climate models project that the northeastern U.S. will experience warmer and more humid conditions, resembling the climate of the Southeast in the coming decades. This is also driving species to expand or shift their ranges into new areas. Future casting to identify range-shifting species is crucial for preventing biological invasions as it allows for proactive management strategies that anticipate and mitigate risks before species establish and spread in new environments. Horizon scanning is a process for identifying unknown risks, emerging issues, and opportunities to inform policy, decision-making, and research prioritization. We adapted existing horizon scanning methods to conduct a horizon scan that explicitly accounts for the impact of climate change on biological invasions, extending the scope beyond previous assessments. We assessed 80 species for their likelihood of range expansion, likelihood of establishment and spread in expanded range, and the magnitude of potential ecological and socioeconomic impacts. Results identified 8 high-risk, 18 moderate-risk, and 54 low-risk species. Additionally, we estimated the confidence of our predictions and found most low confidence species were in the low-risk category, and all high-risk species had medium to high confidence. We recommend full risk analysis and increased surveillance for the high-risk species, and periodic review and revision of the list. Our findings underscore the importance of integrating climate-informed horizon scanning into invasive species management, enabling proactive risk assessment and targeted interventions to mitigate future biological invasions.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

KNOW THEM TO STOP THEM! THE FIRST WORLD DATABASE ON BIO-ECOLOGY AND DISTRIBUTION OF SCOLYTINAE

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ABSTRACT

Scolytinae (Coleoptera: Curculionidae) are one of the most successful groups of invasive forest species (Haack 2001, Sauvard et al. 2010). They generally move among continents transported within live plants, timber and wood-packaging materials (Humble 2010, Meurisse et al. 2019). This grants them protection from adverse travel conditions and allows them to often go unnoticed by phytosanitary inspections at points of entry. The economic and ecological damage caused by these insects results from the direct action of burrowing within host plant tissues and by the plant pathogens vectored by some species. The knowledge of their bioecological traits, as well as their origin, is essential to prevent the introduction of new and potentially harmful species by planning effective monitoring strategies (Poland and Rassati 2019, Lantschner et al. 2020). This kind of information is scattered through a large amount of papers, catalogs and books, and is not always easily available.

For this reason, an online open access database collecting information for all the 6,493 Scolytinae species currently known was created: “Scolytinae hosts and distribution database” (<https://www.scolytinaehostsdatabase.eu/site/it/home/>). The starting point was the catalog on Scolytinae and Platypodidae (Wood and Bright 1992) and the subsequent four supplements (Bright 2014, 2021; Bright and Skidmore 1997, 2002). These catalogs, in addition to containing a great deal of data on host plant and distribution of scolytins, were also used to compile an initial list of species, especially the latest and most up to date (Bright 2021). The research was conducted through a systematic search, treating individual species one-by-one, using the species name of the scolytine and also its synonyms, in Google Scholar and Google (e.g., “*Xylosandrus amputatus*”). The database contains information on their reproduction, feeding habits (i.e., host tissues used by the insect), host plants, and distribution at a national level. Feeding and reproductive habits classification was obtained from Kirkendall et al. (2015). For the host plant records, all the observations of Scolytinae species boring inside any plant or tissue were considered. Records derived from trapping or other observation of occurrence in plantations (including monocultures) were considered unreliable and therefore not included. Plant taxonomy adopted in the database was based on the information available from the Plant of the World Online (POWO). For the distribution, only the presence of stable and reproductive populations inside the nation was considered; records of interceptions at entry points were not included. Moreover, for each nation, the Köppen–Geiger climate classification was also provided, according to MacLeod and Korycinska (2019). Each record included in the database is associated with the corresponding reference.

It is possible to browse the database by applying filters based on biological traits, host plants, and geographic distribution; finally, it is possible to download the filtered species information in csv format. In addition to the database consultation page (“HOME”), the site has pages concerning the instructions on how to consult the database (“HOW TO CONSULT”), the methodologies adopted to create the database (“METHODOLOGY”), and the publications to be cited for data found in the database (“HOW TO CITE”). The database will be kept current with periodic updates including information from new publications. In this context, another page was added to the website (“CONTACTS”). Users can report any errors or missing information on this page to the site managers to help keep the database accurate and up to date. We also acknowledge the valuable contributions and feedback provided by external experts.

A new three-year project, which has just begun, aims to expand the information contained in the database. It is intended to add the possible presence of diagnostic methods for identification, both morphological (i.e., taxonomic keys) and genetic for each species. In addition, it is intended to provide information on the impact of the species, particularly on the possible transmission of pathogenic fungi, with a list of pathogens transmitted by each Scolytinae species. In this context, any collaboration with other agencies or experts in the field is welcome. Currently, European Union Reference Laboratory (EURL) for Insects and Mites and the Italian National Research Council (CNR) participation in the project is being discussed.

With this database, it will be possible to quickly retrieve a wealth of information on Scolytinae, that will be useful in preventing new introductions and planning effective monitoring methods. By knowing the host plants and the origin of the species of greatest interest, it will be possible to plan more targeted phytosanitary policies and protocols. The data collected have already been used by the European Food Safety Authority (EFSA) to prepare two pest categorizations (of non-EU Scolytinae on conifers and non-coniferous hosts) that identified a list of species at greatest risk of introduction in EU territories (EFSA Panel on Plant Health et al. 2020, 2024).

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ACCURATELY DETECTING FOREST DISTURBANCE FROM SPACE USING CANOPY PHENOLOGY

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ABSTRACT

Moderate, non-stand-replacing forest disturbances are common on the landscape but remain more difficult to detect by traditional remote sensing methods than severe and sudden disturbances such as fire and harvest. Insect-caused defoliation and slow forest decline due to some insects and forest pathogens typically associate specific agents with their preferred host species. Changes in seasonal phenological patterns of the forest canopy are often among the first indicators of such a disturbance. We have developed a computational methodology that combines satellite-derived remote sensing image time series (e.g., Landsat and Sentinel) with weather and climate records to estimate expected phenology in forest areas at the image pixel scale, allowing us to distinguish natural variability from true anomalies in remote sensing observations. These anomalies can indicate new disturbance events and help track the progression of a persistent disturbance, such as insect colonization and establishment, on the forest landscape. We combine these results with an expert-informed pest decision matrix of known native and invasive forest pest species, including their preferred forest hosts and seasonal activity, and new U.S. Forest Service Forest Inventory and Analysis maps of forest species biomass to indicate host abundance. This collection of evidence supports the detection of new and ongoing moderate forest disturbances and our ability to differentiate between likely causes among native and invasive biotic agents (e.g., spongy moth, emerald ash borer, spruce budworm, beech bark disease) and abiotic influences (e.g., heatwaves, flash droughts, frost, windstorms). We conducted ground-based forest health surveys to describe and quantify the composition of both understory and overstory vegetation, as well as site characteristics, damage agents, and canopy condition of overstory species in survey plots that corresponded to Landsat pixels. Forest health survey plot data on species and canopy damage were compared to satellite imagery and phenology model predictions. We found a significant relationship between the proportion of image pixels that had vegetation indices determined by our model to be outside of the expected normal phenological range and the overall canopy damage class observed during ground surveys. Our modeling approach could lead to enhanced tools for early detection of canopy disturbances.

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POSTER

Abstracts

PREVENTING INTRODUCTIONS OF PLANT PATHOGENS–NOW WHAT?

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ABSTRACT

There are many challenges that limit international phytosanitary measures from curtailing introductions of tree diseases that are reshaping Earth's forests (Fei et al. 2019, Gougherty et al. 2023, Martinac et al. 2025, Quirion et al. 2021, Raffa et al. 2023, Weed et al. 2013, Wu 2024) and call for actions that reflect the true threat level and limits of science.

Research is needed to devise workarounds to make progress addressing the classical challenges:

- Most microorganisms are unknown to science–“unknown unknowns”.
- Regarding known microorganisms, scientists usually cannot predict their impact on new hosts under novel environmental conditions.
- The World Trade Organization's Sanitary and Phytosanitary (SPS) Agreement and International Plant Protection Convention (IPPC) demand unachievable specificity regarding pests' impacts.
- Most tree-killing pathogens are detected after they have entered the forest.
- Low priority for protecting natural ecosystems from bioinvasion.
- Unreliable funding/staffing for agencies carrying out the full range of efforts.

Additional new challenges include:

Clarifying the current risk profile: how many pathogens (as distinct from arthropods) are entering via traded goods? Which pathways are the most important?

- Incorporating into risk analyses socio-economic drivers of species' transportation to and establishment in a new region (Bonello et al. 2020, Sitzia et al. 2021, Williams et al. 2023, Wu et al. 2023).
- Applying the full range of assessment tools. Raffa et al. (2023) discuss each tool's strengths.
- Improving Early Detection and Rapid Response. Apply innovative molecular techniques to detect and identify plant pathogens (Sitzia et al. 2021, P. Bonello, personal communication, August 14, 2024).
- Providing reliable funding for rapid responses to terrestrial invasive species not important to agriculture (Invasive Species Advisory Committee National Early Detection Rapid Response Framework; Bonello et al. 2020, Lodge et al. 2006).
- Strengthening management strategies. Increase research into more effective controls on important pathways, and strategies for inspection, early detection, and rapid response. Fund classical biocontrol, sterile-insect release, and host resistance breeding (Quirion et al. 2021).
- Focusing on the host–the best intervention point in the host/disease/pest triangle. Deploy tree hosts' genetic resistance (Bonello et al. 2020).

