2026 Abstract Award Winners

Supplemental materials are not included

1st Place: Paige Alexander

Title: Not Just a Blood Buffet: Assessing Host Immune Responses to Repeated Tick Infestations in White-Tailed Deer

Authors: Paige S. Alexander[1], D.C. Wagner[2], E. T. Machtinger[1]

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Tick-borne diseases are expanding in incidence and geographic range. Yet it is still unknown whether white-tailed deer (*Odocoileus virginianus*), the primary reproductive hosts for many medically important tick species including blacklegged ticks (*Ixodes scapularis)* and lone star ticks (*Amblyomma americanum)*, develop acquired tick resistance (ATR). ATR is well documented in laboratory models and livestock systems. Early studies on guinea pigs and cattle showed that repeated tick infestations lead to notable declines in tick fitness. Across various mammalian hosts, ATR aligns with shared immune traits, including basophil recruitment, histamine-driven tick rejection, antibody involvement, and coordinated cytokine signaling. These findings have informed the development of anti-tick vaccines, including Bm86-based vaccines and newer methods targeting salivary antigens. In contrast, little is known about whether wildlife hosts, especially deer, develop ATR. Although deer are usually considered tolerant hosts supporting high tick loads, this idea has seldom been tested experimentally. Recent studies connecting deer-associated microbiomes and host-derived odors to tick attraction highlight the role of deer at the host-tick interface. However, these studies do not address how deer respond immunologically to repeated tick feeding. This study provides the first experimental evaluation of ATR in deer, with the goal of determining whether repeated tick infestations impact tick feeding success, reproductive output, local skin responses, and whether observed effects differ between tick species. In year one, twenty white-tailed deer (WTD) were assigned to infestation groups receiving either blacklegged (BLT*)* or lone star tick (LST*)*, or to control groups, across three successive infestations separated by two-week intervals. Tick recovery, engorged female weights, and egg mass production were recorded after each infestation. Blood draws and skin biopsies were collected at baseline and post-infestation to assess systemic and localized immune responses, and attachment sites were visually documented throughout. Overall tick recovery was low and declined across infestations, likely due to grooming behavior rather than immune rejection. Mean engorged weights of LST females declined significantly across all three infestations ($p < 0.001$), suggesting host-mediated constraints on feeding. BLT showed no consistent weight decline. Lighter females in later infestations often produced equal or greater egg masses, suggesting a possible reproductive compensation under immune pressure, a phenomenon not previously documented in these species on deer. Visual examination revealed increasing scabbing, inflammation, and basophil infiltration at LST attachment sites across infestations. These results demonstrate that deer are not immunologically passive hosts. The second year of this study will further explore these reactions through histology and

transcriptomic analysis. These methods will also be repeated; however, infestations will now be LST-LST-BLT and BLT-BLT-LST to understand potential cross-resistance. These findings have implications for tick population dynamics, host-vector modeling, and wildlife-targeted anti-tick vaccine development. While vaccine work on WTD is underway, no prior experimental reinfestation studies have evaluated ATR in white-tailed deer, despite decades of work in livestock and laboratory mammals. By demonstrating that repeated infestations can alter feeding efficiency, reproductive allocation, and local skin responses, particularly for A. americanum, this study provides the first experimental evidence that deer are not immunologically inert in tick–host interactions.

2nd Place: Ashani Hangawatte

Title: From Parasite to Immune Signature: A Serological Approach to Detecting Nasopulmonary Mite Exposure in Southern Sea Otters

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Nasopulmonary mites (hereafter, mites; *Halarachne halichoeri*) have been increasingly recognized as a significant yet underdiagnosed ectoparasitic threat to southern sea otters (*Enhydra lutris nereis*). Infestations can contribute to severe respiratory illnesses and mortality under severe conditions. Current diagnostics rely primarily on direct parasite detection (e.g., necropsy or limited clinical visualization), restricting large-scale surveillance and potentially missing subclinical or low-burden infestations. A serological tool detecting mite-specific antibody responses would improve early exposure detection, enhance rehabilitation triage, and support population-level acarological surveillance.

This project aims to develop and optimize a mite-specific serological assay to detect exposure to *H. halichoeri* in sea otters using broadly available reagents. I hypothesize that otters with confirmed mite infestations will exhibit stronger antibody responses to mite proteins than (a) healthy otters and (b) sick otters without mite infestation, allowing discrimination of mite exposure from generalized inflammation. A successful assay would permit detection of both active and prior exposure, even when mites are not directly observed.

