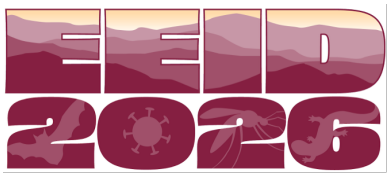

Poster Abstracts

Tues June 2 2026 5:00-6:00 PM (evens); 6:00-7:00 PM (odds)

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Katie Schroeder	63	Impacts of Daily Temperature Fluctuations on Disease in Host Individuals, Populations, and Communities	Thurs	5:30
Jason Sckrabulis	64	Invasive Plant Species as Conduits for Pathogen Spillover Between Natural and Agricultural Systems	Thurs	4:30
Carly Scott	65	Environment and Priority Effects Jointly Predict Multi-Pathogen Dynamics	Thurs	5:30
Monica Shah	66	Quantifying Seasonal Avian Influenza Virus Transmission Among Dabbling Duck Species at a North American Stopover Site	Thurs	4:30
Anna Shattuck	67	The Effect of Dengue Infection and Relative Humidity on the Thermal Preferences of Aedes Albopictus	Thurs	5:30
Clara Shaw	68	Maternal Age Effects on Offspring Virus Susceptibility and Infection Outcomes	Thurs	4:30
Yike Shi	69	Genetic Drift Acts Strongly on Within-Host Influenza Evolution but not Alone, Motivating Models of Respiratory Virus, Cancer, and Immune Interactions	Thurs	5:30
Carleen Silva	70	Burning Down the Mouse: Effects of Wildfire and Post-Fire Reseeding on Sin Nombre Virus Prevalence in Its Reservoir Host	Thurs	4:30
Molly Simonis	71	A Modeling Framework for Cross-Species Transmission in Co-Roosting Host Communities	Thurs	5:30
Brandon Simony	72	How Many Drugs are Enough? a Branching Process Model for Evolution of Resistance	Thurs	4:30
Vanessa Slack	73	Increases in Blastomycosis Incidence in Humans and Dogs by Ecoregion in Minnesota, 1999-2023	Thurs	5:30
Gabrielle Smith	74	Computational Evidence of Population Resilience Mechanisms in Banded Mongoose (Mungos Mungo) in Northern Botswana	Thurs	4:30

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Sam Smith	75	Estimating Slaughter Surveillance Coverage in the United States	Thurs	5:30
Ipsita Srinivas	77	Land Use Change: Implications for Host-Parasite Dynamics	Thurs	5:30
Aleksandra Stamper	78	Spatial Patterns and Environmental Influences of Covid-19 Outbreaks in the United States, Post-Omicron	Thurs	4:30
Alice Stitzer	79	The Role of Population Bottlenecks in the Recovery of Small Populations Affected by Disease	Thurs	5:30
Bengisu S. Subasi	80	Cuticular Microbiota Limit Pathogen Virulence Evolution in Drosophila Melanogaster	Thurs	4:30
Sachin Subedi	81	Inferring Anatidae Connectivity from Occurrence Data Using Seasonal Migration Networks to Inform 2.3.4.4b H5nx Spread	Thurs	5:30
Rahul Subramanian	82	Quantifying the Magnitude of Short and Long-Term Immunity Following Sars-Cov-2 Ancestral Booster Vaccination	Thurs	4:30
Ruijiao Sun	83	Joint Impacts of Temperature and Water on Within-Host Dynamics and the Heterogeneity of Infection Intensity	Thurs	5:30
Yining Sun	84	Zika Virus in the Americas: A Decade of Surveillance, Gaps, and Future Public Health Response	Thurs	4:30
Alicia Surratt	85	Feeding Disease: Threshold Conditions for Bird Feeder-Mediated Epidemics	Thurs	5:30
Zachary Susswein	86	Real-Time County-Level Effective Reproductive Number (Rt) Estimates for Seasonal Respiratory Epidemics Using Hierarchical Generalized Additive Models	Thurs	4:30
Sydney Szwed	87	Picking a Fight: Investigating Aggression-Immune Trade-Offs in the Jamaican Field Cricket (Gryllus Assimilis)	Thurs	5:30
Cecilia A. Sánchez	88	The Macroecology of Viral Coinfection	Thurs	4:30
Lucía Sánchez-Trejo	89	Modelling the Influence of Spatial Coupling on Pathogen Dynamics Between Natural and Anthropogenic Roosting Molossid Bats	Thurs	5:30
Nusrat Tabassum	90	Lagged Temperature Effects on Seasonal Mosquito Dynamics	Thurs	4:30
Luna Taguchi	91	Ecological Interactions in Malaria Coinfections	Thurs	5:30
Katherine Talbott	92	Prior Pathogen Exposure Induces Higher Heterogeneity in Future Susceptibility Among Male Compared to Female Songbirds	Thurs	4:30
Itamar Talpaz	93	Social and Ecological Traits Along with Network Structure Predict Viral Exposure in a Rural Human Population	Thurs	5:30
Himel Talukder	94	Cross-Species Transmission of Avian Influenza Between Wild Birds and Feral Pigs in Dynamic Environmental Systems	Thurs	4:30
Eliza Tarimo	95	Using Phylogenetics to Predict Bat Species' Adaptability to White-Nose Syndrome	Thurs	5:30
Anthony Taylor	96	Coexistence, not Extinction: Tombusvirus Lycopersici and Its Defective Interfering Rna Di72 Form a Stable Equilibrium in Planta	Thurs	4:30
Ibukunoluwa Tella	97	A Comparative Transcriptomics Approach to Elucidate Differences in Chagas Disease Vector Capacity Among Rhodnius Species	Thurs	5:30
Ellie Timmins	98	Pathogen Invasion and Establishment Modifies the Effects of an Environmental Driver of Disease	Thurs	4:30
Ravi Timsina	99	Social Resurrection: Social Interactions and Restoration of Disturbed Bumble Bees Microbiota	Thurs	5:30
Megan Tomamichel	100	Filtering Disease: Do Eastern Oysters Exhibit a Dilution Effect for Hematodinium Perezi in Blue Crabs?	Thurs	4:30
Beth Tuschhoff	101	The Role of Livestock in Shaping Rift Valley Fever Dynamics	Thurs	5:30
Marta Valldeperes	102	Take the Ibex by the Horns: A Mechanistic Basis for Sarcoptic Mange Dynamics in Iberian Ibex Populations	Thurs	4:30
Paige Van de Vuurst	103	A Preliminary Assessment of Population Genetic Structure of Rabies Reservoir, Desmodus Rotundus, in Colombia	Thurs	5:30
Medhavi Verma	104	Parasite-Induced Hormonal Manipulation Associated with Severe Reproductive Costs in a Wild Male Primate	Thurs	4:30
Taylor Verrett	105	Urbanization and Vector-Borne Parasitism in Overwintering Sparrow Assemblages	Thurs	5:30
Gabriella Veytsel	106	Coccidioidomycosis Epidemiology and Seasonality, Utah, 2009-2023	Thurs	4:30
Santiago Villamil-Chacón	107	Human Behavioral Dynamics and Vector Awareness Shape Aedes-Borne Disease Transmission: An Evolutionary Game Theory Approach	Thurs	5:30
Charlie Voirin	108	Seasonality of Sarbecovirus Seroprevalence in Cambodian Horseshoe Bats	Thurs	4:30
Jason Walsman	109	How are Endangered Frog Populations Recovering from Chytridiomycosis?	Thurs	5:30
Jasmine Wang	110	Surviving Maternal Infection During Lactation: Post-Infection Energetic Deficit Explains Increased Mortality – a Modeling Study	Thurs	4:30
Yintong Rita Wang	111	Estimating Vaccination- And Infection-Induced Protection Accounting for Heterogeneous Exposure Histories	Thurs	5:30
Maggie Weber	112	Within-Host Interactions Affect Both Parasite Density and Fecundity with Compounding Effects on Transmission Potential	Thurs	4:30
Fu Wen	113	Co-Occurrence of Endemic, Expanding, and Invasive Tick Species Across an Urban Gradient	Thurs	5:30
Mark Wilber	114	Disease-Associated Mortality Reduces Yukon River Chinook Salmon Escapement: A Novel Method for Quantifying Parasite Suppression of Host Populations	Thurs	4:30
Syd Wilson	115	Novel Management of Haemaphysalis Longicornis Using Baling:	Thurs	5:30

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Presenter	Poster Board	Title	Session	Time
Wenfei Xiao	116	Sources of Stochasticity Shaping Within-Host Viral Evolution in Acute Respiratory Infections	Thurs	4:30
Olivia Yancey	117	Evidence of Enteric Pathogens and Their Antibiotic Resistance Genes Escaping Wastewater Treatment Plants in Riverine Microbial Communities	Thurs	5:30
Qiqi Yang	119	Epidemiology and Control of H5 Avian Influenza in a Conserved Pelican Population	Thurs	5:30
Yang Yang	120	Heat-Sensitive Pathogens in a Warming Word: Effect of Thermal Fluctuations, and Potential for Adaptation.	Thurs	4:30
Ao Yu	121	Plastic Pollution Amplifies Schistosomiasis Risk by Altering Snail Host Life-History	Thurs	5:30
Yizhi Zhang	122	Heterogeneity of Airborne Virus Transmission in the Built Environment	Thurs	4:30
Kejia Zhang	123	Changes in Individual Susceptibility Across Reinfection Histories Shapes Epidemic Dynamics	Thurs	5:30
Xinyi Zhou	124	Characterize Molecular and Antigenic Evolution of Avian Influenza Virus H5 2.3.4.4b in North America	Thurs	4:30
Julia Zulawinska	125	Adaptation of Malaria Parasites Through De Novo Copy Number Variations Studied Through Long-Read Sequencing	Thurs	5:30
Carol de Souza Moreira	126	Context-Aware Machine Learning for Differential Classification of Dengue, Zika, and Chikungunya in National Surveillance Data	Thurs	4:30

Poster Sessions

Tues Poster Session

The Role of Flower Patch Composition on Transmission Dynamics and Spillover of Bee Pathogens

Presenter: Austin Acree

Coauthors: Bartlett, L. J.

Affiliation: University of Georgia; Athens, GA

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Session: Tues

Time: 6:00

Bee species are known to host a suite of pathogens, some of which are detrimental to individual health and may drive population declines or reduce ecosystem services. Flower patches, bee foraging sites, are a key site for indirect contacts between bees and have been shown to facilitate pathogen transmission from one bee to another. Accordingly, flower patches are important sites for the pathogen spillover between different bee species and may operate as hotspots for transmission of bee pathogens throughout a community. In this study we built a mechanistic model of pathogens transmission through populations of bees and flowers in a flower patch. Using this model, we demonstrate how changes to individual traits and community composition influence the number of infected individuals. This model highlights the importance of flower density and the frequency of visits to the flower on predicting pathogen outcomes. By expanding this model to multiple species, we have demonstrated that the inclusion of additional plant species can impact pathogen transmission dynamics, potentially leading to a reduction in infected individuals and spillover between bee species. Additionally, we have used a manipulated field experiment to better inform and assess the model. The results of our field experiment demonstrate the impact of planting regime on visit frequencies and the bee community composition.

Machine Learning Approaches to Vaccine Selection for Current and Emerging Strains of Foot and Mouth Disease Virus.

Presenter: Stephen Ross Addison

Coauthors: Haydon, D.T ; Farrell, M.J; Orton,R; Di Nardo, A

Affiliation: University of Glasgow, Glasgow, Scotland

Poster Board: 2

Session: Tues

Time: 5:00

Foot and mouth disease virus (FMDV) is a rapidly evolving virus that infects all ungulate species and has large impacts on domestic livestock worldwide. Vaccines for FMDV are generated by inactivating existing viral strains, but matching these vaccines to circulating FMDV strains is especially difficult, due to highly variable virus genotypes and complex mappings to antigenic phenotypes. Currently, vaccine effectiveness is measured by cross neutralisation tests that indicate the extent of protection provided by a vaccine to a circulating field strain. However, this is notoriously hard to predict, even between genetically similar strains. Here, we implement a novel methodology to predict vaccine efficacy between different viral strains of FMDV serotypes O and A. We do this by estimating cross neutralisation via machine learning. Using genetic and protein distances alone we can predict the vaccine titre value within normal experimental error with 88% accuracy for serotype O and 86% for serotype A. Furthermore, adding structural and protein features obtained from protein language models, we increase the predictive accuracy to > 93% for both serotypes. Our results allow us to predict the effectiveness of vaccines for current and emerging FMDV strains allowing for more informed and accurate decisions when designing vaccines to support targeted veterinary interventions.

A Novel Approach to Modeling Outbreak Risk of Emerging/Expanding Vector-Borne Pathogens

Presenter: Laura Alexander

Coauthors: Bento, A. I.; De Souza, W. M.; Hua, X.

Affiliation: Cornell, Ithaca NY, USA

Poster Board: 3

Session: Tues

Time: 6:00

Emerging and reemerging diseases present considerable threat to human and wildlife populations, through rapid range expansions driven by ecological shifts, land-use changes, and enhanced pathogen dispersal via global travel. . These dynamics challenge conventional suitability mapping and demand quantitative insights into transmission drivers at local scales.. We present a computationally tractable modeling framework leveraging Brazilian Oropouche virus infections surveillance data alongside local climate, weather, land use, and human population factors to uncover municipal-level outbreak predictors. Key positive drivers include peri-outbreak rainfall (30 days before/after first cases), soil properties, and tropical crop cultivation, reflecting ecological niches favoring vector breeding and host exposure. Annual precipitation sums inversely correlated with risk, highlighting nonlinear weather influences on transmission. These findings illuminate economic and ecological drivers of risk, highlight the role of weather conditions in temporal variation of risk, and enable identification of at-risk regions, informing targeted surveillance and vector control strategies to mitigate OROV's expanding threat. Prospectively, the model identified high-risk Brazilian municipalities before documented introductions and flagged transient hotspots tied to weather variability. Extrapolated regionally, it maps OROV invasion potential across South/Central America and the Caribbean, revealing vulnerabilities in under-surveilled areas. This approach advances understanding of land-use feedbacks, climatic modulation, and potential viral adaptations enhancing vector competence in arboviral emergence, with ongoing extensions to Chikungunya's historical spread to test long-term forecasting utility. By enabling targeted surveillance and control, it supports preemptive mitigation of expanding threats in changing ecosystems.

Serotype Succession in the Shadows: Bayesian Inference Reveals Eco-Evolutionary Feedbacks Driving Dengue Turnover

Presenter: Tijs Alleman

Coauthors: Alexander, L; Bajaj S; Vinhal I; Santos M; Bento A

Affiliation: Cornell University, Ithaca, NY, USA

Poster Board: 4

Session: Tues

Time: 5:00

Dengue fever, the fastest-spreading mosquito-borne viral disease, causes roughly 390 million infections per year through four co-circulating serotypes (DENV-1–4). Ecological and evolutionary interactions among these serotypes, shaped by cross-immunity, fitness trade-offs, and competition for susceptible hosts, generate recurrent cycles of strain replacement that restructure population immunity and drive epidemic oscillations. Predicting these emergent patterns remains a central challenge for evolutionary epidemiology and global health.

We developed a spatial Bayesian compositional model to reconstruct serotype-specific dengue incidence across all Brazilian municipalities from 1996 to 2025. We model observed counts with a Dirichlet–multinomial likelihood that captures both sampling uncertainty and overdispersion. To represent eco-evolutionary feedbacks, we coupled a replicator equation from evolutionary game theory with a catalytic epidemiological model linking serotypes' competitive fitness to the depletion and renewal of susceptible hosts. Our framework interprets serotype turnover as a competitive process mediated by host immunity, spatial connectivity, and the rate of immune escape.

To address data sparsity and improve identifiability, we applied a max-p regionalization algorithm that clusters municipalities with similar serotype trajectories, enhancing spatial coherence and signal recovery. The reconstructed latent incidence surfaces uncover the gradual geographic expansion of DENV serotypes, exposing early invasion fronts that foreshadow future dominance and epidemic amplification. By integrating ecological clustering, evolutionary game theory, catalytic models, and hierarchical Bayesian inference, our approach unites population-level immunity modeling with mechanistic models of multi-strain competition. The resulting synthesis provides a quantitative basis for predicting when and where antigenic turnover amplifies epidemic risk, offering a generalizable approach to understanding pathogen diversification and emergence in complex ecological landscapes.

Age Drives Variation in Susceptibility in Experimental Epidemics

Presenter: Irish Amundson

Coauthors: Amundson, I.A.; Kuzminski, S.G.; Gibson, A.K.

Affiliation: University of Virginia; Charlottesville, Virginia; United States

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Session: Tues

Time: 6:00

Heterogeneity in disease transmission shapes epidemics across ecosystems and public health spheres. This heterogeneity is observed in diverse taxa and both ancient and emerging host-disease interactions. One important driver of heterogeneity is host age, which influences both host physiology and social structure. Population age structure is known to be a powerful predictor for epidemic models of diseases such as measles, but experimental epidemics may help parse the effect of individual age and population age structure on infectiousness and susceptibility. To determine the effect of age on these different levels of host-disease interaction, we use the host Caenorhabditis elegans and its natural microsporidian pathogen, with which we can measure individual and population traits over the course of experimental epidemics. We investigated how an individual host's age impacts susceptibility and trajectory of disease burden over time. We found that adult hosts acquire far more of the pathogen than juveniles, by about 7.2 times. Work in other systems suggests that, on the level of a population, highly susceptible hosts can dilute available infectious agents in the environment and thus shield other hosts in the population (Shaw et al. 2024). To test this hypothesis, we assessed experimental epidemics in populations with controlled variation in age structure. Though our results supported the disparity between adult and juvenile susceptibility, we found that age structure had no measurable effect on susceptibility. We hypothesize that this result may be due to the initial density of infectious agents that seed epidemics. It may also be influenced by behavioral changes of hosts in mixed-age populations, as seen in a prior study of C. elegans (Scott et al. 2017). Though age has a profound effect on an individual's disease state, population age structure does not lead to a dilution of disease in our cross-scale study on experimental epidemics.

Impact of Physiological Stress on Coronavirus Infection Dynamics in Neotropical Fruit- And Nectar-Feeding Bats

Presenter: B.R Ansil

Coauthors: Ansil, B.R; Pereira, M.M.T; Vicente-Santos, A; Quintela-Tizon, R.M; Olbrys, B.L; Cummings, C; Heckley, A.M; Sanchez, K; Roistacher, A; Sánchez-Trejo, L; Calderón-Acevedo, C.A; Fenton, M.B; Simon, R; Page, R.A; Simmons, N.B; Banerjee, A; Becker, D.J.

Affiliation: School of Biological Sciences, University of Oklahoma; Norman, OK; USA

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Session: Tues

Time: 5:00

Resource limitation and reproduction are important drivers of viral shedding in bats. These stressors are hypothesized to manifest physiologically as chronic stress, which impairs immunity and increases viral shedding. However, the mechanistic links among these stressors, immunity, and viral replication remain poorly understood. Using coronaviruses and Neotropical fruit- and nectar-feeding bats as a model system, we test this long-standing hypothesis by integrating mathematical modeling, field studies, and in vitro experiments.

We used a susceptible–infectious–recovered–susceptible modeling framework to analyze impacts of stress on equilibrium infection prevalence and the basic reproductive number (R□). This model was parameterized using fruit bats, and we explored varying functional relationships between stress and epidemiological parameters. Preliminary results indicate prevalence is maximized at moderate stress, whereas R□ consistently declines with increasing stress. This reduction in prevalence and R□ are driven by population declines resulting from stress-induced mortality and reduced birth rates. Ongoing Belize and Panama fieldwork aims to validate these findings by investigating variation in the neutrophil-to-lymphocyte ratio and fur cortisol, two stress biomarkers, in relation to reproduction and habitat fragmentation. We also ask how much variation in coronavirus infection is explained by these stress biomarker levels.

Meanwhile, we simulated physiological stress in Carollia perspicillata lung-derived cells by exposing them to cortisol and infecting them with vesicular stomatitis virus (VSV). We expected increased VSV replication in the presence of cortisol; however, we observed no increase in viral titers but detected elevated viral protein expression. A follow-up experiment using polyinosinic:polycytidylic acid, a viral infection analogue, showed increased expression of antiviral genes. These preliminary results suggest a more complex and nuanced impact of cortisol on viral replication in bat cells. We aim to develop additional cell lines from other focal Neotropical bat species and test the relationship between cortisol and coronaviruses to understand species-specific variation in host–virus interactions.

Evaluating the Effects of Climate and Urbanization on the Disease Dynamics of a Wild Plant-Fungal Pathogen System: A Multi-Year Analysis

Presenter: Kaylee Arnold

Coauthors: Morris, Cheyenne M.; Fox, Quinn N.; Penczykowski, Rachel M.

Affiliation: Washington University, St. Louis, MO, USA

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Session: Tues

Time: 6:00

The effects of climate and urbanization on host-parasite dynamics are highly variable across space and time. Cities experience milder winters and higher daily temperatures compared to their rural counterparts due to the urban heat island effect, which influences many factors such as host susceptibility, parasite transmission, and pathogen virulence. However, the mechanisms through which urbanization and climate synergistically affect disease dynamics over time are poorly understood, especially in plant-pathogen systems. Here we investigated the impacts of urbanization and climate fluctuations on disease prevalence in a common plant-fungal pathogen system across multiple years. We conducted monthly field observations of Plantago and their foliar fungal pathogens (powdery mildews) from 2019 to 2024 in the Greater St. Louis region (Missouri, USA). Across all years, mildew epidemics occurred earlier and reached higher disease severity at urban and suburban sites (N = 16) compared to rural sites (N = 6), with greater prevalence in shaded microclimates. However, the magnitude of these effects varied between years and within land use type. Infection prevalence peaked in 2020, reached its lowest point in 2021, and gradually increased between 2022 and 2024. This temporal variability suggests that climate conditions play a critical role in shaping disease dynamics. Using local weather station data, we examined how climate and urbanization influence powdery mildew dynamics. Relative humidity and urbanization intensity were the strongest predictors of mildew prevalence, while maximum daily temperature and precipitation reduced prevalence. This work demonstrates that climate and urbanization interact to shape plant-pathogen dynamics and emphasizes the importance of using multi-year climate data to predict disease risk in future climate scenarios and urbanized landscapes.

The Return Trip: Exploring Viral Spillback Events

Presenter: Akiko Kaitlin Balitactac

Coauthors: Rowell, A; Ghosh, E; Sombito, L; Bono, L.M

Affiliation: Texas Tech University, Department of Biological Sciences; Lubbock, TX; United States of America

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Time: 5:00

Viruses exist in a world where they are constantly exposed to potential hosts—giving viruses the opportunity to shift to novel hosts (spillover) and to re-encounter their ancestral host (spillback). During host range evolution, it is possible that a virus may incur a fitness cost on their ancestral host, i.e. antagonistic pleiotropy. Alternatively, evolution in another host may allow the population to explore sequence space inaccessible in the ancestral host. Many studies focus on spillover events, but little is known about how a virus responds to being returned to its ancestral host (spillback). Here, we aim to evaluate the fitness consequences of spillback. Previously, the host range of the bacteriophage phi6 was expanded across a set of novel hosts: P. syringae pv. tomato and P. pseudoalcaligenes ERA. The initial mutations that enabled host range expansion were costly (antagonistic pleiotropy). These mutants were then evolved on either one novel host or alternating between the two novel hosts for 150 generations. Here, we isolated a single plaque from the end of these evolution experiments and passaged them on their ancestral host P. syringae pv. phaseolicola (Pp) for 100 generations. We found that the populations that experienced spillback maintained a broad host range and had fitness effects that were idiosyncratic compared to the wild-type ancestor. This indicates that phage experienced weak selection during spillback despite long-term adaptation to novel hosts. Currently, we are working on uncovering mutations that arose during evolution on Pp. We are looking to determine whether the populations adapt to the ancestral host via reversions to the wild-type or new mutations in genes associated with attachment. Our results will allow us to assess the impact of a spillback event on the evolutionary trajectory of host range expansion.

Exploring Environmental State Space Anomalies and Filovirus Spillovers in Central Africa

Presenter: Kelsee Baranowski

Coauthors: Bharti, N.

Affiliation: Penn State University; University Park, PA; USA

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Session: Tues

Time: 6:00

Zoonotic filoviruses can cause deadly outbreaks of viral hemorrhagic fevers in humans and wildlife in Africa. Serosurveillance of wildlife confirms that fruit bats are the reservoir hosts for some of these viruses and suggests the same for others. Filoviruses can transmit, or spillover, from fruit bats to humans, or to intermediate hosts, such as non-human primates and antelopes. Previous research has linked spillovers to transitions in rainfall seasonality, changes in vegetation health, and fruit bat birth pulses. To rigorously investigate links between environmental anomalies and filovirus spillover events, we analyzed time series data on vegetation health, rainfall, and temperature around spillovers in Central Africa from 1982-2022.

We used time-delay embedding to create 3D manifolds of monthly vegetation health, rainfall, and temperature in circular buffers of five radii around locations of reported filovirus spillovers from 1982-2022. We calculated the point distance of each month to the 10-year averaged center of the manifold for each variable and buffer size. We performed continuous wavelet transformations on the distance to manifold center and calculated the variance of wavelet power across all frequency scales at each time point. We defined anomalies as months exceeding the 95th percentile of mean wavelet variance. We determined the number of spillovers reported after an environmental anomaly, the spillovers that did not follow an anomaly, and the number of anomalies that did not precede a spillover.

We found that several spillovers were preceded by or coincided with anomalies in precipitation and/or vegetation health while few were preceded by anomalies in temperature. No universal environmental anomaly was associated with all spillover events. Clustering spillovers by common preceding anomalies revealed potential similar environmental processes prior to spillovers. Characterizing the environmental anomalies and temporal lags before reported spillovers is essential for understanding the environmental mechanisms driving filovirus spillovers in Central Africa.

Negative Impacts of Poor Quality Nutrition Outweighs the Benefits of High Supplementary Feed Quality in Social Insect Health

Presenter: Lewis Bartlett

Coauthors: Kaderis, Josiah; Harrod, Audrey; Collins, Ian; Garrison, Jack.

Affiliation: University of Georgia, Athens, GA, USA

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This poster overviews a series of graduate student led experiments contrasting supplementary feeding regimes of both carbohydrates and protein as part of managing social insect pollinators (bumblebees and honey bees). We find that poor quality supplemental feed inhibits social immune investment (indicated by reduced GOX activity in stored honey) and that pathogens show life-mode specific responses in prevalence within populations based on feeding regime. Specifically, gut pathogens seemingly benefit from excess low-quality protein, while hemolymph-associated viruses are either reduced in titre or neutral in response, which we hypothesise is linked to larger population growth rates of the host increasing carrying capacity for virus-vectoring ectoparasitic mites. Our results demonstrate the multiple routes via which supplemental feeding can impact parasite-host population dynamics in two closely related semi-managed, semi-wild system.

Range Expansion or Improved Surveillance: The Curious Rise of Rift Valley Fever Virus in Southwest Uganda.

Presenter: Tegveer Basraon

Coauthors: Clancey, E; Njenga, M.K; Remien, C.H; Nuismer, S.L.

Affiliation: University of Idaho, Moscow, Idaho, United States of America

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Time: 6:00

Rift Valley fever virus, a mosquito-borne phlebovirus, causes significant economic and public health impacts in affected areas through abortion and death of livestock, and hemorrhagic or febrile illness in humans and ruminants. It has long been endemic in East Africa where it is characterized by low levels of spillover interspersed with sporadic climate-driven region-wide epidemics. This pattern of endemic maintenance with episodic epidemics is well documented in much of East Africa. A curious exception to this pattern is Uganda, which despite porous borders allowing livestock and human movement from adjacent Rift Valley fever (RVF) endemic countries, reported no cases of RVF prior to 2016. After its initial detection in 2016 and through 2023, Uganda has reported sporadic human outbreaks and documented widespread seroprevalence in humans and livestock. Because the emergence of RVF in Uganda may be indicative of an elevated regional epidemic risk, it is critical to understand the timing, origin, and transmission dynamics of the disease in Uganda. The prolonged absence and sudden emergence, however, could have multiple plausible explanations. Using mathematical models fitted to age-structured serological data, we tested three competing hypotheses. First, that RVF has been cryptically circulating within SW Uganda but remained undetected prior to 2016 due to under-diagnosis or lack of surveillance. Second, that RVF expanded into SW Uganda in 2016 with a concomitant increase in spillover into the human population. Third, that cases of RVF infection in Uganda detected between 2016-2023 were a transient and short-lived outbreak. By analyzing model predictions and patterns of age-specific serological data, we evaluate relative support for each of the competing hypotheses to identify the scenarios most consistent with the data, and provide insights into RVF emergence and persistence in Uganda.

Edge Ecology of an Emerging Vector: Gulf Coast Tick (Amblyomma Maculatum) Distribution in a Recreational Landscape

Presenter: Evan Behmer Porter

Coauthors: Pesapane, R.

Affiliation: The Ohio State University; Columbus, OH; USA

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Session: Tues

Time: 5:00

Gulf Coast ticks (Amblyomma maculatum; GCT), vectors of Rickettsia parkeri rickettsiosis, are an emerging medical and veterinary public health threat recently identified in Franklin County, Ohio. Given their unknown local ecology, this study sought to characterize GCT habitat selection as it relates to human and animal use of anthropogenic landscapes. We studied the habitat selection of Gulf Coast ticks in relation to high-use pathways bordering field-lawn edges. Weekly sampling occurred between May and September 2024, with each sample consisting of four parallel tick drags along a field-lawn habitat edge. Only adult stage GCT were observed. At this site, GCT exhibited significant accumulation at the field edge. Additionally, relative GCT distribution across the field-edge border varied by macro-level temperature and humidity conditions. Adult Gulf Coast ticks were active between May and late July, though without discernable activity peaks. While this project was limited in its scope, the collected GCT outnumbered those pooled from local and state public health agency surveillance. Densities along the field edge exceeded those observed via non-targeted agency tick drags at the same park. This edge-associated accumulation of Gulf Coast ticks is a phenomenon uncharacterized in previous field studies. Association with human- and pet-frequented areas suggests GCT pose a significant hazard along these habitat borders. Therefore, there exists a need for systematic, habitat-targeted surveillance to quantify the holistic threat that Gulf Coast ticks pose in Ohio and other newly invaded territories.

The Population Dynamics of Human Rhinovirus and Inference of Viral Interaction

Presenter: Wakinyan Benhamou

Coauthors: Park, S.W.; Howerton, E.; Metcalf, C.J.E.; Grenfell, B.T.

Affiliation: Princeton University, Princeton, NJ, USA

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Time: 6:00

Many respiratory pathogens co-circulate within human populations. Yet, how pathogen community structure shapes the dynamics of infectious diseases remains poorly understood. At the population level, investigating polymicrobial dynamics, with potential underlying competitive or cooperative interactions, is challenging because of confounding factors such as differing seasonality. This is particularly true for endemic pathogens which typically exhibit stable periodic dynamics. The disruption due to the implementation of non-pharmaceutical interventions during the COVID-19 pandemic thus represents a unique large-scale natural experiment that can be leveraged to provide valuable insights into the complex interplay between respiratory pathogens. Here, we focus on the population dynamics of human rhinovirus (RV, common cold) and on the potential viral interference of influenza A virus (IAV, flu A), which is hypothesized to account for their asynchronous circulation. Using a Bayesian framework, we first show based on simulated data that perturbations can be a powerful tool to disentangle the contribution of pathogen interaction from other epidemiological factors. We then apply our framework to pre- and (post-)pandemic surveillance time series from the US and Canada. We estimate key parameters of RV but find no support for an influence of IAV at the population level.

Functional Tests of Immune Gene Divergence Between Closely Related Drosophila Species

Presenter: Camila S. Beraldo

Coauthors: Nabors, M.; Patch, K.B.; Unckless, R.L.

Affiliation: Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

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Infectious diseases impose strong selective pressures on host populations and are a major driver of evolutionary divergence between species. Consistent with this, immune genes are among the fastest-evolving genes in the genome. Despite this pattern, the genetic basis of species-level differences in immune defence remains poorly understood, as relatively few studies have functionally tested how divergence at specific immune loci contributes to variation in resistance among closely related species. Here, we investigate the functional consequences of immune gene divergence using two closely related species, Drosophila simulans and Drosophila mauritiana, which differ in their responses to bacterial infection. We focus on a duplicated antimicrobial peptide gene as a tractable system to test how gene copy number and sequence divergence contribute to immune function. Antimicrobial peptides are central components of insect innate immunity and provide a powerful framework for experimentally dissecting immune divergence. To do so, we use CRISPR/Cas9 genome editing to systematically replace individual copies of this immune gene in both species with fluorescent markers (DsRed or GFP). Each native copy is deleted and replaced via site-specific integration, allowing precise control over genetic background and direct functional comparisons among gene copies between species. Ongoing work focuses on establishing all engineered lines in a homozygous state. Future experiments will assess immune function by infecting males from each line with a bacterial pathogen and quantifying survival outcomes. Together, this approach will provide direct functional insight into how immune gene duplication and divergence contribute to the evolution of host defence.

When There's an Eviction Notice for Bats, What Happens to Pathogen Dynamics?

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Many wildlife species live communally in human-made structures, often leading to conflict with humans. Bats in particular can form large colonies in houses and are frequently evicted from these anthropogenic roosts. While bat roost removals are common, the consequences for pathogen transmission are poorly understood. Bats may experience increased physiological stress from removal and more interactions with infected individuals, impacting susceptibility to pathogens. Here, we develop compartmental models to investigate how increased stress impacts roost-level infection prevalence following an eviction event. We ran these models under different assumptions about the stress impact of eviction, the infection status of the evicted roost, and the occupancy of the roost that the evicted bats move into. Our initial two-roost models show that pathogen prevalence is maximized following eviction when uninfected bats are evicted into an infected roost. Epidemic sizes are maximized when stress impacts to susceptibility were increased, with the strongest effects for the scenario where infected bats are evicted into an unoccupied roost. When susceptibility is increased due to stress, the timing of maximum epidemic size occurs sooner following eviction. Future work will include varying the timing and duration of eviction as well as the duration of increased susceptibility due to stress. This work will provide insight into the stress and timing-related consequences of eviction on transmission dynamics across a suite of pathogens. Additionally, this framework could be extended to study the implications of eviction to cross-species transmission or local and regional consequences of eviction on pathogen dynamics using spatially explicit frameworks.

The Effects of per- And Polyfluoroalkyl Substances (Pfas) on Amphibian Infectious Disease Dynamics

Presenter: Olivia Biasetti

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Emerging infectious diseases and environmental contaminants are recognized as co-occurring stressors that influence host-pathogen interactions. Per- and polyfluoroalkyl substances (PFAS) are persistent pollutants that negatively impact both human and wildlife health. Previous studies in amphibian models show that chronic PFAS exposure can impair immune function and fitness. However, most toxicological research focuses on single chemical exposure scenarios, which don't reflect the variable and intermittent nature of PFAS. To address this gap, we investigated how the timing and duration of exposure to an environmentally relevant PFAS mixture influence fitness metrics and susceptibility to ranavirus infection in amphibian larvae. We evaluated this across three species, bullfrogs (Lithobates catesbeianus), wood frogs (L. sylvaticus), and crawfish frogs (L. areolatus), using 30- and 42-day laboratory experiments. A 4×2 full factorial design was implemented, with eight treatment groups and a total of 720 tadpoles. PFAS treatments included early (days 0-20 or 0-28), late (days 20-30 or 28-42), and continuous (days 0-30 or 0-42) exposure; ranavirus was introduced on day 20 or 28. We hypothesized that continuous PFAS exposure would lead to higher ranavirus prevalence and load compared to early or late exposure and that both continuous and early exposures would reduce fitness metrics, such as scaled mass index (SMI), snout-vent length (SVL), and mass. Results found that there were no generalizable trends across the three species; effects were species and life history characteristic-dependent. There was an interactive effect found in SMI for crawfish frogs, primarily driven by early PFAS exposure. Furthermore, there was significantly lower viral load in the late PFAS treatment in the wood frog experiment when compared to other treatments. This study focuses on the importance of incorporating realistic contaminant scenarios into disease ecology research, highlighting that disease agents interact differently within hosts and the need for further mechanistic insight into co-occurring stressors.

Impact of Rna Interference on the Outcomes of Within-Cell Competition Between Sylvatic and Human-Endemic Strains of Dengue Virus

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Dengue virus (DENV) has previously emerged from the sylvatic (wildlife) cycle at least four times, resulting in the four serotypes that circulate today in the human-endemic cycle. The ancestral sylvatic transmission cycle involves non-human primates and forest-dwelling Aedes mosquito species, while the human-endemic cycle involves humans and the peridomestic mosquito species Aedes aegypti and Aedes albopictus. The sylvatic cycle of DENV remains extant in both Asia and Africa, and spillover into humans occurs with some regularity, but these events have not led to emergence of new human-endemic lineages of DENV in recent times. A major focus in our lab is understanding the factors that limit DENV emergence, one of which may be within-mosquito competition. We have previously demonstrated that sylvatic DENV are competitively inferior than human-endemic DENV in Ae. albopictus C6/36 cells. However, subsequent studies revealed that this cell line lacks a functional RNA interference (RNAi) pathway, the main defense of mosquitoes against arboviruses. In the current study, we quantified the outcome of concurrent and lagged co-infection of sylvatic and human-endemic DENV strains in Ae. albopictus U4.4 cells, which are capable of mounting an RNAi response to infection.

Comparison of Alternative Models of Human Movement and the Spread of Disease

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Predictive models for the spatial spread of infectious diseases have proved indispensable in recent years as tools for the management of infectious disease outbreaks. In particular, various versions of the so-called gravity model—borrowed from transportation theory—have figured prominently. However, the original literature suggests that this model is misspecified inasmuch as it fails to capture higher-order interactions among population centers. The fields of economics, geography, and network sciences have derived alternative formulations that offer more realistic descriptions of human movement within and among conurbations. These include Stouffer's rank model, Fotheringham's competing destinations model, and the radiation model of Simini et al. We fit these models, and variants on them, to the uniquely detailed dataset of prevaccination measles incidence in the 954 cities and towns of England and Wales over the years 1944–65, comparing them within a consistent likelihood framework. We find that while the gravity model is a reasonable first approximation, both Stouffer's rank model, an extended version of the radiation model, and the Fotheringham competing destinations model provide significantly better fits, Stouffer's model being the best. Through a new method of spatially disaggregated likelihoods we identify regions of relatively poor fit, and show that it is indeed in densely-populated conurbations that higher-order spatial interactions are most important. Our main conclusion is that there is scope within infectious disease modeling for a broader class of models of human mobility and its role in shaping spatial spread of infection.

Vaccine Strains of Influenza a Virus Acquire More Genetic Diversity by Embryonated Chicken Egg Propagation than by Mammalian Cell Propagation

Presenter: Juliette Blais-Savoie

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In disease ecology and evolution, host heterogeneity is thought to be protective against infectious diseases at a population level. In medicine, reducing heterogeneity is often the goal, e.g., generating a fully protected population through vaccination. Yet sources of heterogeneity cannot always be controlled. The majority of seasonal influenza vaccines contain viral antigens from viruses propagated in embryonated chicken eggs (ECEs), where egg-adaptive mutations in the hemagglutinin (HA) surface antigen protein are known to occur. Though these are often considered problematic for disease control, recent theory demonstrates that variation in the antigens received by individuals through vaccination can lead to increased population immunity, ergo greater overall vaccine effectiveness. What remains unclear is how much diversity is generated over the course of vaccine production, what frequency new mutations can achieve during the process, and whether the answers to these questions depend on if the viruses are grown in eggs (the historical standard) or in mammalian cells (a relatively new approach).