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EL NINO-SOUTHERN OSCILLATION MODULATED OUTBREAKS OF A PINE CATERPILLAR, *DENDROLIMUS SPECTABILIS*, OVER 600 YEARS IN KOREAN PENINSULA

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ABSTRACT

The aim of our study is to identify climatic drivers of a pine caterpillar (*Dendrolimus spectabilis*) outbreaks based on its long-term outbreak history over several centuries. The outbreak history of the pine caterpillar was constructed based on its outbreak records extracted from History of Goryeo Dynasty (918–1392) and Annals of Joseon Dynasty (1392–1910), official records for Goryeo and Joseon Dynasty, respectively. The past climatic records were selected to represent influencing factors at different geographical scales. El Nino-Southern Oscillation (ENSO), the sea ice extent (SIE) of Barents-Kara Sea (B-K) region and Palmer drought severity index (PDSI) in Monsoon Asia Drought Atlas (MADA) were selected as proxies of climate at the global, continental and local levels, respectively. The first outbreak of the pine caterpillar in Korea was reported in 1150, and historical records of the pine caterpillar showed 110 outbreaks from 1150 to 1910. The year of and one year before the outbreaks of the moth occurred during negative ENSO phase, suggesting La Nina phase was a potential climatic driver of the outbreak. In negative ENSO phase, the weather of Korea is warm and dry in summer, suggesting that warm and dry conditions were favorable for the moth outbreaks. In addition to ENSO, the influence of SIE of Barents-Karra Sea, an indicator of dry summer was only partially observed during current year of outbreaks, whereas PDSI in MADA, an indicator of local summer drought, was not observed during outbreaks. Our historical review showed that moth outbreaks from 1150 to 1910 were tele-connected to ENSO phase and that the outbreak pattern of the moth over 600 years was modulated by global climate, and this modulation was detectable using outbreak history constructed by ancient records.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

PERSISTENCE AND EFFICACY OF EMERALD ASH BORER PARASITOIDS

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ABSTRACT

Four species of parasitoid wasps (*Tetrastichus planipennisi* Yang, *Spathius galinae* Belokobylskij and Strazanac, *Spathius agrili* Yang, and *Oobius agrili* Zhang and Huang), have been released across North America as a biocontrol measure to reduce the spread and damage of the invasive emerald ash borer (*Agrilus planipennis* Fairmaire; EAB). EAB larvae may overwinter in either the phloem or the xylem of an ash (*Fraxinus* spp. L.) tree. It has previously been determined the proportion of EAB larvae overwintering in the xylem increases as accumulated growing degree days (GDD base 50F) increases. These larvae in the xylem are inaccessible to the released parasitoid wasps, as they are too deep in the tree for oviposition by the parasitoids. However, previous work has determined that populations of one parasitoid, *Tetrastichus planipennisi*, are still able to establish and persist in areas with a high proportion of inaccessible larvae when the total EAB population is large. Here, we sought to determine how the dynamics of parasitoid populations behave when EAB populations crash post-invasion. We focused on eight sites along the suitability gradient modeled by Gould et al. (2020). We monitored EAB populations using baited Lindgren funnel traps, parasitoid populations using yellow pan traps, sentinel logs, and bark scraping, assessed the health of adult ash trees at each site, and surveyed for ash seedlings and saplings. Our results show that *Tetrastichus planipennisi*, *Spathius galinae*, and *Oobius agrili* have established and persisted at all sites, but *Spathius agrili* has not been recaptured. We determined that *T. planipennisi* population trends tend to follow those of EAB populations; however, there seems to be a lower limit to the amount of accessible EAB larvae needed for this parasitoid to persist. We are currently working on a life table study to determine the effectiveness of these parasitoids across the suitability gradient.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

NOVEL METHOD OF IDENTIFICATION FOR INVASIVE KNOTWEED

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ABSTRACT

Invasive Knotweed describes three species (*Reynoutria japonica*, *R. bohemica*, *R. sachalinensis*) of highly invasive plants in the buckwheat family that have caused significant damage to riparian areas globally. Knotweed's powerful growth cracks through concrete foundations and extensively devalues property. Control of invasive knotweed is nearly impossible, due to its tendency to grow in dense and resilient monocultures. The only economically viable option for a hearty infestation is biocontrol. Currently the knotweed psyllid (*Aphalara itadori*) is the only biological control agent approved for knotweed, but its establishment in the Northeastern U.S. has not met expectations (Grevstad et al. 2018). One possible explanation is that the strain we call "Japanese Knotweed" is mostly a hybrid of *R. japonica* and *R. sachalinensis*. Despite field observations that Japanese knotweed is the dominant species in our region, genetic analyses have revealed that they are mostly the hybrid species *R. bohemica*, and a possible explanation for the failures of the knotweed biological control program to date is that the target species and the agent are mismatched. Therefore, we hypothesized that our biocontrol efforts may be ineffective without a reliable way to monitor hybridization. This experiment evaluates the effectiveness of klason lignin as a biomarker for species identification. Klason lignin is the acid insoluble lignin that makes up a large portion of lignocellulosic biomass. While other fractions require chromatography or UV spectroscopy to quantify, klason lignin isolation involves taking the weight of a residue left behind after acid hydrolysis and is an inexpensive and reliable method (Li et al. 2016). Results confirmed the hypothesis that a difference could be measured between the two species. A larger sample size is needed to set thresholds and use klason lignin to identify knotweed, but this experiment confirms that this method may be used to quantitatively distinguish between the species *R. sachalinensis* and *R. japonica*.

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RECONSTRUCTING THE INVASION HISTORY OF *MICROSTEGIUM VIMINEUM* USING PLASTID GENOME SEQUENCING

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ABSTRACT

Invasive species impart negative impacts on biodiversity and economies globally. The ecological impacts of invasive species have been the focus of many studies in recent years, however, less is known about their evolutionary history and spread in new environments. One such species native to eastern Asia, stiltgrass (*Microstegium vimineum*), was first discovered in the U.S. approximately 100 years ago around Knoxville, Tennessee. Based on a previous study using digitized herbarium records, it is hypothesized that there were at least two introductions from genetically distinct source populations in Asia based on a pattern of awn versus awnless phenotype. However, few genomic studies across space and time for invasive species have been conducted, including on stiltgrass. We hypothesize that multiple introductions have occurred leading to the genetic diversity present in the invasive range. Illumina sequencing via genome skimming was focused on plastomes, which are highly conserved in land plants and uniparentally inherited. They can be used as a proxy to track seed dispersal between the native and invasive ranges and across the invasive range post-establishment. DNA was extracted from over 200 contemporary field collections and historical herbarium samples, and Illumina libraries were generated from all sampling locales collected and sequenced on an Illumina NextSeq2000. Plastomes were assembled with GetOrganelle and aligned with Multiple Alignment using Fast Fourier Transform (MAFFT), and haplotype networks were drawn with Population Analysis with Reticulate Trees

Population Analysis with Reticulate Trees (PopArt) using Templeton, Crandall, and Sing (TCS) parsimony networks, in four “time slices” of approximately 30 years starting with the original collection in 1919. Nucleotide diversity was calculated in the Trait Analysis by Association, Evolution, and Linkage (TASSEL) over each time slice. Plastid haplotype relationships were used to characterize geographic patterns of important traits (e.g. awn presence/absence) across space and time in the Eastern U.S. and Asia and determine how genetic diversity differs from the native to invasive range, as well as between the two awn phenotypes. Constructed haplotype networks were used to trace the ancestry of individuals in the invasive range, using the native-range samples as a comparative reference for total plastome diversity. Historical samples are split into four time slices of approximately thirty years. Higher nucleotide diversity was observed in the Northern U.S. than the Southern U.S. Northern U.S. nucleotide diversity was similar to that observed in the native range, although it may be biased by sample size. Nucleotide diversity in the Southern U.S. spiked in the most recent time slice. While the awn phenotype retains its north-south gradient there is clear evidence of long-distance seed dispersal as Northern haplotypes are being found in the Southern U.S. and *vice versa*. All Southern U.S. accessions appeared to initially comprise the same haplotype, indicating a single introduction, possibly from Japan. Northern U.S. accessions revealed multiple haplotypes that are most closely related to accessions in China, Japan, and Taiwan. Additionally, new haplotypes appeared over time, suggesting multiple introductions or a more diverse initial introduction than what would be expected under a severe genetic bottleneck resulting from a single introduction. Furthermore, there is evidence for long-distance seed

dispersal as new haplotypes are found in increasingly large areas over time. This indicates that the invasion of stiltgrass in the U.S. has a complex invasion history, involving multiple introductions and long-distance seed dispersal, adding to a growing body of studies that implicate multiple introductions in invasion success. Understanding this pattern can help develop better strategies for managing current and future invasive species. By using stiltgrass as a model, we can gain insight into how other potentially invasive species may establish and spread, informing efforts to contain and control them effectively.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

ASSESSING THE RISK POSED BY SPONGY MOTH TO CANADA'S FORESTS

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ABSTRACT

An assessment was conducted triggered by recent increases in detections of spongy moth (*Lymantria dispar dispar*), an invasive species, in uninfested areas of Canada, as well as outbreaks in areas where this pest is considered established. The objective of the assessment was to characterize the risk posed by spongy moth's spread to currently uninfested forested areas across Canada, including the effect of climate change on the risk of spread and establishment of this insect. The assessment also identifies information needs that, once addressed, will help reduce existing uncertainties around spongy moth risk, and ultimately, will enhance prevention and management of spongy moth in Canada. The report has a primary focus on spongy moth, a subspecies of European origin that is currently present in eastern Canada. The report concludes that without control, spread of spongy moth to currently suitable but uninfested areas of Canada is highly likely and the negative consequences of the insect's establishment in these areas could be substantial, particularly from trade and ecological standpoints. Climate change is expected to exacerbate risk progressively during the next 30 years and to play a role in increasing the severity of outbreaks in areas where spongy moth is already established. Examples of successful eradication programs across Canada demonstrate the feasibility and efficacy of managing risk of spongy moth introductions. Existing prevention strategies to limit spongy moth spread to uninfested areas of Canada, although imperfect, should be maintained, and, where possible, reinforced through institutional partnerships to enhance their effectiveness. The project was led by the Invasive Species Centre, run in collaboration with the Canadian Forest Service of Natural Resources Canada, and under the guidance of a task team.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

MOLECULAR IDENTIFICATION OF THREE FUNGAL PATHOGENS RESPONSIBLE FOR INVASIVE OAK WILT DISEASES IN JAPAN, KOREA, AND THE USA

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ABSTRACT

The Oak wilt diseases caused by three invasive insect-vectored foreign fungal pathogens are a growing concern to the health of oak trees in the central and eastern U.S., Canada, and Europe. Currently, each species of these foreign pathogens is localized to a single geographic region. North American oak wilt (NOW) caused by the fungus *Bretziella fagacearum*, entered the U.S. in the 1960s and is a significant concern for Canada, where the disease was first identified in Niagara Falls in 2023, and in Europe where the disease is not yet present. Two newly emergent oak wilt diseases in Japan (Japanese oak wilt, or JOW) and Korea (Korean oak wilt, or KOW) are responsible for high levels of oak tree mortality and are rapidly expanding their geographic range. These fungal pathogens (*Dryadomyces quercivorus* and *D. quercus-mongolicae*, respectively) have caused severe damage and death to healthy oak trees in urban and landscape forests in Japan and Korea since the 2000s. If these pathogens were to spread to North America, there is the potential for devastating damage to oak forest ecosystems and the oak hardwood industry. Given that the eastern U.S. and eastern Asia have similar temperate biomes conducive to the survival of the beetle vectors and the pathogens, there is real concern that introduction of either of the JOW or KOW pathogens to North America would be devastating to U.S. eastern white oak, northern red oak, and pin oak forests. However, the susceptibility of North American oak species to JOW and KOW is not known.