Completed Phase one of this project established a reliable enzyme-linked immunosorbent assay

(ELISA) to measure total immunoglobulin G (IgG) in sea otter serum using commercially available anti-dog IgG antibody that has shown to cross-react with marine carnivores. Phase one optimized assay conditions and demonstrated reproducibility, providing a foundation for mite-targeted testing. Phase two (the focus of this submission) will adapt this platform into a mite-specific assay. Proteins extracted from *H. halichoeri* mites will be used to coat high-binding microplates, with protein concentration standardized prior to coating to ensure reproducibility. Plates will then be treated with blocking agent to reduce nonspecific binding, followed by incubation with sea otter serum. If an otter has mounted an immune response to mites, antibodies in its serum will bind to the coated mite proteins. Bound antibodies will be detected using anti-dog IgG secondary antibody, producing a measurable color change following substrate development. Optical density (OD) will be read at 450 nm to quantify antibody binding. Control wells lacking mite antigen will account for background signal and improve specificity. Comparisons will include healthy otters, sick otters without mites, and otters with confirmed mite infestations.
Mite-infested otters are expected to exhibit significantly higher antibody responses to *H. halichoeri* proteins than both comparison groups. Ill but mite-free otters are anticipated to show low reactivity to mite proteins, demonstrating assay specificity to mite exposure rather than generalized immune activation. Antibody magnitude may also vary with infestation severity, suggesting utility as both an exposure marker and a quantitative indicator of host response. From an acarological perspective, this study introduces a practical tool for detecting mite exposure in a marine wildlife host where direct parasite recovery is often limited. By shifting detection from parasite visualization to measurement of host response, this approach enables population-level surveillance and identification of subclinical or prior infestations. Adapting a crude mite-protein ELISA, widely used in terrestrial mange systems, to a marine respiratory mite expands diagnostic capacity within wildlife acarology and illustrates a practical approach for developing mite-specific diagnostics in non-model wildlife species where species-specific reagents are limited.

3rd Place (Tie): Pedro Conceição

Title: Insights on population structure and diversification of two Nearctic species of moss dwelling *Dinychus* (Acari:Uropodina) using DNA barcoding

Authors: Pedro Conceição[1] and Dr. Zoë Lindo[1]
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Most of Canada is located in the Nearctic realm that is characterized by diverse ecosystems and a recent post-glacial history supporting a unique biodiversity that remains underexplored, especially soil mites. The genus *Dinychus* (Acari:Uropodina), often associated with northern latitudes, has a worldwide distribution with 35 known species; out of these species, only two have been described for the Nearctic realm. However, it is estimated that there are at least 15 species undescribed in Canada and publicly available DNA barcode data (BINs) suggest an even higher number of species. Therefore, using morphological and molecular approaches, we investigated intra- and inter-specific patterns of *Dinychus* spp. from *Sphagnum*-moss dominated peatlands across a large geographical range in Canada. **Methods:** 82 individuals from genus

Dinychus spp. were collected from moss/peat samples of six peatland sites across Ontario, CA (max. distance between sites: 1000 km). Specimens were morphotyped and sent for DNA extraction and COI gene sequencing at the Canadian Centre for DNA Barcoding (CCDB). Barcode Index Number (BIN) assignment and gene tree reconstruction were used to assess interspecific limits. To investigate intra-specific genetic diversity and spatial structure of the two most abundant species, haplotype networks were generated using two most abundant species and the relationship between genetic distances and geographic distances was tested using a Mantel correlation test. **Preliminary results:** Three morphospecies were identified. Species 1 (n=46) was widely distributed except for one site and overlapping with Species 2 in two sites. Species 2 (n=32) was restricted to two sites and Species 3 (n=6) was the only species in the northern-most site. Morphological inspection suggests that all three are undescribed species, but deeper investigation is still ongoing. BIN assignment was supported by the genetic clustering and morphological identification (Figure 1), suggesting that DNA barcodes might be precise and aligned with traditional taxonomic methods, at least for the genus *Dinychus*. Intra-specific patterns: Most of haplotypes where restricted to one site (Figure 2A) and Species 1 showed lower nucleotide diversity (ϖ=0.656) when compared to Species 2 (ϖ=2.64) likely due the higher number of haplotypes with few mutations' steps. Pairwise genetic distances in Species 1 were weakly correlated to geographic distance (Mantel r= 0.12, p= 0.004) (Figure 2B). Species 2 showed a stronger correlation with distance (Mantel r= 0.62, p= 0.001) (Figure 2C), besides the maximum distance between the sites was less than 160km compared to over 800 km of Species 1 range this data suggests that Species 2 might be under different dispersal pressures.
Significance: My study aligns with the urgent need to describe and understand biodiversity patterns in a human induced mass extinction context. While genetic diversity loss is already a concern for conservation of many species, we have not even scratched the surface when it comes to soil dwelling organisms. Understanding the nuances of genetic and spatial constraints can help to better assess how vulnerable they are to current and ongoing anthropogenic threats such as habitat fragmentation. Finally, the true contribution of the Nearctic realm to the *Dinychus* diversity is yet to be unveiled.