We propagated WHO-recommended vaccine seed strains of H1N1 from previous influenza seasons as well as a pandemic vaccine candidate strain of H5N1 in ECEs and Madin-Darby canine kidney (MDCK) cells and compared the genetic diversity of HA between propagation methods for each strain.

The mean pi nucleotide diversity index of H1N1 HA sequences increased incrementally across five passages in ECEs, while remaining significantly lower across five passages in MDCK cells. Conversely, egg-grown H5N1 retained consistently lower pi values across several passages. Mutations on antigenic sites of the HA gene with known impact on antigenic drift of circulating influenza viruses were observed in egg-grown H1N1. These preliminary findings suggest that ECE-based vaccine manufacturing methods may lead to more antigenically diverse influenza vaccines than propagation in MDCK cells in seasonal influenza vaccines, though this may not be the case for pandemic influenza vaccines.

Increasing Complexity of Selective Pressures Mediates Coevolution Between Phage and Host

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Translating virus-host dynamics between the lab and nature has been difficult, suggesting that simplified lab environments impose relaxed selective pressures relative to more complex environments experienced in nature. In previous experiments, the bacterium Pseudomonas syringae pv phaseolicola, a plant pathogen, can rapidly evolve resistance to the bacteriophage (bacteria-infecting virus) phi6 by altering the phage attachment site (the type IV pilus) in liquid cultures, frequently leading to the phage extinction. However, such evolution is unlikely in nature as pilus function is essential for locomotion within plants, so we imposed selection for the maintenance of pilus function using a bead transfer. We experimentally (co)evolved the host 1) with the phage using a bead transfer, 2) with the phage but without the bead as in previous experiments, and 3) alone with the bead. We found that phages are significantly less likely to go extinct with bead transfer. We also found that the host is more likely to form a pellicle biofilm with bead transfer and that these biofilms formed earlier in the treatment with phage. We characterized host phenotypes at the end of the experiment as either non-piliated or super piliated (resistant), partially piliated (partially resistant), or fully piliated (susceptible) to phage. Preliminary results show that bead transfer was associated with an increase in susceptible phenotypes, whereas no-bead controls showed greater diversity among host phenotypes. We are currently assessing the pilus function and maintenance of these phenotypes using twitching motility assays and quantitative PCR. In conclusion, we demonstrated that increasing the complexity of selective pressures can alter the evolutionary dynamics and outcomes, even in simple models of phage-host coevolution. We found that using the bead transfer imposed selection for pilus maintenance and that this increased the coexistence of phage and host.

The Evolution and Spread of Crimean-Congo Haemorrhagic Fever Virus (Cchfv) Across Multiple Centuries

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Crimean-Congo haemorrhagic fever virus (CCHFV) is a re-emerging tick borne zoonotic virus of global public health concern, with increasing incidence and geographic expansion across Europe, Asia, and Africa. While previous phylogeographic studies have established broad patterns of CCHFV diversification, they do not explicitly investigate the ecological and anthropogenic processes shaping viral dispersal, particularly over its extended evolutionary history. Here, we reconstruct the full-scale dispersal history of CCHFV over thousands of years by integrating genomic data and spatiotemporal predictors in a phylodynamic framework. To capture changes in dispersal mechanisms through time, we analyzed viral movement across ancient and modern periods, enabling direct comparison of processes operating over different time scales. We curated a unique set of covariates explicitly aligned to these periods of time, including historical livestock trade connectivity, modern livestock imports and exports, migratory bird flyways, and vector habitat suitability. Embedding these predictors within a discrete phylogeographic reconstruction and generalized linear diffusion model, we quantified the relative impact of these covariates driving CCHFV movement throughout historical ecological and anthropogenic developments. Temporal stratification of migration processes allowed us to disentangle ancient diffusion pathways from drivers of contemporary spread. By combining genomic data with ecologically and historically informed predictors, this study establishes the evolutionary and ecological backbone of CCHFV, providing a time-calibrated history of the processes structuring viral spread. This data-driven approach enables mechanistic inference into how ecology and connectivity contribute to the emergence and expansion of zoonotic pathogens.

Overcoming Detection Lag in a Cryptic Panzootic: Chytrid Fungus Linked to Historically Enigmatic Amphibian Declines in the Brazilian Atlantic Forest

Presenter: Jack Boyette

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Human activity increasingly facilitates the global spread of non-native species at a speed that outpaces our ability to detect and respond to these biological invasions. This dynamic often creates detection lags that obscure our understanding of the critical early stages of invasion, especially for pathogens, which are easily transported, difficult to detect, and inherently harmful to their hosts. Consequently, many pathogen invasions must be reconstructed retrospectively. Such retrospective approaches are essential for inferring the early dynamics of pathogen emergence and spread, as well as understanding subsequent host responses. Reconstructing undetected invasions of Batrachochytrium dendrobatidis (Bd), a fungal panzootic responsible for mass amphibian biodiversity losses, is necessary to infer its role in historical amphibian declines. Here, we use museum specimens to reconstruct Bd dynamics across declines observed at the Borac,àö¬©ia Biological Station within the Brazilian Atlantic Forest. Two conflicting hypotheses explain Bd,Äö√Ñ√¥s dynamics in this region: (1) Bd is enzootic, with historically stable prevalence, or (2) Bd invaded recently, driving regional amphibian declines. To test these, we swabbed 365 museum specimens and 286 modern frogs collected at Borac,àö¬©ia and used molecular and histological methods to infer temporal patterns of Bd infection prevalence, lineage identity, and allele frequency. Infection was not detected among specimens collected before the decline, whereas infection was detected in 58.8% of post-decline museum specimens. Infection prevalence differed between observed-decline and no-decline species, likely reflecting species-specific interactions between natural susceptibility and ecological exposure risk. Only the global panzootic lineage of Bd (Bd-GPL) was detected in the first post-decline sampling period. In modern frogs, infection prevalence was 34.3% and did not vary by decline history. Our results provide the first direct, site-specific evidence linking Bd-GPL invasion to historically enigmatic declines in the Atlantic Forest, while modern prevalence patterns suggest evolution of infection tolerance among species that historically declined.

Informing Preparedness: Structural Sensitivity and Feral Swine Risk in Simulated African Swine Fever Outbreaks

Presenter: Christopher Brandon

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The United States is closely monitoring several transboundary animal diseases. Among these, the U.S. Department of Agriculture has identified African Swine Fever (ASF) as a critical threat due to the lack of an effective, approved vaccine and the severe economic impacts an outbreak could cause. Using a national-scale, premises-level livestock disease spread model, we simulated ASF outbreaks in the contiguous U.S. These simulations indicated limited options among ASF control measures and revealed consistency in regions sparking the most consequential outbreaks. We used our simulation results to understand the uncertainty and sensitivity of ASF outbreaks in the U.S. by conducting sensitivity analyses on our model parameters. We found that infrastructure parameters – those describing the spatial configuration, connectivity, and demography of the U.S. swine industry – have a greater effect on disease outcomes than parameters surrounding ASF virology. This indicates that the structural features of the swine industry play a larger role in outbreak dynamics than uncertainty surrounding the virus alone. These results highlight that the location of ASF introduction is consequential to disease outcomes. While our disease model simulates transmission among domestic swine, feral swine are known reservoirs and transmitters of ASF. Given the importance of infrastructure on outbreak progression, we integrated model-based projections with spatial data on feral swine population density to identify regions where introduction risk in domestic and feral swine may coincide. By linking sensitivity-driven insights on industry structure with feral swine distributions, this work identifies areas of heightened vulnerability to ASF emergence and transmission.

Seasonal Differences in West Nile Virus Prevalence in Mosquitoes Collected from Urban and Rural Areas

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West Nile virus (WNV) is the leading cause of domestically acquired arboviral disease in the continental United States. The virus is transmitted to humans by mosquitoes in the genus Culex. Mosquitoes are most active during spring and summer when temperatures are higher, and days are longer. When mosquitoes enter a state of dormancy (diapause) in late fall and winter, WNV transmission ceases. Previous laboratory studies demonstrate that light pollution and higher temperatures prevent Culex pipiens from entering diapause, suggesting that urbanization could extend the period of viral transmission in the fall. In Ohio, public health agencies collect and test Culex mosquitoes for WNV from mid-May through the end of September. Mosquito pools typically test positive for WNV during late summer and early autumn. However, it is currently unknown when and where mosquitoes contract the virus and begin circulating it, and whether WNV prevalence differs between urban and rural areas. To address these questions, we continuously collected mosquitoes from urban and rural sites in Northern and Central Ohio from October 2024 through December 2025 (n = 4 urban and rural sites at each region; 16 total sites). Temperature, humidity and light levels were continuously monitored using Hobo data loggers at each site. Culex mosquitoes were identified using a morphological key and pooled by sex and species. RNA was extracted from pools of female mosquitoes, and samples were tested for viral RNA using reverse transcription qPCR. Out of 843 tested pools, 32 were positive for WNV (3.8% positivity). Although higher numbers of Culex mosquitoes were collected from rural sites, 72% of WNV-positive mosquito pools were collected from urban sites. The earliest and latest WNV-positive pools were collected in April and September 2025 at urban sites. Overall, this project is increasing our understanding of spatiotemporal differences in WNV prevalence in Ohio.

Revealing the Connection Between Extrachromosomal Dna and Copy Number Variations as a Rapid Adaptation Mechanism of the Malaria Parasite

Presenter: Noah Brown

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Malaria continues to impose a substantial global disease burden, infecting more than 240 million people each year. Plasmodium falciparum alone is responsible for over 500,000 deaths annually. Despite sustained global control efforts, its persistence is largely attributed to its remarkable capacity to acquire genetic resistance. Investigations of the parasites extreme AT richness, combined with error-prone DNA repair, indicate that the rate of copy number variation (CNV) is elevated at a basal level. CNVs are well understood to confer innate fitness advantages, but more recently, our laboratory has identified extrachromosomal DNA (ecDNA) containing genetic material identical to CNV sequences. Initial investigations have led us to hypothesize that the extensive regions of homology generated by CNVs create opportunities for ecDNA formation. Using an in-vitro model, we identified an ecDNA species that served as a marker of extreme drug resistance, independent of chromosomal copy number. We further determined that P. falciparum ecDNA is structurally complex, containing both single- and double-stranded elements, and that existing ecDNA enrichment strategies were insufficient to capture these rare and transient molecules. Here, we establish a pipeline capable of isolating ecDNA with reproducible patterns across experimental replicates and controls, revealing variant ecDNA populations that differ in size and conformation. Using droplet digital PCR, we demonstrated comparable or greater sensitivity and consistency than the previous field standard, without introducing technical noise from pre-sequencing amplification of low-abundance ecDNA. We used short read sequencing to fully explore the abundance and variety of ecDNA species in the parasite. Finally, using a custom, optimized computational analysis framework, we validated the performance of our enrichment method and shed new insights into ecDNAs derived from CNVs. Together, these findings advance our understanding of ecDNA biology and suggest broader mechanisms by which organisms may leverage under-regulated ecDNA for adaptive advantage.

Incorporating Thermal Performance Curves into Population Dynamic Models for the West Nile Vector, Culex Pipiens

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Culex mosquitoes are a growing concern in North America given their ability to transmit diseases such as West Nile Virus and adapt their thermal tolerances. Culex pipiens, one species found in temperate environments, is predicted to continue to spread north and south of the equator as environmental conditions become more favorable. As climate change persists, it is of high importance to understand how temperature influences Culex pipiens life-history traits and what impacts this might have on transmission of West Nile and other pathogens. In this work, we explore potential functional forms of thermal performance curves (TPCs) for key traits of Culex pipiens by fitting TPCs to temperature-dependent trait data. We found the best-fitting TPCs for the following traits: age-specific mortality, fecundity, juvenile development, and survival to adulthood. We then incorporated TPCs for each trait as a parameter function in a system of stage-structured differential equations of Culex pipiens population dynamics and we explored potential impacts on population dynamics of different TPC curves. Separately toggling both rates yielded notable differences in projected population counts and predicted peaks. We also compared the adult population projections from our model to surveillance data to find the best fitting model and see which fits were strongly supported by the data. Mathematical models such as ours are useful for predicting the potential population dynamics of Culex pipiens in specific geographic regions and for informing public health interventions. Further investigation is needed from additional data collection to explore other potential TPCs which may help to further improve these mathematical models.

Comparing the Consumptive and Non-Consumptive Effects of Parasites

Presenter: Julia Buck

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Over two decades ago, ecologists realized that while predators can kill their prey (“consumptive effects”), they can also cause their prey to adopt defensive strategies that reduce the likelihood of predation (“non-consumptive effects”). Reviews and meta-analyses have generally concluded that predator avoidance exerts a widespread and important influence in ecological communities. In fact, predator-induced non-consumptive effects are often thought to be as strong or stronger than consumptive effects, a realization which shook predator-prey ecology to its foundations. Here we apply this framework to parasites and their hosts. Although parasites are appreciated mainly for their consumptive effects (i.e., infection), like predators, they can also cause non-consumptive effects. Specifically, hosts reduce the likelihood of becoming infected by 1) avoiding conspecifics, especially if they show signs of infection, 2) directly avoiding parasites or species which vector parasites, 3) using cues to avoid objects and situations of infection risk, and 4) altering their niche to discourage parasites. However, avoiding infection is difficult and costly, so hosts should only display avoidance behaviors when parasites are avoidable and worth avoiding. Thus, hosts live on a “landscape of disgust” akin to the predator-induced “landscape of fear.”

To explore the consumptive vs. non-consumptive effects of parasites, we quantified the infection-induced vs. risk-induced trait responses of a copepod (Acartia tonsa) to its parasite, the bopyrid isopod Probopyrus pandalicola. This system is well-suited to answering questions about parasite avoidance because the parasite is large and therefore highly avoidable, and infection reduces host fecundity, making it worth avoiding. We found that the risk-induced trait response is greater in magnitude than and in the opposite direction as the infection-induced trait response, suggesting that parasite-induced non-consumptive effects might overshadow consumptive effects, as has been shown for predators. This work advances recent efforts to unite predator-prey and parasite-host theory under a general consumer-resource framework.

Demography, Rather than Density, Drives Population-Level Disease Dynamics in Wild Bank Vole Populations

Presenter: Sarah Budischak

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Understanding the factors that influence disease dynamics at the population-scale is a central goal of disease ecology. While laboratory and modeling studies have contributed significantly to this question, it is logistically challenging, and thus understudied, in natural systems. Using data from 12 wild bank vole populations sampled monthly across three years, we determined which demographic, density, and infection parameters were associated with metrics of month-to-month disease dynamics for an endemic zoonotic infection, Puumala hantavirus (PUUV). We examined four metrics of disease dynamics: disease introduction into a previously uninfected population, disease fadeout, R0 direction (>1 vs. ≤ 1), and change in prevalence. Demographic and infection characteristics from the prior month often influenced disease dynamics. Disease introduction was more likely in populations that previously had a high proportion of females. Whereas, fadeout was more likely in populations that previously had fewer infected voles or had a high number of non-resident adults. R0 was more likely to be greater than one in populations with a previously low proportion of reproductive individuals, and that subsequently had high density. Prior incidence, proportion reproductive, and the proportion of voles with maternal antibodies were all negatively correlated with change in prevalence. Notably, different infection characteristics from the prior month best explained each disease dynamic metric (# infected voles for fadeout, incidence for change in prevalence, and none for R0 direction). Overall, we found little evidence of density-dependent transmission (previous population size was never significant), but rather that reproductive status, resident status, and sex ratio strongly influenced population-scale disease dynamics. Maternal antibodies also seemed to provide some population-scale protection against infection. These types of demographic characteristics are not typically considered as important as density and case data, but they may provide important insight into the likelihood of disease introduction, fadeout, and change in prevalence in wild populations.

Linking Behaviour and Space Use to Parasite Infection in Free-Roaming Sheep

Presenter: Mercedes Burgueño

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Individual and spatial heterogeneity shape host-parasite dynamics. Parasites that use invertebrates as their intermediate hosts are more sensitive to environmental variation and often demonstrate greater heterogeneity in their spatial distributions. The liver fluke is an ideal model as its intermediate host, a mud snail, requires water-land interface habitats for survival, which serves as a proxy for parasite risk. In this study, we examine how space use and foraging behaviour in risk-associated (snail) habitat drive observed parasite infection patterns in free-roaming sheep, a definitive host of liver flukes. Initially, we treated each individual sheep with Triclabendazole to remove their liver flukes, and then periodically collected faecal samples at 3-week intervals for 4 months to obtain faecal egg counts (FEC). In addition, each individual sheep was fitted with a collar that had GPS and accelerometer sensors to infer space use and foraging behaviour in the risk-associated habitat, which was our main input for our analysis. Using Ordinary Differential Equations within a Bayesian framework to model individual sheep-parasite dynamics, we could successfully estimate the consumption rate of metacercaria (infective stage), suggesting that foraging time in risk-associated habitat influences parasite infection patterns. Unexplained variation in FEC was also found, which was expected and may be related to other factors, like differences in susceptibility, not measured at this time. This study demonstrates a novel approach for linking behaviour and space use to parasite infection dynamics by integrating GPS, accelerometer, and parasite infection data within a Bayesian mechanistic modelling framework.

Cross-Immunity and Asymmetry as Important Drivers of Dengue Virus Invasion and Transient Dynamics

Presenter: Holly Burrows

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Infectious disease invasion dynamics provide ecological and epidemiological insights about a pathogen. In the case of multi-strain pathogens such as dengue virus, invasion and re-invasion dynamics may be driven in part by immune-mediated interactions between strains, such as cross-immunity and immune enhancement. While previous modeling work has found cross-immunity to be important in reproducing observed epidemiological dynamics, there is a lack of consensus on its strength and duration, which may lead to disparate effects on invasion. Using several deterministic, SIR-like models, we deploy invasion simulations as a probe to resolve the accuracy of cross-immunity assumptions and their effects on model predictions. We find that models producing realistic dynamics feature strong cross-immunity of long duration, and asymmetry in the strength of cross-immunity depending on the serotype pair. Our results suggest the structure and parameterization of cross-immunity, rather than just its presence/absence, may be an important driver of dengue ecology and epidemiology, and that cross-immunity may be stronger than often assumed in previous models. These findings have implications for future model development for predicting dengue dynamics and intervention effectiveness.

Dynamically Optimizing Genomic Surveillance to Control the Spread of Antimicrobial Resistance

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Antimicrobial resistance (AMR) is a global threat that has direct impacts on human, animal, and plant health, and the environment. Though much research has been done to determine the best strategies to manage resistance across many settings, the best strategy will generally depend on what we know about the evolutionary dynamics of resistance. Genomic surveillance allows us to monitor the evolutionary dynamics of resistant strains and quantify the relative benefit of resistance to pathogen fitness versus the costs of resistance in the absence of treatment. Understanding the costs and benefits of resistance can help predict how resistant strains will react to treatment and thus inform the design of treatment strategies to better control resistance. However, how to optimize genomic surveillance to uncover these dynamics is not well understood. Additionally, determining what treatment decisions are beneficial in the short-term versus the long-term is difficult. For example, increasing treatment rates may reduce AMR in the short-term, but also increase selection pressure for resistance in the long-term. Determining optimal strategies is further complicated because resources are finite and must be dynamically allocated between surveillance (sampling) and control (treatment). To address these challenges, we developed a sequential decision-making framework based on a partially observed Markov decision process (MDP) to find optimal strategies to manage AMR. We combine these models with Deep Q-Learning (DQL), a form of reinforcement learning that can compute the expected value of different strategies to the long-term goals of disease and resistance management. Using our DQL framework allows us to answer questions related to sampling design, resource allocation, and the amount of information needed to optimize strategies to reduce AMR in the long-term.

Survival of Legionella in Droplets Exposed to Sulfur Dioxide

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Legionnaires' disease (LD) is a severe form of pneumonia caused by Legionella bacteria, and its incidence has increased dramatically over the past two decades in the United States, particularly in the Northeast where ambient sulfur dioxide (SO2) concentrations have decreased substantially due to regulations on coal-fired power plants. LD outbreaks have been linked to building water systems, such as cooling towers, where Legionella can grow and become aerosolized in water droplets. In the atmosphere, droplets can absorb gases from the surrounding air, including SO2, which can lower droplet pH and potentially affect bacterial viability. The objective of this study is to investigate the impact of gas-phase SO2 on Legionella pneumophila (Lp) viability in droplets. One microliter droplets of L. pneumophila strain ATCC 33823 were pipetted onto polystyrene surfaces under different relative humidity (RH) conditions (30%, 50%, and 80%) and exposed to SO2 at concentrations of 50 ppb, 100 ppb, and 1 ppm. Results show that in bulk buffer medium, Lp maintained more than 50% viability at pH 5.0–7.0 for up to one week, whereas viability decreased to 6% at pH 4.0 and was completely lost at pH 3.0 and 2.0 within 6 hours. In 1-µL droplets without SO2 exposure, bacterial viability was lowest at 30% RH and increased at intermediate to high RH. We expect that higher SO2 concentrations will further reduce Lp viability due to enhanced droplet acidification. Such a finding would support the hypothesis that air pollution control measures that reduce SO2 concentrations in ambient air could have the unintended consequence of increasing the risk of airborne Legionella transmission. More broadly, this study illustrates the importance of understanding the role of atmospheric chemistry on pathogen survival.

Stochastic Within-Host Dynamics and Climate-Sensitive Traits Generate Predictable Patterns of Variation in Disease Outcomes

Presenter: Andrew Carlino

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Understanding how climatic variables impact host-pathogen relationships in temperature-sensitive ectothermic host organisms is crucial under global change. Few studies have explored how temperature gradients generate inter-individual variation in epidemiological traits like host susceptibility or pathogen replication. Here, we develop a mathematical model to explore a novel hypothesis: stochastic within-host dynamics and simulated thermal mismatches between host and pathogen traits generate predictable variation in infection outcomes among hosts and across thermal gradients. Our model demonstrates that varying trait thermal optima in host immunity and pathogen replication, and stochastic within-host processes produced variation in infection outcomes. Variability was low when temperatures strongly favored host or pathogen traits, but high and diverse when their performance was similar across a broad thermal range. In contrast, when trait performance was equal across all temperatures (no mismatch) variability remained low at all temperatures. Further, the magnitude of variation, quantified by entropy, exhibited predictable patterns depending on host-pathogen thermal mismatches. We conclude that interactions between trait thermal mismatches and within-host stochasticity provide a theoretical framework to improve ectotherm disease models under climate change, providing a valuable tool for exploring the impacts of environmental change on epizootic or epidemic dynamics, particularly in vulnerable marine ecosystems.

Estimating the Generation Time for Influenza Transmission Using Household Data in the United States

Presenter: Louis Yat Hin Chan

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The generation time, representing the interval between infections in primary and secondary cases, is essential for understanding and predicting the transmission dynamics of seasonal influenza, including the real-time effective reproduction number (Rt). However, comprehensive generation time estimates for seasonal influenza, especially since the 2009 influenza pandemic, are lacking. We estimated the generation time utilizing data from a 7-site case-ascertained household study in the United States over two influenza seasons, 2021/2022 and 2022/2023. More than 200 individuals who tested positive for influenza and their household contacts were enrolled within 7 days of the first illness in the household. All participants were prospectively followed for 10 days, completing daily symptom diaries and collecting nasal swabs, which were then tested for influenza via RT-PCR. We analyzed these data by modifying a previously published Bayesian data augmentation approach that imputes infection times of cases to obtain both intrinsic (assuming no susceptible depletion) and realized (observed within household) generation times. We assessed the robustness of the generation time estimate by varying the incubation period, and generated estimates of the proportion of transmission occurring before symptomatic onset, the infectious period, and the latent period. We estimated a mean intrinsic generation time of 3.2 (95 % credible interval, CrI: 2.9–3.6) days, with a realized household generation time of 2.8 (95 % CrI: 2.7–3.0) days. The generation time exhibited limited sensitivity to incubation period variation. Estimates of the proportion of transmission that occurred before symptom onset, the infectious period, and the latent period were sensitive to variations in the incubation period. Our study contributes to the ongoing efforts to refine estimates of the generation time for influenza. Our estimates, derived from recent data following the COVID-19 pandemic, are consistent with previous pre-pandemic estimates, and will be incorporated into real-time Rt estimation efforts.

Gene by Environment Drivers of Immune Phenotypic Variation Shape Parasite Burden of Trichuris Muris in Rewilded Mice.

Presenter: David Chang van Oordt

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Genes and the environment are well known drivers of variation in immune function and resistance to disease between individuals and populations. However, it remains unclear how the current state of the immune system ultimately shapes infection dynamics. For example, clearance of Trichuris muris, an intestinal nematode of mice, relies on activation of the type 2 T-helper cell (Th2) response to drive parasite expulsion. Theoretical studies of this response suggest that proper activation of the Th2 response depends on the baseline immune conditions of the system at the time of infection. We studied how genes and the environment shape the baseline immune conditions of a host and its subsequent response to a T. muris infection in rewilded resistant and susceptible strains of laboratory mice. Rewilded mice, which are housed in outdoor pens, show distinct white blood cell distributions and reduced resistance to T. muris in both susceptible and resistant genotypes. Th2 polarization in response to infection, measured via plasma IgG isotype ratios, was less responsive in rewilded or susceptible mice. We then used linear mixed regression to investigate the role of baseline immune phenotypes on worm clearance and burden to understand how the state of the immune system can impact downstream parasite expulsion. We found that baseline blood leukocyte levels can predict worm burden, but the effects are context dependent: lymphocytes are more important when mice receive large infective doses, but the innate compartment is more important at small doses. Within rewilded and conventionally housed mice, however, burden is better correlated with baseline basophil numbers indicating that innate components remain important when controlling for environmental effects on immune phenotypic variation. Our work shows that baseline immune conditions can predict the direction and success of the immune response linking standing immune phenotypic variation with downstream infection dynamics.

Keeping Time with the Host: Reconstructing the Developmental Rhythms of Malaria Parasites

Presenter: Nancy Chen

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In a world governed by circadian rhythms, strategic life cycle timing provides fitness advantages for hosts and their parasites. Malaria parasites, for instance, often synchronize their development within red blood cells to multiples of 24 hours. However, identifying the fitness consequences of developmental rhythms is challenging because 1) parasites sequester in blood vessels and tissues as they mature, making them difficult to sample directly, and 2) many Plasmodium species cannot be cultured in vitro, making it difficult to isolate the timing of parasite expression of proteins that enable sequestration. To address these challenges, we fit a mathematical model tracking the timing of parasite development and sequestration to high-resolution time series data from the rodent malaria parasite Plasmodium chabaudi. We show that parasites shorten their developmental cycles to realign with host rhythms when perturbed, at the cost of reduced multiplication rates. Our approach enables, for the first time, reconstruction of sequestration patterns across different parasite and host genotypes. The results reveal substantial variation, suggesting that the timing of sequestration depends on host and parasite strain, patterns impossible to measure directly in vivo or in vitro. Together, this approach provides a framework for linking parasite developmental timing to within-host fitness, informing strategies to disrupt parasite development and reduce disease severity.

The Thermal Performance of a Fungal Plant Pathogen Under Controlled Conditions Matches the Seasonality of the Disease Epidemic in the Field

Presenter: Dalia Chen

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As global temperatures increase, the severity of an epidemic could change. The infectivity of a pathogen is affected by the environmental temperature under which the pathogen encounters its host. Thus, it is critical to understand how temperature affects the host-pathogen interaction. We investigated how temperature affects symptom development of the seasonal fungal pathogen Rhizoctonia solani which causes brown patch disease in the plant host tall fescue. The R. solani epidemic peaks in the tall fescue population during mid-summer, suggesting that R. solani infections are favored under warmer temperatures. We hypothesized that the optimum temperature for R. solani infections in the lab will match the temperature conditions under which infections occur in the field. We tested this hypothesis using thermal performance curves (TPC) with the prediction that the TPC of R. solani would be left skewed with a thermal optimum located towards warmer temperatures (25°C -32°C). To test our hypothesis and prediction we inoculated tall fescue plants with R. solani at 9 temperatures (spanning 10°C to 36°C) in controlled growth chambers. Symptom development was recorded over 2 weeks for each temperature and a TPC was built. Results support a left skewed curve with a thermal optimum between 27°C to 29°C and a thermal maximum around 34°C to 36°C supporting our prediction about how temperature would affect the infectivity of R. solani. This matches what we find in the field where brown patch prevalence peaks at daily average temperatures around 25°C and daily maximum temperatures around 31°C. Under warming temperatures, the heat tolerance of R. solani could lead to a longer epidemic or shift in the epidemic peak. Additionally, during the summer months the heat tolerance of R. solani could give it an advantage in pathogen competition within the host against pathogens that are less heat tolerant.

: Spatial Dynamics of Dengue Transmission Driven by Human Movement in Córdoba, Argentina

Presenter: Mohammad Mihrab Uddin Chowdhury

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Human movement plays an important role in dengue virus (DENV) transmission. Movement determines where outbreaks begin and how they spread across space. We studied the impact of human movement on dengue spread in the city of Córdoba, Argentina. We paired a spatially explicit mosquito–human transmission model with a temperature-dependent mosquito population dynamics model. We incorporate spatially heterogeneous population data and spatiotemporal dengue case data from the 2023–2024 outbreak into the model. We estimate a movement matrix using a gravity-based mobility framework. We simulated introductions of infectious individuals at different locations and tracked the impact on outbreak size, spatial spread, and epidemic timing. Our results show that both mobility patterns and introduction location and timing shape dengue dynamics. Different introduction locations facilitate different patterns of spread throughout the city. Our framework highlights the importance of accounting for human movement and spatial structure when analyzing dengue emergence in temperate regions.

Phylogenetic and Ecological Structuring of Bat-Associated Rabies Virus Across the Americas

Presenter: Analorena Cifuentes-Rincon

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Rabies virus (RABV; Lyssavirus) is a fatal zoonotic pathogen that causes significant human and economic losses worldwide and is also an emblematic study system to understand host-pathogen ecology and evolution. In the Americas, bat-associated rabies transmission represents a burgeoning public health and veterinarian threat. Despite its importance, the ecological and evolutionary processes enabling RABV emergence in vampire bats and its spread across diverse landscapes remain poorly understood. This study investigates the host and environmental factors driving the origin, diversification, and spillover of bat-associated RABV across taxa and the landscape. We reconstructed viral evolutionary relationships across multiple phylogenetic scales, including Lyssavirus genus trees of an intra-species high-resolution analyses that comprised 1203 RABV nucleoprotein gene sequences collected between 1975 and 2024 across ten countries in the Americas. Maximum likelihood phylogenies inferred with 1000 bootstrap replicates in IQ-TREE were geographically contextualized with ecological niche models by analyzing the environments occupied by each lineage in terms of of MERRAclim bioclimatic data, thereby mapping the potential range of RABV clades. Phylogenetic analyses indicate that early-diverging RABV lineages in the Americas are predominantly associated with insectivorous bats, while vampire bat-associated lineages emerge within more recently-derived taxa, which radiated to more ecologically diverse biomes. A strongly supported mixed-host clade containing Tadarida brasiliensis and Desmodus rotundus suggests a historical host-switching event likely facilitated by ecological and geographic overlap. Climatic models identify regions of viral lineage richness where bat distributions intersect, highlighting potential hotspots of viral diversification and zoonotic spillover. By integrating viral phylogenetics, host ecology, and spatial modeling, this study provides fundamental signal of viral evolution, actionable insights for rabies surveillance, and data-driven zoonotic disease prevention in the Americas.

Does Integrating Multiple Sources of Information Correct Detrimental Host Behavioral Responses to Perceived Disease Risk?

Presenter: Dale Clement

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Host behavior plays an important role in driving patterns of transmission, and incorporating host behavior is a pressing goal in epidemiological modeling. Many epidemiological models developed with behavior assume that hosts react to aggregate community-level prevalence. For many infectious diseases, transmission is based on fine scale contacts and so community-level prevalence may provide little information about risk to any given host. However, fine-scale spatial information of infection risk is rarely available and hosts must instead rely on proxies, such as host density or environmental conditions, that may not reliably correlate with actual infection risk. Prior work shows that disease avoidance behavior, when based on a single risk proxy rather than actual risk, can lead to higher disease burden at the population level if the risk proxy lacks pertinent information or incorporates extraneous information. We extend this work to examine how multiple risk proxies interact to determine disease spread by asking: When can misleading risk proxies be “fixed” by considering additional information? When can otherwise accurate proxies be made misleading through extraneous information? We considered three risk proxies: fixed place-based information, local host density, and local prevalence. We found highly variable effects of adding additional information. In some cases, it is beneficial. For example, behavior that increases disease prevalence when based only on placed-based risk proxies can decrease prevalence after incorporating information about host density. In other cases, additional information seems ineffective. For example, misleading risk proxies utilizing density-based information remained inaccurate even after incorporating information about place and prevalence. These results suggest that host movement behavior in response to disease may nonetheless prove ineffective at reducing prevalence, even if hosts use multiple sources of information. Moreover, our results raise questions about what cues hosts use to perceive risk and whether these are valuable at the individual and population levels.

Spatiotemporal Dynamics of Questing Activity by Four Tick Species in the Central Great Plains

Presenter: Marlon E. Cobos

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The expansion of medically relevant tick species across the central Great Plains creates a complex and shifting landscape of disease risk. Traditional modelling approaches provide a general picture of distributional potential, but predictions are often static representations of species ranges. As pathogen transmission is directly linked to tick questing activity, characterizing the spatiotemporal heterogeneity of this behaviour is essential for a better understanding of transmission risks and planning of interventions in the area. In this study, we integrated novel ecological niche modeling frameworks to characterize the spatiotemporal dynamics of questing activity in four tick species across the central Great Plains. We processed data from two years of field tick surveillance to derive detection and non-detection records, thereby making model evaluation more robust. We coupled sampling events with time-specific environmental covariates to leverage longitudinal data. We also constrained model response curves to align with fundamental niche theory within a strong conceptual framework. Our results reveal distinct interspecific differences and pronounced seasonal shifts in the geographic potential of questing behavior. Predictions of activity show higher values for Dermacentor variabilis and Amblyomma maculatum during warmer periods, contrasting with predictions for Ixodes scapulatis with picks of activity during temperate and cold conditions. These modeling approaches provide a more robust basis for understanding the ecological drivers of tick questing activity and characterizing the shifting landscape of vector-borne disease risk.

Terminal Investment and Energy Allocation Tradeoffs in Amphibians: Biases, Gaps, and Research Priorities

Presenter: Zuania Colon-Pineiro

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Life-history theory predicts that immunity competes for energy with reproduction, leading to trade-offs that may be exacerbated under stressors such as food scarcity or pathogen exposure. The terminal investment hypothesis (TIH) proposes that organisms facing infection-induced mortality risk should increase reproductive effort, yet empirical evidence remains inconsistent. We conducted a meta-analysis integrating data across ecological, evolutionary, and physiological studies to evaluate support for TIH in amphibians, focusing on compensatory reproductive responses to pathogen infection. The evolution of reproductive modes (diversification from their ancestral aquatic larvae) has enabled amphibians to adapt to different environments and even avoid aquatic parasites. However, this diversity has also challenged how reproductive effort is quantified across taxa. We identified ~90 reproductive traits used in the amphibian literature and found highly variable reproductive responses to infections, with no consistent support for TIH. Available data represent less than 0.5% of frog and salamander species and none of the caecilians, revealing a broad absence of information across biological scales, from individual traits and reproductive modes to evolutionary lineages and geographic distributions. These data gaps limit our understanding of lethal and sub-lethal effects contributing to amphibian declines and extinctions. Our synthesis underscores the need for holistic approaches capable of detecting emergent patterns from multiple interacting processes. We outline priorities for future research, including expanding work to neglected taxa (e.g., caecilians) and reproductive modes (e.g., direct-development, live-bearing, or paedomorphic), incorporating multi-trait and longitudinal datasets, and leveraging tools such as OMICS and causal inference frameworks. An integrative approach is essential for understanding how reproductive responses to infection influence long-term fitness and species persistence, with broad implications for evolutionary ecology and conservation strategies.

Unraveling Climatic Factors Influencing Prevalence and Severity of Infection in Snake Fungal Disease

Presenter: Dane Conley

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Following the invasion of a novel pathogen identifying the most affected species and determining the ecological factors that influence infection are crucial for understanding and mitigating disease impacts. Snake fungal disease (SFD), caused by the multi-host fungal pathogen Ophidiomyces ophidiicola, is widespread across North America. However, many of the impacts from this disease were likely overlooked during initial pathogen invasion due to the cryptic nature of its hosts. In addition, despite the broad distribution of O. ophidiicola, the effect of climate on infection dynamics has not previously been examined. We compared variation in infection in 47 species of North American snakes at 14 sites spanning a 2000 km north-south gradient. We found strong differences in infection prevalence and severity among species indicating which species may be most at risk from SFD impacts. In addition, we find that longer winters resulted in higher infection prevalence and intensity across all species. This suggests that longer brumation periods for overwintering snakes may result in increased O. ophidiicola infection. More broadly these results highlight the role of climate in shaping disease patterns across the landscape.

Using Bacterial Epidemiology to Track Pathogen Transmission Potential Among Wildlife at the Agricultural Interface

Presenter: Corinne Conlon

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Agricultural landscapes impact wildlife pathogen transmission dynamics through the modification of habitat, aggregation of resources, and the concentration of livestock. These landscapes create interfaces that facilitate increased interactions among wildlife, livestock, and humans, presenting novel opportunities for pathogen spillover and transmission. Understanding how wildlife interactions at agricultural interfaces alter pathogen transmission dynamics within the wildlife reservoir population is essential for predicting pathogen spillover. However, surveillance for wildlife pathogens and transmission at this interface tends to occur after disease outbreaks, and the typically low prevalence of many pathogens limits statistical power for identifying risk factors associated with contemporary transmission dynamics. Alternatively, infectious agents occurring at high prevalence and across multiple host species, such as commensal enteric bacteria, may serve as pathogen proxies for predicting pathogen transmission. Here, we apply techniques from bacterial epidemiology and network analysis to model potential pathogen transmission dynamics in wild birds across agricultural landscapes in Michigan. Using mobile genetic element (MGE) sharing patterns from commensal Escherichia coli isolated from wild birds at farm and natural sites, we construct transmission potential networks to quantify the likelihood of pathogen transmission between hosts. Our objectives were to: 1) evaluate whether E. coli MGE sharing represents an epidemiologically meaningful proxy for pathogen transmission dynamics in wildlife hosts and 2) identify host, environmental, and landscape factors that influence connectivity and transmission potential in hosts across agricultural landscapes. We identified significant heterogeneity in connectivity and MGE communities in E. coli isolates from birds across our farm sites, with specific farm interfaces contributing to increased transmission potential in wild birds utilizing these spaces, suggesting that environmental and farm characteristics may alter connectivity and disease risk in agricultural landscapes. This approach provides a quantitative measure of host connectivity and transmission potential at diverse interfaces, enabling identification of characteristics that confer increased spillover risk.

Integrating Epidemiology and Genomics to Identify Sources of Coccidioides Exposure

Presenter: Lisa Couper

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Coccidioidomycosis (Valley fever) is a serious and emerging human fungal disease caused by inhaling spores of the soil-dwelling fungus, Coccidioides. Despite over 200,000 infections estimated to occur each year in the U.S., we have very little understanding of how and where people are exposed to Coccidioides spores due to major limitations in both epidemiological and environmental surveillance. This presentation will address results and methodologies for identifying sources of human exposure through two recent works. In the first, we identify the impact of oil and gas development on coccidioidomycosis infection in California by using a case-crossover study design–an epidemiological approach to inference wherein individuals (here, coccidioidomycosis patients) serve as their own controls. We estimated that the odds of coccidioidomycosis were 11.0% higher in the 90 days following exposure to at least one preproduction well within 5 km of the patient's residence and increased by 0.7% for each additional preproduction well within this distance. While oil and gas development has previously been linked to increased air pollution, preterm birth, asthma, and childhood cancer, this is the first study to identify its potential role in pathogen transmission. In the second, we develop the first genomes (n=17) of Coccidioides immitis from its endemic environment, finding high levels of genetic diversity across small spatial scales. We then use publicly available Coccidioides genomes from patient isolates in southern California (n=20) to identify the most likely sources of environmental exposure for each infection, finding this is most commonly the highly endemic region of the San Joaquin Valley. Together, these works demonstrate how ecological, evolutionary, and epidemiological approaches can be integrated to advance understanding of fungal pathogen transmission and emergence–critically needed as human fungal infections remain vastly understudied and under-resourced relative to other pathogenic taxa.