Understanding the biology and pathogen-host interactions allow for the development of robust rapid detection tools for these pathogens that currently do not exist and are necessary for early detection and spread mitigation. This international research project has three main objectives: (1) determine if host range of oak wilt pathogens extends to ecologically and economically important North American red and white oak species; (2) improve genomic resources for the oak wilt pathogens using hybrid assemblies of Oxford Nanopore Technology (ONT) and Illumina based sequencing and full-length transcripts; and (3) develop and validate laboratory (ONT and real-time PCR) and field (LAMP and RPA) diagnostic assays to detect the three oak wilt pathogens using multiple platforms (e.g., metagenomics, metabarcoding [*tefla*, *rpb2*, and the ribosomal RNA operon consisting of the SSU, ITS, and LSU loci]), and real-time PCR, LAMP, and RPA primers including a lateral flow component to meet the varied needs of different stakeholder groups. Laboratory validation is being conducted using extracted DNA and artificially inoculated plant samples. Field validation of the LAMP and RPA assays will be conducted in the U.S. and Korea using a crude DNA extraction targeting symptomatic and asymptomatic trees.

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DOUBLE TROUBLE FOR HEMLOCKS: IMPACTS OF HEMLOCK WOOLLY ADELGID DAMAGE ON HEMLOCK BORER INFESTATION

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ABSTRACT

Understanding the interplay of native and invasive pests is crucial for preserving ecosystem health. Eastern hemlock, *Tsuga canadensis* L. Carrière, is an important native conifer in eastern North America that is suffering severe mortality due to the invasive hemlock woolly adelgid (HWA), *Adelges tsugae* Annand. This study investigates the relationship between the native hemlock borer (HB), *Phaenops fulvoguttata* Harris, that attacks weakened eastern hemlock, and the invasive HWA. Recently, an unusual number of HB outbreaks have been detected in New York State. This study assessed HB infestation across three health stages of eastern hemlock trees to understand if HB prefers trees with increased HWA damage. It was found that HB more frequently fly toward eastern hemlock trees with more severe HWA. This study offers insight into the role of secondary pests in the HWA system and underscores the need for pest management strategies tailored to dual threats.

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OVIPOSITIONAL BEHAVIOR, PHENOLOGY, AND NATURAL ENEMY RESPONSE OF THE FLATHEADED HACKBERRY BORER (COLEOPTERA: BUPRESTIDAE: *AGRILUS MACER*), A SECONDARY PEST OF SUGARBERRY (CANNABACEAE: *CELTIS LAEVIGATA*), IN SOUTHEASTERN LOUISIANA

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ABSTRACT

Forests provide critical ecosystem services, including supporting biodiversity, providing recreational and cultural spaces, regulating air and water quality, and contributing to the production of wood and wood products. However, rapid global change is increasing the frequency and severity of drought events, which increase the susceptibility of trees to pest damage and mortality, threatening these ecosystems and their essential services. The flatheaded hackberry borer (Coleoptera: Buprestidae: *Agilus macer*; FHB) is a secondary pest that has been associated with the widespread mortality of sugarberry trees (Cannabaceae: *Celtis laevigata*) in the southeastern U.S. Sugarberry trees are a critical component of bottomland hardwood ecosystems. These trees provide habitat for specialist herbivore taxa, and their wood is important for the production of furniture and other wood products (Tirmenstein 1990).

In this study, we simulated drought by girdling, and thus disrupting the movement of water and nutrients, of 10 healthy sugarberry trees to examine how abiotic stressors influence the population dynamics of FHB and responses by its natural enemies. Our findings suggest that FHB's oviposition is influenced by host tree chemical and tactile cues. We also identified a complex of natural enemies, including an unidentified egg parasitoid likely in the genus *Oobius*, an identified larval parasitoid in the family Bethyridae, and five morphospecies of ants (Hymenoptera: Formicidae) predating on FHB egg masses. Our results suggest the presence of trade-offs between oviposition density and predation, indicating potential predator dilution effects. Future research will further investigate the drivers of FHB's oviposition variability and predator-prey dynamics.

This study contributes to our understanding of top-down and bottom-up regulation of FBH in response to global change and the broader impacts of abiotic stressors on the population dynamics of woodboring pests of broadleaf trees in bottomland hardwood ecosystems.

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The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

FACTORS AFFECTING HOST EGG SELECTION OF *APROSTOCETUS FUKUTAI*, AN EGG PARASITOID OF CITRUS LONGHORNED BEETLE

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ABSTRACT

The invasive Asian longhorned beetle *Anoplophora glabripennis* (ALB) and citrus longhorned beetle *A. chinensis* (CLB) are high-risk invasive beetles worldwide (Haack et al. 2010) to hardwood forests and citrus crops. Both beetles attack a wide range of tree species including maple (*Acer*), willow (*Salix*), elm (*Ulmus*), and citrus (*Citrus*). *Aprostocetus fukutai* (Hymenoptera: Eulophidae) is an egg parasitoid of CLB and other longhorned beetles (such as *Apriona germani*) in its native range (Asia) (He et al. 2000). This parasitoid has also become an important natural enemy of CLB in Europe, where it was accidentally introduced with CLB-infested plant materials from Asia. However, its association with ALB has not been confirmed. In the present study, we expose *A. fukutai* to CLB and ALB eggs under different conditions (naked eggs, naturally laid eggs, and artificially inserted eggs) to evaluate effects of CLB and ALB host-oviposition substrates on host egg attack rates, aiming to gain insights into the host selection behavior and specificity of *A. fukutai*.

Findings from our study show that *A. fukutai* do not attack viable host eggs removed from the hosts' oviposition substrates. However, *A. fukutai* can attack both host (CLB) and non-host (ALB) eggs that are artificially inserted into host plant material, indicating that host plant (oviposition) substrate may play a critical role in the parasitoid's host selection and specificity. Our findings also showed that *A. fukutai* attacked fewer CLB eggs artificially inserted into host plant material (17.9 percent, n=28) than those naturally laid in the host plant material (40 percent, n=30), indicating that natural oviposition substrate is more favorable to *A. fukutai* parasitism. It is known that CLB has a broad host range, attacking several dozens of host tree species. How the host tree species of longhorned beetles may affect *A. fukutai*'s ability to attack and control target hosts is unknown and should be studied in future experiments. This will allow for a better understanding of the viability of *A. fukutai* as an effective control agent against CLB or other related longhorn beetle hosts.

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THE REGIONAL SEX PHEROMONE RESPONSES OF INTRODUCED SATIN MOTH (*LEUCOMA SALICIS*)

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ABSTRACT

Satin moth (*Leucoma salicis* L.) (Lepidoptera: Erebidæ) is a defoliating pest of poplar (*Populus*) and willow (*Salix*) species. Native to the Palearctic region, it was introduced simultaneously to the east and west coasts of North America in 1920, creating geographically distinct eastern and western populations. The geographic origins of each population, and whether they share a common place of origin, is unknown. Regional differences in pheromone response may provide answers to these questions. Previous work has shown that males from the western satin moth population in British Columbia, Canada, exhibit preference for a different stereoisomer of its sex pheromone than in Hungary, part of its native range. These results suggest that the western population did not come from this region, but elsewhere in its native range. However, the pheromone preference of the eastern population of satin moth has yet to be determined. To this end, we conducted a behavioral choice assay by baiting delta flight traps with each of four stereoisomers of satin moth sex pheromone in Isle Royale National Park, Michigan, a current outbreak site that represents the leading edge of the eastern population as of 2024. We found that eastern males showed preference for the same isomer as western males, indicating a common place of origin that is likely outside of central Europe. Our identification of the preferred sex pheromone isomer of the eastern satin moth population in North America sheds light on the origin of this non-native pest and supports further investigation of possible points of origin in its native range.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

DOUBLE THE TROUBLE: USING NEAR INFRARED SPECTROSCOPY TO SCREEN FOR CO-OCCURRING DISEASE IN BEECH TREES

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ABSTRACT

American Beech trees (*Fagus grandifolia*) are severely impacted by two different forest diseases, Beech Bark Disease (BBD) and Beech Leaf Disease (BLD). Beech Leaf Disease, caused by an invasive foliar nematode, *Litylenchus crenatae mccannii*, predominately impacts the leaves of the tree. Whereas BBD involves an invasive scale insect, *Cryptococcus fagisuga*, and native fungi, *Neonectria* spp., and predominately impacts the tree bark. An important component in managing forest pathogens is early disease detection. Developing tools that can screen for diseases like BLD before the trees become symptomatic is critical to implementing effective management strategies. Early detection tools using near-infrared (NIR) spectroscopy have previously been developed for BLD in Ohio and Pennsylvania, near where BLD was first detected, but have not been tested in other states. Additionally, these tools have not been implemented in areas where high levels of BBD co-infect beech trees. Connecticut is an optimal state to test how robust these screening tools are since both diseases have been well established since the 1900s (BBD) and 2019 (BLD). In this study our objectives were to collect foliar spectra from beech trees that are symptomatic and asymptomatic for BLD and BBD, including trees that are co-infected; collect bark and sapwood spectral data using NIR; and evaluate the accuracy of spectral data to distinguish between trees with BLD and/or BBD. We selected trees in four sites within Connecticut: Wadsworth Falls, Giuffrida Park, Stratton Brook, and Shades Swamp. Within each forest we established three plots with 10 trees per plot (n=120). Phenotypic data was collected including diameter at breast height (d.b.h.), percent live canopy, percent healthy leaves, percent low severity leaves, percent high severity leaves, and a beech bark disease rating. Bark plugs were collected on the north and south side of the bole at breast height using a sterile leather punch. Near-infrared spectral measurements of the bark and sapwood were taken with a NeoSpectra Scanner. Preliminary results show that the intensity and shape of the spectral profiles differ between the bark and sapwood and that the bark spectral profiles are similar across canopy class groups. Principal component analysis based on transformed spectral profiles shows no clear separation of groups based on site or BBD rating, nor site vs. canopy rank status suggesting that the spectral tool is robust across different geographic locations within our study area. A sparse partial least square discriminant analysis was used to classify sapwood spectra data based on BBD and results showed that our model has a 21 percent error rate at classifying trees into groups with lower levels of scale insects (N=47), and a 61 percent error rate at classifying trees into groups with higher levels of scale insects (N=28). These results suggest that our model does a better job at classifying trees with lower BBD severity (based on scale insects). Measuring scale insects is an indirect measure of BBD; therefore, repeated screening for cankers and scale insects may be needed to more accurately and precisely assess disease severity overtime.