3rd Place (Tie): Monique Raymond

Title: Host Shift and Specialization in a Novel Spider Mite Pest of Florida Blueberries

Authors: Monique Raymond[1] and Oscar E. Liburd[1]
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We report the first known occurrence of *Eotetranychus carpini* (Oudemans) (Acari: Tetranychidae) functioning as a pest of cultivated southern highbush blueberry *Vaccinium corymbosum* x *V. darrowii* (Ericales: Ericaceae) in Florida and the first record of this species causing economic injury to any cultivated blueberry crop worldwide. Field surveys revealed a strong association with early-developing cultivars under high tunnels, which is common in north-central Florida's blueberry production systems.
Laboratory colonization attempts demonstrated extreme host specificity: mites failed to survive or reproduce on multiple alternative hosts and were maintained only on blueberry foliage. In contrast, European populations of *E. carpini* are associated with European hornbeam *Carpinus*

betulus (Fagales: Betulaceae) and are major pests of the common grape vine *Vitis vinifera* (Vitales: Vitaceae), where host-switching experiments have revealed variable performance, which may suggest cryptic host-associated genetic divergence. Neither host occurs naturally in Florida, raising questions about host adaptation following introduction into blueberry agroecosystems.

To evaluate host-associated performance, host range potential, and blueberry cultivar-level resistance, we conducted replicated no-choice host-switching, antixenosis (preferential oviposition and feeding), and antibiosis (population growth rate) assays using multiple southern highbush blueberry cultivars, the American hornbeam *Carpinus caroliniana*, greenhouse-grown *V. vinifera*, and native muscadine grape *Vitis rotundifolia*. We additionally conducted genetic sequencing of the ITS region to assess similarity between Florida blueberry-associated mites to published *E. carpini* sequences from other regions and host plants. We hypothesized that the Florida population exhibits host specialization to blueberry, and reduced performance on Nearctic relatives of European hosts, consistent with host-associated divergence following introduction.

Preliminary results indicate strong host fidelity to blueberry, reduced survival on non-blueberry hosts, and differential performance among blueberry cultivars, suggesting potential for cultivar-mediated suppression. Together, these findings identify *E. carpini* as an emerging pest of southern highbush blueberry in Florida, provide evidence of host-associated specialization, and highlight risks of within-crop spread and spillover to other cultivated or native hosts. These results directly inform cultivar selection and spider mite pest monitoring, and establish a foundation for resistance screening and development of targeted integrated pest management strategies (IPM) in blueberry production.

4th Place (Tie): Ningzhu Bai

Title: Developing a standardized, visual method for assessing engorgement in host-derived ticks

Authors:

Ningzhu Bai[1] and Risa Pesapane[1,2]

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Accurate assessment of tick engorgement is fundamental to studies of tick feeding biology, pathogen acquisition, and host reservoir competence. In field-based studies and natural xenodiagnosis, host-derived ticks are frequently classified as “fed” or “engorged” without standardized criteria, despite strong evidence that the probability of pathogen acquisition increases with attachment duration and blood meal volume. Quantitative approaches such as scutal indices provide valuable estimates of feeding duration, but they require time-intensive morphometric measurements and lack standardized calculation methods across studies. Consequently, there is a

need for a rapid, reliable, and broadly applicable method to categorize engorgement levels in field-collected ticks.

Here, we developed and validated a visual scoring system to categorize engorgement in larval and nymphal hard ticks removed from wild avian hosts. Ticks representing three species, *Ixodes scapularis*, *I. dentatus*, and *Haemaphysalis leporispalustris*, were assigned to one of four visual engorgement categories (0–3), ranging from unfed to fully engorged, based on qualitative changes in body color and three-dimensional expansion. To validate whether visual scores captured biologically meaningful morphological change, a subset of ticks from each species, life stage, and engorgement score category was photographed under a digital dissecting microscope and measured for scutum width, body length, body width, and (for nymphs) coxal distance. Scutal indices were calculated as ratios of body dimensions relative to scutum width, which serves as a rigid reference structure during blood feeding.