Combining Remotely-Sensed and Ground-Truthed Data to Determine Waterbodies at-Risk or Protected from Infection by Guinea Worm Parasites

Presenter: Jeremiah Cox

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Guinea worm disease (GWD), caused by the nematode Dracunculus medinensis, has rapidly declined from an estimated 3.5 million cases in 1986 to just 15 human cases in 2024 thanks to the Guinea Worm Eradication Program (GWEP). Working towards the GWEP's goal of eradication means preventing future human cases and animal infections. While larvicides may reduce GWD case counts by acting on the intermediate zooplankton host, the cyclopoid copepod, our knowledge surrounding their preferred habitats and how it affects Guinea worm (GW) DNA presence and abundance is currently limited. To that end, with a large portion of GWD cases happening in Chad, Africa, we conducted our research in waterbodies along the Chari River. This study allowed us the opportunity to combine ground-truthed data with remotely-sensed information to determine what characteristics of waterbodies were most impactful on the presence or absence of GW DNA. To better understand the ecology, we conducted sampling at 59 locations in 46 waterbodies during November 2024, at the end of Chad's rainy season. Waterbodies with a history of nearby GWD were sampled between the hours of 0800 and 1300 over the course of ten days. We collected paired water samples, measured Dracunculus spp. DNA and cyclopoid copepod concentrations, and took measurements on the temperature, fecal contamination, chlorophyll-a concentrations, pH, and other water quality characteristics. Preliminary results show that the turbidity, chlorophyll-a, and dissolved organic matter from remotely-sensed indices are inversely predictive of both Guinea worm DNA presence and magnitude, while the ground-truthed data showed that copepod population densities are inversely predictive while the presence of dog fecal bacteria and being located within a six-kilometer distance of recent infections was indicative of higher risk of GW DNA presence. While outcomes differ by method, neither are contradictory of the other and both appear to be complementary to each other.

Emergence of D1.1 Reassortant H5n1 Avian Influenza Viruses in North America

Presenter: Alvin Crespo-Bellido

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Since 2021, highly pathogenic avian influenza viruses (HPAIV) belonging to H5Nx clade 2.3.4.4b have caused high mortality in North American wild birds and poultry. In 2025, a new D1.1 genotype caused two human deaths and host-switched to dairy cattle. However, the evolutionary origins and dynamics of D1.1 have not been fully characterized. Here, our phylogenetic analysis of 17,516 H5N1 genome sequences uncovers how D1.1 introduced a major shift in the antigenic diversity and ecology of the H5N1 epizootic in North America. D1.1 is the first major H5N1 genotype to (a) emerge in the Pacific flyway and spread west-to-east faster than any prior genotype; (b) antigenically shift via reassortment with the North American N1 segment, displacing the previously fixed Eurasian N1; and (c) transmit to a broader range of host species than any H5N1 genotype to date.

Eco-Evolutionary Feedbacks Shaping Yellow Fever Virus Dynamics

Presenter: Elvira D'Bastiani

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Yellow fever virus (YFV) is primarily maintained in sylvatic cycles among non-human primates and canopy-dwelling mosquitoes (Haemagogus and Sabethes spp.), with occasional spillovers to humans. The resurgence of YFV across South America, driven by ecological disruption driven by climate change and environmental degradation, reveals how eco-evolutionary feedback loops reshape zoonotic risk. However, these links remain poorly understood, limiting our ability to anticipate outbreaks and protect at-risk populations.

To address this gap, we developed a mechanistic framework that couples ecological, climatic, epidemiological, and evolutionary processes to predict YFV spillover and outbreak risks across Brazil (2010-2025). To develop the model, we used a municipality-level dataset that includes vector and host distributions and abundances, environmental and climatic covariates, genomic and epidemiological surveillance data, vaccine coverage, and socio-demographic factors.

Analyses uncover marked spatial and temporal variation in vector-host ecologies. Epizootic hotspots exhibit high primate richness and overlapping suitability for sylvatic (Haemagogus and Sabethes spp., as well as Aedes scapularis), transitional (A. albopictus), and urban (A. aegypti) vectors. Critically, land-use intensification and climate precede viral amplification, providing quantifiable early-warning signals for spillover.

Our coupled eco-evolutionary model quantifies how primate population declines, shifts in vector communities, and landscape connectivity sustain YFV persistence and emergence under environmental perturbations. Preliminary results demonstrate that forest fragmentation amplifies spillover probability by enhancing vector-host encounter rates and viral invasion potential.

Our data-driven framework advances understanding of how rapid habitat alteration accelerates the emergence of zoonotic arbovirus threats. By linking environmental drivers to evolutionary processes, it identifies leverage points for proactive surveillance and intervention, with applicability to other emerging pathogens in transforming ecosystems.

Frequent, Seasonal Reassortment Between High and Low Path Viruses Drives the Diversification of Influenza a/H5n1

Presenter: Lambodhar Damodaran

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Since 2021, highly pathogenic H5N1 viruses have spread across the Americas, diversifying via reassortment into novel genotypes that have spilled into humans and agriculture. Reassortment allows genetically novel viruses to form rapidly, posing a challenge for risk mitigation, but is poorly understood. Using a dataset of 9,052 full genome sequences and a set of novel, Bayesian phylodynamic approaches, we show that reassortment and genotype formation are well predicted by seasonal variation in low pathogenicity avian influenza (LPAI) cases and by the spatial and host distribution of viral transmission. We pinpoint ducks and the Central flyway as frequent sources for new genotype formation, suggesting surveillance in those species for identifying new reassortants. Ducks support transmission earliest each season and generate approximately half of all reassortants, while the Central flyway contributes 1.5-2.5 more reassortants than expected ($p<0.0001$), putatively reflecting its role as a central breeding ground for North American waterfowl. Reassortment rates exhibit seasonal peaks in late summer that precede fall surges in case, frequently involving the mixing between HPAI and LPAI, and are best explained by LPAI cases, implying improved understanding of LPAI circulation as key for studying HPAI reassortment. Finally, our data show that viruses evolving during particular time periods are highly likely to involve reassortment, regardless of the fitness impacts of those events. These data imply that reassortment in the history of a novel lineage is not itself an indicator of an unusual evolutionary event with epidemiologic or phenotypic significance. Instead, the likelihood of reassortment is well-described by spatial, temporal, and host-specific patterns of transmission, supporting prevalence as a key predictor for reassortment frequency. These data suggest that the timing and host origins of reassortment may be somewhat predictable, and that targeted surveillance of key species and time periods may improve reassortant virus detection.

Migration and Colder Temperatures Constrain Microsporidian Parasite Outbreaks in Zooplankton Populations

Presenter: Elizabeth Davenport

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Prey frequently encounter multiple natural enemies, so an avoidance behavior in response to one natural enemy, such as diel vertical migration, may alter the conditions in which an encounter with another natural enemy occurs. For instance, zooplankton change their habitat use in response to fish predators and experience daily temperature fluctuations associated with this vertical migration, particularly in thermally stratified lakes. While migrating to avoid predators, zooplankton continue to encounter parasites throughout the water column. Many aspects of host-parasite interactions are influenced by temperature (e.g., host susceptibility, transmission, parasite burden, etc.), so daily temperature fluctuations associated with host diel vertical migration could affect disease dynamics. Furthermore, disease outbreaks often occur seasonally. To test how temperature fluctuations associated with daily vertical migrations and seasonal declines in temperature affected disease outbreaks of the microsporidian Ordospora pajunii in Daphnia dentifera populations, we conducted a multi-phase microcosm experiment motivated by field observations. The first phase focused on the effect of daily temperature fluctuations versus a constant temperature on parasite prevalence. We found that parasite prevalence decreased in the temperature fluctuation treatment, suggesting that diel vertical migration in response to high predation risk reduces parasitism. The second phase was motivated by a field study for this host-parasite system, which suggested strong decreases in parasite prevalence associated with a seasonal decline in temperature. Our experimental results showed that seasonal drops in temperature ended disease outbreaks. Moreover, as parasite prevalence declined, host density rebounded. Overall, our study experimentally tested the impacts of ecologically relevant temperature treatments related to migration and seasonality on parasite prevalence, and our results confirmed that temperature is a strong driver of disease for this host-parasite system.

Terrestrial Winter Dormancy is Key to Fungal Pathogen Spread in a Threatened Amphibian

Presenter: Dave Daversa

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The spread and impact of wildlife pathogens is often seasonal, and identifying the seasons of high impact is critical to biodiversity and public health management. This presentation will feature new evidence that winter host dormancy is a critical season of infection spread for the globally threatening amphibian fungal pathogen, Batrachochytrium dendrobatidis (Bd). Surveillance of Bd in Yosemite toads (Anaxyrus canorus), a species of special conservation concern, showed that Bd prevalence and intensity increased four-fold during their first winter brumation, a hibernation-like form of dormancy in terrestrial refugia. High prevalence and intensity of Bd infections immediately following winter dormancy was observed in young-of-the-year metamorphs across multiple sites and three consecutive years, and the infections persisted into the active season. Post-dormancy Bd prevalence in metamorphs was much higher than that observed in aquatically breeding adults during the same timeframe. This discovery calls for a reconsideration of the seasons enabling the proliferation of Bd and identifies a new overwinter Bd reservoir in terrestrial metamorphs. According to these results, the importance of host dormancy to pathogen persistence and seasonal infection spread may be more general than previously thought.

Sentinel Cages Improve Identifiability of Transmission Models from Field Data

Presenter: Turner DeBlieux

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Parasite transmission mode is often inferred, rather than observed, meaning even in well-studied diseases systems, robust estimates of wild transmission remain elusive. Additionally, existing weak transmission rate estimates hamper our ability to understand and forecast disease outbreaks. In part, transmission estimates are fraught because it is difficult to discern transmission mode (e.g., density- or frequency-dependent or environmental transmission) from observations of prevalence over time. Worse, when hosts have widespread populations without clear boundaries (e.g. some marine fish), replicated sampling risks pseudoreplication. Alternatively, when populations are isolated (e.g. pond systems), susceptibility to parasites may vary, complicating estimates of average transmission. Both issues may be resolved by employing ‘sentinel cages’. In these cages, healthy hosts are briefly exposed to wild populations, allowing for an independent measure of force of infection. Historically, few studies have used sentinel cages to estimate transmission. However, we believe they can be leveraged to augment wild surveys and lend power to transmission estimates. We tested this approach by simulating surveys of wild epidemics, then estimating both transmission mode and rate with and without sentinel cages. We found adding sentinel cages to wild surveys improved our ability to distinguish transmission mode. When fitting competing models to only the wild survey data, we correctly identified the transmission mode with only 55% accuracy. However, with sentinel cages, we improved model identification to over 80%. Sentinel cages also improved our ability to accurately estimate transmission rates. Without cages, median relative error for transmission rate estimates was 57%; but with sentinel cages, this dropped to 16%. Overall, we find that sentinel cages significantly improve our ability to distinguish transmission modes and rates, relative to wild surveys alone. For systems in which sentinel cages are feasible, they can provide robust estimates of transmission rate and sufficient leverage to distinguish transmission mode.

Speed, Strength, and Stealth: Rethinking the Controllability of an Infectious Disease Outbreak

Presenter: Michael DeWitt

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Successful containment of infectious disease outbreaks requires strategies that identify outbreaks early and allows for timely deployment of control measures. Typically, outbreak “controllability” is thought to depend on the basic reproduction number and pathogen stealth, defined as the proportion of infections caused during any asymptomatic period. However, recent work identifies pathogen speed (i.e., the rate of new infections) as an additional, less appreciated, axis that can be used to evaluate the potential success of interventions, such as vaccination campaigns and mobility restrictions. It remains unclear which dimension(s) should be prioritized in surveillance and control strategies across pathogens. To answer this question, we developed a framework to measure the relative contribution of each of these dimensions of pathogen spread (i.e., speed, strength, and stealth) to the final fraction infected. Across select pathogens, we examined the relative importance of intervention delays (and thus speed) versus stealth on epidemic spread. We assess the relative risk of infection due to delays in an intervention and separately, the partial relative risk of infection due to failure to identify asymptomatic infections to compare the contribution of each, showing that different pathogens require strategies that emphasize different dimensions of pathogen spread. In the case of H5N1 in dairy cows, we find that under typical surveillance approaches, the relative risk contribution of delayed interventions often far outweigh the relative risk contribution of asymptomatic infections, even for significant asymptomatic proportions (up to 40%). As such, detections of an outbreak on a farm come too late for interventions to be effective to stop single-farm outbreaks and pathogen speed is the critical factor in control. By decomposing the contributions of pathogen speed, strength, and stealth, we provide a framework for answering the quantitative problem of designing effective surveillance and outbreak control response.

Unpicking the Relationships Between Host Contact Rates, Infectiousness and Parasite Superspreading

Presenter: Andrew Dean

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Identifying superspreaders – individuals disproportionately responsible for disease transmission – is considered of great potential importance to disease control. However, the metrics used to identify superspreaders must be chosen with care, as superspreading is inherently multidimensional and context-dependent, only being defined relative to the population under consideration. Two traits which likely determine superspreader status are contact rate and infectiousness: the opportunity to transmit and effectiveness in doing so. We investigate the theoretical basis of the relationship between these traits and superspreading by carrying out stochastic simulations of susceptible-infected disease dynamics in a variety of host population structures and covariant trait distributions. We show that not only is superspreader prevalence context-dependent, but so is the contribution of each trait to superspreader status. Moreover, in certain circumstances superspreaders have neither very high contact rate nor very high infectiousness, but instead are those which are simultaneously “good enough” in both traits. Thus, interventions based on identifying superspreaders by a single trait may not always be appropriate.

Ecological Drivers and Dynamics of Viromes in Wildlife

Presenter: Luisa Maria Diele-Viegas

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Most studies on infectious disease ecology in wildlife are limited to single-virus frameworks, failing to capture the complex interactions within entire viral communities (viromes). While virome research is expanding, a critical gap remains in understanding how host and environmental factors drive virome composition and structure. The goal of this study is to conduct a systematic review to synthesize knowledge on the diversity, structure, and ecological drivers of wildlife viromes. We performed a comprehensive literature search and implemented a novel, two-phase machine learning (ML) approach for article screening. First, we trained a binary classification model (LinearSVC) on a manually labeled dataset of 600 articles to distinguish relevant wildlife virome research from non-relevant studies. The optimized model was then applied to the entire corpus, successfully filtering it down to a high-quality dataset of 2,080 relevant studies. This curated collection was subjected to a detailed content analysis to identify dominant ecological themes. Most papers were classified as Viral diversity and structure (N=1173), followed by Host ecology and migration (N=489), Environmental factors and habitat (N=304), and Community dynamics and coinfection (N=114). The extent of research on co-infection dynamics was also assessed, and future directions for predictive modeling of viral spread in key wildlife groups, such as bats and birds, was pinpointed.

Modeling Antibody-Dependent Enhancement: Implications for Understanding Immunologic Heterogeneity

Presenter: Riley Drake

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Dengue virus (DENV) infection is a significant and growing global health threat. DENV is associated with a broad range of clinical outcomes. The relative risk of the most severe disease manifestations increases in the presence of sub-neutralizing dengue-specific antibodies from prior dengue virus infection or vaccination. These antibodies can exacerbate pathology in a phenomenon known as antibody-dependent enhancement (ADE). ADE complicates dengue vaccine development because vaccine-elicited antibodies, while initially protective, may wane over time into a range that enhances the pathology (and the risk of hospitalization) from subsequent infections. To examine how humoral and cellular immunity jointly shape within-host infection outcomes, we developed a mechanistic model of dengue infection dynamics that includes innate immunity, humoral immunity, and dengue-specific CD8+ T-cells. We used our model to understand how infection dynamics and infection pathology change when an infection begins with varying levels of humoral (B-cell) and CD8+ T-cell immunity. We found that enhanced pathology occurred most consistently when humoral immunity was low to intermediate, and CD8+ T-cell immunity was minimal. Increasing pre-existing CD8+ T-cells reduced infection pathology in a dose-dependent manner, and high B-cell or high CD8+ T-cell immunity alone prevented productive infection. We apply our simulation results to interpret previous studies of ADE in natural infection, to understand divergent outcomes of two live-attenuated vaccine trials, and to provide an potential evolutionary reason for branchwise immunologic heterogeneity among humans.

Plastic Transmission Investment: Impact of Parasite Density and Immune Killing

Presenter: Weixin Du

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Within their hosts, malaria parasites experience a growth-reproduction trade-off as they invest red blood cells into one of two mutually exclusive pathways: asexual replication (growth) or production of sexual transmission stages called gametocytes (reproduction). Past experimental rodent malaria (Plasmodium chabaudi) infections show that transmission investment strategies are plastic, changing in response to red blood cell (RBC) availability and drug treatment, but the impact of immune clearance remains unclear. Previous methods allow disentangling of resource availability versus immune removal on parasite populations within the host via effective propagation numbers, but those methods could be biased by neglecting transmission investment. Using two P. chabaudi datasets with different inoculation dosages, we estimated transmission investment and effective propagation over the course of infection. We first confirmed that incorporating transmission investment has minimal impact on estimates of immune killing. Next we determined how transmission investment in varied with replication rates, RBC availability, and immune killing. Consistent with previous findings, we found that transmission investment initially declines as asexual replication rates decrease (reproductive restraint) and then increases sharply if replication rates drop precariously low (terminal investment). Similarly, we found that transmission investment initially declines as immune killing increases, but parasites invest more into transmission when immune killing intensifies further. As inoculation dose increases, parasites exhibit greater transmission investment at very low replication rates and at high rates of immune removal. Our results add to growing evidence that parasites alter transmission investment in response to their population dynamics within the host and show further that parasites strategies also depend on initial inoculum dose.

Rift Valley Fever Dynamics and Drivers Vary Across East Africa

Presenter: Evan Eskew

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Rift Valley fever (RVF) is a viral disease of livestock and humans that affects Africa and the Arabian Peninsula. Classically, RVF epidemiology has been described using the concept of epidemic-interepidemic cycles: large, multi-country RVF epidemics can be sparked by environmental drivers, specifically heavy rainfall that facilitates mosquito breeding, while epidemics are separated by interepidemic periods characterized by limited RVF virus circulation. Recently, however, researchers have begun to recognize an alternative RVF epidemiology: some regions may exist in a hyperendemic disease state typified by sustained virus circulation in the absence of explosive epidemics. To better understand variation in RVF dynamics in East Africa, we leveraged data from 122 RVF interepidemic disease events spanning 2008-2022 across Kenya, Tanzania, and Uganda. Critically, this outbreak dataset contains countries with both classical (Kenya, Tanzania) and putative hyperendemic (Uganda) disease patterns. We used a suite of > 30 predictor variables in a machine learning framework to understand the environmental and biological drivers of RVF. When we fit a model to the full dataset using a leave-one-country-out training approach, data from Kenya was consistently the most difficult to predict, suggesting distinct RVF dynamics or reporting infrastructure in Kenya. Further, country-specific models revealed differences in RVF drivers. For example, in the Kenya-specific model, slope (-), elevation (-), and human population (-) were among the top 10 most important predictors along with three precipitation variables. These results are consistent with macro-scale disease patterns given RVF is often reported in the sparsely-populated, arid plains of east Kenya. By contrast, the Uganda-specific model included elevation (+), two precipitation, and four temperature variables among the top 10 most important. Our results highlight how RVF disease dynamics and drivers can vary even across neighboring countries in East Africa, with implications for identifying and managing hyperendemic zones.

Determinants of Hemoparasite Co-Infections in Free-Ranging Lemurs

Presenter: Kayla J. Evans

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Co-infection by multiple parasites is increasingly recognized as a key driver of host health, disease severity, and infection dynamics in wildlife. Lemurs, a unique primate radiation endemic to Madagascar, host a diverse assemblage of hemoparasites, including Plasmodium species, the causative agents of malaria, and Babesia sp, a tick-borne apicomplexan parasite. Despite the potential impacts of these parasites on lemur health, fitness, and conservation, the understanding of the ecological and evolutionary dynamics of hemoparasitism in lemurs is limited. In this study, we characterize the prevalence, diversity and co-infection patterns by Plasmodium and Babesia among free-ranging lemurs across Madagascar. We test the hypothesis that behavioral and ecological factors affect the likelihood of infection by either parasite alone or by both Plasmodium and Babesia. We screened 442 whole-blood samples from 13 free-ranging lemur species, using PCR assays targeting a 1,000 bp region of the cytb gene of Plasmodium and the 18S rRNA of Babesia. Positive samples were sequenced using Sanger sequencing techniques and single strand Oxford Nanopore to analyze patterns of parasite diversity, host specificity, and geographic distribution. Plasmodium infection was common (60%) but varied significantly among host species, sites, and seasons. Phylogenetic analyses revealed stable host-parasite associations and limited cross-species transmission by Plasmodium. Together, our findings suggest that hemoparasite ecology in lemurs is shaped by host behavior, environmental context, and evolutionary relationships between parasites and their lemur hosts.

Seasonal Immune Timing Alters Parasite Growth and Transmission in a Multi-Host System

Presenter: Chloe Fouilloux

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Immune defenses are costly and therefore vary in intensity across ontogenetic and seasonal time. Although theory and empirical work have independently shown that juveniles are often more susceptible to infection and that immune investment tends to peak when parasite exposure is highest, how immune expression changes with host age across seasonal environments remains poorly understood. Resolving this interaction is critical for understanding the evolution of immune timing and parasite transmission. To address this need, we quantified infection and immunity in a trophically transmitted system linking the cestode Schistocephalus solidus with its obligate second intermediate host, the threespine stickleback (Gasterosteus aculeatus). In this system, stickleback have evolved anti-growth resistance via fibrosis, an immune response that constrains parasite development and can be visually quantified. We sampled eight lake populations on Vancouver Island (BC) monthly over one year, tracking parasite size, infection prevalence, and fibrosis expression in mixed-cohort populations. In highly-fibrotic populations, peak immune activation synchronized with peak parasite:host ratios, the result of which suppressed parasite growth quickly, and rarely resulted in transmissible tapeworms. In contrast, low-fibrosis lakes had higher parasite:host biomass ratios that peaked later in the season, despite similar seasonal timing of immune expression. These lakes contained substantially more transmissible parasites, with peak transmission potential coinciding with the seasonal arrival of definitive hosts to Vancouver Island. Together, these results demonstrate how population-level variation in the timing and magnitude of anti-growth immunity shapes transmission potential in the wild.

Identification of a Novel Immune Handoff in a Wild Population of Hantavirus Reservoir Hosts

Presenter: Christina Fragel

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Traditional immunology provides an important foundation to manage, treat, and monitor emerging infectious diseases, but the applicability of lab findings to the study of viral immunology in wild populations is unclear due to the difficulty of experimental manipulation and the complexity of the challenges that a wild immune response faces. Advances in genomic techniques are providing new insights into how the host immune response prevents, restrains, or even facilitates viral transmission in wild reservoir hosts. In this study, I utilize genomic tools to characterize the immune response of wild bank voles to Puumala hantavirus, an important emerging viral infection in Europe.

My work captures the real-time immune responses mounted by bank voles as they move through phases of Puumala infection, observing traditional immunology principles playing out in nature. Using metatranscriptomic and pathway enrichment analyses I identified the active immune pathways and cellular responses for key stages of hantavirus infection; when voles first contract Puumala and are actively shedding virus and when voles shift into a chronic stage of infection. Pathway enrichment identified a classic inflammatory Th1 response from cells of the adaptive immune system when voles are shedding virus. New to our understanding of reservoir immune responses, I identified a hand off to the innate immune system and enrichment of immune pathways associated with inflammatory interferons and phagocytosis as individuals move into the chronic stage of infection. Working from these results, I was additionally able to isolate hantavirus RNA from the vole shotgun RNA sequencing output to construct genomes for the strains infecting voles in the chronic and shedding stages of infection. The results of this project add to the scaffolding of traditional laboratory studies by establishing methods that allow us to study the immune response of wild populations and link those responses to viral evolution and environmental variables.

Centering Human Cognition in Epidemiological Models

Presenter: Ari Freedman

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Epidemiological models have increasingly recognized the importance of human behavioral processes as modulators of transmission dynamics, especially since the COVID-19 pandemic. However, models typically include a small subset of the range of behaviors humans exhibit in response to disease, and generally assume risk perception is a static function of a population's disease state which translates directly to behavioral responses. While such approaches are crucial to understanding how behavior affects disease dynamics in specific, idealized scenarios, we stress the need for epidemiological models which can encompass a wide variety of behaviors simultaneously; allow for discrepancies and heterogeneities in how behavioral responses cognitive elements like risk perception; and are more closely informed by experts and data from the social sciences. As a mixed group of epidemiological modelers and social scientists, we will present two general "cognitive epidemiological models" which seek to incorporate these concepts to illustrate this new paradigm in behavioral epidemiological models, with cognitive processes parameterized by discrete choice test surveys.

Linking Disease Prevalence to Wildlife Spatial Organization Using High-Resolution Satellite Imagery

Presenter: Bowen Gao

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Pathogen infection can cause profound shifts in how animals interact with one another. However, whether such disease-associated changes in individual behavior can scale up to detectable differences in population-level social and spatial organization is an open question. To address this question, we used a combination of experimental and field studies to investigate the effects of bovine tuberculosis (TB, Mycobacterium bovis) on individual- to population-level spatial organization of wild African buffalo (Syncerus caffer) in Kruger National Park (KNP), South Africa. First, by experimentally infecting 16 buffalo with TB in captivity, we found that the average pairwise distance between individuals progressively increased during infection. Next, we tested >500 buffalo for TB across 17 herds in KNP to estimate TB prevalence at the home range scale, and paired these data with high-resolution satellite imagery to generate herd-level datasets on TB prevalence and animal spatial patterning. We found that both average nearest neighbor distance (NND) and variability in NND were significantly greater in groups from high-prevalence home ranges vs. low-prevalence home ranges. Overall, our results suggest that TB infection affects host spatial interactions, and that effects on individual buffalo scale up to herd-level spatial organization in the wild. These findings also suggest that for diseases like TB, social behavior may serve as a useful tool for indirect disease monitoring.

Fine-Scale Movement Patterns Reduce Sars-Cov-2 Persistence in White-Tailed Deer

Presenter: Billy Gardner

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Understanding how pathogens invade and persist in wildlife populations has important implications for mitigating the risk of spillover and spillback of pathogens to humans and wildlife. SARS-CoV-2 (SCV2) is a virus of considerable importance to human health that infects wildlife. An outstanding challenge is understanding under what conditions, if any, a wildlife species can act as a reservoir for SCV2. White-tailed deer (WTD, Odocoileus virginianus) are a competent wildlife host of particular interest due to high observed infection rates. We combine a novel modeling approach with a dataset from nationwide targeted surveillance (12 sites and >1000 collared deer) to scale up from empirically observed individual deer movements to landscape-level transmission patterns. We used this model to assess i) the plausibility SCV2 could persist independently in observed WTD populations for three years following introduction and ii) how variation in landscape structure, population density, and empirical movement patterns affected within-group and between-group transmission. We found that between-group R0 (number of new infections produced in groups not belonging to the index case), and not total R0, was a strong predictor of persistence. For example, we predicted a 11.7-fold higher probability of three-year persistence at a site in Tennessee (TN) compared to one in Illinois (IL), despite the Illinois site having a 1.6-fold higher total R0. Model-predicted between-group transmission was lower in IL 21.1% of total R0) compared to TN (34.1%). The observed differences in SCV2 dynamics were largely a result of smaller activity ranges in IL compared to TN (0.98 vs 2.13 km2). Our work demonstrates that fine-scale movements can drastically reduce SCV2 persistence probability in WTD populations, suggesting that if WTD are acting as a reservoir for SCV2, they are likely doing so at broader spatial scales than the areas inhabited by most managed deer populations.

Trait-Based Assessment of West Nile Virus Impacts in Pennsylvania Wild Bird Populations

Presenter: Brock Geary

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Pathogens that infect multiple host species may exhibit host-specific disease outcomes, leading to variable impacts at the community or landscape scale. This may occur as a result of interactions between hosts, vectors, and their environment, and long-term monitoring efforts are often required to accurately characterize these dynamics. Understanding how pathogens can have differential effects based on hosts' life histories or behaviors can serve as a path of inquiry to direct limited management resources to more imperiled species and promote overall ecosystem health.

West Nile virus (WNV) has occurred throughout North America for over 20 years, and can represent a threat to wild birds in environments that promote large, persistent mosquito populations. Following an analysis of how environmental conditions favorable to WNV occurrence influenced bird population trends in Pennsylvania, we evaluated the relationship between species-specific ecological traits and state level measures of WNV impact . Using databases such as AVONET and EltonTraits, as well as additional information acquired from resources such as Birds of the World and the broader literature, we constructed phylogenetically explicit models to assess how bird characteristics and behaviors potentially influence interspecific variation to mosquito exposure and WNV effects. Beyond detecting a phylogenetic signal in our observed patterns of WNV response, we found increased effects in ground-nesting birds, vertivores, and species that exhibited more gregarious behaviors during the nesting season. Additionally, we found that species nesting in cliffs and comparable human structures showed reduced effects, possibly reflecting their relatively low accessibility to WNV vectors. Further analysis of community composition in areas where WNV effects are pronounced, along with future field-based validation of model estimates, will contribute to management strategies by adding to our understanding of how the virus shapes population trends relative to other threats such as habitat loss.

“Everything Sensor”: A Multimodal Sensing Platform for Environmental and Bioacoustic Monitoring

Presenter: Julia Gersey

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Monitoring bat activities in the wild is important for understanding ecosystem health, biodiversity, and the ecological dynamics that influence infectious disease risk. Traditional monitoring approaches such as mist-netting, thermal imaging, and acoustic recording provide valuable information, but they primarily focus on a single sensing modality, limiting the ability to capture the full spectrum of bat behaviors and environmental interactions. In this work, we propose a multimodal “Everything Sensor” that integrates particulate matter, gas concentration, environmental conditions (e.g., temperature, humidity, pressure), and acoustic sensing on a single sensing platform. Bat activity is inherently multimodal: flight and roosting behaviors are accompanied by ultrasonic vocalizations, wing-induced airflow, and changes in the surrounding micro-environment. By simultaneously capturing these co-occurring signals, our system improves the robustness and accuracy of bat activity recognition beyond what is possible with any single modality alone. We validate the feasibility of this approach through preliminary field deployments using a subset of the sensing modalities. Data were collected in collaboration with partners at Colorado State University and Pinnacles National Park, as well as through deployments conducted with the San Diego Zoo Wildlife Alliance. These early results demonstrate the potential of multimodal, synchronized sensing to provide richer and more resilient measurements of bat activity in complex, real-world environments.

Vegetation Preferences and Dispersal Behaviors of Dermacentor Andersoni: A Mark-Release-Recapture Study

Presenter: Sabrina Gobran

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Tick-borne diseases (TBDs) constitute a greater threat to human health within the contiguous United States than mosquito or flea-borne viruses, bacteria, and parasites. From 2001-2023, vector-borne disease cases more than doubled in the U.S., with TBDs garnering the highest case reports. In the mountain west, the primary tick vector is Dermacentor andersoni (Rocky Mountain wood tick), which is capable of transmitting Rickettsia rickettsii (Rocky Mountain spotted fever) and Colorado tick fever virus. Geographic distribution of numerous tick species and overall TBD incidence in the U.S. has been increasing, attributed to climate warming, reforestation efforts, and human encroachment into tick habitat. It is thus important to understand how changing landscape and climate conditions will impact tick behaviour and TBD risk. Mark-release-recapture (MRR) is a commonly used tool in ecological research to study animal movement, estimate population sizes, and quantify survivorship. We used tick MRR to quantify D. andersoni dispersal distances and vegetation preferences in Northern Colorado. We constructed five continuous 10 m2 study plots in Rustic, Colorado, which were surveyed by active dragging 1-3 times per week for 8 weeks. Ticks were marked with nail polish using a unique 3-color system and released onto predetermined vegetation sites representing the overall diversity of plants in the area. Recaptured ticks were identified based on their unique markings. We recorded the vegetation type each tick was recollected from and the straight-line distance to its prior release site. We found that D. andersoni ticks exhibit directed movement towards preferred vegetation (i.e., grass, leaf litter) and away from non-preferred vegetation (e.g., shrub). The average rate of movement was 0.67 m/day (SD = 1.2), with most ticks moving <2 m/day. Overall, we were able to determine fine scale vegetation preferences and dispersal behaviors of individual D. andersoni ticks.

Estimating Effective Reproduction Numbers Using Multiple Data Streams, Including Wastewater and Case-Counts

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Traditional methods for estimating the effective reproduction number (Rt) rely on case-count data, which, in many instances, can be unreliable due to wide spatial and temporal dispersion in reporting rates. Recognizing this limitation, viral concentrations measured from wastewater samples have emerged as an alternative dataset, providing researchers with a cost-effective and scalable data stream for the quantitative monitoring of infectious viral pathogens. Here, we first briefly present a review of the latest methodological developments in wastewater epidemiology to identify best practices for estimating time-varying Rt. Next, we present a semi-mechanistic Bayesian state-space model that incorporates these best practices and builds on them to estimate Rt using wastewater data either alone or jointly with case count data. To achieve joint inferences, we specify separate infection, shedding, and detection dynamical layers that share common incidence rates but differ in the timescales of how an individual progresses through these layers. This provides us a parsimonious way to constrain timescales of infection, shedding, and detection dynamics using empirically estimated generation time distributions, shedding profiles, and infection-to-reporting distributions, respectively, while allowing information to flow through different data streams via common incidence rates to inform Rt. We extensively test our method using mock data and further apply it to empirical SARS-CoV-2 data.

Cross-Scale Selection Pressures on Pre-Symptomatic Transmission

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Disease spread is amplified when infected hosts can transmit before symptoms (pre-symptomatic transmission). Pathogen traits that facilitate pre-symptomatic transmission could evolve in response to selection pressures at multiple scales. Recent analysis of controlled human infection trial data suggests that faster replication can extend the duration of pre-symptomatic infectiousness, the time until symptom onset and, potentially, associated changes in host behavior that reduce the probability of onward transmission. Theory suggests faster within-host replication can enhance both R0 and the risk of stochastic extinction at the between-host scale, creating a tradeoff between invasion and persistence in host populations. However, it remains unclear how within-host replication rates influence persistence at the between-host scale when symptom-driven behavioral changes constrain transmission. For example, symptom-induced transmission changes could impose selection on replication rate, potentially favoring replication rates that enable more efficient transmission before symptoms manifest. Here, we use a multiscale model to couple within-host replication and between-host transmission to examine 1) how optimal pathogen replication rates differ at the within- and between-host scales and 2) how these strategies might evolve given symptoms,Äö√Ñ√¥ impact on transmission rate. Ultimately, this study will provide insight on how pre-symptomatic transmission could evolve in response to selection pressures across scales.

Integrated Farmer-Led Strategies to Optimise Sustainable Control of African Animal Trypanosomosis

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Background: African animal trypanosomosis (AAT) remains a major constraint to livestock productivity in rural sub-Saharan Africa, reinforcing poverty and food insecurity. While large-scale vector control strategies such as aerial spraying have historically reduced transmission, these approaches require sustained political and financial commitment, which has in recent decades declined. Control is now largely farmer-led, relying on trypanocides and small-scale insecticide use, often without evidence-based guidance. Aim: The study aims to identify combinations of existing control strategies that achieve sustainable and cost-effective AAT control across different epidemiological and agro-ecological settings. Methods: We developed a livestock-vector-wildlife epidemiological model to simulate the farmer-led control strategies. Scenarios included responsive treatment with diminazene or isometamidium and prophylactic isometamidium combined with insecticide coverage. An economic framework was layered onto the model to quantify direct costs (drug and insecticide expenditure) and indirect costs (production losses). Benefits were calculated as averted production losses relative to the baseline scenario with 0% drug treatment and 0% insecticide coverage. Economic efficiency was assessed using the benefit-cost ratio (BCR), with BCR > 1 indicating efficiency. Results: Without vector control, case treatment alone was inefficient at reducing disease burden, requiring significantly high case treatment coverage (>95%) for responsive treatment or high frequency for prophylactic treatment (~8 treatments per year). When combined with vector control, >40% insecticide coverage was required to reduce prevalence below epidemiologically relevant levels, eliminating the need for drug treatment (Figure 1). Benefit-cost ratios showed that curative treatment alone was rarely cost-efficient, whereas combining responsive treatment with ~30% insecticide coverage restored cost-efficiency at prevailing case treatment proportions (Figure 2). Prophylactic treatment exhibited declining BCRs with increasing treatment frequency. Conclusion: Integrated farmer-led strategies combining moderate insecticide coverage with targeted drug use achieve sustainable and cost-effective control of AAT, while reliance on drug treatment alone requires unrealistically high coverage to remain efficient.

Modeling Fomite Transmission Between Individuals Quantifies Efficacy of Milk Last Intervention in Reducing Contagious Mastitis in Dairy Cattle

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Managing bacterial infection by pharmaceutically treating symptomatic individuals is often insufficient to suppress transmission and can encourage antimicrobial resistance. The intentional ordering of contacts is an alternative fomite transmission control strategy that is not confounded by antimicrobial resistance. To investigate the relative efficacy of potential implementations of one such non-pharmaceutical control, we develop an individual-based model that explicitly accounts for fomite transmission of contagious mastitis via dairy milking equipment. Our model tracks specific exposures and disease states of each immunologically variable animal at each milking session throughout an entire lactation period. The conventional Milk-Last Intervention temporarily “isolates” animals by milking them last during each milking session, as long as they remain visibly inflamed. We investigate the impact of isolating all animals that have been visibly inflamed for the remainder of the lactation period, as well as the impact of instituting a temporary post-inflammation “quarantine.” Permanent isolation requires infrastructure, but we show it is the most effective at preventing transmission by apparently healthy carriers, assuming there is a single pathogen of concern. In certain labor/infrastructure environments, only temporary sorting is feasible. We find that adding a temporary quarantine group is still more effective than the conventional implementation alone. Additionally, an emergent property of this sorting may be helpful in designing phenotypically relevant stocking and breeding plans for a facility’s specific microbiotic context. Our results highlight the importance of accounting for individual heterogeneity and apparently healthy carriers in evaluating non-pharmaceutical interventions.