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BTK (*BACILLUS THURINGIENSIS KURSTAKI*) FOR SPONGY MOTH CONTROL IN MINNESOTA: FIRST YEAR ASSESSMENT OF EFFECTS ON NON-TARGET LEPIDOPTERA

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ABSTRACT

The spongy moth (*Lymantria dispar dispar*; previously known as European gypsy moth), an invasive defoliator of over 300 tree and shrub species, has been a persistent ecological challenge in North America since its introduction in the late 19th century (Elkinton and Liebhold 1990, Liebhold et al. 1997) and Renate R. Bush since 1868 or 1869, when it was introduced near Boston, the gypsy moth has been slowly expanding its range to include the entire northeastern U.S. and portions of Virginia, West Virginia, North Carolina, Ohio, and Michigan (Liebhold et al. 1992, 1996). In Minnesota, where populations have established permanently since 2005 (Streifel et al. 2019); the primary management strategy for satellite infestations involves aerial applications of *Bacillus thuringiensis kurstaki* (Btk), a microbial pesticide that selectively targets Lepidopteran larvae (Reardon et al. 1994). However, public opposition to Btk treatments, often fueled by concerns about non-target effects on beneficial Lepidoptera, has created challenges for implementation. While non-target Lepidoptera can be temporarily affected by Btk treatments (Venables 1990, Reardon et al. 1994, Rastall et al. 2003, Scriber 2004, Wayland et al. 2015), no comprehensive studies have been conducted in Minnesota to assess these impacts.

To address this knowledge gap, we conducted a field study in the summer of 2024 to quantify the short-term effects of Btk applications on non-target Lepidoptera populations in Minnesota. We established 16 study sites across areas designated for treatment with Btk ($n = 8$) and control ($n = 8$), ensuring an average one kilometer separation between sites. Sampling was performed twice: once approximately 10 days prior to Btk application and again one week after the final treatment. Two sampling methodologies were employed to maximize the detection of larval Lepidoptera: (1) branch collection, where caterpillars were collected from randomly selected tree branches using pole pruners, and (2) beatsheet sampling, which involved dislodging caterpillars from understory vegetation using a dowel and beatsheet. Following collection, larvae were reared in laboratory until adult emergence to facilitate taxonomic identification to the family level.

Our preliminary results revealed that caterpillar abundance declined in both treated and control sites following Btk application, such that there was no treatment effect. These findings were consistent across sampling methods. Taxonomic analyses are ongoing.

Decline in caterpillar abundance in both treatment and control plots could be caused by several mechanisms. First, spray could have drifted from treatment to control plots during application, reducing numbers of Lepidoptera in all locations. We view this phenomenon as unlikely, however, given the precision of aerial applications and distances between plots. Second, decreases in caterpillar abundance may reflect development to and dispersal of adults away from the plots. Finally, it is possible that Btk may have killed caterpillars feeding in the treatment plots while those in the control plots developed to adults and left, obscuring any treatment effects. To determine adult abundances later in the summer, blacklight trapping was conducted. Identifications are currently ongoing. Further study in 2025 will resample all sites to evaluate longer-term impacts.

By empirically evaluating the non-target effects of Btk under local ecological conditions, this study contributes to an evidence-based framework for forest pest management in Minnesota. Continued monitoring will permit evaluation of potential cumulative effects on Lepidoptera populations and their broader ecological roles. Given the increasing public scrutiny of aerial insecticide applications, studies such as this are critical for fostering informed decision-making and enhancing public trust in pest management interventions.

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EVALUATING THREE MECHANISMS OF RESISTANCE IN LINGERING HEMLOCKS

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ABSTRACT

Hemlock woolly adelgids (*Adelges tsugae*; HWA) are invasive insects that kill eastern and Carolina hemlocks, which are keystone species. However, some trees survive in stands where most hemlocks have died. These are called “lingering hemlocks” and may be resistant to, or tolerant of, HWA feeding. It is unknown whether lingering hemlocks provide resistance to HWA. To test whether lingering hemlocks are resistant to HWA, we propagated 200 hemlock trees comprising 48 genotypes from 10 locations. One hybrid variety acted as our resistant control, and one group of wild-type eastern hemlocks as our susceptible control. The hybridized trees, known to be resistant, provide a comparison for our lingering genotypes. We tested the primary types of host plant resistance: antibiosis, antixenosis, and tolerance. To test antibiosis, we measured HWA density, survival, and fecundity on different hemlock genotypes by caging infested branches on each tree and counting HWA as nymphs and adults. We found that wild-type eastern hemlocks (susceptible control) do not reduce HWA survival, but the hybrid (resistant control) and 11 lingering hemlock genotypes do. To test antixenosis, we conducted a preference experiment in which HWA nymphs could choose between lingering and non-lingering hemlock cuttings. This experiment showed that HWA does not demonstrate a preference between lingering and wild type genotypes. To test tolerance, we measured hemlock growth relative to HWA density. We found three lingering hemlocks with significantly more growth than our wild-type eastern hemlocks. We think antibiosis is playing a role in lingering hemlock resistance because we have 11 genotypes decreasing HWA density across multiple life stages, whereas the mechanisms of preference and tolerance have no influence. These experiments will be repeated so we can compare HWA sistens and progrediens generations. The results of this study should help determine which lingering hemlock trees exhibit resistance that can be propagated for reforestation and for breeders to use. Having resistant hemlocks in the field can help manage HWA populations in the future.

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INVESTIGATING THE FUNCTION OF THE AWN AND ITS ROLE IN INVASION SUCCESS OF *MICROSTEGIUM VIMINEUM* (STILTGRASS)

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ABSTRACT

Invasive species can disrupt ecosystem processes and reduce biodiversity, but mechanisms underlying many invasions remain unknown. We focused on *Microstegium vimineum* (stiltgrass) and the role of awns in its invasion success. This species is expanding both northward and westward in the U.S., and one possible explanation for northward expansion is the distribution of awn types across the invasive range. Awns are bristle-like extensions from the floret that respond to changes in moisture and can aid in dispersal/burial in some grasses, but their function in *M. vimineum* remains unresolved. *M. vimineum* has multiple awn forms (awned, awnless, short-awned) with a distinct awned-awnless distribution from north-south in the native and invasive ranges, suggesting awns may be favored by selection in certain conditions. We hypothesize that awns facilitate floret small-scale dispersal to safe sites and subsequent burial, which protects seeds from freezing at high latitudes, increasing survival and promoting northern expansion. Our goal is to elucidate awn function and its role in invasion success through reciprocal transplant and dispersal experiments examining the effects of awn type on germination, survival, and dispersal capabilities. Reciprocal transplant experiments were conducted over three years at four locations across the U.S., including sites at low/high latitude/elevation (Erie, Pennsylvania, Morgantown, West Virginia, Davis, West Virginia, and Clemson, South Carolina). Awn treatments included awned, awnless, and awn-removal to account for trait differences in the awned-type not due to the awn itself. In year one, the awned-type had the greatest germination at high latitude, and the awnless-type had the greatest mortality at high latitude/elevation, supporting the hypothesis of an advantage for the awned-type in higher soil freezing conditions. However, the awn-removed treatment had the greatest germination at high elevation, suggesting that the awn itself may not confer this advantage. In years two and three, we investigated awn function in seedbank survival over multiple winters. The awned-type had significantly greater germination in year two than the awnless and awn-removed treatments, suggesting the awn itself increases seedbank survival over multiple years. Year three of this experiment showed no difference in germination between the awn treatments, likely due to a lack of remaining seeds in the seedbank. Ongoing dispersal experiments investigating dispersal of awn treatments on various substrates will further clarify awn function. Awn treatments include awned, awnless, short-awned, and awn-removed, while substrate treatments include hardboard (Masonite), soil, and soil with leaf litter. Preliminary results suggest the awned-type has the greatest dispersal ability, supporting the function of *M. vimineum* awns in small-scale dispersal via hygroscopic movement. This research uses the well-established *M. vimineum* as a study system to shed light on the dynamics of the invasion process, and the outcomes of elucidating *M. vimineum* awn function will provide insights into mechanisms behind northern range expansion.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

THE SILENT INVADER: UNCOVERING THE LOCAL DISPERSAL OF *LITYLENCHUS CRENATAE* SSP. *MCCANNII* IN U.S. FORESTS

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ABSTRACT

Beech leaf disease (BLD), caused by the *Litylenchus crenatae* ssp. *mccannii* (Lcm) nematode, is an emerging threat to beech trees. This disease is characterized by distinct leaf symptoms, including leaf interveinal banding and thickened leaf texture, which leads to eventual tree mortality. Understanding Lcm dispersal mechanism(s) is crucial for managing BLD, yet these remain largely unknown, posing a major barrier to its effective management. This study represents a pioneering investigation into the abiotic and biotic vectors that potentially contribute to the local dispersal of Lcm in natural American beech (*Fagus grandifolia*) forest systems in the Northeastern United States. An experiment was set up in Stone Valley Forest, Pennsylvania, using four funnel stands placed at variable distances from naturally BLD-infected beech trees. This approach enabled the recovery of active Lcm nematodes from each funnel, demonstrating their ability to naturally disperse at least 11.74 meters (38.52 feet) from the nearest BLD-infected tree. In addition, birds were investigated as potential dispersal vectors of Lcm via external and internal mechanisms. The objectives were to determine if Lcm can be detected from ectoparasites, feathers or feces collected from wild birds caught in BLD areas. The findings highlight the role of abiotic factors involved in the dispersal dynamics of Lcm, especially wind and humidity, as indicated by a generalized linear model. The current study also uncovered the incidental association of Lcm with other organisms beneath the canopy of BLD trees, including spiderwebs and caterpillars. The detection of Lcm DNA in seven ectozoochory and fourteen endozoochory samples from six different bird species further supports the idea that birds may play a role in transmitting the nematode. To our knowledge, this is the first study to document the potential vectors involved in the local dispersal of Lcm, offering valuable information for the biology of this nematode. The findings contribute to broader efforts in advancing the understanding of the local spread of BLD, highlighting the complex interplay of abiotic and biotic factors in this disease dispersal.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

MOLECULAR AND BIOCHEMICAL INSIGHTS INTO THE BEECH LEAF DISEASE PATHOSYSTEM

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ABSTRACT

American beech (*Fagus grandifolia*), a keystone species in eastern U.S. Forest ecosystems, is currently threatened by beech leaf disease (BLD). BLD, caused by the foliar nematode *Litylenchus crenatae* ssp. *mccannii* (LCM), has significantly impacted the health of mixed eastern hardwood forests since 2012 and raised concerns among foresters, ecologists, and private landowners. The disease alters bud and leaf physiology, with a distinctive symptom being the hypertrophy and hyperplasia observed in bud tissues following infection. LCM infection also contributes to tree decline and mortality.