Scutum width varied predictably among species and life stages but showed no biologically meaningful expansion with engorgement, supporting its use as a stable reference dimension. In contrast, scutal indices that incorporated scutum width increased monotonically with the visual engorgement score across species and life stages. Body length and body width were strongly correlated and expanded proportionally during feeding, indicating that their ratio did not provide additional information on engorgement progression. Principal component analysis of scutal indices revealed a strong alignment between visual engorgement scores and a continuous morphological gradient, with the primary axis explaining over 97% of total variation. Patterns of engorgement-associated change were consistent across tick species and life stages, indicating that visual scores reflect a generalizable feeding process rather than taxon-specific scaling differences.

Comparisons with previously published scutal index thresholds further demonstrated that visual engorgement categories correspond to reported feeding durations and probabilities of *Borrelia burgdorferi* acquisition. Fully engorged larvae consistently fell within scutal index

ranges associated with high infection probability, whereas unfed and slightly engorged larvae corresponded to low-risk categories.

This study provides a practical, standardized visual approach for assessing engorgement in host-derived ticks that is rapid, repeatable, and compatible with field-based and large-scale studies. By linking qualitative visual assessment with quantitative morphological validation, this approach improves comparability across studies, supports standardized tick selection for pathogen screening, and enables more robust inference in xenodiagnosis, surveillance, and ecological studies of tick–host–pathogen systems.

4th Place (Tie): Marie Yanchak

Title: Developing a standardized, visual method for assessing engorgement in host-derived ticks

Authors: Marie Yanchak[1] and Cameron Jack[1]

[1] Entomology and Nematology Department, University of Florida

Managed honey bee (*Apis mellifera*) colonies in the United States continue to experience high losses, largely driven by the ectoparasitic mite *Varroa destructor* (Acari:Mesostigmata). Synthetic acarides are commonly used to control *V. destructor*, however due to overuse and often off-label application by beekeepers, acaricide resistance has been documented in nearly every synthetic acaricide approved for use for *V. destructor*. Oxalic acid (OA) is an organic acid that is widely used for *V. destructor* control due to its efficacy and lack of documented resistance; however, much is still unknown regarding how application methods perform in control of *V. destructor* infestation. These studies evaluated a novel OA formulation, as well as assessed impacts of application temperature on OA vapor efficacy. These studies also evaluated impacts of application methods on colony health.

The first study evaluated a newly approved glycerin-based OA formulation, Api-Bioxal™ RTU Beehive Solution (OA RTU), designed to extend OA exposure within colonies. Fifty-five colonies were assigned to OA RTU, OA vaporization, OA sugar syrup trickle, Apivar®, or an untreated control. This study is unique in that a new rapid brood uncapping technique was used to quickly assess *V. destructor* infestation of immature honey bees. All treatments significantly reduced brood mite infestation, whereas other OA methods and Apivar® did not significantly affect brood-level infestation. Adult bee mite infestation declined over time across treated colonies, and all miticides increased 72-hour mite fall at different timepoints throughout the study, relative to untreated colonies. None of the treatments evaluated adversely affected colony strength as measured through visual estimation of bee population, brood area, and honey and pollen storage area.

In the second study, laboratory trials quantified the time required to vaporize 4 g of OA at three temperatures, revealing a strong temperature dependence: 161 s at 180°C, 107 s at 230°C, and 37 s at 280°C. A subsequent field experiment assessed colony health and mite control across these vaporization temperatures. Colonies receiving OA vapor treatments applied at any temperature showed significant reductions in adult and brood mite infestation and increased short-term mite fall relative to untreated controls, while colony strength parameters were unaffected by treatment temperature. Despite OA's known thermal decomposition threshold, vaporization at 230°C did not reduce efficacy, indicating that higher temperatures can substantially reduce application time without compromising control. ASA 2026 Marie Yanchak

Collectively, these findings demonstrate that OA is effective across a range of vaporization temperatures and that extended-exposure OA formulations may provide additional benefits for managing *V. destructor,* particularly within brood cells. Together, these studies offer practical guidance for optimizing OA-based *V. destructor* treatments for beekeepers to implement into their larger integrated *Varroa* management programs.