Characterizing the Emergence of Antimicrobial Resistance in Marine Ecosystems

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Marine mammals harbor microbiomes that co-evolved with them for millions of years, partly shaped by phylosymbiosis, correlations between host phylogenetic relationships and microbiome composition, and diet. Antimicrobial resistance (AMR) is an immediate concern in these populations, mirroring trends observed in humans, including multi-drug resistance. Despite the well-studied occurrence of AMR in humans and domesticated animals, there is an overall lack of literature pertaining to the distribution of resistance among marine mammals, as well as the associated environmental burden on already fragile marine ecosystems. Here, we carried out a longitudinal bioinformatic analysis over the course of 2+ years aimed at characterizing AMR dynamics within the gut excreta of captive beluga whales (Delphinapterus leucas) held at Mystic Aquarium in Mystic, Connecticut. We find that gut microbial community structure concords with that of other carnivorous whales, largely dominated by gram-positive bacteria in the phyla Firmicutes and Actinomycetota. Automatic binning for the construction of metagenome-assembled genomes within these phyla resulted in the recovery of 100+ genome bins, revealing novel lineages largely pertaining to the family Mycobacterium. Further classification of antibiotic resistance within these assembled genomes reveals multidrug resistance toward clinically relevant antibiotics, including fluoroquinolones and cephalosporins. To date, no existing studies have evaluated beluga whales for their capacity to harbor or transmit antimicrobial resistance. Further, evolutionary consequences of such resistance – including the selective pressures shaping microbial fitness and heritable antimicrobial resistance gene (ARG) persistence – remain entirely unexplored in this system. By investigating the distribution and evolutionary behavior of cetacean-associated ARGs, we can better elucidate our understanding of marine ecology and the interplay between marine animals and human health.

Understanding the Role of Wild Suids in Mycobacterium Bovis Transmission in Multi-Host Systems: A Systematic Review

Presenter: Natalia Grazda-Valdez

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Mycobacterium bovis is the main cause of animal tuberculosis in livestock and wildlife, which can also infect humans causing zoonotic tuberculosis. The issue surrounding this mycobacterium lies with spread and control of animal tuberculosis at the wildlife, livestock, and human interface, presenting a global economic and public health challenge. Maintenance hosts are species that sustain a pathogen in an area regardless of whether there are other species present that can disseminate the pathogen. Wild suids (i.e., wild boar [Sus scrofa] natively and invasive wild pigs [S. scrofa x domesticus] elsewhere) serve as M. bovis maintenance hosts. A thorough understanding of the factors promoting maintenance host status is necessary to improve disease control. In this study, we aim to define the epidemiological, ecological, and behavioral factors that promote wild suids as maintenance hosts for M. bovis transmission. We conducted a systematic review, following the Preferred Reporting Items of Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines and utilizing the Population, Exposure, Comparison, and Outcome (PECO) search method for determining keywords. These keywords were used to systematically pull references from several databases. A total of 1,517 references were identified through our initial search. Utilizing Rayyan, duplicates (n=551) were removed from the literature collected, leaving a total of n=1,219. Once initial abstract screening was complete, n=127 references were left. Of these, 88 met the inclusion criteria and were included for analysis. We identified 42 variables of interest in these references divided into the following categories: Diagnostics, Demographic, Behavioral, Environmental, Ecological, and Epidemiological. A meta-analysis is being performed to determine the risk factors underlying M. bovis infection (based on prevalence) in wild pig populations. This study will allow us to address M. bovis transmission in wild suids populations globally, informing guidelines applicable to different regions for efficient prevention and control.

Generating Informative Sub-Sampled Networks to Study the Spread of Outbreaks Across Explicit and Network Space

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Directly transmitted pathogens are often transmitted by a mixture of processes. Direct transmission is best characterized by a network or by a spatial/proximity kernel, depending on the exact transmission mechanism. Studying the relative contribution of network structure and proximity to outbreak risk in realistically large networks is challenging. Large observed networks are often only a single realization of a contact process and not necessarily reflective of future contacts. Generating full size stochastic realizations of the original network is computationally expensive and unnecessary for characterizing early transient phenomena, like the probability of a major outbreak. In this study, we compare various approaches for subsampling and simulating small networks that replicate the node and network properties of a large, real-world cattle shipment network from the Republic of Türkiye. We then simulate outbreaks of foot-and-mouth disease on the resulting smaller networks. We show that while various algorithms are capable of generating networks that replicate properties of the original network, most are incapable of replicating the dynamics of outbreaks observed in the full network. We show that forest fire subsamples retain network structure, spatial arrangement and correlations between nodal attributes and network parameters. We then show, using algorithms that either retain the original networks structure, correlation among nodal properties, or the spatial arrangement of nodes, that all three properties are necessary in sub-networks to replicate the outbreak probability observed in the original network. We find that replicating the specific correlation structure (between network parameters and nodal attributes) of the original network is necessary for replicating the duration of infection observed in simulations on the original network and that changing the nearest neighbor distribution of the nodes has a large impact on the proportion of nodes infected. This methodology helps us identify which networks properties are most relevant for the initial stages of outbreak spread.

Estimating Risk of Blacklegged Tick-Borne Coinfections Across Counties in the Eastern United States.

Presenter: Alexander Grimaudo

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Coinfection with tick-borne pathogens, which can result from the bite of a single tick or sequential tick bites, can complicate the diagnosis and treatment of tick-borne diseases. However, the distribution and prevalence of coinfecting pathogens in tick populations is incompletely understood in the United States, despite determining local risk. We leveraged tick surveillance data in the ArboNET Tick Module to develop habitat suitability models to estimate the geographic overlap (i.e. coinfection zones) of nymphal blacklegged ticks (Ixodes scapularis) infected with Anaplasma phagocytophilum human-active variant (Apha; Anaplasmosis), Babesia microti (Bam; babesiosis), Borrelia burgdorferi sensu stricto (Bbss; Lyme disease), and Borrelia miyamotoi (Bmiya; hard tick relapsing fever) in the eastern United States. Further, we used Bayesian zero-inflated binomial models to estimate coinfection prevalence in nymphal tick populations within coinfection zones. The suitability models predicted widespread co-occurrence of the pathogens examined, particularly throughout the northern Midwest, Northeast, central Appalachia, and northern Ohio Valley regions. Bbss-Bmiya was predicted to be the most geographically widespread coinfection, though it had the lowest predicted prevalence of the coinfections examined. Bam-Apha was predicted to be the most geographically constrained coinfection, while Bbss-Bam had the highest predicted prevalence in nymphal populations. Importantly, field data suggested coinfections in nymphs form more often than expected by chance. Ultimately, the findings presented here characterize regional variation in tick-borne coinfection risk, useful to raising awareness of tick-borne coinfections among medical providers.

Stress Induced Genome Dynamics Reveal Rapid Adaptive Potential of the Malaria Parasite

Presenter: Jennifer Guler

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Genome structural variation, particularly copy number variation (CNV), is increasingly recognized as a major contributor to rapid evolutionary change in pathogens. Yet rare de novo CNVs, or those present in only a few individual cells within a population, remain largely unexplored. This reservoir of genetic variation has the potential to fuel adaptive responses but detecting these variants is especially challenging in microbes with small and base-skewed genomes. Our work focuses on the single-celled malaria parasite, Plasmodium falciparum, whose highly AT rich genome and unusual mechanisms of genome maintenance create a distinctive landscape for CNV generation. To sequence rare CNVs at single genome resolution, we optimized a whole genome amplification protocol that minimizes amplification bias and host contamination and enables robust CNV discovery. We paired this approach with two novel complementary computational tools, HapCNV and SVCROWS, designed to detect and quantify CNVs in complex single cell datasets. Together, we dramatically increased our ability to recover known CNVs present across parasite populations and provided confidence for discovering novel variants. Using this framework, we mapped de novo CNVs and found that replication stress markedly elevates CNV generation over normal conditions. Variants were distributed broadly across the genome and affected genes tied to diverse pathways essential for parasite survival. These observations suggest that P. falciparum has evolved genome features and repair strategies that actively promote CNV accumulation, generating standing structural variation. We are currently exploring other conditions that may shape genome plasticity in pathogen populations. Characterizing CNV dynamics provides a mechanistic foundation for predicting how microbial pathogens expand host range, navigate fluctuating environments, and evolve resistance in real time.

Basil: Bayesian Source Inference and Localization for Spatial Epidemiology

Presenter: Fangfang Guo

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Abstract Identifying spatial sources of biological invasions, disease outbreaks, or environmental contaminants from spatial observations is critical for intervention, yet existing methods fail to resolve overlapping signals from multiple sources or handle extreme boundary inflation in bounded data. We developed BASIL (BAyesian Source Inference and Localization), a hierarchical framework that jointly infers source locations and mechanistic dispersal kernels from zero-one-inflated spatial observations. Systematic validation across 2,300 simulations spanning localized to long-distance dispersal regimes, foci weight mixture compositions (0.5/0.5 to 0.95/0.05), and sample sizes (N = 50 to 500) demonstrates robust model selection via leave-one-out cross-validation: 100% correct kernel identification in well-specified scenarios, 100% and 98% (2% predictively equivalent) with under-and over-parameterization, and appropriate parsimony in null scenarios (80% predictive equivalence). Median source localization bias was 0.13 units (90th percentile: 0.78 units), with successfully resolved minority sources contributing only 5% of observations. The framework provides intrinsic self-diagnostics, signaling model complexity mismatch through posterior bimodality (under-parameterization scenario) or parameter collapse (over-parameterization scenario). When applied to experimental field data of cucurbit downy mildew, the framework achieved an 80% reduction in source uncertainty despite environmental heterogeneity and sparse sampling, validating its capacity to isolate biological signals from real-world noise. BASIL is available as open-source Python software enabling inverse spatial inference across ecology, epidemiology, and environmental monitoring.

Keywords: Spatial epidemiology; Zero-one-inflated data; Dispersal kernel; Bayesian inference; Inverse problem

Don’t Spend It All in One Place: Variation in Immune Function Allocation Drives Infection Dynamics of an Intermittently Shed Pathogen

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Many wildlife pathogens with zoonotic potential (e.g. rodent hantaviruses) exhibit intermittent shedding, characterized by an initial infectious phase, followed by a latent phase until a change in the internal condition causes the host to become infectious again. Periods of low or high food availability could influence the ability of hosts to reduce shedding, increase clearance and suppress future infection relapse, but how variation in food availability influences these different components of immune defense remains unknown.

Here, we develop a mathematical model to explore how resource allocation to immune defense, alters the infection dynamics and zoonotic potential of an intermittently shed pathogen in variable environments. We co-vary mean annual resource availability and the magnitude of weekly fluctuations in availability, and how these resources are allocated to reducing (i) shedding intensity, (ii) infection duration and (iii) relapse rate; we use the timing of peak population-level shedding, and the cumulative number of infections as metrics of instantaneous and season-long human exposure risk.

Environments with low resource availability and low fluctuations resulted in the greatest instantaneous and cumulative zoonotic exposure risk, but increasing fluctuations lessened these impacts through temporary immune benefits. The magnitude of this effect depended on how host immunity responded to resources; zoonotic exposure risk was greatest when prolonged food scarcity primarily acted to increase the duration of host shedding. Conversely, high resource availability reduced infections, but these benefits were eroded by large fluctuations and periods of immunocompromise. Our results highlight the importance of quantifying variation in resource availability for reservoir hosts as well as the pathways through which resources influence immune function.

Modeling the Consequences of Infection During Migratory Stopover

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Animal migration shapes exposure to pathogens, and in turn, pathogen infection can influence the timing and extent of migratory movements. Prior theory linking migration and infection outcomes focuses on the effects of habitat switching (e.g. migratory escape and recovery from infection), or active periods of migratory movement, and the lethal or sub-lethal consequences of moving while infected (e.g. migratory culling and relapse). However, many migrants break up their long-distance journeys with sometimes-protracted stays at stopover sites to rest, refuel and repair. By aggregating high numbers of migrants, stopover sites can act as transmission hotspots; however, we lack a theoretical framework for understanding how infection influences an individual host's stopover behavior, and in turn how decisions about stopover departure influence infection duration and host survival at the stopover site, and during subsequent migration. Here, we develop a model linking the intensity and duration of pathogen infection to stopover activities such as foraging activity, and resource allocation tradeoffs between refueling and immune response. We calculate the consequences of stopover-infection feedbacks for host survival under different scenarios for decisions relating to stopover duration, where individuals prioritize (i) keeping to a migratory schedule, (ii) recovery from infection before departure or (iii) maximizing fuel load prior to departure. We find that the relative advantages of each scenario for survival across the annual cycle are influenced by the environmental context of the migration, such as cost-distance between stopover sites, the seasonality of resources at stopover sites and favorable conditions for migration. Tracking these associations between host condition, infection and stopover behavior are a critical first step for understanding infection patterns at stopover sites and across the migratory range.

Vsv Moves in Mysterious Ways: Epidemiological Studies of Vesicular Stomatitis Virus Reveal Evidence of a Sylvatic Cycle

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Vesicular stomatitis virus (VSV), a vector-borne pathogen of hoofed livestock, circulates endemically from southern Mexico south to northern South America, and emerges periodically to cause outbreaks in northern Mexico and the US. VSV includes two species (Indiana (VSIV) and New Jersey (VSNJV)) with overlapping endemic ranges. While a sylvatic, enzootic cycle of VSV in its endemic region has long been suspected, proof remains elusive. Our epidemiological investigations of VSV in foci of endemic transmission in southern Mexico and Costa Rica together reveal strong, albeit circumstantial, evidence of sylvatic circulation. In Chiapas, Mexico, VSV cases, evident from cutaneous lesions on the mouth, teats and/or legs, were detected at five target ranches nearly annually during the rainy season but were absent during the dry season. However, VSNJV RNA was detected in a panel of haematophagous insect taxa implicated in transmission (sand flies, biting midges, mosquitoes and black flies) year-round. Since experimental studies have shown that vectors can only acquire VSV from lesions, the occurrence of VSNJV RNA in insects during the dry season suggests that the virus is either being acquired from wildlife or maintained exclusively in insects via vertical or co-feeding transmission. To pursue the former hypothesis, we trapped haematophagous insects at distances up to 500 m into forests abutting the target ranches and detected VSV RNA at depths in the forest where livestock were never detected via wildlife cameras. While VSIV was largely absent in our collections from Chiapas, a study of passive case reports followed by RT-qPCR confirmation in Costa Rica revealed circulation of both VSIV and VSNJV. Although the ranges of both viruses overlapped, the relative proportion of VSIV cases was significantly higher in dryer habitats and higher elevations, suggesting either different wildlife reservoir hosts or different suites of vectors are involved in transmission of the two viruses.

Parasite Traits Shape Forest Loss–Infection Associations: A Global Meta-Analysis of Mammals

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Forest loss can affect host–parasite dynamics, posing risks to wildlife and human health. Most work investigating the effects of forest loss on parasite infection outcomes has examined how host traits moderate forest loss—prevalence associations. However, the role that parasite traits play in moderating these associations is less understood. To address this knowledge gap, we synthesized parasite prevalence and parasite trait data from global, publicly available databases including carnivore, ungulate, and primate host species. We combined these data with open-source, remote-sensing forest loss data and conducted multi-level phylogenetic meta-analyses. Overall, across 5017 parasite prevalence records, we found no association between forest loss and prevalence across mammalian parasites. However, forest loss effects on prevalence varied by parasite group (i.e., arthropod, bacteria, fungus, helminth, protozoa, or virus). Moreover, while we also found no evidence that prevalence responses to forest loss vary by transmission mode (i.e., close, non-close, intermediate, vector), responses varied by transmission mode within some specific parasite groups. As one example, prevalence decreased with forest loss for closely transmitted helminths but increased for not closely transmitted helminths. These results illustrate that parasite traits must be considered to understand complex associations between environmental change and infection outcomes. Our study highlights several avenues for future work on this topic, including a need to address key data gaps and for focused studies to identify the mechanisms underlying how parasite traits moderate forest loss—prevalence associations.

Insecticide Deltamethrin Shifts the Thermal Performance of Key Transmission-Linked Traits in Aedes Aegypti Mosquitoes

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Understanding the influence of environmental heterogeneity on mosquitoes is essential to effectively implementing interventions, such as insecticides, to reduce arbovirus transmission. As mosquitoes are ectotherms, temperature-explicit frameworks have been extensively employed to link temperature-dependent mosquito and pathogen traits to transmission through a generalized R0 model. While previous approaches have treated insecticides as external factors influencing transmission in isolation, insecticide exposure has recently been proposed to influence R0 internally by interacting with temperature. The extent to which insecticides can alter the transmission landscape with temperature remain unknown, however. To explore the temperature- and insecticide-explicit framework, we implemented a response-surface experimental design on Aedes aegypti mosquitoes to examine if deltamethrin (a widely used pyrethroid adulticide) interacts with temperature to alter adult transmission-linked traits (lifespan, egg laying, and biting rate). We found that deltamethrin exposure decreased the thermal breadth of all three traits, lowered the thermal optimum for egg laying and biting rate, and increased the thermal optimum for lifespan. Our results provide further evidence that low levels of insecticide exposure can alter the thermal response of Ae. aegypti mosquitoes, and they stress the importance of expanding the abiotic gradients considered in the arbovirus R0 framework to better understand the impact of vector control.

Portrait of Viral Communities in Deer Upper Respiratory Tracts Across the United States

Presenter: Axel Hoarau

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As a result of anthropogenic change, North American deer are increasingly exposed to pathogen spillover from humans and domestic livestock. For instance, cases of pneumonia associated with pathogens common to cattle, as well as evidence for transmission of SARS-CoV-2 amongst deer, have been reported. However, the diversity of microparasites circulating in deer remains incompletely understood. In this study, we use metagenomics to characterize viral communities in the upper respiratory tracts of white-tailed deer (Odocoileus virginianus) and mule deer (O. hemionus) across the United States. We sequenced 21 pooled RNA libraries derived from 210 nasopharyngeal swabs collected at 14 sites across 9 states, representing diverse geographic and ecological contexts, including rural versus urban populations and varying degrees of interaction with humans and domestic animals. Our aims were to identify known and unknown/rare viruses, assess how geography influences viral community composition, and compare viral communities between deer species. We found a wide range of viruses, including those commonly associated with cattle (e.g., bovine coronavirus, bovine parainfluenza virus 3) and humans (e.g., SARS-CoV-2), as well as viruses recently identified in deer, such as CHeRI orbivirus 1. In addition, we discovered a novel Aphthovirus tentatively named “Deer aphthovirus”, related to bovine rhinitis A virus. These findings expand our understanding of deer viral diversity across the United States, providing important insights for managing pathogens at the wildlife, livestock, and human interface.

Assessing Environmental and Biological Controls on Eelgrass Wasting Disease – a Modeling Study

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Eelgrass wasting disease, caused by the marine protist Labyrinthula zosterae, is globally distributed with temperate Zostera marina and outbreaks intermittently, including along the Pacific coast from California to Alaska. Laboratory and field-based studies of eelgrass wasting disease provide insights into the effects of single or limited combinations of environmental and biological factors on the eelgrass wasting disease process. However, disease progression and severity are outcomes of the interactions of multiple factors that reflect environmental conditions, host-pathogen interactions, and seagrass community structure. This study used a coupled eelgrass leaf-L. zosterae model to simulate the growth of an individual leaf, transmission of L. zosterae to the leaf, proliferation of L. zosterae, and disease progression to assess controls by environmental and biological interactions individually and in combination on eelgrass wasting disease. The simulated progression of eelgrass wasting disease resulted from a balance between leaf growth rate and L. zosterea doubling rate; both are temperature controlled. The rate of infection acquisition by a leaf and L. zosterae virulence were the primary controls on disease severity. Comparison of simulated and observed leaf lengths showed the potential role of L. zosterae virulence and transmission rate in structuring eelgrass communities.

Use of Modeled Acarological Risk to Identify Counties with Emerging Lyme Disease Incidence in the Eastern United States

Presenter: Karen Holcomb

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Acarological metrics collected through tick surveillance are used to assess the risk of acquiring tickborne diseases but can be difficult to interpret. Lyme disease, caused primarily by the bite of a nymphal Ixodes scapularis tick infected with Borrelia burgdorferi sensu stricto, is the most commonly reported vector-borne disease in the United States. Although several acarological risk metrics are calculated using tick surveillance data, previous work demonstrated that the density of host-seeking B. burgdorferi s.s.-infected I. scapularis nymphs (DIN) is the most predictive metric for human Lyme disease incidence. We sought to identify a threshold in DIN that accurately separated high from low incidence counties. Using this threshold, we could identify areas with elevated acarological risk that have the potential for increased case counts and become classified as high incidence. Because tick surveillance is not conducted uniformly, estimates of DIN are sparse ("observed DIN"). To fill these gaps, we developed models to estimate DIN in all counties ("modeled DIN") and identified a threshold of modeled DIN that accurately discriminated counties with low vs. high Lyme disease incidence (2022-2023). Applying this threshold back to the observed DIN values, we found weak agreement between the categorization of modeled and observed values, largely driven by outdated density estimates of zero in counties reporting high incidence. We also identified counties in Ohio, Michigan, Indiana, and Illinois estimated to be suitable for elevated incidence (modeled DIN above threshold), but with low observed risk (low observed DIN and incidence). These counties could be targeted with longitudinal tick surveillance to monitor for increasing DIN heralding a subsequent increase in incidence. Our results provide a threshold that can be used in communicating acarological risk for Lyme disease and identifying counties where Lyme disease incidence is likely to increase, areas that could benefit from intensified tick surveillance.

Patterns of Parasite Diversity Across Mammalian Threat Classes

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Understanding patterns of parasite diversity is a central aim of disease ecology. This aim is particularly pertinent for species whose populations may be especially vulnerable, such as those which are already considered threatened. Host species are considered 'threatened' by the International Union for the Conservation of Nature (IUCN) when they meet at least one of the criteria for extinction risk (e.g., small global population size, restricted geographic range, declines, or fragmentation). Meeting one, or multiple, of these criteria can influence host-parasite associations and may cause threatened species to exhibit distinct patterns of parasite diversity. A barrier to characterizing patterns of parasite diversity across threat statuses is undocumented host-parasite associations. Undocumented associations can be substantial and are likely non-randomly distributed, with sampling disparities across host species and geography (e.g., small ranged or cryptic hosts, and remote or less surveyed regions). In this study, we leveraged a bipartite link prediction model to predict the potential missing associations in the London Museum of Natural History's global host-helminth dataset. Paired with threat statuses from the IUCN, we examined how patterns of parasite species richness, parasite community similarity, and parasite biogeography differed across mammalian threat statuses. We found no significant difference in parasite species richness or the patterns of parasitic community similarity across host threat status. Europe was consistently associated with high parasite diversity across threat classes, though some regions differed. These results suggest that patterns of parasite diversity may be broadly consistent across threat classes and demonstrate how host-parasite associations vary across host species and geographic space.

Pandemic Impacts on Protected Rainforests and Rural Communities with Health and Livelihood Support: A Mixed-Methods Approach

Presenter: Skylar Hopkins

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Community support programs can simultaneously improve human and ecosystem health, but it is unclear if and how supported communities maintain these sustainable trajectories during major disruptions. Here, we document how the COVID-19 pandemic impacted rural communities and protected rainforests in West Kalimantan, Indonesia. We surveyed 1016 households across six villages with NGO-affiliated health–livelihood support and four nearby unaffiliated villages to understand their pandemic experiences and logging activity. We also independently estimated weekly forest loss in protected rainforests in 28 NGO-affiliated villages and 698 unaffiliated villages using satellite imagery. The pandemic created an economic shock, whereby half of households lost income, struggled with increased costs of basic needs, or both. We expected this to increase logging, but average forest loss across West Kalimantan decreased 39% after the pandemic declaration. These declines were due to the global timber market crash in early 2020, pandemic travel restrictions, and heavy precipitation in 2020 and 2021. Average rates of forest loss were 52% lower in NGO-affiliated villages before the pandemic, and this difference increased to 68% during the pandemic. Correspondingly, NGO-affiliated households were more likely to report having alternative sustainable livelihoods, several sources of external support (e.g., loans), and access to affordable healthcare, and they were less likely to report increased spending on basic needs during the pandemic. Health and livelihood support can buffer communities during major disturbances, sustaining progress toward improved human well-being and forest conservation.

Is the Honeymoon Over? Dynamic Impacts of Abrupt Reductions in Vaccine Uptake

Presenter: Emily Howerton

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The current landscape of global health suggests the possibility of rapid declines in vaccination coverage, potentially compounding the slow declines that have been observed in countries across the globe. Rich theory has been developed to evaluate the consequences of increases in vaccination coverage, including counter-intuitive outcomes such as the honeymoon effect. Yet, the consequences of rapid reverses in the gains in global vaccination coverage have been less explored, especially where they may interact with honeymoon dynamics. While equilibrium analyses support the intuition that following vaccine reduction the eventual onset of major epidemics is inevitable, in practice, major outbreaks occur after a longer honeymoon period and are seemingly less explosive than would be predicted by standard theory. Here, we present a theoretical framework for understanding how honeymoon dynamics interact with declining vaccination coverage, including an evaluation of various heterogeneities that could delay rebound outbreaks. Prevailing uncertainties around vaccination coverage and the history of infection make serological measurement of susceptibility a vital component for predicting risk and timing of subsequent outbreaks.

Exposure Heterogeneity and Outbreak Dynamics of Environmentally Persistent Pathogens

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Infectious diseases caused by environmentally persistent pathogens can strongly impact host populations because transmission occurs not only through direct host-host contact but also via indirect exposure to contaminated environments. Understanding how variation in exposure dose, frequency, and duration, together with temporal changes in host susceptibility, shapes transmission across different routes remains an important challenge in environmentally transmitted disease systems. To address these challenges, we develop a stochastic model that integrates host infection dynamics with an explicit environmental pathogen reservoir characterized by time and dose-dependent exposure. Transmission occurs through both direct contact with infectious hosts and indirect environmental exposure, with infection probability governed by dose-response functions. This formulation captures transmission dynamics when host or pathogen densities are low and allows infection risk to depend on accumulated exposure rather than contact alone. Using branching process approximations, we derive outbreak probability from the underlying continuous-time Markov chain model. We extend the framework to include seasonality in host susceptibility and environmental exposure, reflecting empirically documented seasonal patterns in environmentally transmitted diseases. As a case study, we apply the model to snake fungal disease. Numerical simulations are used to illustrate how seasonality and the relative contributions of environmental and host-driven transmission pathways, as well as the choice of dose-response function, can influence outbreak probability. Together, these results illustrate how incorporating environmental pathogen reservoirs and seasonal exposure processes may affect inferences about outbreak dynamics in systems dominated by environmental transmission.

Investigating Spatial and Behavioral Drivers of Sars-Cov-2 Exposure in Urban White-Tailed Deer (Odocoileus Virginianus)

Presenter: Yen-Hua Huang

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In urban environments, wildlife movement and contact patterns determine transmission opportunities for zoonotic pathogens. White-tailed deer (Odocoileus virginianus) across the United States are frequently exposed to SARS-CoV-2 (SCV2), yet the specific pathways of viral exposure in urban environments remain undetermined. Exposure may occur through contact with humans and human-derived waste or via intraspecific transmission among deer. We investigated SCV2 exposure dynamics in the New York City borough of Staten Island, NY, a highly fragmented urban region with interspersed forest habitats. While no active viral shedding was detected in 111 captured deer, 30.6% (n = 34) were identified as being at least seropositive once during the study, and the longitudinal monitoring of 43 recaptured individuals (mean: 2.72 captures) identified five instances of seroconversion. To explore behavioral predictors of prior SCV2 exposure, we integrated high-resolution GPS telemetry with local convex hulls and resource selection functions. We examined home range size, habitat preference (anthropogenic and natural areas), and conspecific contact probability across varying temporal windows prior to recapture. Preliminary analyses suggest a complex exposure dynamic in which intraspecific transmission appears to be the more prominent pathway. First, seropositive individuals, particularly males, exhibited a trend of intermittent, stronger selection for anthropogenic areas relative to seronegative individuals, and these behavioral occurrences aligned with periods of increasing local human COVID-19 cases and wastewater SCV2 RNA concentrations. Additionally, seropositive deer exhibited significantly higher contact rates with other individuals 10–14 weeks prior to recapture, suggesting that conspecific transmission may be the dominant pathway in this environment. Together, these results suggest that urban deer exposure to SCV2 in Staten Island is likely driven by deer-to-deer interactions, possibly occurring after initial human-derived viral spillover. Future research will focus on characterizing spatiotemporal serodynamics and pathogen spillover risk at the urban wildlife-human interface.

Evolution in a Warming World: Feedbacks Between a Changing Environment and Host Resistance to Infection

Presenter: Samuel Hulse

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Disease ecologists have long recognized that environmental conditions play a central role in determining dynamics of disease transmission. In light of climate change, there is an ongoing debate over whether a warmer world will be a sicker world. For example, warmer temperatures might allow vector-transmitted disease to expand into more temperate regions but limit the spread of heat-sensitive fungal pathogens. However, current investigations have not yet considered the impacts of rapid host and pathogen evolution in response to a changing environment. If pathogens become less transmissive due to warmer conditions, this could lead to weakened selection for host resistance, ultimately minimizing climate's impact on disease prevalence. To test this hypothesis, we developed a seasonally forced SI model, based on the temperature-sensitive fungal pathogen anther-smut and its flowering plant host. In this model, we assume that hosts can evolve costly resistance against anther-smut infection, but disease transmission is constrained by high summer temperatures. With our model, we investigated the impacts of various warming scenarios. Overall, our model supports our hypothesis that host evolution can have significant feedbacks with a changing climate, leading to a reduced impact on disease prevalence than non-evolutionary models would predict.

Environmental Air Sampling Captures Coronavirus Shedding and Host Population Dynamics in Cave-Roosting Bats

Presenter: Caleb Huntington

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The frequency of viral spillover from wildlife is expected to increase in the coming decades. Traditional surveillance methods require large-scale efforts to detect rare, intermittently shed viruses, highlighting the need for new technologies to improve viral discovery and monitor viral dynamics. Environmental air sampling offers a complementary approach that has been utilized in indoor and agricultural settings but has yet to be systematically applied in wildlife. As a non-invasive sampling tool, it would reduce risk to both animals and researchers and minimize disturbance to bat populations. Additionally, there has been growing interest in this tool for capturing terrestrial animal environmental DNA (eDNA) for biodiversity surveys. In this study, we collected 90 air samples over a two-month period to track viral shedding and host population dynamics in a bat cave in Puerto Rico. As a comparison, 1,948 bats were captured and sampled for viral screening. We also conducted assemblage composition studies to determine the relative abundance of the bat assemblage at the end of the first and second month. By using next-generation sequencing (NGS) on coronavirus PCR-positive samples, we generated near-complete genomes of both alphacoronaviruses and betacoronaviruses. We then mapped NGS reads from air samples to these viral genomes, and subsequently to host cytochrome B sequences, to determine the presence of viruses and host eDNA. Our results show overlapping peaks in the shedding of both the alphacoronavirus and betacoronavirus in air samples during a biologically relevant period (during late-pregnancy and weaning). For the host assemblage, air samples detected all bat species and reflected the shift in relative abundance observed between the two assemblage composition studies. This study demonstrates that environmental air sampling could be a powerful addition to wildlife viral surveillance, capturing both viruses and hosts. Future work will refine this approach to enhance viral discovery, transmission monitoring, and ecological surveillance.

Effects of Snake Fungal Disease on Wild Snake Growth, Body Condition, and Movement

Presenter: Jacob Hutton

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Emerging infectious diseases pose serious threats to biodiversity and ecosystem stability worldwide. Yet, their behavioral and physiological effects on wild populations remain difficult to identify and quantify, particularly in cryptic taxa such as snakes. Snake fungal disease (SFD), caused by Ophidiomyces ophidiicola, is a widespread pathogen of conservation concern across North America and Europe. Recent evidence suggests that SFD infection reduces survival in two semi-aquatic snake species from central Kentucky, USA. Building on this prior work, we used multi-year capture-mark-recapture (CMR), passive integrated transponder (PIT) telemetry, and repeated diagnostic swabbing across three stream communities in central Kentucky from 2016–2018 to assess how consecutive SFD infection states (e.g., Negative-Negative, Positive-Positive) influence growth, body condition, and movement behaviors in two stream-dwelling snake species: the Northern Watersnake (Nerodia sipedon) and the Queensnake (Regina septemvittata). Using robust Bayesian modeling approaches, we predicted species-specific daily changes in (1) growth rates, (2) body condition (Scaled Mass Index, SMI), and (3) individual movement distances as functions of mean size, consecutive SFD infection pair, age, sex, environmental conditions, and time between captures. Across both species, SFD infection was associated with strong negative effects on mean delta daily growth rate (-0.09 to -0.27 mm/day), overall snout-vent length (-28.5 to -96.6 mm), and body condition (-0.01 to -0.16 ΔSMI/day), while infection was associated with increased daily movement distances (2.0 to 5.2 m/day). Our results demonstrate that SFD substantially affects key physiological and behavioral processes with considerable potential consequences on long-term survival and population viability. This integrative modeling framework, which links CMR, PIT telemetry, disease diagnostics, and robust Bayesian inference, provides a transferable approach for quantifying hidden effects of disease mechanisms across taxa and can be applied broadly to other emerging wildlife disease systems.

Mojiang-Like Henipavirus Spillover in Rural Communities of Bangladesh

Presenter: Ariful Islam

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Nipah virus (NiV) has caused recurrent fatal encephalitis outbreaks in Bangladesh since 2001. Recent detection of a Langya-like henipavirus in shrews in Bangladesh, together with reports of Langya virus spillover in humans in China, highlights the broader diversity of henipaviruses with zoonotic potential. However, the extent of human exposure to non-Nipah henipaviruses in Bangladesh remains poorly understood. We conducted a serology-based biosurveillance study to assess whether additional henipavirus strains had spilled over to humans. Serum samples from 1,320 participants were tested using a multiplex microsphere-based immunoassay to detect immunoglobulin G reactivity against soluble envelope glycoprotein ectodomain trimers of multiple henipaviruses. Antibody responses were quantified as median fluorescence intensity (MFI). Linear mixed-effects models were used to examine associations between MFI values and demographic or exposure variables, including age, sex, district, occupation, and self-reported rodent exposure. Age and occupation were significantly associated with increased reactivity to Mojiang-like henipavirus antigens. MFI values rose modestly with age, suggesting cumulative or long-lasting exposure. Participants engaged in agricultural work showed higher reactivity than other occupational groups, consistent with increased contact with rodents, the putative reservoir of Mojiang virus. Self-reported rodent exposure was associated with increased MFI but was not statistically significant, possibly reflecting widespread and unrecognized indirect exposure. These findings suggest serological reactivity consistent with exposure to Mojiang-like henipaviruses in the population, with agricultural occupation and age as key correlates. The results indicate that non-Nipah henipaviruses may be circulating undetected in rural communities. Integrating serological surveillance with ecological and virological investigations will be essential to identify reservoirs, characterize viral diversity, and understand spillover pathways. Such approaches are critical for early detection of emerging henipaviruses and for strengthening One Health preparedness in Bangladesh and similar high-risk settings. Further multidisciplinary studies are needed to quantify transmission risk and inform targeted prevention strategies across high-risk landscapes globally.

Biodiversity Linkages with Wildlife Host Prevalence and Human Spillover

Presenter: Shariful Islam

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Lyme disease, caused by Borrelia spp. and transmitted by Ixodes scapularis, continues to rise across the United States. Prior studies in small mammals have shown that rodent and tick infection rates decline with higher species richness (“dilution effect”). However, mechanisms linking Borrelia circulation in wildlife to human spillover remain elusive. This study examined Borrelia prevalence in rodents and ticks, their interrelationship, and their linkage with human Lyme disease incidence across the U.S. We utilized National Ecological Observatory Network rodent and tick data and CDC Lyme surveillance data (2020–2023). Polymerase chain reaction tested 12,762 rodent blood samples from 20 species across 35 sites and 1,211 I. scapularis ticks sampled at eight sites. Linear regression assessed associations between Borrelia prevalence in rodents, ticks, and county-level human Lyme incidence (per 1,000 people). We also evaluated relationships between rodent diversity metrics and human incidence.

Results: Rodent species richness ranged from five species in Konza, Kansas to one in Moab, Utah. Peromyscus leucopus (34.2%,n=4370) and P. maniculatus (32.8%,n=4191) were most common. Seven species were Borrelia-positive, with overall prevalence of 0.52% (n=66) in rodent. Treehaven, Wisconsin had the highest rodent prevalence (2.04%). Onychomys torridus showed the highest species-level prevalence (2.56%). Among ticks, 246 (20.28%) were positive, with the highest prevalence in Maryland (29.20%). Rodent–tick infection prevalence showed a positive but non-significant association (coefficient=5.012,P=0.2656,adj. R2 =0.0675). The strongest model predicting human incidence included rodent prevalence and the first PCA of diversity component (Adj. R^2 = 0.31,P = 0.001). Rodent infection prevalence showed a statistically significant positive association with human incidence (coefficient =7.33,P = 0.0004). We found no evidence of a dilution effect which might be related to larger geographical scale and no relationship between tick infection prevalence and human incidence. Rodent infection prevalence was the strongest predictor of human Lyme incidence, highlighting rodents as key sentinels of Lyme disease risk.

Within- And Between-Host Dynamics of Highly Pathogenic Avian Influenza in Domestic Birds in Pennsylvania

Presenter: Anna Jaeger

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Since late 2021, highly pathogenic avian influenza viruses (HPAI) of the H5 subtype clade 2.3.4.4b have spread across the Americas, devastating wildlife, agricultural animals, and resulting in dozens of human spillovers. Unlike previous outbreaks, which were maintained predominantly in commercial poultry, extensive culling has not been sufficient to quell this outbreak. National surveillance strategies generally provide only a single sequence per poultry outbreak, precluding the study of fine-scale geographic transmission or analysis of viral evolution within an infected premise. To address these gaps, we have produced high-quality deep sequence data in technical replicate from 36 Galliformes and Anseriformes infections from commercial farm and live bird market outbreaks in Pennsylvania from 2022-2025. We constructed maximum likelihood phylogenetic trees, placing these sequences within the larger North American tree of 2,588 sequences. H5N1 viruses were introduced into Pennsylvania at least 27 independent times. Most Pennsylvania clusters represent independent introductions into either domestic or wild birds, indicating that control measures in agricultural settings likely limited spread. By building full-genome divergence trees, we found that in agricultural outbreak clusters, ducks are basal to chickens across 4 outbreaks in 2023 and 2025, suggesting that ducks are infected before chickens. In preliminary analyses of within-farm variant populations, we found that diversity is generally low in these samples, but there is a high level of within-host variant sharing between samples, suggesting that within-host variants may be propagated between infections during these outbreaks. Our findings support the hypothesis that ducks are a bridge to chicken infections, requiring increased biosecurity between these species in mixed farm and market settings. Our results also suggest wide bottlenecks in commercial outbreaks, increasing the risk of minority variants being transmitted between infections. These data can help inform biosecurity measures and assess the risk of viral adaptation during agricultural outbreaks.

Host Physiological Variation in a Wild Reservoir of Sin Nombre Virus

Presenter: Nelle Jenkins

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Physiological stress is widely hypothesized to influence immune function and disease susceptibility in a variety of systems, yet empirically testing this relationship remains limited in free-ranging wildlife. The Sin Nombre virus (SNV) – Deer mouse (Peromyscus maniculatus) system provides a natural framework for exploring how host physiology relates to infection status under ecologically relevant conditions. In this study, we assessed variation in physiological stress, immune metrics, and condition among wild-caught deer mice sampled across multiple sites in Western Montana. We quantified stress and condition using circulating corticosterone responses to a standardized suppression challenge, hematocrit, white blood cell profiles, and biometric measurements to explore their relationship with SNV infection status. Using these data, we explore whether physiological indicators differ between infected and uninfected individuals, and whether these relationships vary across sites. Across the study period, SNV prevalence was 13.5%, and stress-regulation phenotypes differed among hosts. Females – particularly lactating females – more frequently exhibited altered stress regulation. By integrating endocrine and immune data, this work aims to characterize how individual-level physiological variation may be associated with SNV infection patterns in natural populations.