Our research utilizes transcriptional data from bud tissues to explore the host response to LCM infection. Additionally, we analyzed buds from trees treated with Polyphosphite (PP30), a biostimulant widely used in agriculture to enhance plant growth, yield, and resistance to various pathogens. Private industry has experimented with PP30 as a potential management option to mitigate beech leaf disease and protect high-value trees. Our findings indicate that PP30 application leads to the upregulation of key plant defense genes, including the induction of salicylic acid pathways and the biosynthesis of nematocidal compounds such as linamarin, suggesting the elicitation of systemic induced resistance (SIR). Furthermore, glycosyltransferase and quercetin glucosyltransferase activity were identified as key pathways affected by PP30 application.

Our analyses reveal that LCM influences molecular pathways related to defense and the cell cycle, primarily through the differential expression of genes involved in various metabolic processes. Analysis of infested tissue shows upregulation of brassinosteroid and auxin biosynthesis, coupled with heightened expression of key cell cycle genes such as *Bub1* and *MCM*. This was accompanied by the downregulation of defense pathways related to salicylic acid biosynthesis. As part of this research, we generated a *de novo* assembly of the LCM transcriptome and mapped the reads back to our bud transcriptome libraries. Our data suggests that PP30 application slightly decreases LCM titer in bud tissue. This research provides insights into the host response to the nematode and changes likely induced by LCM effectors. Ultimately, our research aims to develop a model that enhances our understanding of the factors driving host susceptibility in American beech. This foundational research informs future resistance-based management strategies for combating BLD and explores approaches to protect high-value trees, such as those in arboretums or breeding programs.

The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.

ELUCIDATING DISEASE ETIOLOGY OF BEECH LEAF DISEASE IN NORTHEAST OHIO

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ABSTRACT

Beech leaf disease (BLD) was discovered in Lake County Ohio by Lake Metroparks naturalist John Pogacnik in 2012. BLD is caused by the nematode, *Litylenchus crenatae mccannii* (LCM), which is native to Japan and naturally occurs as a parasite on Japanese beech trees. BLD causes tree mortality and has spread very quickly through northeast Ohio to neighboring states and Canada. Although the modes of transmission remain poorly understood, nematodes travel through the soil and groundwater typically, so BLD movement may be aided by a vector. This research focuses on potential aerial transmission and disease etiology. Spore traps developed at the University of Florida (Quesada et al. 2018) were placed among symptomatic trees over a 15-week period, at one-week intervals, starting August 19 through December 2, 2025. Three sites at the University of Mount Union Huston Brumbaugh Nature center in Minerva, Ohio were chosen and two spore traps, each with two membranes for collection, were set out at these locations. Each week half of the membranes were examined microscopically, and half were used for qPCR detection. The molecular methods are being improved, and data collection is ongoing. From weeks 2 to 8, nursery grown American beech saplings were placed at two of the sampling locations (three saplings per location) and maintained in a closed glasshouse until each weekly exposure. Each set of saplings was then returned to the glasshouse and maintained in a separate closed room until fall, when they were placed in a cold storage facility for dormancy. The exposure saplings will be evaluated for symptoms in spring of 2025. These studies aim to provide new insights into nematode dispersal, disease transmission and infection timing in BLD and further our understanding of this emerging disease affecting eastern North America.

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The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.

COLD DURATION AFFECTS SURVIVAL OF ELONGATE HEMLOCK SCALE, A HITCHHIKER TO THE UPPER MIDWEST ON IMPORTED CHRISTMAS TREES

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ABSTRACT

Elongate hemlock scale, *Fiorinia externa* (Hemiptera: Diaspididae), is an alien invasive insect that occurs in the eastern United States, primarily within the range of eastern/Canadian hemlock. In these areas, the insect also can infest Fraser fir, grown for Christmas trees and holiday greenery. *Fiorinia externa* has been detected repeatedly in Minnesota and Wisconsin on this cut host material imported from eastern states. However, the insect has not established in the Upper Midwest. Our previous research demonstrated that brief exposure to temperatures below -25 °C (-13 °F) can cause substantial mortality of overwintering females. The current study measures the effect of prolonged exposure to temperatures > 25 °C [-13 °F] (i.e., not immediately lethal) on the survival of overwintering females. Branch tips of eastern hemlock and Fraser fir infested with *F. externa* were collected in winter and early spring from North Carolina, shipped to a quarantine laboratory in Minnesota, and held at constant +3, -10, or -20 °C (+37, +14, or -4 °F). Survival of females was measured periodically for up to eight weeks by using a biochemical viability test, a colorimetric measure of ATP (adenosine triphosphate) levels. Regardless of collection month, exposure to +3 or -10 °C (26 or 14 °F) caused little mortality within five weeks, but some thereafter. Scales collected in mid-winter survived longer at -20 °C (-4 °F) than scales collected in spring but experienced complete mortality by eight weeks. Warming winters may create opportunities for new insects like *F. externa* to establish in the Upper Midwest.

The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.

HERBIVORE DIET AND PLANT DAMAGE ASSOCIATED COMPOUNDS ALTER SEED GERMINATION, GROWTH, AND HERBIVORY

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ABSTRACT

While plant defense against herbivory is primarily thought to occur following attack, there is also evidence that plants can detect and respond to pre-attack cues. These cues include chemicals released from damaged conspecifics and kairomones, non-attack-related substances emitted by an herbivore that plants can detect and use to their benefit. It is unknown, however, whether or how plants react to the interaction of these pre-attack cues. In the summer of 2024, we measured germination, growth, and herbivore susceptibility of *B. nigra* seedlings in an experiment that crossed the presence/absence of crushed *B. nigra* leaves with exposure to the mucus of a generalist herbivore, *A. subfuscus*, that have been fed either closely- or distantly-related species (*B. nigra* and iceberg lettuce, respectively). Seeds exposed to slug mucus germinated more quickly than control seeds; crushed *B. nigra* leaves only increased germination speed in combination with mucus. The same pattern was found in herbivore bioassays: *Spodoptera exigua* only avoided seedlings exposed to both slug slime and crushed leaves. There was no difference in the final biomass of mature plants, suggesting that plants exposed to herbivore cues early in their development can increase defense without a measurable cost in size at maturity.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

HERBIVORE KAIROMONES AFFECT GERMINATION SPEED, SEEDLING GROWTH, AND HERBIVORY

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ABSTRACT

Seeds and seedlings are particularly vulnerable to herbivory. Unlike mature plants, which can wait until herbivory is experienced to induce defense, seeds and seedlings face mortality if they wait. Slug mucus functions as a kairomone, a non-attack-related substance emitted by consumers that is detected by a prey species (in this case, plants). While snail mucus has been shown to induce defense in seedlings, it is not widely confirmed whether slugs have the same effect and whether seeds can also detect and react to such herbivore cues. We investigated how exposure to *Arion subfuscus* mucus affected growth and defense in *Brassica nigra* seeds and seedlings. Seeds exposed to slug mucus germinated five percent faster than control (water only) seeds, but the resulting seedlings weighed 16 percent less than control seedlings. To test whether this difference results from herbivore-exposed plants allocating energy from growth to defense, we conducted choice bioassays assessing slug preference for control seedlings versus seedlings that were either (A) exposed to mucus only as a seed; or (B) exposed to mucus as a seed and seedling. While slugs did not differentiate between control seedlings and ones exposed to herbivore cues only as a seed, they ate 88 percent less biomass of seedlings exposed to mucus as both seeds and seedlings. These results suggest that slug mucus induces changes in plant traits related to defense and growth/competitive ability. Future research should determine the chemical mechanisms of this induced defense.

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EFFICACY OF BRIEF HEAT TREATMENTS FOR NON-NATIVE AMBROSIA BEETLES

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ABSTRACT

Ambrosia beetles (Curculionidae: Scolytinae) are among the most destructive and abundant tree pests in the U.S. With many non-native ambrosia beetle species arriving inside solid wood packaging material, biosecurity measures for that pathway are vital for preventing invasions. However, even with International Standards for Phytosanitary Measures No. 15 (ISPM 15), which requires wood packaging materials to be treated with heat or methyl bromide, some species appear to bypass biosecurity measures and invade. Therefore, we investigated the heat tolerance of two non-native ambrosia beetles in their larval and adult life stages (*Xylosandrus crassiusculus* and *Anisandrus maiche*) to determine their potential for surviving current ISPM 15 standards (56° C [132.8 °F] for over 30 minutes). The two species were reared on branches from common hosts, red maple (*Acer rubrum*) and American beech (*Fagus grandifolia*), and then warmed to randomly determined target temperatures between 40 and 60° C (104 and 140 °F). Survival status was determined upon completion of each bioassay following tactile stimulation. Our preliminary results indicated the upper lethal limit of adult (43° C [109.4 °F]) and larval (40-44 °C [104-111.2 °F]) *X. crassiusculus* and larval (below 40 °C [104 °F]) *A. maiche* are below ISPM 15 heat treatment standards. This provides foundational knowledge for determining the temperatures required to kill these two ambrosia beetle species and indicates that it is unlikely these beetles survive ISPM 15 compliant heat treatments.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

ASSESSMENT OF SPATIAL DISTRIBUTION PATTERNS AND INFESTATION RISK OVER TIME OF SPOTTED LANTERNFLY (*LYCORMA DELICATULA*) IN NEW YORK STATE