Opposing Effects of Environmental Drivers Generate Heterogeneity in Epidemics Across an Elevational Gradient

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Infectious diseases often vary in intensity across their range. One potential driver of this heterogeneity could be the environment, which can simultaneously alter host and pathogen traits. However, environmental effects on disease can be hard to disentangle from innate properties of host and pathogen populations, making it difficult to predict outbreaks and forecast how they might shift under climate change. On one hand, rising temperatures might lead to a decrease in disease prevalence because environmental conditions become unsuitable for pathogens. On the other hand, pathogens may be able to expand their presence in areas that were once marginal habitat, infecting hosts that are poorly defended. Steep elevational gradients provide an opportunity to study host–pathogen interactions across environments and pinpoint the conditions that contribute most to disease prevalence. We studied natural variation in disease outbreaks of a fungal pathogen, Melampsora lini, in its wildflower host, Linum lewisii. We tracked weekly prevalence and disease load of the conspicuous orange rust in populations spanning an elevational gradient over 3 years. We find that neither disease prevalence or load vary consistently with elevation. However, in a common garden experiment, we found that fungal development was inhibited in low elevation gardens. We hypothesize that the dampening effect of high heat is tempered by earlier emergence times for the pathogen at lower elevation. These results suggest that different aspects of global change may pull epidemics in different directions, and that there is a need to understand the underlying mechanisms that drive disease to understand how prevalence and severity will shift.

Using Life History Theory to Assess Covariation Across Key Transmission Traits in Anopheles Stephensi

Presenter: Britny Johnson

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Vector-borne diseases present significant challenges to public health worldwide, and our current understanding of pathogen transmission relies heavily on mechanistic mathematical models such as those derived from r-naught and the SIR framework. Because mosquitoes are small-bodied ectotherms, physiological processes like reproduction and immunity are strongly influenced by ambient temperature. In addition, the pathogens they transmit are also subject to the thermal environment experienced by the mosquito. However, current temperature-dependent models typically assume that traits for the mosquito (e.g., fecundity, survival, vector competence) and pathogen (e.g., development rates) vary independently, overlooking correlations that can generate life history trade-offs. To gain a better understanding of how temperature modifies the correlation between mosquito and pathogen traits we will infect Anopheles stephensi females with Plasmodium falciparum and measure mosquito fecundity, lifespan, and time to infectiousness across a range of temperatures. The results from this work will represent the first, non-destructive assessment of both mosquito and parasite traits within individual females. Further, establishing correlations across mosquito and pathogen traits will provide evidence for how life history trade-offs emerge and inform key assumptions in transmission models.

The Presence of Non-Lethal Parasites Equalizes Biomass Distribution Across Host Stages – a Stage-Structured Biomass Model for “mild” Parasites

Presenter: E. Rosa Jolma

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Most parasites do not kill or castrate their hosts but rather limit host energy available for other processes like growth and reproduction. While virulent parasites are known to be capable to regulate host populations, the impact of “mild” energy-tapping parasites on host populations and their structure is less well known. Often parasites infect only certain stages of a host’s life history so potentially affecting intraspecific competition and the resulting host population structure. We built a stage-structured biomass model that was parameterized to fit a model system consisting of blue mussel (Mytilus edulis) hosts and intestinal copepod parasites which have simple life cycles. The model included three host stages, two of which were susceptible, and three parasite stages. All energy fluxes were accounted for including feeding, maintenance, growth, reproduction, mortality, immune response and parasite feeding. Without parasites the host population was dominated by the small adult stage for most of the ranges of the intraspecific competition factor and host mortality rate parameters, while with parasites host population biomass was relatively evenly distributed across juveniles, small adults and large adults at a wider range of parameter values. This implies that the presence of typical “mild” parasites can prevent host population stunting so affecting the food availability of predators that consume only certain host stages and the host availability for other parasites that rely on certain host stages for the completion of their life cycles.

Quantifying the Effects of Predation on Disease-Imperiled Host Populations

Presenter: Chris Kailing

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Infectious diseases are a key threat to wildlife populations. Following novel pathogen invasion and subsequent host declines, remnant populations that survive the epidemic trough can have adaptive traits that reduce disease burdens which can aid in population recovery. For example, white-nose syndrome (WNS), caused by the invasive fungal pathogen, Pseudogymnoascus destructans, has caused dramatic and widespread declines in many cave dwelling bat species resulting in regional extirpation in certain cases. However, some populations have stabilized and are beginning to recover following initial declines, although remnant populations are small fractions of their former size and likely sensitive to additional stressors. Predation is a source of non-disease mortality that has been suggested to either weaken or strengthen host adaptation to novel pathogens depending on if predation occurs primarily on healthy or sick individuals. Therefore, we quantified predation on remnant bat populations to assess whether population adaptation to disease might be weakened or strengthened in the presence of predation. We measured animal activity at cave and mine entrances using trail cameras to record videos of predation on bats. We found that most predation events occurred during fall swarm, a time when bats are first exposed to the pathogen but not suffering disease symptoms yet, suggesting that predation on bats is unlikely to have a positive effect on host populations by removing the most infected individuals. Of the predators observed at these entrances, we found that domestic cats, barred owls, screech owls, raccoons, and rat snakes were all successful at capturing bats, although domestic cats killed the largest number of bats despite low capture efficiency. Ultimately, our results suggest that introduced predators could serve as an important stressor for disease-imperiled populations and underscore the importance of quantifying non-disease related threats even in instances where pathogens are a primary cause of population decline.

Seasonality Varies Epidemic Outcomes in an Environmentally Transmitted Wildlife Disease

Presenter: Macy Kailing

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How seasonal processes scale to population outcomes is poorly characterized in most natural systems, particularly for wildlife diseases with environmentally persistent pathogens. Here, we explore the role of seasonality in shaping sarcoptic mange in bare-nosed wombats, a disease caused by the environmentally transmitted parasitic mite, Sarcoptes scabiei. We test standing hypotheses that variations in wombat population trajectories are influenced by seasonal constraints to mite survival and host-pathogen encounter rates, as measured by the ratio of burrows to wombats, using an empirically informed deterministic model. We demonstrated three possible long-term outcomes of wombat-mange that differed between seasonal environments with fluctuating mite survival and stable environments with constant mite survival: host and parasite extinction, endemic disease, and parasite extinction. We found seasonal environments narrowed the range over which host-pathogen encounter rates supported S. scabiei persistence relative to stable environments, and prevalence and population sizes varied more in seasonal compared to stable environments except under moderate host-pathogen encounter rates when seasonal effects were reduced. Our results are broadly consistent with field observations and can help inform which populations may require interventions and the ecological contexts in which abiotic reservoirs may be a conservation target. Of broad significance, we demonstrate that seasonal effects on host-pathogen interactions can temporally decouple from climate cycles and vary population responses. Efforts to scale seasonality to a population outcome should consider the relative importance of interacting seasonal mechanisms and the time scale over which hosts and pathogens are affected.

From Patterns to Processes: Meta-Analysis and Experiments Reveal Cumulative Damage Drives Infection-Induced Mortality

Presenter: Canan Karakoc

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Understanding how within-host infection processes translate into mortality patterns remains a central challenge in infectious disease biology. Meta-analysis of 209 experimental infections across diverse host-pathogen systems revealed that instantaneous mortality risk increases approximately exponentially following infection, analogous to aging dynamics. This universal pattern raises a fundamental question: what biological mechanisms drive accelerating mortality, and do these mechanisms vary across host and pathogen taxa? Phylogenetic comparative analysis revealed weak taxonomic signatures in mortality dynamics. While pathogen phylogeny showed modest signals in mortality acceleration rates, host-pathogen identity explained minimal variation compared to within-system heterogeneity. This suggests mortality patterns reflect general infection processes rather than taxon-specific mechanisms, but the meta-analysis alone cannot distinguish between alternative mechanistic explanations. To resolve underlying mechanisms, we developed a Galleria mellonella– Pseudomonas aeruginosa system tracking mortality, morbidity, and pathogen dynamics in parallel cohorts. Pathogen burden increased logistically while host health declined monotonically. Causal analysis using directed acyclic graphs and structural equation modeling demonstrated complete mediation: pathogen burden affects survival entirely through deteriorating host physiological condition, with no direct effect. Critically, systematic model comparison revealed mortality depends on cumulative pathogen exposure rather than instantaneous bacterial density. This cumulative damage framework exhibits hysteresis, time- dependent health deterioration beyond current pathogen burden, indicating irreversible physiological damage accumulation. Timed antibiotic interventions validated this framework: early treatment dramatically improved outcomes, while delayed treatment failed to rescue hosts despite reducing bacterial burden. Late-treated larvae with lower burdens than early-stage untreated larvae still exhibited poor outcomes, confirming accumulated damage determines survival. Our integrated approach demonstrates how combining comparative pattern analysis with mechanistic experimentation resolves fundamental questions about infection biology. The universal pattern of accelerating mortality reflects progressive, cumulative health deterioration rather than simple tracking of pathogen burden, a finding with implications for understanding therapeutic windows and treatment timing.

Host Habitat Specialization Determines Where Multihost Parasite Sharing Occurs Along Forest-Agriculture Boundaries

Presenter: Kayla Kauffman

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Parasite sharing among wildlife species shapes biodiversity outcomes and offers broad insights into the mechanisms and geography of cross-species transmission. Transmission among wildlife hosts is widespread, tractable to study, and directly relevant to conservation. We combined parasite infection data with spatial analyses to test whether parasite sharing in a diverse community of endemic and invasive small mammals in Madagascar is associated with forest-agriculture boundaries. We defined a “primary host” for each parasite as the host species in which the parasite is most frequently detected and all other infected host species as “secondary hosts.” We used species distribution models to map where primary hosts and infected primary hosts were likely to occur. Then we evaluated where infected secondary hosts occurred in relation to primary host occurrence and infection and distance to forest-agriculture boundaries. Guided by theory linking community assembly, contact structure, and transmission, we predicted that parasite sharing increases where primary and secondary hosts co-occur and is elevated at forest-agriculture boundaries where edge effects may increase interspecific contract rates and parasite diversity. Across host species and parasite taxa, we detected patterns consistent with edge-associated parasite sharing, but the degree of edge association depended strongly on the level of secondary host habitat specialization. Thus, multihost parasite sharing reflects interactions between landscape configuration and host ecological niches. These results indicate that habitat modification can restructure host overlap and parasite sharing, and that combining edge effects with species-specific habitat associations can improve spillover risk assessment. This framework can also help identify permeable areas for cross-species transmission in wildlife communities and inform conservation planning.

Seasonal Dynamics Driving Persistence of Coronaviruses in Malagasy Fruit Bat Populations

Presenter: Gwenddolen Kettenburg

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Endemic fruit bats (Eidolon dupreanum, Pteropus rufus, and Rousettus madagascariensis) from Madagascar host divergent coronaviruses (subgenus Nobecovirus). Here, we used individual capture data from a longitudinal field study to decipher the dynamics of seasonal virus shedding and serological response for four coronaviruses circulating among three bat species. Fecal (N=1952) and serum (N=1383) samples were collected from individual bats over six years (2013-2016, 2018-2020, 2021-2022). We performed metagenomic Next Generation Sequencing on a subset of fecal sample, from which full-genome Nobecovirus sequences were used to design primers and soluble spike glycoproteins for subsequent qPCR and Luminex serological screening, respectively. We then used generalized additive models to evaluate correlates of binomial infection and serological status, and identify correlates of quantitative metrics of viral load (Ct)/antibody response (MFI). Finally, we fit epidemiological compartmental models to time series data to evaluate the transmission dynamics by which coronaviruses are maintained in this system. Seasonal dynamics of virus shedding and corresponding serological response were observed in all three species. Viral shedding peaked in the nutritionally-stressed winter season in male bats and energetically-demanding reproductive period in female bats. Higher individual-level viral loads preceded peaks in population-level prevalence, and age-structured seroprevalence showed a pattern of declining antibody-prevalence in older individuals, consistent with the dynamics of persistent coronavirus infections which undergo seasonal cycles of latency and recrudescence. Longitudinal studies pairing molecular and serological data are critical to deciphering the stressors that underpin seasonal shedding of potentially zoonotic viruses from fruit bats, as well as the transmission dynamics by which these viruses are maintained. Only two previous compartmental models of coronaviruses in wild bats exist, and to our knowledge, no prior published studies have evaluated coronavirus serology in bats. Here, we provide a comprehensive evaluation of transmission dynamics of multiple coronaviruses co-circulating in three bat species using longitudinal field data.

Changes in Pathogen Survival Rates Following Emergence and Establishment of the Fungal Disease, White-Nose Syndrome

Presenter: Oleksandra Klynova

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Environmental persistence of a pathogen is an important trait in infectious disease systems, as it directly influences the likelihood of host infection. Pathogen survival time in the environment can be a critical determinate influencing the speed and extent of an outbreak. For Pseudogymnoascus destructans, the causative agent of white-nose syndrome, spore survival determines whether environmental reservoirs persist through summer and enable reinfection when bats return to hibernacula in autumn.

Bat populations affected by WNS often experience severe initial declines, followed by an increase in survival within several years after disease arrival. Several mechanisms have been proposed to explain this pattern, yet the contribution of spore environmental persistence remains unexplored.

In this study, we quantified long-term spore viability for 17 isolates of P. destructans: six US historical (2007-2016), seven US contemporary (2020-2024), and four isolates from the endemic region (Eurasia). We used an in vitro spore survival experiment to estimate strain-specific viability by storing spores under controlled environmental conditions and quantifying colony-forming units over time. Inactivation curves were fitted using a generalized nonlinear model with a Fermi distribution. The time at which 50% of spores remained viable was estimated and compared among strains using the multcomp package in R with Bonferroni correction.

When comparing paired historical and contemporary isolates from the same study locations in the United States, three pairs showed significantly higher spore survival in historical isolates relative to contemporary ones. These results suggest that some P. destructans lineages may have evolved reduced spore survival over time, implying that long-term persistence carries fitness costs. Such evolutionary change could contribute to reduced host mortality during the established period of WNS, highlighting spore survival as a potentially important trait linking pathogen evolution to long-term disease outcomes.

Host-Symbiont Interactions Across a Sociality Continuum in Halictid Bees

Presenter: Charlotte Knopp

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Most studies of parasitism and disease in pollinators are focused on a small number of eusocial, commercially important honeybees and bumblebees. As a result, little is known about how parasitism varies across the social landscape of the nearly 20,000 other bee species. My goal is to understand how social structure impacts where symbionts fall on the mutualist-to-parasite continuum, and how virulence and transmission optimums are influenced by variation in social behavior. Halictid bees (‘sweat bees’) provide an ideal system for such comparative studies – this species-rich family includes species whose life histories range from solitary individuals to eusocial colonies of ~400 workers. Some halictid species host over 4500 non-feeding Acrostichus spp. nematode dauers in an exocrine organ called the Dufour’s gland. These host-specific nematodes are vertically transmitted from the Dufour’s gland into the brood cells, where they feed and reproduce sexually. Juvenile nematodes will molt into dauer and enter the bee shortly before eclosion. Despite their high numbers, these nematodes are generally considered commensal, and their impact on their hosts remains poorly understood. Here, I compare four solitary, social, and socially flexible sweat bee species within the tribe Augochlorini (Hymenoptera: Halictidae) and assess how nematode burden impacts host body condition, reproductive capacity, and immune response across different bee species and social forms. This work provides new insights into how nematode prevalence, infection intensity, and virulence vary across social scales and highlights how key aspects of disease ecology can be influenced by the social structure of the host.

Multiscale Biodiversity Effects from Forests to Host Microbiomes on Fungal Pathogen Dynamics in Tropical Amphibians

Presenter: Kathryn Koo

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Hypothesized associations between biodiversity and pathogen risk have long been debated. However, how biodiversity across multiple biological scales affects wildlife health remains to be explored. The waterborne fungal pathogen Batrachochytrium dendrobatidis (Bd) has caused global declines in amphibian species. Habitat complexity, amphibian community diversity, and the amphibian skin-associated microbial community (skin microbiome) diversity can affect Bd dynamics in amphibian communities. At the macroscopic scale, diverse life history strategies (e.g., reproductive modes) and microhabitat specializations influence pathogen exposure and disease dynamics. At the microscopic scale, the amphibian skin-associated microbial community (skin microbiome) can have complex and sometimes inhibitory interactions with Bd. Not only can habitat complexity shape amphibian species diversity and composition through available microhabitats, but habitat complexity (e.g., plant diversity) may also impact the environmental microbial pool available for recruitment to the skin microbiome. Our objective is to test whether biodiversity effects at one of these biological scales (habitat, host, and microbiome) amplify or dampen diversity at other scales, and if these cross-scale interactions ultimately increase or reduce Bd prevalence in amphibian communities in the Atlantic Forest in Brazil. We expect habitat complexity to indirectly reduce disease prevalence in amphibian communities by enhancing both host species diversity and skin microbiome diversity. Preliminary analyses using Generalized Linear Mixed Models (GLMMs), accounting for the effects of season, transect, and sampling campaign, indicate that increased plant community richness and increased transect-wide skin microbiome richness are linked to reduced Bd prevalence within a transect. Our results will provide insight into the relationships between multiscale biodiversity effects on host-pathogen dynamics in wildlife.

Perceptions of Tick Encounter and Tickborne Disease Risk Across Two Urban Gradients

Presenter: Heather Kopsco

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Lyme disease (LD) is the most common vector-borne illness in the United States, with an estimated 476,000 cases diagnosed annually. Although LD is typically associated with Ixodes scapularis encounters in rural settings, urban greenspaces increasingly provide suitable habitats for multiple tick species, raising exposure concern for densely populated areas. We surveyed residents in 10 counties across the New York City (five counties) and Boston (five counties) metropolitan areas to assess how experiences with and perceptions of tick exposure and LD risk vary across low, medium, and high housing unit density (HUD) levels derived from census data. To capture perspectives of individuals actively using urban greenspaces, we also recruited park-goers in both cities. Multivariate logistic and ordinal generalized linear regression models were used to examine demographic, behavioral, and geographic predictors of tick encounters and perceived risk. A total of 4,486 adults completed the online survey between June and August 2024 and were proportionally represented across low- (33%), medium- (33%), and high-HUD (34%) tertiles. Overall, 66.5% of respondents reported having encountered a tick on themselves or someone in their household in their lifetime. Recent tick encounters (limited to 2023–2024) were more likely to be reported by residents in low-HUD areas, dog owners, and individuals with annual incomes over $100,000 compared with those earning less than $50,000. Despite higher reported exposure, residents in low-HUD areas perceived their risk of a tick encounter to be significantly lower than those in medium-HUD areas. Similarly, respondents with a prior LD diagnosis reported lower concern about infection risk than those without a diagnosis. These findings demonstrate a disconnect between self-reported tick exposure and perceived risk, particularly among populations with higher exposure. Reframing LD as an emerging concern within higher-density urban settings underscores the need for targeted strategies to better align risk perception with actual exposure.

Environmental Associations with Winter Tick (Dermacentor Albipictus) Occupancy, Abundance, Survival, and Reproduction in Jackson Hole, Wyoming

Presenter: Troy Koser

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Environmental factors like temperature and moisture availability are known to limit key processes in tick life cycles but scaling findings from small-scale field or laboratory studies to landscape-level patterns in tick occupancy and abundance has proven difficult. Local adaptation in tick populations to regional climate conditions could partially explain difficulties in expanding findings in broadly distributed tick species. The winter tick (Dermacentor albipictus) is a widespread one-host tick species with a range spanning from the Yukon territory in northern Canada as far south as the Mexican state of Chiapas. Winter ticks infest a wide range of wildlife host species in North America but are notorious for infesting moose (Alces alces) at rates high enough to cause negative health impacts including anemia, early spring hair loss (alopecia), and even death. We hypothesized that although previous research on winter ticks has shown high sensitivities to snow presence in spring, desiccating conditions in summer would be a stronger driver of winter tick population dynamics in western, mountainous systems where populations may be locally adapted to high snow volumes in spring. We used hierarchical N-mixture models to examine relationships between snow water equivalent, minimum spring temperatures, maximum summer temperatures, and vapor pressure deficits with winter tick occupancy and abundance in Jackson Hole, Wyoming from 2020-2022. We found winter tick occupancy to increase with warmer summer temperatures and decrease with drier summer conditions. Spring conditions had little affect on occupancy rates and neither suite of environmental variables fit the abundance data well. Fitting models to tick data, which is typically highly over dispersed, remains challenging even when accounting for imperfect detection biases with hierarchical N-mixture models. Future studies on tick-climate relationships should consider imperfect detection, the potential for local adaptation, and explore new methods for handling highly heterogeneous tick data.

Dispersers and Residents Differ in Infection Prevalence and Reproduction Regardless of Exposure Duration

Presenter: Aaron Krivchenia

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Dispersal - the movement of individuals among habitat patches - is a key life-history trait that shapes population persistence, metacommunity connectivity, and community stability. Dispersal behavior can be influenced by local patch conditions as well as by the presence or density of heterospecifics. In host-pathogen systems, infection risk may modify dispersal through avoidance behaviors or through physiological constraints that reduce energy investment in movement. Hosts may therefore face a trade-off between resistance and avoidance, while from the pathogen's perspective host dispersal can either limit or facilitate spread into new habitats depending on the infection status of the host. Understanding how hosts alter dispersal behaviors in the presence of a pathogen is crucial information as it may illustrate how dispersal in turn mediates these host-pathogen interactions. In this experiment, we investigated infection rates between residents and dispersed individuals of Tribolium castaneum and T. confusum. Beetles were assigned to one of two treatments: individuals were either pre-exposed to the fungal pathogen, Beauveria bassiana, 24 h before dispersal or were exposed during the dispersal phase. We also tested for differences host fitness via reproduction and assessed the infection prevalence in the offspring generation. Preliminary results indicate that dispersed individuals of both species showed significantly lower infection rates compared to residents, suggesting an avoidance behavior. The presence of B. bassiana also caused a reduction in dispersal and reproduction, but there was no significant difference between pre-exposed and not pre-exposed populations for both variables. Though, residents, on average, had greater reproductive output than dispersers. In the subsequent generation, infections were again significantly lower in the emigrant offspring than for resident offspring. Together, these findings suggest that pathogen presence can depress movement and fecundity while simultaneously generating spatial structure in infection through dispersal behavior.

Multi-Species Infections and Host Range Evolution of an Insect Baculovirus

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Nuclear Polyhedrosis Viruses (NPVs) in butterflies are often specialist viruses that have co-evolved with one or a few host species. Most data on host ranges of NPVs comes from laboratory infections, and little is known about how overlapping geographic distributions of host species might affect the evolution of the virus in nature. We asked whether the NPV that infects Gulf Fritillary butterflies (Dione vanillae, Nymphalidae), is also able to infect related species of butterflies with shared larval food plants. After infection through consuming contaminated leaf tissue, the NPV causes internal melting and death of the host. We collected 503 larvae from natural populations of D. vanillae, Heliconius charithonia (Zebra Longwings), Euptoieta claudia (Variegated Fritillary), and Dryas iulia (Julia,Äö√Ñ√¥s Butterfly) in the southeastern U.S. Of these, 162 of 424 Gulf Fritillary and 32 of 59 Zebra Longwing larvae died of NPV, based on the presence of viral particles (occlusion bodies). No Julia,Äö√Ñ√¥s Butterfly or Variegated Fritillary larvae had evidence of NPV infection (n=6 and 14 larvae collected, respectively). After extracting viral DNA, we sequenced whole genomes for 19 virus isolates collected at multi-host sites (D. vanillae: 12 isolates; H. charithonia: 7 isolates). Preliminary results showed that virus isolates collected from H. charithonia larvae tended to be more similar genetically to isolates collected from D. vanillae hosts at the same site than to each other. This suggests that a single species of NPV is able to successfully infect multiple related host species. We are currently analyzing whole genomes to determine whether certain gene variants are associated with successful infection of a particular larval host species, or with a specialist or generalist strategy. Understanding the ecological factors that affect evolution of pathogen host ranges is crucial, particularly as climate change and anthropogenic introductions lead to distribution changes for many species.

Immune Selection and Co-Infection Decouple Resistance Establishment from Post-Establishment Spread

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Antimalarial drug resistance spreads unevenly across regions. Several lineages rose to high frequency in low-transmission Southeast Asia and later appeared in high-transmission Africa (e.g., pfcrt-associated chloroquine resistance). Yet resistance frequency is often lower in high-transmission settings, despite a high burden of resistant infections and more opportunities for resistant mutants. Previous work suggests immune selection and within-host competition slow resistance spread in hyperendemic settings, but how they jointly shape establishment and post-establishment frequency across transmission gradients remains unclear. We ask whether factors associated with resistance establishment differ from those associated with post-establishment frequency across transmission settings. For this, we use an agent-based model of Plasmodium falciparum with generalized and strain-specific immunity, multi-gene antigenic repertoires, mixed infections, and drug treatment with resistance costs. After endemic equilibrium, we introduce a rare resistant genotype and quantify (i) establishment (non-zero resistance at 10 years) and (ii) post-establishment frequency (mean over final 5 years among established runs). We fit Gaussian Process emulators and use global sensitivity analysis to rank the drivers. Preliminary results show establishment probability varies most with standing antigenic gene richness (first-order Sobol = 0.457; positively related) and daily treatment rate (0.252; positive). Because biting rate and initial richness co-vary, this ranking reflects a transmission-diversity gradient. Post-establishment resistance frequency varies most with biting rate (0.398; negative): higher transmission sustains mixed infections and within-host competition, limiting fixation and keeping resistance at lower frequency. Together, these results suggest phase-specific drivers: new resistant genotypes are more likely to survive early stochastic loss under strong selection (higher treatment) and a high-transmission background (larger parasite population). Yet in high-transmission settings they rarely fix, instead persisting at lower frequency. Also, widespread resistance in low-transmission regions may reflect conditions that permit higher post-establishment frequency (e.g., lower fitness costs or higher drug survival), rather than fewer establishment opportunities in high-transmission regions.

Strain-Resolved Analyses Reveal Bacterial Transmission from Humans to Captive Mammals

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Captive animals experience sustained exposure to human-associated environments, diets, and microbial sources, creating opportunities for cross-species transmission of gut microbes. Across diverse taxa, captivity is frequently associated with a shift toward “humanized” gut microbiomes, yet the ecological and evolutionary mechanisms underlying this convergence remain unresolved. In particular, it is unclear whether microbiome shifts in captivity arise primarily through parallel ecological selection or through colonization by human-associated microbial strains. Here, we present a comparative meta-analysis of publicly available mammalian gut metagenomes from wild and captive conspecifics, and human hosts, to quantify microbiome convergence and assess evidence for cross-host microbial transmission. Using species- and genome-level taxonomic profiles, we show that captivity consistently alters gut microbiome composition across host species and increases similarity to human microbiomes relative to wild conspecifics. Multivariate analyses indicate that captivity status explains significant variation in microbiome composition independent of host species identity, while distance-based metrics reveal that captive individuals are, on average, closer to humans than wild individuals in community composition. Leveraging strain-resolved profiling with inStrain, we further find that captive animals harbor a higher prevalence of human-associated species genome bins (SGBs) and share closely related strains with humans more frequently than wild counterparts. Notably, the magnitude of microbiome convergence and strain sharing varies substantially among host species, suggesting host-specific barriers or susceptibility to colonization by human-associated microbes. Ongoing work integrates metagenome-assembled genomes (MAGs) into phylogenetic frameworks to test whether convergence reflects replacement by human-derived strains or parallel adaptation of resident microbes. Together, these results provide a comparative framework for understanding how captivity reshapes gut microbiomes and highlight the importance of host identity in mediating microbial spillover in human-dominated environments.

Host Pace of Life and Evolutionary History Shape Within-Host Interactions

Presenter: Nichole Laggan

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Interactions among free-living species tend to become more facilitative in stressful environments that create opportunities for mutually beneficial niche modification. Similarly, within-host interactions may become increasingly facilitative in hosts that are more resistant to infection when one pathogen modifies its host in a way that benefits another pathogen. Slow-growing hosts are likely to allocate more resources to resistance than fast-growing hosts. Thus, host pace of life may shape within-host interactions. Yet, the degree to which this relationship is influenced by host evolutionary history remains unresolved. For example, in novel ranges, hosts can experience pathogen release, and weaker pathogen selection may disrupt relationships between host life-history, infection, and within-host interactions. To investigate how host life-history and evolutionary history moderate within-host interactions, we performed inoculation experiments with a globally distributed host grass, Dactylis glomerata, using 25 accessions that vary in pace of life and span native and introduced regions. We measured infection by the agriculturally and ecologically significant necrotrophic fungal pathogen, Rhynchobrunnera orthospora, and tested the effects of previous infection of the host by the rust fungus, Puccinia striiformis, or exposure with inactive P. striiformis spores. We found that slow-paced hosts were most resistant during single infections, but also exhibited the greatest facilitative interactions when coinfected. In contrast, priming the host with inactive rust spores weakened the relationship between host life-history and disease by reducing disease burden across all host pace of life strategies. Moreover, host pace of life differentially modified within-host interactions across native and introduced ranges, such that disease burden in introduced hosts was independent of host life-history strategy. Together, these results suggest that the nature of within-host interactions may be governed by host evolutionary context, with host pace of life structuring disease in coevolved hosts but not in introduced hosts released from pathogen-mediated selection.

Assessing the Impact of Vector Control Interventions on Dengue Incidence in Guatemala Using a Bayesian Hierarchical Model

Presenter: Julieta Lamm-Perez

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In the past decade, Guatemala has experienced a marked resurgence of dengue fever, a vector-borne disease transmitted by Aedes aegypti and Aedes albopictus mosquitoes, with thousands of cases reported annually. Historically, dengue has followed a quadrennial pattern of infection peaks in Guatemala; however, the expected periodicity was recently disrupted when cases reached a record high in both 2023 and 2024. The Guatemala Ministry of Health has deployed a variety of vector control interventions to reduce dengue transmission, but the efficacy of these interventions remains largely unmeasured during this most recent outbreak as well as historically. In this study, we combine monthly dengue case counts from the Guatemalan Ministry of Health (2012–2024) with monthly records of household-level vector control interventions (including fogging and insecticide application), and high-resolution environmental data (temperature, precipitation) extracted from Google Earth Engine. We then build a Bayesian hierarchical spatiotemporal model to evaluate the effectiveness of vector control interventions on reducing dengue transmission and to assess how climatic conditions may modulate the efficacy. We examine both lagged and non-linear relationships between climate, interventions, and disease incidence. We directly test different lag lengths to determine how long vector control may remain effective. Initial results demonstrate that temperature has the greatest effect on dengue risk, but that lagged vector control is a significant predictor of dengue incidence, indicating that the vector control may reduce dengue transmission for at least 3 months. We also explore where these interventions have been most effective, controlling for characteristics that may affect baseline differences in dengue burden. Our study aims to provide evidence on where and when vector control interventions should be implemented at the household level to have the greatest impact on local dengue burden in Guatemala.

Effects of Snake Fungal Disease on Snake Density, Space Use, and Detection

Presenter: Eleanor Lane

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The emergence of Snake Fungal Disease (SFD), caused by the fungal pathogen Ophidiomyces ophidiicola (O.o.), is considered a significant conservation threat for snake populations. However, evaluating the population-level impacts of SFD remains challenging due to the cryptic behavior and low detectability of free-ranging snakes. In this study, we utilized three years of passive integrated transponder (PIT) tag telemetry, disease monitoring, and multi-session spatial capture-recapture (SCR) models to investigate changes in snake population densities, the effects of SFD status on spatial scale of detection (σ) values, and factors influencing detection probabilities (g0) for Northern Watersnakes (Nerodia sipedon) and Queensnakes (Regina septemvittata) in three central Kentucky streams with known SFD prevalence. Although most changes were not statistically significant, mean population density declined for both species between survey years and across study locations. O.o.-positive N. sipedon exhibited significantly smaller spatial scale of detection values than uninfected snakes (33 m ± 2.59 m vs. 45 m ± 2.09 m), while spatial scale of detection did not differ between infected and uninfected R. septemvittata (45 m ± 2.09 m vs. 51 m ± 2.52 m). Snake detection probability was significantly influenced by day of year, time since last rain, and rainfall accumulation, but not by O.o. infection. Our findings demonstrate that combining PIT telemetry with SCR modeling provides an effective framework to quantify population-level impacts of SFD and advance understanding of disease ecology in wild snake populations.

Incorporating Sociodemographic Heterogeneity into Transmission Models for Respiratory Diseases

Presenter: Soren Larsen

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Infectious diseases exhibit complex dynamics which are shaped by both biological and behavioral/environmental factors. Ecological studies across multiple domains find that host resource quality influences pathogen transmission, underscoring the importance of considering heterogeneous host factors as a core driver of infectious disease dynamics. In the context of human respiratory pathogens, structural factors such as housing conditions or mobility patterns have been shown to drive different transmission risks across sociodemographic groups. Yet, social heterogeneity remains underexplored as a fundamental cause of respiratory infectious disease. To better understand the social and behavioral factors driving ecological dynamics of human respiratory pathogens, in 2024-2025, we fielded a statewide survey in Illinois to capture health status, health-seeking behaviors, and motivations across sociodemographic groups. We first analyzed vaccination across age, finding adults are more likely to be vaccinated for SARS-CoV-2 than influenza, while the reverse is true for their children. When analyzing reasons for vaccination behavior, over 70% of vaccinated respondents in each age bracket cited protecting themselves or others. Conversely, unvaccinated individuals reported highly heterogeneous motivations such as safety concerns, skepticism, or resource constraints, with no single motivation shared by the majority of respondents in any age group. Therefore, campaigns to increase vaccination coverage must be targeted to populations with distinct concerns. Second, across households with children, 19% of SARS-CoV-2 vaccinated adults live with an unvaccinated child, and 5% of vaccinated children live with an unvaccinated adult. We implemented transmission models to explore indirect effects of excluding children and young adults from vaccine eligibility, finding that associated absolute increases in deaths would be greatest for those over 65. These findings highlight the crucial role of considering sociodemographic heterogeneity in disease dynamics.

Genomic Signals of Disease Adaptation Reflect Ecological Drivers of Pathogen Exposure

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Global patterns of pathogen prevalence are shifting in response to climate change. Despite the health and biodiversity implications of shifts in the distribution of infectious agents, we lack a strong understanding of the most important ecological factors driving these patterns worldwide. This makes it difficult to predict, plan for, and mitigate these potential shifts and resulting changes in infectious disease exposure. Here, we develop a framework and models to link the ecology of pathogen prevalence to the genomics of disease adaptation to identify the key ecological, host life history, and pathogen traits driving global patterns of pathogen prevalence. We use host genomic adaptation to viruses to quantify the impact of virus exposure across species and environments using genomic adaptation at virus-interacting loci (VIPs) of more than 200 host mammals species. We develop hierarchical Bayesian regressions and correspondence analyses to link ecological factors such as host range-wide climatic factors and host and virus life-history traits with viral impact across evolutionary time. We show that there are broad, general effects of these ecological factors, including specific climatic variables, host range overlap, and both host and virus life history on the impact of virus exposure as measured through host genomic disease adaptation. Our work has important implications for understanding the distribution of viruses across host and virus types worldwide, and for predicting future changes in virus exposure both to humans and other organisms in response to changing environments. In addition, this model can be generalized to other questions for which genomic adaptation is an expected response that can be correlated to ecological conditions.

The Effects of Abnormal Temperature Patterns on Batrachochytrium Dendrobatidis Density and Size in Vitro

Presenter: Megan Lawson

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Amphibian species throughout the world have been declining at increasing rates due to infections from the fungal pathogen, Batrachochytrium dendrobatidis (Bd). Bd is found on every continent that has amphibians, and has adapted to a wide range of temperatures with maximum growth rates between 17°C - 25°C. As global temperatures increase and fluctuate, it is important to consider how these shifts can influence the survival and growth of Bd. Organisms can increase their tolerance range of an abiotic factor, such as temperature, through an increase in phenotypic plasticity, gaining the ability to survive in a larger temperature range. To evaluate Bd growth in hypothetical scenarios of warming and fluctuating climates, the pathogen's growth rate and size were measured in varying temperatures. Over the course of 10-11 days, Bd samples in liquid media were exposed to four temperature treatments: constant temperatures at 22°C or 26°C, and fluctuating temperatures from 20°C to 24°C and 24°C to 28°C. Temperatures of the fluctuating treatments were changed every 24 hours. Following the exposure period, Bd zoospores were quantified and compared to the original zoospore count prior to treatment. Samples were preserved, and zoospore and zoosporangia size were measured using fluorescence microscopy. Results are expected to show that when exposed to fluctuating temperatures at a higher range (24°C to 28°C), Bd samples will have higher zoospore densities compared to those kept at a constant temperature outside of the pathogen's preferred range (28°C). Bd zoospores exposed to higher temperature ranges are expected to be larger in size, but at lower densities, compared to those in lower temperature ranges. When exposed to temperatures within the preferred range, Bd zoospores are expected to be smaller in size, but at higher densities.

Fear Factor: Human Behavior Shaping Epidemic Dynamics

Presenter: Leah LeJeune

Coauthors: Ghaffarzadegan, N; Childs, L. M; Saucedo, O

Affiliation: VIrginia Tech; Blacksburg, VA; United States

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Human behavior plays an integral role in the spread of infectious diseases, a reality that the world observed during the COVID-19 pandemic. Human behavior has long been incorporated into disease models, but recent efforts have sought to improve upon past methods and models, formulating behavior mechanisms to better understand human behavior's influence on disease outcomes. One promising mechanism is the behavior-transmission feedback loop, which captures how changes in human behavior drive changes in the amount of infections, which in turn drives changes in human behavior. A simple mechanism when considered in the framework of a deterministic compartmental model, this tool has strong fitting and forecasting capabilities and provides important insights into how adaptation of behavioral responses impacts short-term, transient disease dynamics and long-term disease outcome in the context of single- or multi-disease outbreaks.

Ecological Drivers of Backyard Tick-Borne Disease Hazard and Tick Management Optimization

Presenter: Sung-Joo Lee

Coauthors: Wu, L; Kopsco, H.L; Brown, J.E; Bailey, N; Linske, M; Williams, S.C; Diuk-Wasser, M.

Affiliation: Columbia University; New York, NY; USA The Connecticut Agricultural Experiment Station; New Haven; USA

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Residential backyards are a primary interface where humans are exposed to tick-borne hazards, yet the ecological drivers of tick-borne disease hazard at the individual yard scale remain poorly understood. Because methods to reduce tick-borne disease risk target either the tick vector or a particular host, linking property characteristics with host community assembly and visitation patterns could enable better targeting interventions. Here, we statistically assessed how landscape patterns affect observed host visitation and tick-borne disease hazard (measured as density of infected I. scapularis nymphs) and used these data to parameterize a process-based mathematical tick population-infection model to evaluate how host community heterogeneity influences the cost-effectiveness of tick control strategies. We sampled mice and ticks via mouse trapping and tick dragging in 112 participating properties in Connecticut, USA. Among those, a camera trap was installed in 41 properties to quantify the visitation rates (proxy for relative abundance) of medium and large mammalian hosts. We found that white-tailed deer (O. virginianus) visitation exhibited strong edge effects, with visitation increasing with forest edge length within 500 m of a property. Eastern chipmunks (T. striatus) and eastern gray squirrels (S. carolinensis) showed positive associations with total forest area at a 500 m scale, with a stronger effect observed for chipmunks than for squirrels. Northern raccoon (P. lotor) visitation showed no significant relationship with measured covariates, indicating ubiquitous use of residential landscapes. We parameterized and calibrated a tick population–infection model to reflect the observed host community composition and tick-borne disease hazard. By manipulating host abundances in ways that captured realistic variation among residential properties, we evaluated the performance of multiple tick control interventions, including area-wide acaricide applications and host-targeted approaches, using cost-effectiveness ratios (CERs). Substantial variation in CERs across property types and host assemblages will highlight the need for yard-specific, ecologically informed decision frameworks to optimize tick management in peridomestic landscapes.

Linking Disturbances and Microbiome Dynamics to Disease Epidemics in a Multi-Pathogen System

Presenter: Josh Leon

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Infectious diseases rarely occur in isolation, for example, many hosts experience sequential epidemics caused by different pathogens throughout a growing season, such that may interact with host-associated microbial communities and other pathogens. In North Carolina, the grass species tall fescue (Lolium arundinaceum) experiences three seasonal foliar diseases each year: anthracnose (caused primarily by Colletotrichum cereale) in early spring, brown patch (Rhizoctonia solani) in early summer, and crown rust (Puccinia coronata) in late summer. This predictable disease succession offers an opportunity to investigate how disturbances influence disease epidemics and host-associated microbiomes at different times in the year. This system also allows us to investigate how pathogen interactions and the microbiome jointly structure disease dynamics. We conducted a field experiment implementing short-term fungicide application and mowing as disturbance events, in a factorial design, at multiple points throughout the growing season to evaluate their effects on disease severity and the foliar fungal microbiome. Fungicide and mowing treatments were applied to replicated tall fescue plots, and disease severity for each pathogen was quantified throughout the season. Leaf tissue was collected to characterize temporal shifts in microbial community composition using high-throughput sequencing. Fungicide application significantly reduced severity of all three diseases, demonstrating consistent efficacy throughout the season. In contrast, mowing had disease-specific effects, with a significant reduction in anthracnose severity but limited effects on later-season diseases. These results demonstrate that the timing of disturbances can shape disease dynamics.

Ecological Drivers of Nematode Parasite Community Composition

Presenter: Alec Leonetti

Coauthors: Snyder, P; Senso, B; Trentinus, A; Sabuni, P; Donaldson, J.E; Anderson, T.M; Holdo, R; Ezenwa, V.O.

Affiliation: Yale University; New Haven, CT; USA

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Both biotic and abiotic factors influence parasite community composition in host populations. However, non-invasively characterizing endoparasite communities in wild populations is a challenge that has limited our understanding of the drivers of variability in wildlife parasite communities. The Nemabiome protocol has emerged as a useful tool for high-throughput characterization of parasitic nematode communities in wildlife. We will use this DNA metabarcoding approach to investigate ecological drivers of parasite community composition among ungulates in Serengeti National Park, Tanzania. Fecal samples were collected quarterly between 2021 and 2025 from five sympatric herbivore species (wildebeest, topi, buffalo, hartebeest, Grant's gazelle) and are being used to characterize nematode community composition. Using multivariate analyses, we will test how host species identity, host density, rainfall, and temperature influence parasite community composition, providing insights into the ecological processes structuring parasite communities in this herbivore community. Additionally, we will examine how parasite host range modulates these associations.

A Systematic Review of Hantavirus in Small Mammals in America

Presenter: Manuel Lepe

Coauthors: Moran, D.; Medizabal, R.; Paiz, C; Brennan, R.; and Escobar, L. E.

Affiliation: Universidad del Valle de Guatemala, Guatemala City, Guatemala

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Hantavirus is an emerging zoonosis that is transmitted through the inhalation of aerosols containing viral particles from the excrement of infected rodents. These viruses challenge the assumption that each pathogen is specific to a single reservoir species, as they interact with multiple hosts across distribution gradients. However, our understanding of the hosts involved in the Americas is limited to certain species in some countries. In this systematic review, we examined evidence of the diversity of small mammal species infected in the Americas between 1985 and 2026. Following the PRISMA protocol, we searched peer-reviewed articles in PubMed, SpringerLink, Scielo and Web of Science (n = 327). Of these, 125 articles involving live mammal trapping, species specifications, samples, and serological or molecular positivity counts were eligible for this review. These studies identified 134 species with evidence of infection in 15 out of 22 countries in the Americas. The largest group was the Cricetidae family of rodents (78.4%, or 105 species), followed by the Heteromyidae family (6%, or eight species), the Soricidae family (4.5%, or six species), the Muridae family (3%, or four species), and the Sciuridae family (3%, or four species). The smallest group was the Chiroptera class, with the Phyllostomidae (1.5%, 2 species), Molossidae (1.5%, 2 species) and Emballonuridae (0.7%, 1 species) families identified only in Brazil and Panama. The number of positive individuals per species varied widely (29.5 ± 104.7), and there was no correlation between the number of positives and sample size by species (Kendall tau = 0.5). To improve our understanding of the ecology of Hantavirus hosts and the occurrence of human outbreaks, we must consider opportunistic contact within the Cricetidae family and monitor seven countries lacking data.

Spatio-Temporal Modelling of in Vitro Influenza a Virus Infection: The Impact of Defective Interfering Particles on Type I Interferon Response

Presenter: Yimei Li

Coauthors: Nielsen, B.F.; Levin, S.A.; te Velthuis, A.J.W.*; Grenfell, B.T.*

Affiliation: Princeton University

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Influenza A virus (IAV) infection outcomes vary across hosts in viral-load kinetics and innate immune responses. One potential driver is heterogeneity within the viral population, especially defective interfering particles (DIPs). DIPs can change IAV outcomes in both directions

They can suppress standard virus output by competing for replication resources. They can also trigger stronger type I interferon (IFN) responses, which may help control viruses but can also contribute to inflammatory pathology.

However, this can sustain low-level viral replication and has been reported to promote viral persistence both in vitro and in vivo, suggesting they may also support longer-term virus maintenance within host populations.

In this talk, I will present a spatiotemporal, spatially explicit stochastic model of in vitro IAV infection to study how DIPs shape IFN response. The model integrates virus and DIP replication, IFN signalling, and different dispersal modes, and it reproduces key experimental plaque features such as ring-like and patchy morphologies.

We show two main results:

First, long-range dispersal (“jumps”) of virus and DIPs can reshape spatiotemporal dynamics by seeding new foci beyond the contemporaneous local IFN front. Increasing IFN range improves containment, but does not eliminate the impact of jumps.

Second, IFN production peaks at an intermediate DIP ratio. This reflects a trade-off between early immune activation and sufficient co-infection. I will illustrate these effects with simulation videos.

I will end by briefly discussing how these effects differ across scales, from within-host dynamics to the population level, and why this matters: ignoring DIPs can bias inference and transmission estimates. I will also discuss the potential of DIPs as an intervention (e.g., as an antiviral or vaccine-like strategy).

Assessment of Invasive Wild Pig (Sus Scrofa) Wallows as an Environmental Source for Aspergillus Fumigatus

Presenter: Taylor Fisher

Coauthors: Beasley, J.C.; Brewer, M.; Callaham, L.; Haynes, E.; Momany, M.; Stanislaw, J.; Yabsley, M.J.; Cleveland, C.A.; Peach, D.A.H.

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Aspergillus fumigatus is an environmental fungus that can cause disease in animal species including humans. There are increasing reports of antifungal resistance, posing management challenges. Invasive wild pigs (Sus scrofa), are found throughout much of the U.S. and through their wallowing behavior, may create environmental conditions fostering increased growth of A. fumigatus, facilitating exposure pathways to wildlife that visit wallows. To investigate this relationship, we evaluated wild pig wallows as environmental reservoirs for A. fumigatus and azole-resistant isolates. The following soil samples were collected from wallow sites (n=15) in 2024–2025 across three locations in Georgia and South Carolina: the wallow perimeter, the wallow center (when water was present), and 5 m outside the wallow. Samples were cultured in triplicate on amended Sabouraud dextrose agar (aSDA) and on tebuconazole-amended SDA (tSDA) to assess azole resistance. Colony-forming units (CFU) per gram of soil were quantified. Wallows (n=4) had repeat sampling. Preliminary results demonstrate low recovery of A. fumigatus with CFU counts ranging from 0–6, with positive cultures from 11/19 wallow samples and 8/19 samples outside of the wallow, with one sampling event yielding >50 CFU. No growth occurred on tSDA plates, suggesting an absence of azole-resistant isolates from our sites. Preliminary results reveal wild pig wallows harbor A. fumigatus, but do not appear to harbor azole resistance under employed sampling conditions. Further analyses are required to understand the role that pig created wallows has on A. fumigatus growth. Future work should target wallows within agricultural landscapes where fungicide application may select for resistance and consider increasing soil volume to enhance fungal recovery.

Chagas Disease Ecology in the Us: Stage-Structured Parasite Prevalence Suggests Vertical Resource Partitioning Between Adult and Juvenile Vectors

Presenter: Jennifer K. Peterson

Coauthors: Kelley, A.; Cortes, H.; Kinnaird, H.

Affiliation: University of Delaware

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The Chagas disease system consists of the parasite Trypanosome cruzi, its triatomine bug vectors, and mammal hosts. Chagas disease is most associated with Latin America where triatomine bug diversity is concentrated, but T. cruzi and its vectors range as far north as the Mid-Atlantic United States, where the system is understudied. After finding a T. cruzi-infected triatomine bug under someone's pillow in a million-dollar Delaware home, we set out to investigate the eco-epidemiology of the Chagas disease system on the Delmarva Peninsula. Over two years, we collected 155 triatomine bugs of the species Triatoma sanguisuga in 31 sites throughout all three counties of Delaware. We discovered that juvenile triatomine bugs inhabited standing dead trees in forest fragments while adults foraged in human homes and other human-dominated areas. Trypanosoma cruzi prevalence in the vectors was stage structured, with fewer than 3% of nymphs infected but over 60% of adults infected. Blood meal analyses suggested that the stage-structured infection prevalence reflected resource partitioning of arboreal hosts and habitats between adult and juvenile vectors; wingless nymphs remained under the bark in lower portions of tree trunks feeding on reptiles and other insects, which are not competent T. cruzi hosts. Adult vectors fed on mammals, namely raccoons and squirrels, which nest in the tree canopy. Our findings suggest a vertical shift in the bugs' habitat and host use (from the lower trunk to the canopy) after the larger, winged adult stage of the bug is reached. This is the first study of triatomine stage-driven behavior and host and habitat partitioning in any North American species, which have different cold weather adaptations than their warmer climate counterparts. The patterns observed in our study can be used to inform future studies of vector ecology in temperate regions.

Virulence and Phylogenomics of Galápagos Avian Poxvirus

Presenter: Allyson Placko

Coauthors: Weiler, I. L. G; Loyola, D. C; Tutivén, Y; McNew S. M.

Affiliation: University of Arizona; Tucson, Arizona, US

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Emerging infectious diseases pose a significant threat to global biodiversity. Island endemic species with limited prior exposure to pathogens are particularly vulnerable. Avian poxvirus was introduced to the Galápagos Islands in the late 1800s, where two viral strains, Gal-1 and Gal-2, are now endemic; however, little is known about their evolutionary history or relative virulence. We investigated differences in disease severity associated with these strains across a community of Darwin's finches and Galápagos mockingbirds on Santa Cruz Island. We found that Gal-1 is associated with significantly larger lesion sizes in Galápagos mockingbirds compared to Gal-2, while no significant differences in lesion size were observed between strains in Darwin's finches. To explore the evolutionary origins of these strains and their relationship to other avian poxviruses, we sequenced reference genomes for both Gal-1 and Gal-2 and compiled all available avian poxvirus whole-genome sequences, comprising 45 genomes isolated from 25 bird species. Using Bayesian phylogenomic analyses of 49 conserved poxvirus genes, we reconstructed the evolutionary relationships among avian poxviruses. Gal-1 and Gal-2 form distinct clades within clade B (canary poxviruses), with Gal-1 clustering most closely with viruses isolated from Australia and New Zealand, while Gal-2 groups with viruses primarily from North America. Together, these results suggest that Gal-1 and Gal-2, while typically seen and treated as one disease, potentially have different pathology, particularly in the Galápagos mockingbirds. Additionally, our data suggests these viruses did not diverge following a single introduction to the Galápagos, but instead represent independent introductions from distinct geographic regions. This work highlights how repeated pathogen introductions and strain-level variation can shape disease manifestations and evolutionary dynamics in isolated island populations.

Feeding Patterns of Aedes Aegypti Vary Across Human Use and Socioeconomic Landscape

Presenter: Daniel Suh

Coauthors: Johansson, M.A.

Affiliation: Northeastern University; Boston, MA; USA

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Host feeding choice by disease vectors is mediated by ecological factors, such as host availability and the innate feeding preferences of vector species. Aedes aegypti, a key vector of dengue virus (DENV) and other arboviruses, primarily feeds on humans in some locations but on non-human animals in others. For DENV, subsequent feeding on multiple humans is required for transmission, and lower human feeding may explain why DENV is not prevalent in certain regions despite availability of vectors and hosts. To understand what may be driving variations in feeding patterns of Ae. aegypti, we considered how human use factors and socioeconomic status may predict whether mosquitoes are feeding on humans. Higher density of human hosts can increase contact rates between humans and mosquitoes, but contact can also be mediated by the built environment, such as when humans spend more time in indoor environments protected by screens and air conditioning, which are tied to socioeconomic status. Using Ae. aegypti bloodmeal data from eight studies across the contiguous US and Puerto Rico, we analyzed how the proportion of single-family homes and median income across census tracts could predict the proportion of bloodmeals that contained human blood. Overall, we found that Ae. aegypti were more likely to feed on humans in areas that were characterized by denser housing structure and lower socioeconomic levels. However, due to the limited number of existing studies, it was difficult to account for differences between urban and rural settings, indoor and outdoor collections, the US and Puerto Rico, and endemic and non-endemic areas. These results highlight a critical knowledge gap in our understanding of vector feeding patterns across human use and socioeconomic landscape and can be used to inform management and surveillance of DENV.

Signatures of Selection by Viruses in Avian Genomes

Presenter: Isabella Weiler

Coauthors: McNew, S. M.; Enard, D.

Affiliation: University of Arizona; Tucson, AZ, USA

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Viruses are powerful evolutionary forces and are responsible for an estimated 30% of all adaptive protein adaptations in humans. Their impact on mammalian evolution has been well-characterized, but less is known about their impact on other taxa such as birds. A powerful method of gaining insight into the selective pressures imposed by viruses is analyzing specific protein-coding sequences that are known to interface directly with viruses, termed “virus-interacting proteins”, or VIPs. By analyzing the changes in these sequences over time or across a phylogeny, we can determine whether specific species or lineages have experienced significantly higher pressures from particular viruses. We investigated the diversity and evolution of VIPs across the avian tree including genomes of 62 bird species representing 85% of all avian orders. Across our phylogeny, we identified 8,567 orthologous genes. Approximately 554 of these genes are putative VIP orthologues. Selection analysis revealed that birds have experienced significant selective pressures as the result of viruses, with many VIP sequences across birds demonstrating signatures of episodic diversifying selection. We further discuss the impact of particular viral families on species with known ecological relevance, i.e. influenza-associated VIPs and seabirds, to identify whether deep coevolutionary history with related viruses can provide increased contemporary resistance. This work provides insight into the evolutionary forces that have shaped avian genomes and may inform our understanding of current disease dynamics.

Exploring Prolactin as a Mediator of Avian Malaria Tolerance in a Novel Host, the Hawaii Amakihi

Presenter: Gabrielle Names

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Following the introduction of avian malaria to Hawaii in the early 1900s, many native Hawaiian honeycreepers have declined. The Hawaii Amakihi (Chlorodrepanis virens) is the only species that has maintained stable populations at low elevations, where avian malaria is prevalent. Previous studies suggest low elevation populations have evolved increased malaria tolerance and have higher levels of some measures of immunity compared to birds at high elevations, where avian malaria is absent. However, the mechanisms underlying increased tolerance remain largely unknown. Endocrine mechanisms may contribute to increased tolerance by driving changes in immunity. Prolactin is a peptide hormone that regulates parental care, but it also stimulates immune function through its effects on immune organs, cells, and inflammatory responses. The goal of our project was to explore relationships among prolactin, immunity, and avian malaria infection in Amakihi, predicting that prolactin would vary positively with immunity and be higher in low than high elevation Amakihi. To test this, we collected small blood samples from adult and juvenile free-living Amakihi at high and low elevation to measure circulating prolactin, innate immunity, and avian malaria infection. Innate immunity was measured as agglutination score (a measure of natural antibodies via the hemagglutination assay) and circulating white blood cells (WBCs). Agglutination score was best predicted by an interaction between prolactin and elevation (P=0.027), where a significant, positive relationship between agglutination score and prolactin was found for birds at low (P=0.025) but not high (P=0.83) elevation. In juveniles, WBCs tended to increase as prolactin increased, but not significantly (P=0.098). Surprisingly, prolactin was lower in low compared to high elevation birds (P=0.059), while also significantly higher in infected than uninfected females (P=0.0096) but not males (P=0.60). These results provide some support of a mechanistic role of prolactin in mediating immunity in response to avian malaria.

Trait-Based Transmission Models for Climate-Driven Seasonal and Interannual Urban Malaria Dynamics

Presenter: Leonardo Souto Ferreira

Coauthors: Murdock, C.; Baharia, R. K.; Sharma, R.; Vaishnav, K.; Kohli, V.; Desai, V.;Mohanty, A. K.; Sharma, S.; Wimberly, M.; Pascual, M.

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Rapid urbanization and the spread of the truly urban vector Anopheles stephensi from Asia into Africa motivate a closer examination of how climate variability shapes malaria transmission in cities. Temperature dependent trait-performance curves for mosquito vectors and the pathogens they transmit, open the door to confront mechanistic temporal transmission models to time series data. We formulate a stochastic climate-driven SEIR-type model in which an effective transmission rate incorporates temperature-dependent mosquito and parasite traits and a precipitation-driven formulation of larval carrying capacity. The model relies on (1) a dynamical equation for carrying capacity whose inferred parameters set the timescale of rainfall effects, and (2) a fast,Äö√Ñ√¨slow dynamics approximation collapsing the vector equations into a transmission rate. We ask whether this approximation is sufficient to reproduce the temporal patterns of urban malaria at seasonal and interannual timescales in two cities of India. We demonstrate that the temporal resolution of climate forcing is critical for causal inference. When climate covariates are supplied at hourly resolution, the effective transmission rate peaks one month before the observed cases, consistent with biological delays, whereas monthly-aggregated inputs shift this peak to after the outbreak. Thus, sub-monthly temperature variation matters for mechanistic inference, even when the model is fitted to monthly data. We further show that the fitted model captures both seasonality and interannual variability from 1997 to 2016. Using a likelihood-based attribution method to quantify the contribution of climate drivers, we find that rainfall plays a dominant role in shaping the interannual variability of the disease, challenging the prevailing assumption that urban malaria is weakly sensitive to precipitation but consistent with recent findings on relative humidity. Our results show that trait-based, climate-driven models with explicit timescale separation can capture the temporal patterns of malaria in urban settings, providing an alternative to higher-dimensional coupled human-vector models.

Post Job Opportunities Here

Presenter: Job Board

Coauthors: Contact Job Board

Affiliation: EEID

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NA

Thurs Poster Session

Genetic and Phenotypic Changes of Multi-Host Viruses Lacrosse and Jamestown Canyon Virus After Adaption to a Single Host

Presenter: Daniel Little

Coauthors: Jones, E.; KC, S.; Taylor, K.

Affiliation: Towson University; Towson, MD; USA

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Time: 5:30

Orthobunyaviruses like LaCrosse virus (LACV) and Jamestown Canyon viruses (JCV) are mosquito-borne arboviruses. They are endemic to the United States and contribute to the overall burden of neurological infectious disease. Yet, they remain understudied. Arboviruses are multi-host pathogens that must replicate in both vertebrate and invertebrate hosts to sustain the transmission cycle. Understanding the phenotypic consequences of interactions between mosquito and mammalian hosts have important implications for predicting the evolution and emergence of Orthobunyaviruses and of their subsequent epidemiological patterns. Here, we tested the hypothesis that adaptation to a single host, either mosquito or mammalian, would result in a loss of fitness of the virus both in virulence and in the ability to infect the alternate host (i.e. mosquito mammal or mammal mosquito) Strains of LACV and JCV isolated from either a human or mosquito host were serially passaged 10 times in either mosquito (C6/36) or mammalian (Vero and BHK) cells and observed for phenotypic and genotypic changes. We saw changes in plaque phenotype and overall replication kinetics for those viruses serially passaged in mammalian cells in comparison to the same isolates cycled between insect and mammalian cells. This suggests out hypothesis that host switching between insect and mammalian hosts constrain viral diversity and subsequent evolution. Our ongoing studies aim to define the viral dynamics of host switching during sustained arbovirus transmission cycles of Orthobunyaviruses and how it aids in or restricts the emergence or re-emergence of significant human pathogens.

Modeling Within-Herd Infection of High Pathogenic Avian Influenza H5n1 in Dairy Cattle—The Roles of Stochasticity and Heterogeneity

Presenter: Jiawei Liu

Coauthors: Rodriguez, Z; Picasso, C

Affiliation: Department of Large Animal Clinical Science, College of Veterinary Medicine, Michigan State University; East Lansing, MI; USA

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The emergence of Highly Pathogenic Avian Influenza (HPAI) H5N1 in U.S. dairy cattle has raised concerns in both dairy industry and public health, particularly regarding cross-species transmission and zoonotic spillover. Despite experimental and epidemiological efforts to understand HPAI transmission in this new host system, the lack of longitudinal, individual-level data and mechanistic models limits detailed local outbreak evaluation and the assessment of surveillance and control strategies. To fulfill this gap, we aimed to develop a mechanistic model to understand the within-herd HPAI transmission pathways and mechanisms.

We collected longitudinal data from intra-ruminal automated sensor devices measuring cow body temperature during an outbreak in 2024 on a commercial dairy farm in Michigan. By comparing the data with post-outbreak HPAI-antibody test results through ELISA, we defined a temperature indicator for HPAI diagnosis. We fitted compartmental models including Susceptible, Exposed, Infected and Recovered classes (SEIR) to this indicator to provide farm-level epidemiological parameter estimates. Sensitivity analysis using partial rank correlation coefficients (PRCCs) were performed to show the parameters' effects on the outbreak dynamics.

Sensor data showed an initial disease peak in May (week 1-2), followed by minor proportions of infections until October with an ELISA relative-sensitivity of 0.78. A SEIR-structured model is sufficient to reproduce the outbreak onset and duration. Additionally, the scattered fever and the late-season fluctuations in minor infections are reproduced by including stochasticity and host heterogeneity, which reflect the farm herd management practices. Preliminary results suggest a daily transmission rate of 0.6-0.8, with relatively short incubation period (2-9 days) and long virus shedding time (15-30 days). These parameters greatly alter the outbreak dynamics (with |PRCC|s of 0.83, 0.43, and 0.61). We are further exploring the sources of heterogeneity, followed by more rigorous model fitting. Results will help guide control strategies for HPAI in dairy systems in the U.S. and globally.

Climate Change and Urbanization Effects on the Evolution of an Insect Virus: A Landscape Genomics Approach

Presenter: Kayla Lizaola

Coauthors: Fleming-Davies, Arietta E (co-presenter)

Affiliation: University of San Diego, San Diego, CA, USA

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The dynamics of disease transmission are shifting in response to climate change. Cities and similarly urbanized areas provide novel environments which exacerbate these symptoms of climate change by altering microclimates and changing the connectivity of the landscape in which pathogens evolve. Spatiotemporal elements of the environment, including anthropogenic factors, strongly influence selective pressures across taxa and can associate themselves with fitness-related traits of an organism, leaving a traceable genetic footprint in the form of local adaptation. The field of landscape genomics increasingly has been used to analyze the genetic changes associated with environmental selective pressures. We used a landscape genomics approach in a highly variable Lepidopteran baculovirus to characterize genetic signatures of interacting climate and urbanization factors in 72 whole genomes from 72 viral isolates of DijuNPV. We sequenced genomes of virus isolates from a subset of 403 Dione vanillae specimens collected from natural populations across the southern United States. We then conducted an environmental association analysis (AMOVA; poppr package in R) to separate neutral population structure from potentially adaptive genetic variation associated with bioclimactic variables (WorldClim; e.g. annual mean temperature, total summer precipitation, etc), urbanization variables (e.g. human population density, percent impervious surfaces), host subspecies, and host food plant species. We identified 17,274 SNPs across the 122Kbp genome, 1,910 of which occurred within previously-described viral genes from the published DijuNPV reference genome. We found evidence of strong population structure at nested spatial scales (site, metro area, and U.S. state), and preliminary results also suggest adaptive variation in important viral genes such as egt, which controls the host behavior post-infection. Identifying this variation is a first step in understanding how urbanization might affect the evolution and the maintenance of genetic diversity in pathogen populations, particularly for wildlife pathogens with limited dispersal across patchy urban landscapes.

Quantifying Effects of Temperature on the Distribution of Host Susceptibility in Pacific Herring (Clupea Pallasii) Across Viral Exposure Doses

Presenter: Malina Loeher

Coauthors: Hershberger, P.; Carlino, A.; Grady, C.; DeBlieux, T.; Wolf, N.; Mihaljevic, J.; Páez, D.

Affiliation: Alaska Pacific University; Anchorage, AK; USA. USGS Western Fisheries Research Center; Seattle, WA; USA.

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Susceptibility to disease naturally varies across individual hosts, and the degree of variation can be shaped by environmental conditions such as temperature. There is currently a limited understanding of how temperature effects the distribution of host susceptibility, especially in marine ectotherm systems. To accurately predict host-pathogen relationships like transmission and epidemic risk, host-level variability and environmental factors should be considered concurrently. In the marine forage fish Pacific herring (Clupea pallasii), recurring seasonal epidemics caused by viral hemorrhagic septicemia virus (VHSV) can cause massive fish die-offs along Pacific Northwest coasts. With increasing ocean temperatures, herring are anticipated to face shifting VHSV disease risk. We investigate how shifting temperatures modulate host susceptibility to pathogen infection by using a model that explicitly estimates the distribution of host susceptibility from dose response data. We first quantified the statistical power to estimate the distribution of host susceptibility under different experimental scenarios and parameter values. From this, we found that estimation uncertainty in the parameters increased as the average and variation in host susceptibility increased, and as the number of doses and samples per dose decreased. Then in our empirical work, we found that both the average and variation in host susceptibility were highest in the intermediate temperature treatment, and that this temperature also had the lowest overall infection prevalence. Higher infection prevalence was noted among both the cold and warm treatments and this corresponded to lower average and variation in host susceptibility. Overall, our simulation work identifies experimental designs and analytical strategies to reduce the uncertainty around parameter estimation. By applying these strategies, our empirical work shows that host susceptibility can change non-linearly with temperature in a marine host-pathogen system.

Host-Associated Beneficial Gut Microbiota Boosts Induced Immunity and Limits Immune Deployment Costs in Bumblebees

Presenter: Brenna Long

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Ecological immunology posits that variation in host resistance to infection may be attributed partly to the ecological and evolutionary costs of immunity. While the deployment of immune defense is necessary to combat pathogenic infection, hosts pay energetic and other costs for activation. Host-associated beneficial microbiota have been shown to affect multiple host traits, including immunity, but how interactions with these microbial communities may mitigate the costs of immune activation remains an open question. For apid bees, including eusocial bumblebees, core members of the adult gut microbiota contribute to a variety of fitness-relevant traits and provide a key ecological and evolutionary relationship contributing to ecological success. Here we test the hypothesis that the host-associated microbiota provides benefits to bumblebee immunity, including the mitigation of the costs associated with inducible immune responses. Freshly emerged germ-free adult workers were supplemented with their native microbiota via experimental fecal transplants from nestmates or kept deprived of their native microbiota inoculum. We assessed functional measures of induced immunity and assessed the costs of nonpathogenic immune activation for survival. In support of our hypothesis, we find that microbiota supplementation strengthened functional antibacterial immunity. Moreover, although we observed a cost of immune activation for survival, the cost was much greater for bees deprived of their native gut microbiota compared to those supplemented. Thus, we provide evidence that in addition to other roles, the microbiota mitigates costs of immune deployment. This demonstrates a key role for host-associated microbiota in the realization of induced immune defense, and contributes more broadly to our understanding of microbiota-immune interactions in the context of ecological immunology.

Cyanide Adaptation in Bamboo Lemurs: Variation in Ectoparasite Distribution Across Species

Presenter: Jenna Lopez

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Ectoparasites play a critical role in pathogen transmission and host health. Although some primates have been shown to self-medicate to treat pathogen infections by supplementing their diet, the role of long-term daily host diet in ectoparasite and vector-borne pathogen load remains poorly explored. Investigating the relationships between host ecology, ectoparasites, and pathogens is critical to understanding infectious disease risks in wildlife populations. Lemurs (Order Primates) exhibit diverse ectoparasite interactions that negatively impact hosts through pathogen transmission, skin damage, and blood loss. One clade, the bamboo lemurs, consumes exceptionally high amounts of cyanide as a natural component of their bamboo diet. While cyanide is toxic to most eukaryotes, as it inhibits aerobic cellular respiration, bamboo lemurs and a few plant-feeding arthropods have adapted a tolerance to chronic cyanide exposure. These adaptations provide a useful system to examine the impact of host ecology on ectoparasites. Using previously collected field data from Madagascar, I analyzed the relationships between ectoparasite load and host diet. Ectoparasite load was modeled using separate zero-inflated negative binomial models in brms with host species or parasite type as predictors, while incorporating host phylogeny. The results suggest species-specific patterns in ectoparasite load, with the bamboo lemur Prolemur simus exhibiting significantly lower ectoparasite loads in comparison to other lemur species. This pattern suggests cyanide consumption may influence host-ectoparasitic interactions, reducing ectoparasite burden in bamboo lemurs. Ongoing genomic analyses are investigating evolutionary adaptations associated with vector-borne pathogenic interactions with Plasmodium spp. across lemur species.

Sick and Tired: The Impact of Disease on Movement Driven Nutrient Subsidies

Presenter: Allegra Love

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Animals are the lifelines of our planet, linking ecosystems via the transport of nutrients and energy. Animal movement, therefore, dictates where large quantities of nutrients are removed and where they are deposited. However, disease can disrupt this function – altering movement patterns, behavior, and animal health. This ripple effect could influence not only the quantity of nutrients that is transferred but also the precise locations where ecosystems gain or lose them. To investigate the interplay between movement and disease and how this interaction modulates underlying mechanisms in zoogeochemical cycles, we developed an agent-based model based on the recent mange outbreak in San Guillermo National Park. In this system, vicuñas (Vicugna vicugna) perform a daily migration between plains and meadows, creating a nutrient subsidy. Typically, in the daytime, vicuñas travel to the meadows where there is abundant high-quality forage but an increased risk of predation. At nighttime, vicuñas travel to plains, where predation risk is lower. However, the recent introduction of a parasite (Sarcoptic Mange; Sarcoptes scabiei) caused a large decrease in vicuña density (~90%) and disrupted the daily migration. To explore the consequences of disease outbreaks for ecosystem functioning, we model daily migration, and several scenarios related to the parasite introduction, aiming to disentangle how the interplay between movement and disease affects zoogeochemical cycles. Specifically, we investigate the impacts of infection on movement (e.g., how many infected hosts move across systems), infection morbidity (e.g., increases in metabolic demand and decreases to grazing time), and infection mortality (e.g., reduction in total population) on the total amount of nitrogen transferred between ecosystems. We find that although morbidity has a relatively smaller magnitude of impact than mortality, both mechanisms impact heterogeneity and total export. By simulating this real-world scenario, we provide insight into how movement and disease can reshape nutrient dynamics in interconnected ecosystems.

Interactive Effects of Alkaloids and the Microbiome on Bd Susceptibility in Phyllobates Terribilis

Presenter: Yanileth López-Tacoaman

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Amphibian skin integrates multiple defensive strategies, including antimicrobial peptides, dietary alkaloids, and a diverse microbiome. Together they can shape susceptibility to pathogens such as Batrachochytrium dendrobatidis (Bd). These defenses are highly plastic and can influence one another, yet their combined effects on disease resistance remain poorly understood. Additionally, it remains unclear whether the alkaloids contribute directly to pathogen resistance, whether the skin or gut microbiome provides measurable protection, and how these two defenses may interact. As a first step toward addressing these questions, we developed and tested a method to experimentally reduce the skin microbiome of the golden poison frog (Phyllobates terribilis). Frogs were exposed to a 0.5% bleach-wash protocol across five treatment groups (n = 10 per group). Individuals tolerated the procedure, survived the experimental period, and exhibited treatment-specific differences in fecal coloration. We collected samples for metagenomic analysis from frogs at late larval (Gosner 39,Äì40) and early post,Äëmetamorphic stages. Ongoing analyses will quantify changes in alpha and beta diversity across treatments and tissues (gut and skin) to provide a foundation for future experiments testing how chemical defenses and microbial communities jointly influence Bd susceptibility.

Adaptable Immunity: Genomic Analysis Reveals Phylogenetically Structured Variation in Immune Gene Family Diversity

Presenter: Ian Magill

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The evolution of the immune system is often understood through the lens of two interacting coevolutionary circuits, with host-pathogen dynamics giving rise to a Red Queen-style arms race which is then heavily constrained by a host-intrinsic pressure to balance pathogen-killing capacity against minimizing autoimmune risk. This framing predicts fluctuating but fundamentally similar immune systems, which is at odds with the presence of taxa with highly divergent (and, by supposition, imbalanced) immune architectures. Given the critical role of the immune system in pathogen defense, as well as aging, metabolism, and tissue remodeling, it is imperative that we understand the conditions that permit such immune innovation. Using publicly available genome data for eutherian mammals, genes orthologous to major immune gene families were identified and quantified for each species. Special attention was given to proteins involved with direct pattern recognition and antigen display, as their copy diversity is likely more tightly linked to functional diversity. The resulting data was mapped to a time calibrated pan-eutherian phylogeny. The results reveal divergent patterns of gene family diversification, as some gene families, including the KLR, MHCi, Siglec, cathelicidin, and defensin families, show strong phylogenetic signal, while others, including the TLR, scavenger receptor, and complement families, show very little. Specific taxonomic groups exhibit dramatic expansions of immune gene families, with the Perissodactyls and talpid moles expanding their defensin and KLR repertoires, respectively. Taken together, these results show widespread, phylogenetically structured differences in immune gene copy number variation across eutherian mammals. These findings could provide insights into the immune capacities of diverse mammal lineages, including those for which detailed immunophenotyping is unavailable. This will also provide a contextual foundation for future, targeted comparative immunology studies.

Characterizing How Reassortment Shapes H3nx Influenza a Virus Evolution Across Diverse Hosts

Presenter: Maria Maltepes

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H3Nx influenza A viruses (IAV) are diverse, avian-derived pathogens with an unusual capacity to jump hosts, yet the evolutionary mechanisms underlying host adaptation remain unclear. One such mechanism is reassortment: when a host is coinfected with different IAV, progeny viruses with new gene combinations and altered phenotypes may emerge. Using 13,000 H3Nx genome sequences, we inferred phylogenies that confirmed continuously circulating clades in humans, equines, canines, swine, and avians, and transient spillovers into felines, camels, mink, and seals. Leveraging this broad host range, we analyzed the contribution of reassortment to H3Nx's evolution by developing a pipeline that infers reassortment across large datasets with measures of statistical uncertainty. Host-specific reassortment rates showed that the low-pathogenic North American avian clade exhibited the highest reassortment rates across the genome (0.35 reassortments/lineage/year), with markedly lower rates among the Eurasian avian and mammalian clades (0.04 - 0.15). For each host clade, we observed that segments reassort nonrandomly relative to a null model, indicating host-specific variation across segment compatibility. We found that neuraminidase (NA) reassorts more frequently than expected in birds, and that reassortment introduces new NA subtypes at frequencies that exceed those expected from the cocirculation of these viruses alone. These findings are compatible with a model in which acquiring new NA genes is beneficial to low-pathogenic avian viruses, potentially by enabling immune evasion. Current work is focused on analyzing reassortment's impact on virus fitness, which can be estimated from the persistence of a reassortant lineage. Preliminary data show that while reassortment occurs most frequently in the North American avian clade, these reassortant lineages are shorter-lived as compared to Eurasian avian or swine reassortants. These data support the ubiquitous role of reassortment in the generation of viral diversity and highlight that these viruses follow host-specific evolutionary patterns that remain relatively understudied.

Hematology of Wild Watersnakes (Nerodia Spp.) Infected with Emerging and Enzootic Pathogens

Presenter: Cory McKinstry

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Hematology is frequently a critical component in health assessments of free-ranging wildlife. However, baseline hematologic values and changes in response to infection with enzootic and emerging pathogens of reptiles are poorly characterized. One such emerging pathogen, Ophidiomyces ophidiicola, causes the necrotizing tissue disease Ophidiomycosis, which is a potential threat to snake populations across the United States. Complete blood counts from wild snakes infected with Ophidiomyces ophidiicola are infrequent and cover few species, as are studies assessing the interactions between Ophidiomyces ophidiicola and enzootic pathogens. Here, we compared the hemogram of uninfected snakes and snakes infected with each of two pathogens: Ophidiomyces ophidiicola and an enzootic blood parasite (Hepatozoon sp.), in wild watersnakes (Nerodia spp.). Using a pooled-analysis, we document baseline hemogram values, including leukocyte counts, erythrocyte counts, and associated ratios, from healthy individuals of four species (N. erythrogaster, N. harteri., N. rhombifer, and N. sipedon) sampled in three geographic regions (New Jersey, North Carolina, and Texas). We then compare baseline hematologic values, values from infected snakes, and infection prevalence for each pathogen across a temporal and regional gradient. Our data revealed that although Ophidiomyces ophidiicola infection was present across all groups, the prevalence varied greatly between species, regions, and seasons, and few individuals showed signs of severe disease. Similarly, the presence of blood parasites and metrics of the hemogram varied widely between individuals, species, regions and seasons. By integrating hematologic analysis with Ophidiomyces ophidiicola and Hepatozoon infection data, this study adds to a growing body of literature about how emerging and enzootic pathogens interact to impact host health.

Using Geospatial Mapping to Understand Differences on Baculovirus Transmission and Insect Outbreak Cycling

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Introduction

The spongy moth (Lymantria dispar), an invasive forest defoliating insect, is strongly affected by its species-specific baculovirus pathogen, which plays a key role in reducing defoliation. The transmission of the baculovirus is modulated by the multiple host tree species the insect feeds on and their differences in leaf chemistry. Therefore, understanding the effect of tree species on baculovirus transmission is important for understanding the mechanisms driving the spread of the virus. Changes in geographic distributions of trembling aspen and red oak, two preferred host trees of the spongy moth, due to climate change and land-use change, may alter the dynamics of baculovirus-driven spongy moth outbreaks. Incorporating spatial data of tree species distributions over time may provide more accurate projections of future spongy moth outbreak dynamics.

Methods

We used geospatial tools to analyze spongy moth outbreaks in North America. Using a combination of experimental data and observations of spongy moth defoliation patterns, we parameterized a long-term host-pathogen model that accounts for transmission differences in host tree species and the effects of host tree species spatial dynamics on spongy moth outbreaks and baculovirus transmission dynamics.

Results/Discussion

Our results suggest that observed dynamics of spongy moth outbreaks differ depending on host tree species predominance in a given geographic area. Previous experimental data we collected showed that both the average baculovirus transmission rate and heterogeneity in the transmission rate are higher on trembling aspen than on red oak. By using parameters estimated from these data, we have been able to show that variation in spongy moth dynamics across forests of different tree-species composition is partly due to the effects of differences in host tree foliage on the transmission of the baculovirus. Our work has important implications for the effects of climate change on spongy moth outbreaks.