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ABSTRACT

Spotted Lanternfly (*Lycorma delicatula*) is an invasive treehopper native to Asia. It was first introduced to Pennsylvania in 2014, and as of 2020 it has expanded to New York. Their preferred host tree is the invasive tree of heaven (*Ailanthus altissima*), but they will feed on over 173 different plants worldwide. Preferred host species in New York state include agricultural vegetation such as grape vines and fruit trees. Positive Spotted Lanternfly site data collected by the New York Department of Agriculture and Markets and iMapInvasives were analyzed using ArcGIS Pro to assess spatial distribution patterns. Spotted Lanternfly egg masses can be unknowingly spread via transportation pathways such as highways and railroads. Using a multi-scale geographically weighted regression, proximity to these pathways and tree of heaven presence were shown to be significant global factors in the location of spotted lanternfly sightings in New York. However, these factors showed little significance at local levels, indicating the need to better understand the local variability of spotted lanternfly occurrences. Additionally, infestation risk was geographically categorized based on proximity to these transportation pathways and agricultural regions.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

EVALUATING THE DEVELOPMENT AND REPRODUCTIVE POTENTIAL OF *DRYINUS SINICUS*, A NYMPHAL PARASITOID OF SPOTTED LANTERNFLY

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ABSTRACT

Dryinus sinicus Ashmead (Hym.: Dryinidae) is an important nymphal parasitoid of the spotted lanternfly, *Lycorma delicatula* White (Hemiptera: Fulgoridae), within its native range in China. We described some aspects of the biology of this parasitoid, including its immature developmental morphology and reproductive potential. Adult *D. sinicus* exhibits sexual dimorphism, with female's protarsus bearing a chela. *D. sinicus* is synovigenic; female emerging with a few mature oocytes. Its larva is ectoparasitic, with the head partly immersed in the coelom of the host and the rest of the body protruding between two of the host's sclerites, covered by the larval exuviae (thylacium). The larva develops through five instars and then crawls out to pupate in a silk cocoon killing its host. At 20° C (68° F), adult females lived 62.7 ± 11.6 d (range = 5 -147 d), parasitized 6- 488 nymphs, laid 6- 623 eggs, and host-fed upon 3- 59 nymphs during their lifetime. Self-superparasitism occurred frequently in the laboratory setting and more than one offspring developed in some cases. The life-time fecundity is positively related to longevity or predation. Overall, *D. sinicus* is a long living, synovigenic and highly fecund parasitoid. In a laboratory setting, it more effectively parasitizes 1st rather than 2nd instars on potted trees of heaven *Ailanthus altissima*. It killed more nymphs by parasitism than by host feeding. Host feeding and oviposition likely prompts egg production. It is a candidate biological control agent and research is underway evaluating its host specificity and improving rearing.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

THE STATUS OF ASH REGENERATION IN SOUTHEAST MICHIGAN

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ABSTRACT

Emerald ash borer (EAB, *Agrilus planipennis* Fairmaire) has been established in North America for over 20 years and has killed hundreds of millions of ash (*Fraxinus* spp.). While most mature canopy ash have died due to EAB, ash seedlings and saplings too small to be colonized have survived in the understory. Ash, especially in swamp forests where they are a dominant species, support unique wildlife communities including insects and birds. This study aimed to characterize the occurrence and health of ash within long-term research plots established in 2004–2005 in southeast Michigan, a region that has experienced the longest duration of EAB impacts. In 2024, we resurveyed forest plots that varied in hydrology, including hydric plots with seasonal standing water, mesic riparian plots, and upland xeric plots. Within these plots, we assessed the abundance and health of ash canopy trees (≥ 10 centimeters d.b.h.), understory trees (2.5 centimeters $\leq$ d.b.h. < 10 centimeters), saplings (≥ 137 centimeters tall and < 2.5 centimeters diameter at breast height, d.b.h.), and percentage cover of ash seedlings (< 137 centimeters tall). Preliminary results indicated that ash were present in the understory of 95 percent of the plots surveyed, but their abundance and size class varied by hydrology. Hydric forests had lower percentage cover of ash seedlings than mesic or xeric forests ($\chi^2 = 12.4$, 2 d.f., $p = 0.002$), but higher densities of understory ash trees ($\chi^2 = 8.38$, 2 d.f., $p = 0.015$). Basal area of ash (≥ 2.5 centimeters d.b.h.) across all plots averaged 0.18 meters²/hectare in 2024, compared to 6 meters²/hectare in 2004–2005 (Smith et al. 2015). Of the 320 ash trees (≥ 2.5 centimeters d.b.h.) found in the 97 plots surveyed, 31 percent showed canopy decline or death. Four black ash (*F. nigra*) trees were found producing seeds near our study plots, and these trees ranged from 6.6 – 11.5 centimeters d.b.h. However, newly germinated seedlings were not observed in any of the plots surveyed. These preliminary findings suggest that ash are abundant in the understory of some forest types, and that there will continue to be scattered pulses of host material available to EAB in the future. Continued surveys to assess ash health over time and the efficacy of natural enemies is required to understand whether ash will persist in or be extirpated from natural forests. The results of this project will provide insights into the status of ash in post-outbreak forests to inform management.

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The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

BIOSURVEILLANCE FOR NATIVE AND INVASIVE FOREST FUNGAL PATHOGENS IN THE U.S. THROUGH SPORE TRAPPING

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ABSTRACT

Forest ecosystems provide essential ecological and economic services, yet they face increasing threats from invasive pathogens and pests. In the Northeastern United States, tree mortality caused by non-native forest pathogens has become a growing concern. While national surveillance programs target invasive insect pests in high-risk areas such as ports of entry and industrial zones, large-scale early detection efforts for forest pathogens remain limited due to their microscopic nature and challenges in traditional morphological identification. DNA-based detection offers a more efficient and scalable approach for identifying these pathogens in environmental samples.

This study aims to (1) establish a baseline of existing forest pathogens in the region, (2) enhance detection efforts for high-priority pathogens such as *Bretziella fagacearum* (oak wilt), *Geosmithia morbida* (thousand cankers disease), *Heterobasidion annosum* s.l. (heterobasidion root disease), and *Litylenchus crenatae* spp. *mccannii* (beech leaf disease), and (3) identify newly introduced invasive fungal pathogens from international sources.

In the first phase of this study, we deployed spore traps in six locations in Ohio (Cincinnati Barge and Rail Terminal, Eden Park, Rocky River Reservation, Hinckley Reservation, Toledo Metroparks Corridor 12, and Maumee State Forest) and six in New Hampshire (Bear Brook State Park—Beaver Pond Campground and Podunk Road Entrance, White Lake State Park, Monadnock State Park, Greenfield State Park). Environmental DNA (eDNA) from the collected spore tapes was extracted and subjected to metabarcoding sequencing targeting the ITS2 region. Additionally, targeted detection of *B. fagacearum*, *G. morbida*, *H. annosum* s.l., and *L. crenatae* spp. *mccannii* (Lcm) was conducted using conventional PCR and quantitative PCR (qPCR).

In New Hampshire, qPCR analysis detected *B. fagacearum* (confirmation through sequencing is ongoing) and *G. morbida* in all six locations. *H. annosum* s.l. was present in five locations (absent in Greenfield State Park), and Lcm was detected in all sampled sites. In Ohio, *B. fagacearum* was not detected in any location, whereas *G. morbida* was found in Eden Park and Rocky River Reservation, and *H. annosum* s.l. was detected in Eden Park. Detection of Lcm in Ohio samples is still under evaluation.

Metabarcoding analyses revealed significant differences in fungal community composition between locations (Adonis, $p < 0.001$), with site identity accounting for 42.5 percent of the variation. Samples from Ohio clustered separately from those in New Hampshire, and within New Hampshire, samples from Monadnock State Park formed a distinct group. When analyzing the relative abundance of amplified sequence variants (ASVs) assigned to *Bretziella*, *Geosmithia*, and *Heterobasidion*, *Geosmithia* was detected in Greenfield State Park and one Ohio site, *Heterobasidion* in White Lake State Park, while *Bretziella* was not identified in any sample via metabarcoding. The most abundant fungal taxa across all sites included members of the genera *Ramularia*, *Dothiora*, *Aureobasidium*, *Cladosporium*, *Taphrina*, *Curvibasidium*, *Hormonema*, *Alternaria* and unclassified members of the families *Phaeosphaeriaceae*, *Didymellaceae*, and the

class *Dothideomycetes*. To refine pathogen surveillance, the curated USDA fungal database was utilized to classify pathogenic species, revealing a high abundance of plant pathogens, including *Aureobasidium pullulans*, *Ramularia nyssicola*, *R. simplex*, *Cryptocline arctostaphyli*, *Curvibasidium cygneicollum*, *Alternaria prinicola*, *Capnobotryella renispora*, *Retiarius bovicornutus*, *R. gaultheriae*, *Taphrina sacchari*, *Neocatenulostroma microsporum*, *Lophodermium nitens*, and *Fusarium tricinctum*.

The results of this study are being incorporated into a geospatial mapping tool to provide a baseline for monitoring potential invasive pathogens that may threaten forest health in the Northeastern U.S. This study demonstrates the efficacy of integrating metabarcoding with targeted molecular detection to enhance early pathogen surveillance. By establishing a comprehensive baseline dataset, these findings contribute to improved biosecurity measures, inform forest health management strategies, and support proactive mitigation efforts against emerging forest pathogens.

The content of this paper reflects the views of the authors(s), who are responsible for the facts and accuracy of the information presented herein.

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Continued on next page.

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FORUM AGENDA

Tuesday Afternoon, February 25, 2025
Poster session–Sheet Vend (Powerhouse, 3rd Floor)
3:00–6:00 p.m.