Quantifying the Public Health Impact of Behavioral Interventions Against Mosquito-Borne Diseases

Presenter: Yuxin Meng

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Host behaviors are significant determinants of infectious disease dynamics, directly shaping disease incidence during transmission and further influencing the speed and magnitude of outbreaks. Yet, behaviors vary as the perceived risk of acquiring infection changes, and are likely influenced by the environment and control strategies under specific social contexts. Specifically, for mosquito-borne diseases (MBDs) in urban settings, which are transmitted by mosquitoes breeding in residual rainfall, waste, and water containers, prevention behaviors such as removing containers or cleaning waste in a timely manner can directly interrupt transmission pathways. Our goal was to quantify how prevention behaviors implemented by individuals impact MBD transmission in the context of Ibagué, Colombia, a city with long-term water infrastructure scarcity and a high dependence on household water storage. We used an agent-based model (ABM), in which human agents implemented prevention behaviors and, in turn, influenced mosquito dynamics. We calibrated our model with reported cases in Ibagué from 2007 to 2024 such that our calibrated ABM reproduces observed epidemic timing and interannual variation. By sequentially turning off prevention behaviors in the model, we conducted counterfactual simulations and revealed how behavior-driven strategies reshape transmission dynamics. By comparing scenarios with different control policies, we found that sustained household practices suppress human infections. These results quantify which control approaches most reliably shift household practices in Ibagué and translate those shifts into sustained reductions in mosquito-borne disease burden.

Uncertainty as Inference in Disease Distribution Models

Presenter: Kaitlyn Mitchell

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Species distribution models (SDMs) are widely used in disease ecology to guide surveillance and risk mapping, yet biotic predictors are often treated as fixed inputs even when pathogens depend obligately on other taxa. This obscures a key source of structural uncertainty: incomplete information about interacting species, which can directly affect spatial inference and downstream decisions. We develop a two-stage SDM framework that explicitly propagates uncertainty from obligate host distributions into predictions of dependent pathogens. Using simulation-based uncertainty propagation, we decompose predictive uncertainty into parametric and host-driven components and translate these patterns into a spatial Survey Priority Index (SPI) that identifies where additional host sampling would most reduce uncertainty affecting suitability classification. We apply the framework to schistosomiasis risk mapping in Madagascar, contrasting Schistosoma mansoni, which depends on a single snail host, with S. haematobium, which depends on multiple hosts. Host-driven uncertainty dominated predictions for the single-host system, producing clustered survey priorities, whereas uncertainty was more diffuse in the multi-host system. Our results show that the structure of obligate biotic dependence governs how uncertainty shapes disease risk inference and surveillance priorities.

Branching Process Model of Potential Undetected Chains of Transmission of Sudan Virus Disease — Uganda, 2025

Presenter: Eric Q. Mooring

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An outbreak of Sudan virus disease was identified in Uganda in January 2025. By March, two clusters had been identified with no known epidemiologic links between them. The Uganda Ministry of Health requested infectious disease modeling support from the U.S. Centers for Disease Control and Prevention. Through this collaboration, we developed a method to estimate the probability of ongoing undetected chains of transmission.

We used a stochastic branching process model to simulate potential transmission trees compatible with the earliest symptom onset date from each of the two clusters. We simulated surveillance for infections that were not descended from a known cluster. In the main analysis, we assumed a 5% per-infection probability of detection from February 1, 2025, onward. If simulated surveillance detected any cases outside the two known clusters, we excluded the corresponding tree since, in reality, surveillance did not detect any additional clusters.

We estimated a 25% probability of ongoing undetected transmission as of April 1, 2025, which dropped to 6% by April 30, 2025. These results were highly sensitive to surveillance assumptions; with a 10% per-infection probability of detection, the estimated probability of ongoing undetected transmission was 9% as of April 1, 2025. We also estimated the number of infections that may have occurred in undetected chains. Assuming a 5% per-infection probability of detection, the median cumulative number of undetected infections as of April 1, 2025, was 22, and 5% of trees had more than 113 infections.

An outbreak of a directly transmitted pathogen such as Sudan virus can be expected to either die out or grow exponentially. Our analysis quantified how sustained surveillance increases confidence that an outbreak has ended, even if some infections are never detected. The approaches used in this analysis could be adapted to other outbreaks to provide quantitative insights for decision-makers.

Disease Ecology in a Changing World (Deco): Transforming Knowledge to Planetary Health Through Stakeholder-Engaged Research

Presenter: Erin Mordecai

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Anthropogenic changes in climate, land use, mobility, population introductions and declines, and behavior are transforming the landscape of infectious diseases for humans, domestic species, and wildlife. As methods for detecting and quantifying these global change-driven disease outcomes mature, we are entering a new era of research that leverages disease ecology knowledge to develop human and planetary health solutions. In this presentation, I will describe a new interdisciplinary research program at Stanford called Disease Ecology in a Changing World (DECO) that is applying disease ecology to develop solutions that improve ecosystem and human health in partnership with local stakeholders and communities. In three cornerstone projects, we: (1) identify win-win water management strategies in sub-Saharan Africa that promote ecosystem integrity, water quality, and food security while reducing parasitic disease burden; (2) develop drone-based trash removal programs that reduce the environmental burden and increase the efficacy of dengue vector control in rural Costa Rica; and (3) operate a black soldier fly farm that transforms organic waste into valuable fertilizer and animal feed, closing a waste loop and reducing disease risk in Kenya. I will share how these projects build upon rigorous disease ecology research to develop novel interventions for disease control via community partnerships that respond to local needs and contexts. Outcomes include data dashboards, process-driven risk models, agricultural outputs (fertilizer, chicken feed, fish and rice biomass), and community-led businesses. While the field of planetary health presents promising opportunities to discover win – win solutions for the environment and health, the evidence base for implementing these ecologically informed nature-based solutions remains an important research frontier.

Evolutionary Trajectory of H5 Hemagglutinin Phenotypes Across U.s. Clade 2.3.4.4b

Presenter: M H M Mubassir

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Linking genetic variation to phenotypic traits remains a major barrier to assessing the risk of viruses with pandemic potential. Here, we map the evolution of predicted phenotypic traits for ~13,000 highly pathogenic avian influenza A H5N1 clade 2.3.4.4b viruses circulating in North America. We identify rapid phenotypic diversification during the initial geographic expansion after introduction. This diversification contracts through selective sweeps in avian hosts. In contrast, following establishment in dairy cattle, circulating lineages exhibit renewed phenotypic diversification, including increased potential for binding human-like α26 receptors despite conservation of the receptor-binding domain. Our framework provides a mechanistic basis for anticipating zoonotic emergence and prioritizing surveillance.

Mosquito Community Structure, Host Use, and Environmental Drivers Across an Elevational Gradient in Virginia

Presenter: John Muller

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Understanding how mosquito community composition, host use, and environmental drivers vary across heterogeneous landscapes is critical for predicting vector-borne disease risk. Virginia spans five distinct ecoregions and a broad elevational gradient, yet statewide mosquito surveillance remains limited and geographically centered around urban centers. We conducted mosquito surveys across four ecologically distinct sites in Virginia during the 2022 active season to assess patterns of mosquito diversity, blood-feeding behavior, and environmental drivers of species occurrence. Using CDC light traps, gravid traps, and supplemental aspiration, we collected 7,781 mosquitoes representing 34 species. Community composition differed markedly among sites, with the Coastal Plain site exhibiting the highest abundance and richness, while montane and urban sites supported less but distinct assemblages. Several medically important and invasive species were detected, including Culex pipiens, Culiseta inornata, Aedes albopictus, Ae. japonicus, and the range-expanding vectors Cx. coronator and Cx. nigripalpus, representing new regional records outside previously documented localities. Blood-meal analysis of engorged females revealed strong mammalian feeding preference, with white-tailed deer (Odocoileus virginianus) accounting for 83.3% of identified hosts across multiple mosquito taxa. Avian and amphibian hosts were detected at lower frequencies, including passerine birds and a green frog (Rana clamitans), highlighting diverse host–vector interactions relevant to enzootic transmission cycles. Random forest models identified elevation and trap type as primary predictors of species-specific occurrence, with climatic variables (temperature, humidity, and precipitation) contributing secondary influences. These results demonstrate that mosquito distribution and host use are shaped by interacting environmental and ecological drivers, with implications for pathogen transmission dynamics. Our findings underscore the need for expanded ecologically-informed surveillance to improve risk assessments for emerging and re-emerging vector-borne diseases in the Mid-Atlantic region.

The Effects of Rate Summation on Predicted Zika Virus Transmission Suitability

Presenter: Laura Multini

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Temperature strongly affects arbovirus transmission. Mechanistic modeling studies commonly estimate arbovirus transmission suitability by fitting thermal performance curves (TPCs) for mosquito and pathogen traits measured under constant temperatures and integrating these relationships into the basic reproduction number (R0). However, mosquitoes experience fluctuating temperatures in the field, and because trait-temperature relationships are nonlinear, fluctuations can shift traits performance. Rate summation provides a way to predict the average trait performance as temperature fluctuates over time. While rate summation has been evaluated for malaria transmission, its performance for arbovirus transmission remains largely untested. In this study, we use modeling approaches to better understand the use of rate summation to predict the thermal suitability for Zika virus (ZIKV) transmission by Aedes aegypti. Using previously published ZIKV-Ae. aegypti TPCs, we generate hourly temperature profiles across a mean-temperature gradient using the Logan-Parton model and implement hourly rate summation trait expectations for field-relevant daily temperature ranges (DTR) scenarios (9°C and 12°C). We then integrate the updated trait curves into an R0 framework to estimate ZIKV transmission suitability under fluctuating temperatures. Preliminary findings indicate that including DTR into the TPCs substantially reduces trait performance relative to constant-temperature curves. Consequently, peak suitability for transmission is drastically reduced under fluctuating conditions, highlighting the potential for bias in suitability analysis based on constant-temperature TPCs alone. Ongoing work will further (i) validate the effects of diurnal temperature fluctuation on predicted transmission suitability against real-world ZIKV transmission data and (ii) generate updated transmission suitability maps that incorporate diurnal temperature fluctuation. Integrating rate summation into established ZIKV frameworks has important implication for understanding how mosquito-pathogen traits and their transmission dynamics under field-relevant conditions can be used as basis for forecasting arbovirus transmission risk under a changing climate.

The Interaction of Temperature and Humidity Impacts Life History Traits and Wnv Infection Rates of Culex Pipiens Mosquitoes

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Environmental variation has a significant impact on numerous aspects of the biology of ectothermic vectors, which in turn influences the transmission potential of vector-borne pathogens. Statistical models demonstrate a significant effect of both temperature and humidity on the transmission of mosquito-borne viruses, including West Nile virus (WNV), yet empirical, lab-based studies that model the effect of environment on vector and pathogen dynamics have focused almost exclusively on temperature. This represents a clear gap in our understanding of transmission theory and a barrier to developing accurate trait-based predictive models. To address this gap, we assessed how the interaction of temperature and humidity influenced life history traits and vector competence of Culex pipiens from Albany, NY. Specifically, replicate populations of 60 mosquitoes each were reared at 20°C, 25°C, or 30°C under high (90%), mid (70%), and low (50%) relative humidity, simulating a simplified climate range during WNV transmission season in New York State. Mosquito development (time to emergence), immature survival, adult survival, blood feeding rates, and fecundity were monitored and recorded throughout the study. Furthermore, lab-raised adult females were challenged with WNV NY10 (2017) (V1C2), representative of currently circulating strains, and held under the same environmental conditions. Vector competence was assessed at 5 and 10 days post-infection. Results demonstrate that temperature and humidity significantly influence mosquito fitness and transmission potential. Specifically, increased humidity enhances adult survivability and blood-feeding rates, while higher infection and dissemination rates were observed at elevated temperature and humidity. Together, these findings highlight the complex effect of temperature and humidity on mosquito biology and WNV transmission, emphasizing the need for updated climate-informed predictive models.

The Effect of Temporal Transmission Changes on P. Falciparum Population Genetic Signals in Ghana.

Presenter: James Myers-Hansen

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The gold standard malaria transmission surveillance methods, such as the estimation of entomological inoculation rate (EIR) and parasite rate (PR) have had challenges. For example, EIR is difficult to implement under low transmission due to low mosquito sampling, and PR estimation with rapid diagnostic test (RDT) has issues with both false positivity (antigens detected by RDT may persist even after the clearance of the parasite) and false negativity (presence of parasites that lack RDT antigen). The evaluation of parasite population genetic signals such as complexity of infection (COI), Linkage disequilibrium (LD), genetic diversity and genetic differentiation (Fst) can accurately assess transmission in humans, and can complement the traditional methods. Reduction in transmission is characterized by declines in COI and genetic diversity, and increases in LD and Fst.

We characterized the population genetic signals in 573 P. falciparum isolates from 2010 to 2017 in the three ecological zones (Coastal, Forest, Savannah) in Ghana via antigenic and neutral loci typing using an Amplicon sequencing technique. Repeated cross-sectional sampling had been carried out amidst control interventions such as Indoor Residual Spraying (IRS) and Chemotherapy with ACT. This study was conducted to track changes in transmission intensity and build on the genomic toolkit for transmission assessment.

Following population genetic analysis of 71 loci, malaria transmission was generally sustained in all three zones, contrasting to the overall drop in PR from 26.1% to 22.0%, 52.4% to 22.2%, and 26.6% to 32.0% in the Coastal, Savannah and Forest zones, respectively. The COI, Nucleotide and Haplotype diversities in the Forest zone however slightly declined over the intervention period.

Overall, we show that population genetics reveal new aspects of malaria transmission when assessing control effectiveness. Similar to previous simulation studies, we observe high antigenic diversity and coinfection rates in endemic regions despite an overall reduced transmission intensity.

Vector–Natural Enemy Dynamics Govern Effects of Host Microbiota on Pathogen Spread

Presenter: Lucas Nell

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Protective factors against vector-borne diseases can have divergent effects on how diseases spread through populations. Host microbiota and pathogens can alter vector host-seeking behavior, and natural enemies that target vectors shape the density and distribution of vector populations. How these complex interactions collectively shape disease spread remains an open question. Common plant epiphytic bacteria in the genus Pseudomonas can repel or kill pea aphids that transmit costly viruses among pea plants. However, repelling of aphids could lead to greater crowding and production of the winged aphids that more effectively vector viruses, potentially increasing aphid-mediated virus transmission in plant populations. Thus, host microbiota could complement or hinder the control of aphid vectors by their natural enemies like parasitoid wasps. We used mathematical modeling to show that Pseudomonas presence can indeed either inhibit or promote virus outbreaks. Pseudomonas inhibits virus outbreaks by killing aphids, which is the more common outcome across starting conditions and parameter values. Yet, Pseudomonas-induced mortality generates spatial variability in aphid densities that can slow parasitoid population growth when parasitoids are relatively ineffective at finding aphids. The net result is amplified crowding in non-Pseudomonas patches, which increases winged aphid production and accelerates virus spread. In this scenario, the more effective Pseudomonas is at killing aphids, the more strongly it generates spatial variability and accelerates virus spread. Our results show how community context changes the outcomes of the Pseudomonas–pea association, such that microbiota protective to a single individual can have qualitatively different effects on disease outbreaks in host populations.

Non-Invasive Methods for Describing Internal Parasite Communities: A Metabarcoding Case Study.

Presenter: Alexandria Nelson

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Internal parasite communities can provide insights into host ecology, including habitat, diet, and health. However, these insights are often logistically impossible using classical parasitological methods. Methods that require necropsies are not feasible for rare or threatened hosts or for study designs that cannot accommodate destructive sampling. Methods that require fecal samples are not feasible for hosts whose feces are difficult to collect, and even when feces can be collected, parasite eggs are difficult to identify beyond the family level. Therefore, we developed and tested a metabarcoding pipeline that can use non-invasive swabs of captured animals to provide high resolution snapshots of internal parasite communities. We developed the pipeline using four snake host species: Timber Rattlesnakes (Crotalus horridus, species of special concern in North Carolina), Northern Pine Snakes (Pituophis melanoleucus, threatened in North Carolina), and Northern and Banded Water Snakes (Nerodia spp., least concern in North Carolina). We first used roadkill snake specimens to compare DNA detected on swabs collected from the stomach, intestine, and cloaca to the internal parasite communities observed with necropsies. We then applied the pipeline to two case studies where full necropsies were not possible: a longitudinal study of live Nerodia spp. caught in Wake County, North Carolina (cloacal swabs only) and an invasive Burmese python (Python bivittatus) removal program with strict regulations regarding specimen disposition (cloacal swabs, gut scrapes, or feces only). Swab preservation medium and snake species had significant impacts on post-extraction DNA concentrations. Without using host-blocking primers, we successfully detected parasite 28S DNA across all necropsied host species, live Nerodia spp., and python samples. The parasite taxa detected from our metabarcoding pipeline aligned well with the parasite taxa detected from necropsies. We will also discuss the benefits, limitations, and challenges of using the pipeline, including necessary steps for adapting it to other host systems.

Determining the Role of Density-Dependent Effects in Disease Induced Population Impacts

Presenter: Rose Newell

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Emerging infectious diseases threaten biodiversity conservation efforts across the globe. Managing infectious diseases in wildlife is challenging due to the complex nature of pathogen transmission in muti-host systems that can lead to varied decline and recovery patterns. Common disease management strategies rely on density-dependent pathogen spread and declines to be effective. Density-dependent contact rates are generally assumed to be the mechanism behind these decline patterns. However, other density-dependent processes that influence transmission probability are rarely investigated. Here we examine the processes by which population density contributes to the observed declines of bats infected with white-nose syndrome, a fungal disease that has decimated bat populations across North America. We evaluated the contribution of both density-dependent transmission rates and density-dependent environmental exposure on host prevalence and population declines. Our analyses indicate that the importance of population density varies depending on the phase of the epidemic, and density dependent declines are not observed in years when we see density dependent transmission. Instead, we found that the amount of pathogen a host is exposed to in the environment was dependent on host density and likely contributes to the observed patterns of decline. This research contributes to our general understanding of the role of density-dependent processes in disease dynamics and can help inform when to focus certain disease mitigation efforts.

Multiscale Immune System Modeling (Mism): a New Nih Center of Excellence and Research Hub

Presenter: Charles Nunn

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The Multiscale Immune Systems Modeling (MISM) “Center of Excellence” is a national hub to advance modeling frameworks that bridge biological scales and deepen understanding and prediction of infectious and immune-mediated diseases (IID). MISM generates and integrates models that span molecular, cellular, tissue, organismal, and population scales, overcoming limitations inherent in single-scale approaches. To do so, we integrate diverse expertise across immunology, computational modeling, data science, and population health, with the goals of creating integrated models, shared resources, and a collaborative community to accelerate translational impact for medical and public health interventions. MISM’s research focuses on three interdisciplinary Research Projects (RPs), each co-led by computational and experimental scientists. RP-1 integrates atomic-scale antigen modeling with repertoire-level protein language models to inform understanding of immune specificity. RP-2 bridges cell and organ scales to model viral, cellular, and environmental determinants of infection outcomes. RP-3 advances multiscale modeling from individual immune responses to population-level transmission dynamics by integrating within-host viral and immune dynamics with contact networks and social behavior. In this way, RP-3 links variation in immune responses, susceptibility, transmissibility, and symptomatic behavior to dynamic contact patterns, with the goal to generate realistic outbreak forecasts and inform control strategies. This poster provides an example from RP-3 that incorporates viral load dynamics into network models of disease transmission. MISM also has a Community Development and Education Core and a Model and Data Sharing Core. Collectively, the RPs and Cores illustrate MISM’s mission to create inter-operable and predictive multiscale models, and to foster a collaborative ecosystem that empowers researchers to tackle complex IID challenges, ultimately enhancing public health preparedness and response. MISM is growing the broader IID research community through graduate internships, seed grants, and a seminar series, and is supported by the NIAID.

Genomic and Phenotypic Characterization of Antimicrobial-Resistant and Virulent Escherichia Coli from Small Ruminants Reveal High-Risk Hybrid Lineages

Presenter: Ivan Odur

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Antimicrobial resistance (AMR) is a critical One Health challenge spanning humans, animals, and the environment. While Escherichia coli from major livestock species have been extensively characterized, small ruminants remain underrepresented in AMR surveillance. Small ruminants merit attention, given their greater tendency for close human contact and as known reservoirs of Shiga toxin-producing E. coli (STEC). Here, we applied an integrated phenotypic and genomic approach to characterize AMR and virulence profiles of E. coli isolated from sheep and goats in Virginia. Twenty-seven E. coli isolates (sheep=13, goats=14) recovered from fecal samples were tested against 12 medically-important antimicrobials using the Kirby-Bauer disk diffusion method. Illumina whole-genome sequencing was performed, followed by de novo assembly and annotation of AMR genes, virulence factors, serotypes, and sequence types. Phenotypically, 29.6% of isolates were multidrug-resistant, with the highest resistance observed to aminoglycosides and β-lactams. Genomic analyses revealed substantial serotype and sequence-type diversity, including both recurrent clonal lineages and genetically distinct strains. Notably, we identified a Locus of Enterocyte Effacement-negative STEC isolate encoding stx2 and subAB, a virulence combination associated with severe human disease. Additional isolates harbored ColV-like plasmid signatures characteristic of extraintestinal pathogenic E. coli, while others encoded Serine Protease Autotransporters of Enterobacteriaceae (SPATEs) and sslE, consistent with Enteroaggregative Escherichia coli-like or hybrid virulence architectures. Co-occurrence of antimicrobial and metal resistance operons was common, suggesting potential for co-selection under multiple environmental pressures. These findings demonstrate that small ruminants harbor genetically diverse E. coli populations, including multidrug-resistant and virulence-convergent lineages with zoonotic potential. Inclusion of small ruminants in One Health AMR surveillance is warranted to better anticipate emerging public health risks.

Tickhunter: A Semi-Targeted Hybridization-Capture Sequencing Approach for the Detection and Characterization of Tick-Borne Pathogens and Blood Meals

Presenter: Ximena Olarte-Castillo

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Ticks are vectors of many debilitating pathogens that are transmitted during blood meal acquisition. As both vector and pathogen species continue to emerge, there is a critical need for improved pathogen diagnostic and host remnant identification methods to develop interventions. Current pathogen detection methods are limited in their ability to subtype and detect emerging variants. Determination of tick blood meal sources is also an elusive step for understanding tick interactions with the biotic community in a given environment, with consequences for environmental management and disease prevention strategies. We have created an accessible hybridization capture next-generation sequencing (HCNGS) panel called “TICKHUNTER” to improve molecular detection and subtyping of bacterial and parasitic pathogens in both clinical and tick samples. The panel targets 43 genes or genomic regions, including highly conserved genes or genomic regions, genes used for multilocus sequence typing, and genes related to pathogenicity, which makes our detection method both precise and comprehensive. For disease ecology studies, the panel also detects host blood meal sources of interest by targeting a variable region of the mammalian mitochondrial 16S rRNA. An alternative method for unbiased blood meal remnant analysis is also presented. We find that the HCNGGS method using the TICKHUNTER is a promising tool for effective and accurate detection of a variety of tick-borne pathogens, based on comparable linearity, limit of detection, sensitivity, and specificity to real-time PCR. Additionally, it can detect and characterize unexpected pathogens due to the large capacity for multiplexing and flexibility in variant detection.

Data-Driven Modeling Suggests Migratory Bat–Bartonella Dynamics are Driven by Vector-Borne Rather than Host–Host Transmission

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Bartonellae are common, Gram-negative bacteria found globally, with some species capable of causing moderate-to-severe disease in humans. While typically associated with vectors such as fleas or lice, some Bartonella species are transmitted through direct contact with an infected individual. These potentially multiple transmission routes complicate understanding Bartonella infection dynamics in ecological communities. An example of this uncertainty is the Mexican free-tailed bat (Tadarida brasiliensis), a migratory species found throughout the southwestern United States and Mexico. Starting in early spring, pregnant females migrate north to give birth, forming dense maternity colonies. Our prior data from 2022 and 2023 in western Oklahoma suggest Bartonella prevalence increases during this summer period, potentially caused by bat population growth. However, this spike in infection prevalence also overlaps with peak prevalence of bat fleas (family Ischnopsyllidae), with both Bartonella and ectoparasite prevalence dropping prior to fall migration. To understand the relative contribution of direct and vector-borne transmission in this system, we built and analyzed a seasonal susceptible–exposed–infected–susceptible model. The model included both direct bat–bat transmission and vector-borne transmission. We used Latin hypercube sampling (LHS) to broadly explore parameter space across different transmission assumptions, retaining those parameterizations for simulations in which equilibrium states fell within the bounds of our empirical infection prevalence and flea intensity data. We found that the flea biting rate and the bat probability of being infected once bitten were the most important parameters, with the inclusion of bat–bat transmission being inconsistent with our seasonal field data. Our data-driven model suggests that bat–bat contact transmission is not a significant driver of Bartonella dynamics and that this pathogen is largely driven by flea-borne transmission.

High Environmental Overlap but Low Geographic Connectivity: Quantifying Niche Conservatism in Peromyscus

Presenter: Paanwaris Paansri

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The genus Peromyscus constitutes a primary reservoir system for numerous zoonotic pathogens, including hantaviruses and the causative agents of Lyme disease. Understanding the evolutionary stability of these hosts' ecological niches is critical for predicting disease-risk landscapes under global change conditions. This study evaluates the hypothesis of niche conservatism across the genus to determine if Peromyscus species retain ancestral climatic preferences during speciation, which ultimately could influence disease maintenance and spread. We obtained Peromyscus occurrence records from the Global Biodiversity Information Facility, the National Ecological Observatory Network, and environmental data from the MERRA-2 bioclimatic dataset. To disentangle environmental adaptation from geographic availability, we quantified pairwise niche overlap among the Peromyscus clade using Schoener's D metric in the environmental (E-space) and geographic (G-space) spaces. Statistical significance was assessed using niche similarity tests with 1000 permutations, and niche similarity networks were constructed to visualize ecological similarity and climatic decoupling. Our results in E-space strongly support the hypothesis of niche conservatism among Peromyscus, with the genus exhibiting a dense, highly connected network topology. Peromyscus species, despite distinct taxonomic identities and phylogenetic divergences (e.g., ecological differentiation between the P. truei and P. maniculatus), occupy a shared subset of environmental conditions that explain. In contrast, the G-space analysis reveals a fragmented pattern in which many species pairs exhibit high environmental similarity but near-zero geographic overlap. The disparity indicates that Peromyscus species have primarily diversified via allopatric and parapatric speciation while retaining their ancestral climatic niche. The strong signal of niche conservatism and spatial isolation suggests could help explain bacterial and viral diversification among Peromyscus, and the different levels of virulence found across the range of the genus. Results support the use of aggregate niche models to forecast spillover risk at the domestic-wildlife boundary for Peromyscus species of limited data.

Elevated Co□ Reshapes Barley Yellow Dwarf Virus Dynamics Across Crop and Non-Crop Grass Hosts

Presenter: Shirin Parizad

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Environmental variability such as rising atmospheric CO□ is expected to alter plant physiology and reshape host–vector–pathogen interactions, potentially influencing infectious disease dynamics in agroecosystems. Barley yellow dwarf virus (BYDV), particularly the BYDV-PAV species, is the most widespread and economically important viral disease of small grains worldwide. It is transmitted by cereal aphids and maintained across landscapes in cultivated and uncultivated grass reservoirs. We examined how elevated CO□ influences plant performance, aphid fitness, and BYDV-PAV accumulation in winter wheat (Triticum aestivum), and the wild host species foxtail barley (Hordeum jubatum) and green foxtail (Setaria viridis). Growth-chamber experiments were conducted under ambient (420 ppm) and elevated (700 ppm) CO□ with aphid-infested and uninfested plants. We quantified plant biomass allocation, transpiration, water-soluble carbohydrates, Rhopalosiphum padi survival and reproduction, and BYDV-PAV titers. Elevated CO□ increased total plant biomass across host species, with green foxtail producing greater biomass than winter wheat and foxtail barley but did not affect transpiration or carbohydrate concentrations. Aphid performance depended on host plant species rather than CO□ level, with higher mortality and lower reproduction on green foxtail. In contrast, elevated CO□ increased BYDV-PAV accumulation, primarily in uncultivated hosts. Our findings indicated that elevated CO□ enhances plant biomass and viral accumulation. Although CO□ had no direct effect on aphid performance, increased virus accumulation in host plants can indirectly affect BYDV dynamics, as aphid acquisition success is known to be positively correlated with virus titer. Considering the roles of non-crop hosts and the effects of environmental drivers in vector–plant–virus interactions can lead to the development of more accurate predictive and risk-assessment models in our dynamic agroecosystems.

Mammalian Parasite-Sharing Across Marine and Terrestrial Environments

Presenter: Andrew Park

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While knowledge of factors governing interspecies parasite sharing has improved in recent years, parasite sharing between animals in marine versus terrestrial environments is less understood. Many animal pairs that span the two environments are more related than pairs that co-occur in the same environment, possibly promoting transboundary parasite sharing. Conversely, ecological opportunity, differences in animal behaviors, and variation in population densities on land and in the sea, together with contrasting environmental conditions, may limit parasites' ability to thrive in both environments. To characterize boundaries and bridges regulating parasite sharing between terrestrial and marine environments, we compiled known mammal-parasite associations from three sources: the Global Mammal Parasite Database, a published complex life-cycle database, and supplemental marine mammal data compiled for this study. Broadly, bacteria are the parasite group that shows the most propensity to infect across environments, and dual transmission modes also promote trans-boundary sharing. When accounting for relatedness of host species, parasite community sharing between host pairs reveals phylogenetic distance decay profiles, suggesting that marine mammals share parasites most readily followed by terrestrial mammals and then marine-terrestrial pairs. Mammals infected by a disproportionate amount of trans-boundary parasites are characterized by maritime mammal status, haul-out behavior, and traits including longevity. Overall, parasite sharing between terrestrial and marine mammals is non-random and explained by both parasite and host factors.

Scavenging Behavior and Non-Typhoidal Salmonella Carriage Among Wildlife and Domestic Animals Utilizing Human Waste in Northern Botswana

Presenter: Lena C. Patino W.

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Scavenging behavior serves as an essential ecological process that facilitates removal of carrion, nutrient cycling, and disease regulation within ecosystems. However, rapid human population growth and expanding urban waste streams have created persistent anthropogenic food resources attracting scavenging species, increasing their exposure to pathogens and antimicrobial resistance (AMR) determinants. To investigate these dynamics, we retrospectively screened archived fecal samples for non-typhoidal Salmonella (NTS) from facultative scavengers (banded mongoose, marabou storks, domestic dogs, and chickens) and non-scavenging wildlife (hippos and elephants) collected in Kasane in northern Botswana (January 2022–May 2023; n=797). NTS was isolated from banded mongooses (17%, 95% CI 13–20%, n=421), marabou storks (5%, 95% CI 2–11%, n=132), dogs (26%, 95% CI 10–48%, n=23), and hippos (7%, 95% CI 1–24%, n=27), but not from chickens (n=77) or elephants (n=117). Serotyping of six banded mongoose NTS isolates identified S. enterica serovars Agona (n=5) as well as Jedburg var 15+ (n=1). Using the disk diffusion method, phenotypic AMR was overall low, detected in only 5% of banded mongoose isolates (95% CI 1–13%, n=62) and 14% of marabou stork isolates (95% CI 0–58%, n=7). Multidrug resistance was not observed. Facultative scavengers consuming human waste were approximately nine times more likely to carry NTS than non-scavenging species evaluated in this study (p=0.0001). NTS carriage varied among scavenging species along a trophic gradient of food waste exposure, from grain- and vegetable-based materials (chickens, no NTS detected) to mixed and meat-derived waste (marabou storks, dogs, banded mongooses), suggesting that differences in food waste composition may contribute to variation in NTS exposure. Our findings suggest that scavenging behaviour can increase exposure to zoonotic pathogens such as NTS for certain scavenging species influenced by local conditions, possibly shaping critical transmission networks for zoonotic pathogens.

Updated Neon Pathogen Datasets Facilitate Cross-Scale Community Disease Ecology Research

Presenter: Sara Paull

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Vector-borne disease burdens continue to rise against a backdrop of global environmental disturbance and change. The U.S. National Ecological Observatory Network (NEON) offers continental-scale long-term pathogen data in mosquitoes, ticks and rodents co-located with other environmental measures with the potential to elucidate key relationships between the environment and pathogen communities. NEON is implementing a shift from PCR-testing to next generation RNA virus sequencing of mosquito samples. Analyses of the pilot results indicate that the virome of Aedes albopictus, Aedes vexans, Culex tarsalis and Culiseta melanura demonstrate differences in virome diversity that are associated with mosquito pathogen niche breadth. In 2020, NEON also began testing rodent blood and ear samples for tick-borne pathogens, enabling cross-species comparisons of rodent pathogen diversity and prevalence. Combining these data with the ongoing tick surveillance and pathogen testing at NEON sites enables a powerful opportunity for analyses of co-infection and community level patterns of infection. Pairing these uniquely in-depth community-level vector and host disease datasets with environmental monitoring data offers a compelling framework for disentangling the environmental drivers of disease burden in wildland communities

Modeling Rare but Explosive Eastern Equine Encephalitis Virus (Eeev) Epidemics

Presenter: Angela Peace

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Eastern equine encephalitis virus (EEEV) is an alphavirus (family Togaviridae) transmitted among wild birds by mosquitoes, primarily Culiseta melanura. Disease outbreaks occur when the virus amplifies to critical levels and spills over to horses and humans. In the Northeast U.S., EEEV transmission is characterized by prolonged interepidemic periods punctuated by intense, single-season outbreaks, making seasonal risk difficult to predict. Understanding the mechanisms that give rise to these episodic epidemics remains a central challenge in EEEV ecology. We present a stochastic modeling framework informed by long-term mosquito surveillance data that integrates continuous-time Markov chain (CTMC) models with Galton–Watson branching processes to quantify seasonal epidemic risk under low-prevalence conditions. Preliminary single-season simulations show that outbreaks are rare but occasionally explosive, even when the basic reproductive number is only slightly greater than one. Replicated CTMC sample paths demonstrate substantial variability in vector infection prevalence. Comparisons between theoretical expectations and simulated dynamics highlight threshold behavior driven by vector–host ratios, biting rates, and avian herd immunity.

Global Modelling of Long-Term Dengue Control Under Combined Intervention Scenarios

Presenter: T. Alex Perkins

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A growing range of control tools for dengue have now demonstrated effectiveness in randomised controlled trials including Wolbachia replacement, dengue vaccines, and improved mosquito control methods. Policy-makers now need to decide which interventions to invest in and how to integrate them with existing vector control programmes to meet their short- and long-term control goals. We developed a compartmental model of dengue transmission with multi-infection dynamics, seasonally varying transmission, and use of enhanced vector control guided by optimal control theory. We implemented this model in 1,634 cities at risk of dengue worldwide with independent validation against reported case count data. For each city, we projected cumulative hospitalisations averted and financial costs of different combinations of enhanced vector control, vaccination, Wolbachia replacement, and urban environmental improvements (“building out Aedes”) over a 25-year time horizon. Wolbachia was predicted to deliver substantial long-term reductions in dengue burden in many locations; however, its performance varied widely across cities. Pairing Wolbachia with enhanced vector control improved and reduced the variance of long-term predicted impact, but required sustained investment and rising operational costs as population susceptibility increased over time. The most effective and sustainable strategy combined novel and conventional approaches with gradual, structural reductions in mosquito habitat suitability through “building out Aedes.” This integrated portfolio produced the largest and most consistent burden reductions (>90% reduction in all cities) and prevented ever-increasing costs of control in other intervention scenarios. Sustainable dengue control will require long-term, integrated strategies that acknowledge changing population immunity and the changing role of routine vector control once novel tools are introduced. Cities should consider integrated strategies that use conventional and novel interventions to suppress dengue transmission in the short term while more permanent changes can be made to remove mosquito habitat in the urban environment to ensure that control remains sustainable.

Spatiotemporal Dynamics of Asian Longhorned Tick Invasion in the United States

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The invasive Asian longhorned tick (Haemaphysalis longicornis) is an economically significant ectoparasite of livestock and a vector of multiple pathogens of medical and veterinary concern. Since its inferred introduction circa 2010, H. longicornis has expanded rapidly across the eastern United States, yet the ecological and anthropogenic drivers governing its spread remain incompletely characterized. Understanding invasion dynamics is essential for forecasting future range expansion, prioritizing surveillance, and designing targeted surveillance and control strategies.

We analyzed county-level invasion dynamics of H. longicornis across the United States using national surveillance data and a Cox proportional hazards modeling framework to estimate time-to-invasion from the onset of the U.S. invasion. Candidate predictors included biotic factors (host availability and habitat characteristics), abiotic variables (climatological conditions), and anthropogenic factors (human population density and land use).

Invasion dynamics were consistent with a stratified diffusion process, incorporating both short- and long-distance dispersal events. The current phase of invasion appears diffusion-dominated, with an estimated mean rate of spread of approximately 48 km per year. County-level invasion risk was positively associated with variables reflecting habitat suitability, host availability, and human population density, whereas spatial proximity to previously invaded counties was not a strong predictor of time-to-invasion.

These results indicate that ecological suitability and anthropogenic processes play a central role in shaping the spread of H. longicornis, with direct implications for the spatial distribution of tick-borne disease risk across emerging invasion fronts. This framework provides a quantitative basis for forecasting invasion risk and informing targeted surveillance and intervention strategies.

Inferring the Relationship Between Prevalence of Malaria Infection and Case Incidence

Presenter: Daniel Petro

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Ecological and individual factors can shape how disease incidence translates into prevalence, producing heterogeneous patterns across populations. The context-dependence of these complementary measures of disease burden means their relationship is rarely constant. For malaria, assuming a stable prevalence-incidence relationship can obscure substantial population-level heterogeneity driven by differences in control measures and ecological factors. Here, we used routine surveillance data from pregnant women attending their first antenatal care visits and confirmed malaria cases reported by all health facilities in Mainland Tanzania between 2014 and 2024 to investigate how ecological and intervention contexts reshape the prevalence-incidence relationship. We estimated population-specific prevalence-incidence curves using nonlinear mixed-effects models with district-level random effects and temporal autocorrelation. We found that prevalence respond to changes in incidence up to a one-month lag ($p<0.001$), and we observed pronounced heterogeneity in prevalence-incidence relationships across districts. Across most districts, a one-percentage-point increase in prevalence corresponded to approximately 17 (range: 10 - 30) additional malaria cases per 1,000 population per year. These results show that similar incidence regimes can generate markedly different prevalence patterns across populations, highlighting the importance of accounting for ecological and intervention-driven heterogeneity when interpreting malaria surveillance data.

Transmission Chains of Canine Distemper Virus Reveal Fine-Scale Structuring by Host Traits in an Urban Patch

Presenter: Laura Plimpton

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Urban landscapes can concentrate wildlife into discrete green patches that provide refuge and abundant anthropogenic resources, often producing elevated but spatially heterogeneous densities and altering movement, space use, and social behavior. For directly transmitted pathogens, this heterogeneity can structure who infects whom and shape outbreak growth, duration, and persistence in ways not captured by classical mass-action models. Understanding transmission at the scale of individuals within patches is therefore central to explaining pathogen spread and persistence in fragmented urban systems. Here, we use a genomic epidemiology approach to reconstruct within-patch transmission during a canine distemper virus (CDV) outbreak in an urban cemetery in Brooklyn, New York City. We used near complete CDV genomes from 14 infected individuals—predominantly raccoons, the primary wildlife reservoir—to infer transmission chains and applied trait-based network analyses to assess associations with age, sex, relatedness, symptom severity, and spatial position within the urban green patch. We found that CDV transmission was non-randomly structured by raccoon sex and age, and capture location. Male raccoons exhibited disproportionately high inferred transmission involvement and elevated male-to-male transmission support, while adults showed elevated transmission support to juvenile raccoons. Transmission was spatially clustered, with individuals captured near the urban edge exhibiting the highest inferred transmission involvement and elevated within-group transmission support, whereas individuals in the cemetery interior played a comparatively peripheral role. Forward simulations of stochastic SIR epidemics on empirically parameterized, sex-structured networks produced larger, longer outbreaks with delayed peaks relative to null networks lacking structure. Together, these results demonstrate that fine-scale, within-patch heterogeneity can amplify and prolong transmission in urban wildlife populations, highlighting a plausible mechanism by which pathogens such as CDV may be maintained in fragmented urban systems.