Wednesday Morning, February 26, 2025
Opening Session–Ballroom
8:15–10:00 a.m.
Moderator:
Scott Pfiste, USDA APHIS PPQ, Buzzards Bay, MA

Time	Session
8:15 a.m.	Welcome–Therese Poland, USDA Forest Service, Northern Research Station, East Lansing, MI
	Mike McManus Memorial Keynote Presentations
8:30 a.m.	Ecology of <i>Sirex noctilio</i> : Toward a better understanding of a global forest insect invasion. Juan Corley Grupo de Ecología de Poblaciones de Insectos, IFAB CONICET-INTA, Bariloche, Argentina
9:15 a.m.	Globalization, plant and insect invasions- where are we headed? Sandy Liebhold Czech University of Life Sciences, Prague and USDA Forest Service, Northern Research Station, Morgantown, WV
10:00–10:30 a.m.	BREAK

Research reports
10:30 a.m.–11:50 a.m.
Moderator:
Andreas Linde, University for Sustainable Development, Eberswalde, Germany

Time	Session
10:30 a.m.	Biological and environmental factors that limit winter moth spread. Jeremy Andersen ¹ , Nathan Havill ² , Alana Russell ³ , Thomas Schmeelk ⁴ , Armand Martinez ¹ , Artemis Roehrig ¹ , Jeff Boettner ¹ , Hannah Broadley ⁵ , Jennifer Chandler ¹ , Joseph Elkinton ¹ ¹ University of Massachusetts, Amherst, MA, ² USDA Forest Service, Northern Research Station, ³ Rhode Island Department of Environmental Management, Providence, RI, ⁴ Maine Forest Service, Augusta, ME, ⁵ USDA, Animal and Plant Health Inspection Service - Plant Protection and Quarantine, Buzzards Bay, MA
10:50 a.m.	Population genomic evidence for a single point origin and local climate adaptation of the dominant beech bark disease pathogen. Eric Morrison ¹ , Tuan A. Duong ² , Berni van der Meer ³ , Philippe Tanguay ³ , Jeff R. Garnas ¹ ¹ University of New Hampshire, Durham, NH, ² University of Pretoria, South Africa, ³ Natural Resources Canada, Québec, QC
11:10 a.m.	Tree invasions as a tool to mitigate climate change: more cons than pros. Martin A. Nuñez ¹ , Romina D. Dimarco ¹ , Kerri M. Crawford ¹ , Kimberley T. Davis ² , Aníbal Pauchard ³ , Jaime Moyano ⁴ , Juan Paritsis ⁴ ¹ University of Houston, Houston, TX, ² USDA Missoula Fire Sciences Laboratory, Missoula, MT, ³ Universidad de Concepción, Concepción, Chile, ⁴ Universidad Nacional del Comahue, San Carlos de Bariloche, Argentina
11:30 a.m.	Changes in tree demographic structure in the face of invasive forest pests. Carlisle Bascom Jr. ¹ , Carrie Fearer ² , Randal Morin ³ , Andrew Liebhold ³ , Songlin Fei ⁴ , Jeff Garnas ¹ ¹ University of New Hampshire, Durham, NH, ² Virginia Tech University, Blacksburg, VA, ³ USDA Forest Service, Northern Research Station, Morgantown, WV, ⁴ Purdue University, West Lafayette, IN
11:50–1:00 p.m.	LUNCH

FORUM AGENDA CONTINUED

Wednesday Afternoon, February 26, 2025

Invasive pathogens

1:00–2:40 p.m.

Organizer:

Elena Karlsen-Ayala, USDA Forest Service, Northern Research Station, Hamden, CT

Time	Session
1:00 p.m.	Discovery and fine-tuning the use of fluopyram and thiabendazole as potent nematocides to include in beech leaf disease IPM programs. Matthew Borden ¹ , Andrew Loyd ² , Matthew Borden ² , Caitlin Littlejohn ² , Beth Brantley ² , Amber Stiller ² , Kelby Fite ² , Paulo Vieira ³ , Mark Ware ⁴ , Cory McCury ⁴ ¹ Bartlett Tree Experts, Charlotte, NC, ² Bartlett Tree Research Laboratories, Charlotte, NC, ³ USDA-ARS, Beltsville, MD, ⁴ Rainbow Ecosciences, Minnetonka, MN
1:20 p.m.	Leveraging climate and disease data to spatially predict risk and uncertainty. Simone Lim-Hing ¹ , Frank Koch ² , Christian Montes ³ , Caterina Villari ⁴ ¹ North Carolina State University, Raleigh, NC, ² USDA Forest Service, ³ Southern Research Station, Research Triangle Park, NC, ⁴ Rayonier Inc., Wildlight, FL, ⁵ University of Georgia, Athens, GA
1:40 p.m.	The impacts of prescribed fire on the spread of laurel wilt in the southeastern United States. Shane Allan , Scott Salom, Adam Coates, Carrie Fearer Virginia Tech University, Blacksburg, VA
2:00 p.m.	Oak wilt detection across scales from leaves to landscapes. Jeannine Cavender-Bares ¹ , Beth Fallon ² , Gerard Sapes ³ , J. Antonio Guzmán Q. ¹ , Jennifer Juzwik ⁴ ¹ Harvard University, Cambridge, MA, ² National Park Service, Mount Rainier National Park, Ashford, WA ³ University of Florida, Gainesville, FL, ⁴ USDA Forest Service, Northern Research Station, St. Paul, MN
2:20 p.m.	The impacts of beech leaf disease on tree carbon balance. Cameron McIntire ¹ , Andrew L. Loyd ^{2,3} , Chad M. Rigsby ^{2,4} , Patrick Lemis ⁷ , Elena Karlsen-Ayala ⁵ , Caitlin Littlejohn ² , Aaron Bertgdahl ⁶ , Jeff Garnas ⁷ , Paulo Vieira ⁸ , Danielle Martin ⁹ ¹ USDA Forest Service, Forest Health Protection, Durham, NH, ² Bartlett Tree Research Laboratories, Charlotte, NC, ³ Botanical Research Institute of Texas, Fort Worth, TX, ⁴ The Morton Arboretum, Lisle, IL, ⁵ USDA Forest Service, Northern Research Station, Hamden, CT, ⁶ Maine Forest Service, Augusta, ME, ⁷ University of New Hampshire, Durham, NH, ⁸ USDA Agricultural Research Service, Beltsville, MD, ⁹ USDA Forest Service, Forest Health Protection, Morgantown, WV
2:40–3:10 p.m.	BREAK

FORUM AGENDA CONTINUED

Wednesday Afternoon, February 26, 2025

Cascading impacts of invasive species

3:10–4:50 p.m.

Organizer:

Toby Petrice, USDA Forest Service, Northern Research Station, East Lansing, MI

Time	Session
3:10 p.m.	The fundamental shift in the parasitoid complex of spongy moth post-arrival of <i>Entomophaga maimaiga</i> . Dylan Parry ¹ , Nate Siegert ² , Ann Hajek ³ ¹ SUNY College of Environmental Science and Forestry, Syracuse, NY, ² USDA Forest Service, State, Private and Tribal Forestry, Forest Health Protection, Durham, NH, ³ Cornell University, Ithaca, NY
3:30 p.m.	Cascading impacts from emerald ash borer-caused black ash mortality. Alexis R. Grinde ¹ , Rob A. Slesak ² , Brian J. Palik ³ , Anthony W. D'Amato ⁴ ¹ Natural Resources Research Institute, University of Minnesota Duluth MN, ² USDA Forest Service, Pacific Northwest Research Station, Olympia, WA, ³ USDA Forest Service, Northern Research Station, Grand Rapids, MN, ⁴ University of Vermont, Rubenstein School of Environment and Natural Resources, Burlington
3:50 p.m.	Effects of decomposing <i>Ailanthus</i> wood on the soil and native species germination and growth. Cynthia Huebner USDA Forest Service, Northern Research Station, Morgantown, WV
4:10 p.m.	Not so it'sy-bitsy: Joro spider biology, management, and impacts in the Southeast. David Coyle ¹ , Angela Chuang ¹ , Beth Donohoe ¹ , David Nelsen ² , Michael Sitvarin ³ ¹ Clemson University, Clemson, SC; ² Nelsen: Southern Adventist University, Collegedale, TN; ³ Union College, Schenectady, NY
4:30 p.m.	Hurry before it's history—generating baseline data on ash associated arthropods prior to invasion by the emerald ash borer in subtropical southeastern Louisiana. Todd D. Johnson ¹ , Andrew Sanford ¹ , Ridley Graudnard ¹ , C. Wood Johnson ¹ ¹ Louisiana State University, Baton Rouge, LA; ² USDA Forest Service, State, Private and Tribal Forestry, Pineville, LA

Wednesday Evening, February 26, 2025

Poster session–Sheet Bend (Powerhouse, 3rd Floor)

5:00–6:30 p.m.

Wednesday Evening, February 26, 2025

Mixer–Atrium.

6:30–7:30 p.m.

FORUM AGENDA CONTINUED

Thursday Morning, February 27, 2025

Wood Boring and Bark Beetles

8:00–10:00 a.m.

Organizers:

Kayla Perry and Sam Ward, The Ohio State University, Columbus, OH

Time	Session
8:00 a.m.	Ash survival and growth response to emerald ash borer invasion in Massachusetts riparian forests: impacts of biological control. Mitchell A. Green ^{1,2} , Jian Duan ¹ , Ryan S. Crandall ² , Roy G. Van Dreische ² , Jeremy C. Andersen ² , Joseph S. Elkinton ² ¹ USDA, Agricultural Research Service, Beneficial Insects Introduction Research Unit, Newark, DE, ² University of Massachusetts, Amherst, MA
8:20 a.m.	What we know about <i>Chlorophorus signaticollis</i> , a new and potentially damaging longhorned beetle detected in New Orleans, Louisiana. Todd D. Johnson , Elise Grossman, Casey Butler, Tanner Sparks, Victoria Bayless, Jonathan Richards, Rodrigo Diaz Louisiana State University, Baton Rouge, LA
8:40 a.m.	longhorned beetle in the United States. Kristy M. McAndrew ¹ , Kevin D. Chase ² , Andrew M. Liebhold ³ , Samuel F. Ward ⁴ ¹ Department of Forestry, Mississippi State University, Starkville, MS, ² The R.A. Bartlett Tree Research Lab, Reading, England, ³ USDA Forest Service, Northern Research Station, Morgantown, WV, ⁴ The Ohio State University, Columbus, OH
9:00 a.m.	Understanding the range and etiology of wilting sassafras in the central hardwood forest region. Matthew Ginzel ¹ , Olivia Bigham ¹ , Tyler Dreaden ² , James Jacobs ³ , Anna Conrad ^{1,4} ¹ Purdue University, West Lafayette, IN, ² USDA Forest Service, Southern Research Station, ³ USDA Forest Service, Forest Health Protection, ⁴ USDA Forest Service, Northern Research Station
9:20 a.m.	Recent invasions in Central Europe of ambrosia beetles and their fungal associates. Eckehard G. Brockerhoff ¹ , José Ribeiro-Correia ¹ , Simon Blaser ¹ , Ludwig Beenken ¹ , Doris Hölling ¹ , Simone Prospero ¹ , Massimo Faccoli ² ¹ Swiss Federal Institute for Forest, Snow and Landscape Research (WSL), Birmensdorf, Switzerland, ² University of Padua, Italy
9:40 a.m.	Using multipherome blends for early detection of non-native longhorn beetle species: is the probability of detection changing with lure ageing? Alain Roques ¹ , Robert Setter ² , Mike Fraser ² , Marie-Anne Auger-Rozenberg ¹ ¹ INRAE, Zoologie Forestière, Orléans, France, ² Synergy Semiochemicals Corp. Delta, BC, Canada
10:00–10:30 a.m.	BREAK

FORUM AGENDA CONTINUED

Thursday Morning, February 27, 2025

Research reports

10:30 –11:50 a.m.

Moderator:

Leigh Greenwood, The Nature Conservancy, Missoula, MT

Time	Session
10:30 a.m.	Optimizing release device technology for a multipheromone blend; notes on chemistry and field trapping of longhorn beetles in British Columbia, Canada. Mike Fraser ¹ , Jorge Macias-Samano ¹ , Nicole Jeans-Williams ¹ , Alain Roques ² , Marie-Anne Auger-Rozenberg ² , Bob Setter ¹ ¹ Synergy Semiochemicals Corp. Delta, BC, Canada, ² INRAE, Zoologie Forestière, Orléans, France
10:50 a.m.	Research progress on the Asian longhorned beetle infestation in South Carolina. Lindsey Stone ¹ , Courtney Johnson ² , Abby Ratcliff ² , R. Talbot Trotter ³ , Kelly Oten ² , David Coyle ¹ ¹ Clemson University, Clemson, SC, ² North Carolina State University, Raleigh, NC, ³ USDA Forest Service, Northern Research Station, Hamden, CT
11:10 a.m.	Ecological Traits and Current Status of Invasive Insects in South Korea. Min-Jung Kim , Youngwoo Nam Forest Entomology and Pathology Division, National Institute of Forest Science, Seoul, Korea
11:30 a.m.	Forest Pest Pathway Risk Levels in Solid Wood Packaging: Quality data in, quality answers out. Leigh Greenwood The Nature Conservancy, Missoula, MT
12:00–1:00 p.m.	LUNCH

FORUM AGENDA CONTINUED

Thursday Afternoon, February 27, 2025

Invasive plants

1:00–3:00 p.m.

Organizer:

Rima Lucardi, USDA Forest Service, Southern Research Station, Athens, GA

Time	Session
1:00 p.m.	Defining the Invasive Front of <i>Oplismenus undulatifolius</i> (wavyleaf basketgrass; invasive nonnative) and Regional Expansion of <i>Oplismenus hirtellus</i> (basket grass; aggressive native). Cynthia Huebner ¹ , Carrie Wu ² , Craig Barrett ³ ¹ USDA Forest Service, Northern Research Station, Morgantown, WV, ² University of Richmond, Richmond, VA, ³ West Virginia University, Morgantown, WV
1:20 p.m.	Leaf damage from extreme heat in native and invasive trees in West Virginia. Evan Rehm USDA Forest Service, Northern Research Station, Morgantown, WV
1:40 p.m.	Advancing our understanding of invasive plants and disturbance interactions in western forests. Becky K. Kerns , Claire Tortorelli, Nathan Wade, Andrew Gray USDA Forest Service, Pacific Northwest Research Station, Corvallis OR
2:00 p.m.	Genetic diversity in the genus <i>Imperata</i> : horticultural cultivars, cooccurring congeners, and the wild-type invasive in the US. Rima D. Lucardi , Daniel C. Oakley, Victor K. Fitzgerald USDA Forest Service, Southern Research Station, Athens, GA
2:20 p.m.	Decoding genomic determinants of invasion risk in <i>Saccharum spontaneum</i> , a federally noxious weed. Santosh Kumar Rana ¹ , Rima D. Lucardi ² , Kristin Saltonstall ³ , Travis D. Marsico ¹ ¹ Arkansas State University, Jonesboro, AR, ² USDA Forest Service, Southern Research Station, Athens, GA, ³ Smithsonian Tropical Research Institute, Balboa, Ancon, Panamá
2:40 p.m.	Harnessing autotoxicity for cogongrass management: Early results and future directions. Elizabeth A. Esser ¹ , Gary Ervin ¹ , Rima D. Lucardi ² , Daniel Oakley ² , Victor Fitzgerald ² , Erika D. Womack ^{1,3} , Ashley Schulz ¹ ¹ Mississippi State University, Mississippi State, MS, ² USDA Forest Service, Southern Research Station, Athens, GA, ³ Mississippi State Chemical Laboratory, Mississippi State, MS
3:00–3:30 p.m.	BREAK

FORUM AGENDA CONTINUED

Thursday Afternoon, February 27, 2025

Early detection and rapid response for non-native invasive forest pests: insights and challenges
3:30–5:10 p.m.

Organizers:

Angela Chuang and Jess Hartshorn, Clemson University, Clemson, SC

Time	Session
3:30 p.m.	Know them to stop them! The first global database on bio-ecology and distribution of Scolytines. Matteo Marchioro ¹ , Virág Kertész ² , Giuseppe Stancanelli ² , Massimo Faccoli ¹ ¹ Università degli Studi di Padova, Legnaro, Italy, ² European Food Safety Authority (EFSA), Parma, Italy
3:50 p.m.	Horizon Scanning for Range-Shifting Forest Pests in a Changing Climate. Deah Lieurance ¹ , Amanda Suzzi-Simmons ¹ , Gabriela C. Nunez-Mir ² , Sarah Romy ² , Renee Ramos ² , Cesilia Aguilar ³ , Coleman R. Earnest ² , Sofia M. A. Al-Shayeb ² , Annette E. Evans ⁴ , Alanna Richman ¹ ¹ Penn State University, University Park, PA, ² University of Illinois, Chicago IL, ³ Northeastern Illinois University, Chicago IL, ⁴ University of Saint Joseph, West Hartford, CT
4:10 p.m.	Reporting Forest Invasives through EDDMapS, Wild Spotter, and iNaturalist. Chuck Barger Center for Invasive Species and Ecosystem Health (Bugwood), University of Georgia, Athens, GA
4:30 p.m.	Developing a decision tool for Early Detection Rapid Response of non-regulated forest pests. Angela Chuang , David Coyle, Jess Hartshorn Clemson University, Clemson, SC
4:50 p.m.	Accurately detecting forest disturbances from space using Canopy-Phenology. Clay Morrow ¹ , Matthew Garcia ² , Brian Sturtevant ¹ , Therese Poland ¹ ¹ USDA Forest Service, Northern Research Station, East Lansing, MI, ² University of Wisconsin, Madison, WI

FORUM AGENDA CONTINUED

Friday Morning, February 28, 2025

Research reports

8:00 a.m.–11:00 a.m.

Moderator:

Sandy Liebhold, USDA Forest Service, Morgantown, WV

Time	Session
8:00 a.m.	Cultural Impacts of Invasive Species. Jessica Raspitha Saint Regis Mohawk Tribe, Akwesasne, NY
8:20 a.m.	Insights from an international sentinel garden project for fungal pathogen surveillance: are we doing everything wrong? Eliana Torres-Bedoya ¹ , Enrico Bonello ¹ , Isabel Munck ² , Marc Digirolomo ² , Duccio Migliorini ³ , Alessia Pepori ³ , Patrick Sherwood ⁴ , Rebekka Schloesser ³ , Michelle Cleary ⁴ , Alberto Santini ³ , Hui Sun ⁵ ¹ The Ohio State University, Columbus, OH; ² USDA Forest Service, Durham, NH; ³ National Research Council, Florence, Italy; ⁴ Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁵ Nanjing Forestry University, Nanjing, China
8:40 a.m.	Dispersal of pioneering mountain pine beetles from active infestations: implications to range expansion for this domestic invasive. Brian Aukema ¹ , August Kramer ^{1,2} ¹ University of Minnesota, St. Paul, MN, ² Minnesota Department of Natural Resources
9:00 a.m.	Hemlock woolly adelgid biocontrol: Signs of hope for eastern forests. Nicholas Dietschler ¹ , Tonya Bittner ¹ , Elizabeth D'Auria ¹ , Melanie Halko ¹ , Nathan Havill ² , Zephyr Zembruski ² , Mark Whitmore ¹ ¹ Cornell University, Ithaca, NY, ² USDA Forest Service, Northern Research Station, Hamden, CT
9:20 a.m.	Connecting the fuzzy dots: Progress towards a dynamic synthesis model of Hemlock Woolly Adelgid dynamics. Talbot Trotter ¹ , Jennifer Chandler ¹ , Joseph Elkinton ² ¹ USDA Forest Service, Northern Research Station, Hamden, CT, ² University of Massachusetts, Amherst, MA
9:40 - 10:00 a.m.	BREAK
10:00 a.m.	Understanding a new pest: Elm zigzag sawfly spread, phenology, and management. Delaney Serpan ¹ , Abby R. Ratcliff ¹ , Kendra Wagner ² , Steve Frank ¹ , Kelly Oten ¹ ¹ North Carolina State University, Raleigh, NC, ² Rainbow Ecosciences, Minnetonka, MN
10:20 a.m.	Five years of methods improvements for mass rearing of <i>Spathius galinae</i> , a parasitoid of emerald ash borer. Andrea Anulewicz ¹ , Faye Meyers ¹ , Ben Slager ¹ , Nicole Sawallich ^{1,2} , Juli Gould ³ ¹ USDA Animal and Plant Health Inspection Service - Plant Protection and Quarantine, Brighton, MI, ² USDA APHIS PPQ, Romulus, MI, ³ USDA APHIS PPQ, Buzzards Bay, MA
10:40 a.m.	Inheritance of female flight capability in spongy moth hybrids. Alex Wu ¹ , Daniel Laffoon ¹ , Megan Doner ¹ , Brian Silva ¹ , Caroline Davock ^{1,2} , Melissa Warden ¹ , Scott Myers ¹ ¹ USDA Animal and Plant Health Inspection Service - Plant Protection and Quarantine, Buzzards Bay, MA, ² University of Massachusetts, Amherst
11:00 a.m.	Concluding Remarks. Nathan Havill USDA Forest Service, Northern Research Station, Hamden, CT

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