Modeling Mosquitoes and West Nile Virus Dynamics in the Us

Presenter: Laura Pomeroy

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Mosquito-borne diseases are an enormous burden worldwide, causing illness and mortality in multiple host species. West Nile virus (WNV), a flavivirus transmitted by Culex spp. mosquitoes, has been detected in North America since 1999 and has caused morbidity and mortality in humans, horses, and multiple avian species. We developed non-linear, dynamical, temperature- and precipitation-dependent models that represent WNV transmission vectored by Culex spp. mosquitoes among multiple bird species and calibrated the models with field-collected data 16 sites (8 urban, 8 rural) from northern and central Ohio. We quantified relative abundance of Culex spp. mosquitoes over space and time and estimated critical quantities like the number of generations per summer active season. We simulated WNV transmission and predicted the size of local outbreaks. This work demonstrates the importance of incorporating temperature-dependence and specific requirements for each mosquito life stage into estimates of mosquito active season durations, establishes a foundation for future computational models of WNV transmission, and can inform decisions about mosquito control.

Temperature-Dependent Wolbachia Interventions on Dengue Dynamics: Optimizing Release Timing in Changing Climates

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Wolbachia-based interventions are an innovative strategy that effectively reduces dengue transmission by Aedes aegypti. However, experimental data show that temperature influences critical Wolbachia mechanisms such as cytoplasmic incompatibility, maternal transmission, and fitness costs, which may hinder its capacity to invade wild mosquito populations and sustain long-term presence. We developed a temperature-dependent compartmental model that incorporates mosquito population dynamics, frequency-dependent cytoplasmic incompatibility, and imperfect maternal transmission. This model aims to determine the establishment time and long-term persistence across various temperature scenarios and connects these processes to dengue transmission in humans. We simulated different release scenarios under both constant and different seasonal temperature regimes.

Our results show that, at constant temperatures, establishment dynamics were similar at 25°C and 28°C, whereas at 30°C, invasion was significantly slowed. Under seasonal temperature fluctuations, Wolbachia invasion was affected by the timing of temperature changes, causing delayed establishment in some cases. Additionally, identical temperature ranges yielded different outcomes depending on whether a high-temperature period occurred.

Temperature plays a pivotal role in Wolbachia-based dengue control by shaping invasion dynamics and persistence and by reducing human transmission. These findings highlight that local thermal regimes, particularly seasonal variability, critically influence release timing and the long-term success of Wolbachia strategies. Effective deployment, therefore, requires tailoring release schedules to regional temperature profiles to maximize Wolbachia establishment and minimize dengue transmission over time

Epidemiological and Clinical Features of Chikungunya in Brazil from 2015 to 2025: Age, Sex, Ethnicity and Spatial Dispersal

Presenter: Zhang Quanqi

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Chikungunya virus (CHIKV) has emerged as a major public health threat in Brazil since its introduction, causing recurrent large-scale outbreaks associated with substantial morbidity. Unlike many other arboviruses, chikungunya is characterized by a high symptomatic rate and durable post-infection immunity, suggesting that population susceptibility and demographic exposure may play an important role in shaping its spatial and temporal transmission dynamics. However, the ecological mechanisms underlying the geographic propagation of chikungunya across Brazil remain incompletely understood. We conducted a nationwide retrospective analysis of laboratory-confirmed chikungunya cases reported to Brazil,Äö√Ñ√¥s national surveillance system (SINAN) from 2015 to 2025, linked with municipality-level population data from the Brazilian Institute of Geography and Statistics (IBGE). We characterized temporal trends, age-, sex-, and ethnicity-specific incidence patterns, clinical symptom profiles, and disease progression using descriptive analyses and survival models. To quantify spatiotemporal transmission dynamics, we fitted a Bayesian hierarchical model implemented in the Integrated Nested Laplace Approximation (INLA) framework, incorporating a Besag,Äö√Ñ√¨York,Äö√Ñ√¨Molli,àö¬© 2 (BYM2) spatial component and a second-order random walk to estimate municipality-level relative risks over time. Model-based spatial risk patterns were confirmed with published regional chikungunya seroprevalence estimates. Chikungunya incidence in Brazil exhibited pronounced epidemic waves rather than stable endemic transmission. Reported cases were consistently concentrated among adults aged 25,Äö√Ñ√¨50 years, with a marked female predominance across most municipalities. Survival analyses revealed strong age gradients in disease severity and mortality, with males progressing faster to hospitalization and death. Spatiotemporal modeling identified a coherent north-to-south propagation of elevated transmission risk, followed by sustained suppression in affected regions, consistent with rapid depletion of susceptible populations after major outbreaks. Our findings indicate that chikungunya,Äö√Ñ√¥s spatial dispersal in Brazil is shaped by regional herd immunity and demographic exposure.

Patterns of H5 Viral Spread and Spillover Risk Across Wild Bird Migration and Poultry Production Landscapes

Presenter: Tanin Rajamand

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Highly pathogenic avian influenza A(H5) has entered an unprecedented panzootic phase since late 2021, with repeated introductions into the United States and Canada and rapid viral spread along migratory flyways, reshaping risk at the wildlife-agriculture interface. Despite extensive surveillance, prevention and preparedness remain constrained by an incomplete understanding of when spillover risk emerges during migration-linked seasonal windows and where it concentrates across migratory bird habitats and poultry production clusters in the United States and Canada. Here, we integrate viral genomic data from wild birds and poultry with phylogenetic inference to identify likely independent introduction events, and relate these events to migration-linked seasonality, migratory bird habitat structure, and spatially clustered poultry production across the United States and Canada.

Preliminary analyses show that viral introductions into poultry are not evenly distributed across space or time but instead concentrate within recurring seasonal windows aligned with avian migration and within specific ecological-agricultural contexts. Introduction events are associated with habitat types commonly used by migratory waterbirds, peak during migratory periods, and appear elevated in regions of dense poultry production. Together, these patterns support an ecological-agricultural framework in which migration-linked viral flux intersects with structured production landscapes to generate predictable spillover risk, providing a basis for risk-informed surveillance and targeted biosecurity at the wildlife-agriculture interface.

Ecological Interventions Underpinning Public Health Interventions

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Environmentally mediated infectious diseases account for nearly 40% of the global disease burden. Ecologically-based interventions, defined as the use of living organisms to suppress pathogens, vectors, or intermediate hosts have gained renewed attention for their low cost, feasibility and alignment with One Health. Despite renewed interest, predicting the effects of biological controls remains difficult for three reasons: similar interventions often yield divergent outcomes across settings, few unifying frameworks generalize across transmission routes, and evaluations rarely track ecological trade offs. Clearly, One Health needs to be operationalized with clear ecological mechanisms, moving from cure first approaches to prevention. To tackle these limitations we examine the mechanistic basis of ecologically-based public health interventions. Our goal is to understand not only what interventions were used but how these interventions potentially rewire underlying transmission dynamics. Using a SIR-inspired compartment model framework, we synthesize the ecological processes associated with interventions applied to >80 environmentally mediated diseases. The diseases span soil-, water, and vector-borne transmission modes, and the interventions involve a range of ecological processes including direct killing, etc., including direct killing, predation, competition, ecosystem modification, symbiosis, and genetic manipulation. We find that most diseases rely on diversified portfolios of ecological control rather than a single strategy. Predator introduction, ecosystem modification, and vector suppression dominate existing approaches, but profiles differ by transmission mode: soilborne diseases rely mainly on direct killing and ecosystem modification, whereas vectorborne diseases use about 4 biological controls on average. We also identify vector groups where biologically plausible intervention types remain unused, and use global disease burden estimates to examine whether intervention diversity tracks public health needs versus historical investment patterns. Taken together, this synthesis provides a mechanistic basis for interpreting existing ecological controls and identifying gaps where additional interventions are plausible.

Evaluating How Demography and Temperature Increase Might Alter the Burden of Congenital Toxoplasmosis in Africa

Presenter: Fidisoa Rasambainarivo

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Climate change is expected to alter the transmission dynamics of many environmentally mediated pathogens, with potentially counterintuitive consequences. Toxoplasma gondii, a globally distributed protozoan parasite, is one such pathogen. Higher temperatures may reduce the survival of T. gondii oocysts in the environment, but reductions in transmission can paradoxically increase disease burden by shifting infections to older ages and increasing the risk of congenital toxoplasmosis. We evaluate how changes in human demography and rising temperatures may reshape the burden of congenital toxoplasmosis across Africa. We synthesize age-stratified seroprevalence data from studies conducted between 1979 and 2023 across 25 countries to estimate the force of infection and its dependence on temperature and the Human Development Index (HDI). Using these estimates, we integrate projected demographic changes in fertility and age structure for 2050 and 2100 with scenarios of increasing minimum and maximum temperatures. Our analyses show that transmission intensity declines with increasing HDI and maximum temperature, while minimum temperature exerts a positive effect, consistent with biological constraints on oocyst survival. When combined with demographic projections, these effects generate substantial heterogeneity in future burden. In many settings, demographic change dominates, leading to either increases or decreases in risk depending on shifts in fertility timing. Temperature increases can either mitigate or exacerbate burden depending on local transmission intensity and reproductive age structure. Together, these results highlight that climate-driven reductions in transmission do not necessarily translate into reduced disease burden. Anticipating future risk of congenital toxoplasmosis will require integrating epidemiological, climatic, and demographic processes to guide surveillance and prevention strategies.

Reconstructing the Evolutionary Dynamics of Artemisinin Resistance in Plasmodium Falciparum Using Recombination-Aware Phylogenetics

Presenter: Valeria Rayo-Solano

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The malaria pathogen Plasmodium falciparum is a globally significant pathogen with a high disease burden. Resistance to antimalarial drugs is also spreading globally. The C580Y mutation in the kelch13 gene is associated with resistance to the most widely used antimalarial medication, artemisinin, and poses a risk to effective treatment and malaria elimination efforts. We explore the evolutionary history of the emergence of the C580Y mutation in P. falciparum strains from Cambodia, and whether this mutation has afforded a selective advantage over time. Looking at 287 malaria sequences from Cambodia, we reconstructed phylogenetic trees for the kelch13 genomic region. To account for recombination across the malaria genome, sequences were extended in either direction of C580Y to the nearest recombination breakpoints— an approach we call “haplotype walking”. Time-calibrated phylogenetic trees were then reconstructed in BEAST 2 to assess node times, resistance trends, and tree topology support values. We identified multiple independent emergence events of the C580Y mutation in closely related genetic backgrounds. Our time calibrated trees suggest that genotypes with resistance emerged about 50-80 years in the past, which places the appearance of these resistant genotypes well before the use of artemisinin proliferated in Cambodia around the early 2000s following regional clinical trials during the 1980-90s. These results suggest that drug resistant genotypes may have had low fitness costs, or potentially even fitness benefits, preceding widespread drug use.

Estimating Contacts of Deer Mice from Long Term Trapping Grids to Track Sin Nombre Virus Transmission

Presenter: Leah Rensel

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Contact rates between animals are key factors in disease transmission, and are one of the fastest and easiest interventions for disease prevention or control. However, quantifying contact rates in any population of wild animals is challenging, especially for small or cryptic rodent species. Sin Nombre Virus, a North American hantavirus that causes a chronic infection in deer mice (Peromyscus maniculatus) but can be fatal in humans. Despite being common hosts for zoonotic diseases around the globe, small rodents like deer mice have been excluded from more rigorous contact studies due to their size and the limits of tracking technology.

We estimated contact rates of deer mice using capture-mark-recapture data collected on long term trapping grids in Montana over 8-10 years. The first step is to determine the deer mouse home range size, and whether sex, age, season, conspecific density and SNV status influence mouse behavior. Our results show that males have larger home ranges than females, but females are more likely to be found near the center of their home ranges. Mouse density was not positively correlated with home range size, suggesting density dependent transmission may be responsible for SNV transmission. We will use this information to predict home range overlap as a proxy for contacts between individuals. Our approach to track potential contacts between cryptic individuals will potentially allow us to predict trends in disease transmission of SNV. However, as trapping grids are common techniques to monitor small mammals, this approach is applicable in taxa and disease systems beyond SNV in deer mice.

Extreme Weather Event Impacts on Human and Nonhuman Disease Landscapes in Madagascar

Presenter: Benjamin Rice

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In addition to gradual warming, climate change is making extreme weather events more extreme. Events such as rapidly intensifying tropical cyclones have broad effects on landscapes, hosts, and vectors in affected areas with downstream consequences for disease. Studies from a handful of individual events indicate extreme weather can considerably alter local vegetation, hydrology, temperature, and vector dynamics in exposed populations, with impacts on pathogen transmission potential. Inferring the scale and generality of the observed effects, however, remains difficult due to the limited, biased sample of events studied to date. Further, studies of human infections cover only a fraction of global pathogen diversity and are subject to strong confounding from changing public health activities and ad hoc disaster response efforts. We present a framework to more systematically sample across climate events and host-pathogen systems, applying this approach to tropical cyclones and vector-borne pathogens in Madagascar. We first use high resolution remote sensing data sets (e.g., ECOSTRESS) to quantify changes in vegetation and surface temperature that occur in the wake of 52 cyclone events. Importantly, analyzing a much larger sample of events allows more robustly characterizing relationships between pre-storm conditions, e.g., forest type and preceding precipitation, and the observed landscape impacts. Next, we leverage mathematical models of vector population dynamics to estimate the range of effects for observed post-storm changes in surface temperature (e.g., due to storm-induced destruction of vegetation reducing shade). We survey a set of human (e.g., falciparum malaria and flaviviruses) and nonhuman pathogens (e.g., Plasmodium and arboviruses in wildlife), and discuss implications for public health and conservation strategy. Such data suggest that efforts to understand the impact of extreme events is urgent for the large fraction of the world's surface that is exposed to extreme weather each year.

National Wildlife Disease Database - Interagency Collaboration for Pandemic Prevention

Presenter: Katherine Richgels

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Emerging wildlife diseases can pose a significant threat to the American public through their potential impacts to human health, food security, and the economy. However, information about wildlife diseases is spread across varying land-owning jurisdictions and to date is not gathered or collated in a comprehensive way. In recognition of the need for real-time, nationwide wildlife disease information to support effective responses to potential pandemics, Congress called for and funded development of a “national wildlife disease database” (NWDD) in 2021. The NWDD will create health intelligence for participating agencies to assess risks, understand potential impacts, and better visualize wildlife disease occurrence in the US by combining multiple existing data streams in a robust data analytic platform. NWDD requirements are guided by a multi-agency steering committee and partnership between USGS and the DOE Pacific Northwest National Laboratories (PNNL). An initial product is expected by September 2026, including data from federal sources, such as USGS (WHISPers and AquaDePTH), USFWS, NPS, and USDA-APHIS-WS, and states, such as Minnesota Department of Natural Resources, Wisconsin Department of Natural Resources, Texas Parks and Wildlife, Nebraska Game and Parks Commissions, and more. The platform is intended to provide real-time information for decision-makers at the local, state, and federal levels to manage wildlife diseases and will not have public access. However, we are looking for feedback from the EEID community a data request process that could be added to the platform that would protect the sensitivity of this information while also empowering it’s collation to be used to further our understanding of wildlife diseases on the landscape.

Cellular and Molecular Immune Variation Across Bat Life-History Strategies in the Families Molossidae and Vespertilionidae

Presenter: Alicia Roistacher

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Immune variation in wild hosts can shape pathogen dynamics by altering susceptibility and shedding, and immune allocation is constrained by trade-offs that can vary with life-history. Bats are key reservoir hosts for diverse zoonotic pathogens, often roost in close proximity to humans, and exhibit multiple life-history strategies (e.g., migration and hibernation); however, the role life history plays in shaping bat immune state remains poorly resolved. Here, we test whether life-history strategy explains baseline immune variation within and among bat species while accounting for season, reproduction, region, and interannual variability. As part of a multi-year project (2024-2027), we are sampling four molossid and four vespertilionid bat species across the U.S. Great Plains, Belize, and Panama. We pair hematology with blood transcriptomics and plasma proteomics from the same individuals to quantify immune cell distributions and molecular immune pathways. Preliminary hematology results indicate that life-history strategy is associated with leukocyte profiles and that some metrics vary by season (in the U.S. Great Plains) and year. For example, neutrophil-to-lymphocyte ratios were higher in Neotropical resident species than in a long-distance migratory species and a Great Plains hibernator. Ongoing transcriptomic and proteomic analyses will test whether these patterns are mirrored in expression of inflammatory and antiviral pathways and whether seasonal and reproductive shifts produce consistent signatures across regions. By integrating cellular and molecular immune measures across species, years, and biogeographic contexts, this work identifies life history drivers of bat immune states and provides a foundation for identifying taxa and forecasting periods of elevated infection risk relevant to both conservation and public health.

Characterization of Movement Networks and Seasonal Corridors of Malagasy Fruit Bats to Inform Viral Transmission Risk

Presenter: Martin C. Roland

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Background: Madagascar hosts three endemic fruit bat species that carry potentially zoonotic coronaviruses, filoviruses, and henipaviruses. Understanding viral persistence and circulation requires detailed knowledge of bat movement and population connectivity. Methods: We deployed GPS tags on 12 Pteropus rufus and 8 Eidolon dupreanum individuals from 9 sites across Madagascar. Tags were active between 2023-2026 for an average duration of 8 months for P. rufus and 4 months for E. dupreanum. We fit continuous-time movement models to irregular, autocorrelated GPS tracks and estimated season- and species-specific home ranges using autocorrelated kernel density estimation (AKDE). We applied dynamic Brownian bridge movement models to identify recurrent nocturnal flight corridors, analyzed roost switching with multi-state models, and used step-selection functions to test how habitat features shape movement decisions. Results: Both species showed pronounced seasonal range expansion during the resource-scarce dry season, with P. rufus expanding home ranges by 33.9% and E. dupreanum by 24.1%. GPS-tracked P. rufus females foraged significantly farther (mean 22.7 km) than males (mean 13.8 km) regardless of season, a pattern mirrored in E. dupreanum. Brownian bridge analyses revealed persistent movement pathways reused across months, with landscape pinch points concentrating bat traffic. P. rufus exhibited higher inter-roost connectivity and broader dispersal than E. dupreanum. Step-selection models showed both species selected structurally complex habitats, with seasonal shifts in selection strength. Conclusions: Dry-season range expansion may increase spillover risk, as bats shed more virus during nutritional stress while simultaneously spending more time in human-modified landscapes. Species differences in roost connectivity and dispersal likely generate distinct spatiotemporal patterns of viral circulation across Madagascar’s fragmented bat populations.

Characterizing Infectious Hematopoietic Necrosis Virus Evolution Following a Host Jump in Salmonids

Presenter: David Romero

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Viral host shifts are a major source of emerging infectious diseases, with potential impacts on public health, biodiversity, and food security. Understanding how viruses evolve during the host shift process is therefore critically important. Experimental studies where viruses are serially passaged in novel host species often show evidence of convergent evolution, suggesting that virus evolution following host shifts may in theory be at least partially predictable. However, the repeatability of evolutionary trajectories following host shifts in the field is still poorly understood due to the rarity of well-documented examples. Here we take advantage of the infectious hematopoietic necrosis virus (IHNV) system, in which there were two distinct viral host shifts from sockeye salmon into rainbow trout. We sequenced a collection of 99 IHNV isolates that were sampled over fifty years from the ancestral and novel host and combined this dataset with an additional 63 previously generated genomes. We then conducted phylogenetic analyses and evolutionary tests, and we used codon evolution modeling tools to identify genomic regions under selective pressure. These analyses revealed rapid evolutionary changes following the host shift events. While we did not find strong evidence of convergent evolution across viral host shifts at the nucleotide or amino acid level, we did find evidence that the nucleoprotein and phosphoprotein genes changed rapidly following both host shift events. We also found evidence of positive selection in the nucleoprotein gene following one of the host shifts. Our data therefore suggest that the precise mutations that arise following host shifts may be unpredictable and different across host shift events in the field, but that the regions of the genome that change may be predictable.

Host and Environmental Factors Influencing Prevalence and Severity of Ophidiomycosis Among Michigan Snakes

Presenter: Hannah Rothkopf

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Wildlife fungal diseases have increased in frequency over the past decade and represent major conservation threats. Of growing concern is ophidiomycosis, a fungal disease specific to snakes, which is caused by the pathogen Ophidiomyces ophiodiicola. O. ophiodiicola has been recorded in 62 species and has been linked to significant population declines, but there has been considerable variation in its population-level impacts. For example, populations of the eastern massasauga rattlesnake (EMR) have experienced localized declines linked to this disease, while for other EMR populations, O. ophiodiicola remains undetected or causes only mild, transient infections. The drivers of this heterogeneity remain poorly understood, making it difficult to quantify population-level disease risks. In particular, little is known about how environmental factors and O. ophiodiicola prevalence at the community level influence population-level risk. To quantify how host species and environment influence ophidiomycosis prevalence and severity, in Michigan and evaluate the influence of host identity and environment, we conducted opportunistic surveys of Michigan snake communities in wetland and dry upland habitats sympatric with three continuously monitored EMR populations. From May-September 2025, 101 snakes representing nine species (excluding EMR) were captured, swabbed, and visually inspected for clinical signs of infection. Preliminary results indicate that 75 snakes (74%) exhibited clinical signs of infection. The southeastern wetland site showed the highest incidence (93%), consistent with recent reports of ophidiomycosis in EMR at that location. High occurrence of clinical signs was observed in Coluber constrictor foxii (63%), Storeria dekayi (100%), Thamnophis sirtalis (76%), and Thamnophis saurita (100%). qPCR confirmation of ophidiomycosis will be followed by O. ophiodiicola strain identification via sequencing of cultured isolates to evaluate host–strain associations. Understanding how ophidiomycosis prevalence and severity vary across hosts and environments will enhance prediction of disease impacts on affected populations, including endangered species such as the EMR, and may help to contextualize similar patterns in other fungal pathogens.

Helminth Parasite Co-Infections Interact with Sin Nombre Hantavirus in Montana Deer Mice (Peromyscus Maniculatus)

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Wildlife populations are exposed to diverse parasite communities, where co-infection is the rule rather than the exception. Understanding the mechanistic effects of co-infection on disease dynamics requires moving beyond the traditional focus on single pathogen - single host systems. We use infection of Sin Nombre hantavirus (SNV) in wild deer mice (Peromyscus maniculatus) as a model system to identify potential mechanistic effects of co-infection on disease dynamics of SNV in its reservoir host. We trapped and removed wild deer mice (n = 1,065) from six sites across western Montana from 2023-2025 and tested individual SNV serostatus (n = 78 seropositive of 1,054 tested to date) and adult helminth infection via gastrointestinal dissection (n = 181 infected of 318 dissected to date). We used joint species occupancy (infection probability) models with symmetric interactions to estimate parameters of non-independent infection (presence/absence) of co-infecting parasites. This approach allows us to describe infection probability of each parasite species conditional on infection with other parasites and is preferable to linear models which assume an effect of one species on another but not vice versa. We compared models to determine whether Trichuris stansburyi, Calodium hepaticum (tissue-invasive helminths), and SNV interact in individual mice and to estimate effects of host characteristics, sex and body length, on independent infection and on interactions. The top model incorporated (1) non-independent interactions between parasite species, (2) a strong positive effect of body length on each infection (likely because older individuals have more time to become infected) and (3) a positive effect of sex (being male) on interactions. Predicted SNV infection probability was significantly higher in mice (especially males) that were co-infected with C. hepaticum. These results confirm that co-infections in this system are not independent and are impacted by host characteristics, emphasizing the importance of integrating co-infection into investigations disease dynamics.

Gulf Coast Tick Movement in the Eastern United States

Presenter: Afsoon Sabet

Coauthors: Sabet, A.; Ward, S.F.; Sovic, M.G.; Peterman, W.E.; Bajwa, W.; Gaff, H.; Gauthier, D.; Goddard, J.; Green, L.; Halsey, S.; Herrin, B.; Kennedy, A.; Loftin, K.; Molaei, G.; Nolan, M.; Navarre, C.; Occi, J.L.; Scimeca, R.; Stone, C.M.; Trout-Frxyell, R.T.; Teel, P.; Pesapane, R.

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The Gulf Coast tick (GCT), Amblyomma maculatum Koch, has undergone a significant range expansion over the last 30 years and is now found well outside of its historic range. Tick dispersal is intrinsically linked to the movement of their hosts. The prevailing hypothesis for GCT range expansion has been tick drop offs from migratory birds as they fly north to their breeding grounds, though other mechanisms may contribute. Gulf Coast ticks have been found on over 70 animal species, representing substantial variation among their dispersal capacities. We assessed the genetic structure of GCT populations across much of the United States. Using a broad network of collaborators, we amassed over 400 individual ticks from 18 states within the current range of GCT, representing over 50 unique sites. We hypothesized that the leading edge of the expansion of GCT would exhibit similar or higher levels of genetic variability than populations in the historical range. This would be consistent with recurring gene flow into the populations at the leading edge and suggest that a mixture of both long distance and short distance dispersal may occur. Our work will help understand the varying mechanisms of tick movement at a broad spatial scale, which can in turn inform potential avenues of intervention to limit tick spread.

Integrating Weather Shocks and Environmental Shifts in a Stochastic Eco-Epidemiological Framework of Zoonotic Spillover

Presenter: Barsha Saha

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Environmental variability and extreme weather events profoundly shape species interactions and the emergence of zoonotic diseases. However, existing eco-epidemic models do not simultaneously account for weather shocks and environmental shifts. To address this gap, we develop a novel stochastic eco-epidemiological framework that (i) couples multi-species competitive Lotka-Volterra (CLV) interactions with Susceptible-Infectious-Recovered (SIR) disease dynamics in the wildlife populations, (ii) incorporates dispersal of wildlife species via advection–diffusion processes, and (iii) includes both wildlife-to-human and environment-to-human transmission routes to compute exposure dose and the spillover risk under various weather and environmental disturbances. The framework integrates Gaussian white noise and Poisson-driven Lévy jumps to represent chronic environmental fluctuations and sudden weather events, respectively. For the reduced forms of the eco-epidemiological framework, we establish conditions for stochastic persistence and extinction, as well as partial coexistence and competitive exclusion among wildlife species. Our analysis of the full framework includes global existence, uniqueness, and positivity of the mild solution of the stochastic SIR-CLV Reaction-Advection-Diffusion system of wildlife species, derivation of the stochastic reproduction number R_0, and local and global sensitivity analyses. Numerical simulations reveal that prolonged environmental stressors (e.g., drought) combined with sudden weather events (e.g., cold snaps) can lead to the extinction of most species, while increasing the survival and re-emergence of infectious diseases, thereby elevating the risk of spillover. This study highlights the nonlinear effects of coupled environmental and climatic disturbances on the stability of wildlife ecosystems and the subsequent elevated risk of zoonotic spillover.

Beyond Static Humans: Integrating Mobility Data into Ecological Models of Vector-Borne Disease

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Vector-borne disease risk emerges from dynamic interaction between ecological conditions and human behavior. While advances in disease ecology have greatly improved spatial predictions of vector and pathogen suitability, the field of EEID often treats humans as static agents, relying on coarse proxies for exposure such as residential location or administrative boundaries. This disconnect obscures the spatial and temporal heterogeneity in risk and limits the translation of ecological models into actionable public health strategies. Here, we present a scalable framework that integrates high-resolution ecological models of infected vectors with dynamic estimates of human activity derived from social media and location-based mobility data. We generate monthly daytime human activity estimates at ~5km resolution and integrate these with existing models of tick habitat suitability and infection prevalence. We apply this approach to the Lyme disease system in the western United States, where exposure is dominated by recreational rather than peri-domestic activity. Using Bayesian hierarchical spatial models, we predict reported human Lyme disease cases as a function of environmental risk and human activity. We identify hotspots of elevated exposure across 221 state parks – settings where targeted interventions such as vegetation management or seasonal risk communication are feasible. While environmental suitability alone predicts disease patterns, model performance greatly improves when dynamic human activity is incorporated. Most interestingly, we find that human mobility covariates are informative only when aggregated over ecologically meaningful spaces (park polygons) rather than administrative units (ZIP codes). This result suggests that human activity translates into disease risk primarily when people overlap directly with environmentally risky areas (i.e., state parks), rather than through general movement (e.g., grocery stores) alone. This work demonstrates a novel, cost-effective pathway for translating EEID models into prioritization tools for public health. More broadly, it highlights the importance of integrating dynamic human behavior into infectious disease ecology.

Prairie Grass Stand Quality and Drought Legacy Drive Accumulation of a Leafhopper-Transmitted Wild Virus in a Multiyear Landscape-Scale Experiment

Presenter: Katrina Sanders

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Plant viruses are ubiquitous in nature, yet we still lack experimentally-grounded understanding of how virus assemblages establish, accumulate, and change over time within wild plant communities. This is particularly true for long-lived native plants which dominate natural landscapes, but differ dramatically from annual crops in their trait suites. To quantify drivers of virus dynamics in perennial-dominated natural habitats, we examined virus colonization of switchgrass (Panicum virgatum), a North American prairie grass. Switchgrass is susceptible to insect-vectored crop pathogens such as yellow dwarf viruses (YDVs) while also hosting less known “wild” viruses. Among these is switchgrass mosaic virus (SwMV), a marafivirus transmitted in a persistent, propagative manner by the leafhopper Graminella aureovittata. For this study, we conducted a novel five-year experiment replicated across 12 sites embedded in diverse landscapes in Michigan (USA). Within these landscape contexts, we experimentally manipulated the complexity of the plant community in which P. virgatum hosts established and performed longitudinal monitoring of virus prevalence, vector abundance, and explanatory variables (plant community composition, abiotic factors, and host chemistry). We found little evidence of YDV spillover from crops. Instead, wild SwMV rapidly colonized switchgrass stands (within three years) with virus prevalence positively associated with vector abundance across landscape contexts, and less influenced by community complexity. Multivariate analysis and structural equation modeling revealed that host stand establishment and realized stand productivity were the best predictors of fourth-year virus prevalence, which in some cases exceeded 50%. Intriguingly, notable legacy effects of establishment-year drought were also evident. At drought-impacted sites, reductions in host height and density likely rendered vegetation initially less attractive to leafhoppers and delayed virus accumulation. Our results reveal multi-year effects of biotic and abiotic factors on virus colonization over seasons and demonstrate that networks of insect-transmitted wild plant viruses can persist even within strongly anthropic landscapes.

Mosquito Diversity, Host-Feeding Patterns, and Arbovirus Surveillance in Western Virginia

Presenter: Gavyn Sanford

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Mosquito-borne arboviruses are a growing concern in the United States, yet surveillance in rural regions often remains sparse. In Virginia, state surveillance is limited to urban centers of the Coastal/Piedmont, leaving inland counties underserved in vector monitoring, with poor understanding of arboviral threats and enzootic transmission. This study aims to fill critical gaps in mosquito species diversity and arbovirus prevalence across western Virginia. Weekly mosquito collections were conducted in summer 2023-2025 in up to five counties along the I-81 corridor, using BG-Pro, CDC light, and GAT traps, deployed in both urban and sylvatic habitats. Specimens were identified to species level, pooled by trap-type, site, and week, and then screened for arboviruses using cell culture isolation methods, with viral species identified molecularly. Blood meal analysis via DNA extraction and amplification of the 16s rRNA gene and Sanger sequencing were also conducted. A total of 997 mosquitoes from 18 species across 7 genera, including Aedes albopictus, Aedes japonicus and Culex pipiens were collected in 2023. Collections in 2024 yielded 1,668 mosquitoes from 22 species of 5 genera, further indicating the presence of known arbovirus vectors (Ae. albopictus, Ae. japonicus, Ae. triseriatus, Ae. vexans, An. quadrimaculatus, An. crucians, Ps. Columbiae). Screened as 424 pools, West Nile virus was isolated from samples from 2023 in Rockingham and Rockbridge counties. In 2024, West Nile and Cache Valley viruses were isolated from Rockbridge County from 362 pools. An analysis of vector community and arbovirus prevalence across all three years will be presented. Results of blood meal analysis indicates feeding on a broad range of hosts, including humans and wildlife. These findings provide the first regional catalog of mosquito diversity and arboviral activity in this underserved region of the Commonwealth. Continued monitoring will enhance understanding of vector-host-pathogen dynamics and inform local public health and vector control strategies.

Identifying Underserved Populations by Mapping Health Care Catchment Areas in the Democratic Republic of Congo

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Background: Human disease data are reported spatially at administrative units, creating a substantial gap in disease reporting for populations with poor access to health care facilities. These populations are overlooked when coordinating outbreak prevention and response efforts, potentially limiting the impact of vaccination efforts and disease control. In the Democratic Republic of the Congo (DRC), health facilities are unevenly distributed across administrative units known as health zones. As a result, the country experiences recurring outbreaks of vaccine-preventable infectious diseases despite intensive prevention efforts. To improve our understanding of the spatial variance of health care access within these health zones, we determined the catchment areas of health care facilities in the Équateur province of DRC. Methods: We used publicly available data of locations of health care centers and transit data to generate health facility catchment areas in the Équateur province of DRC. We modeled the travel time to the nearest health facility using a cost distance algorithm, accounting for factors such as geographic and seasonal barriers. Results: We found unequal access to health care facilities within health zones; many populations experience longer travel times to the nearest health facility, which can subsequently drive disease underreporting. Areas identified as having longer travel times should be considered a high priority for targeted disease surveillance, mobile vaccine delivery, and outbreak response efforts. Defining health facility catchment areas can aid in more equitable access to health care, diagnostics, and disease reporting for populations across the Équateur province.

An Agent-Based Model of Dengue Transmission: Comparing Individual Actions and Collective Measures

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Background: Dengue remains the most common mosquito-borne disease, endemic in over 100 countries and impacting nearly half of the world's population. Its transmission depends on human movement, personal protective measures, and community efforts. Standard mathematical models often overlook individual differences and behavioral influences crucial to dengue spread. In contrast, agent-based models (ABMs) simulate autonomous agents with specific interaction patterns, integrating spatial data, behavioral diversity, and collective strategies. Methods: We created an agent-based model (ABM) that incorporates human spatial movement, behavioral interventions, and mosquito ecology to study dengue spread in Colombia. The model represents households distributed spatially, with each household containing indoor and outdoor vector containers. Human agents are defined by their infection status (S-E-I-R), preventive behaviors (none, protective clothing, repellent, or a combination), and movement patterns. Vector agents progress through different life stages, each with specific survival probabilities. We evaluated individual interventions such as repellent and protective clothing, as well as collective efforts including household and neighborhood sanitation campaigns, and broad policies, under varying awareness levels and implementation frequencies. Results: Individual protective measures alone proved insufficient; universal adoption of combined repellent use and protective clothing would be necessary but is impractical. Collective interventions demonstrated greater effectiveness with increased cleaning frequency (shorter cooldowns) and larger, cohesive scales (from household to neighborhood to system-wide). The highest awareness levels produced the most effective results, although patterns varied unpredictably. Public policy interventions required either 100% efficacy or very high frequency; otherwise, residual mosquito populations maintained low but constant transmission, eventually infecting the entire population. Optimal control involved combining individual and collective measures to significantly reduce dengue incidence. Conclusions: Effective dengue control requires comprehensive, multilevel strategies. Relying exclusively on individual responsibility is insufficient; coordinated community efforts and sustained public health initiatives are essential to effectively reduce transmission in endemic areas.

An Underexplored Theory for Why Culling Has Had Unintended Consequences in Social Animals

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Culling is one of the main ways to manage infectious diseases in livestock and wildlife populations, but its success is dependent on several factors, including the type of pathogen transmission (frequency- versus density-dependent transmission) and population structure. In some cases, such as with vampire bat rabies, culling programs have even led to increased (rather than decreased) pathogen transmission. An underexplored explanation for the failure of culling programs may be the population's social structure. Vampire bats exhibit complex social behaviors, depend on one another for grooming and food sharing, and tend to have a high degree of social structure. Culling-induced loss of social partners is therefore likely to encourage individuals to seek out new connections. These new connections are new edges in the network through which disease may spread. In this work, we develop a generalizable mathematical framework that integrates animal social network data and agent-based modeling to test whether social disruptions from culling programs could explain the unintended consequences of culling as a disease management strategy. Increasing our understanding of why mitigation strategies have not performed as expected will help us improve our current wildlife disease control measures and reduce the economic burden of infectious diseases.

Impacts of Daily Temperature Fluctuations on Disease in Host Individuals, Populations, and Communities

Presenter: Katie Schroeder

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Temperature is a primary driver of host-parasite interactions, but the impacts of daily thermal variation remain poorly understood compared to the effects of differences in mean temperature. Moreover, insights gleaned from individual hosts might not predict outcomes at population or community scales, because individual-level responses often scale non-linearly to population-level outcomes. To address these gaps, we examined how daily fluctuating temperatures influence disease at the individual, population, and community scales in a system of zooplankton hosts (Daphnia and Ceriodaphnia) and a fungal parasite (Metschnikowia). We first quantified life-history traits of focal host Daphnia individuals (i.e. birth and death rates) under three magnitudes of thermal fluctuation. These rates were consistently higher in variable temperature conditions than in constant temperatures. Additionally, at larger fluctuations (□7□C), the cost of infection was eliminated, as fitness between infected and uninfected individuals became indistinguishable. Infected hosts also had increased transmission rates and higher spore yields under variable conditions. To observe the cumulative and dynamic effects of these traits, we conducted experiments in 55-liter buckets to monitor population and community dynamics over time. At the population scale, these fluctuations resulted in sudden population collapses and infection prevalence that was double the level observed under constant temperature with a similar mean. In community trials, thermal variation enabled higher densities of a secondary host (Ceriodaphnia) which often dilutes disease in this system. However, higher densities of this potential diluter did not reduce infection rates in Daphnia focal hosts in this thermally fluctuating environment. These results show that daily variation in temperature can alter host demography, host-parasite interactions, and the persistence of competing hosts. Ultimately, this multi-scale approach suggests that environmental variance can accelerate disease transmission and trigger population-level shifts that are not captured by traditional, constant-temperature frameworks or measurements on individual hosts.

Invasive Plant Species as Conduits for Pathogen Spillover Between Natural and Agricultural Systems

Presenter: Jason Sckrabulis

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Pathogen spillover between host species is a major driver of pathogen emergence in humans, animals, crops, and natural ecosystems. Many human pathogens reflect spillover from wild animal hosts to humans, forest pathogens have spilled over from ornamental plants, and novel crop pathogens have emerged via spillover from wild hosts. However, the mechanisms and eco-evolutionary dynamics of spillover, especially between plants and pathogens, are poorly understood. Invasive species might exacerbate spillover events because they can cross ecosystem boundaries, disrupt natural areas, and establish in disturbed ecosystems. We hypothesize that invasive plants, with dense populations at ecosystem boundaries, facilitate the eco-evolutionary dynamics of pathogen transmission between ecosystems. To examine this, we focus on a natural-agricultural ecosystem boundary with a recent emergence of a novel fungal pathogen of industrial hemp. The fungus Bipolaris gigantea has caused widespread epidemics on the invasive grass Microstegium vimineum in Eastern US forests for over 20 years. After legalization of hemp cultivation in 2014, there were massive outbreaks on hemp of the same pathogen occurring in the same region as diseased M. vimineum. Utilizing this system, we aim to (1) quantify the ecological drivers of pathogen transmission between ecosystems, (2) determine the role of pathogen evolution in disease emergence on novel hosts, and (3) develop eco-evolutionary infectious disease models for coupled natural-agricultural systems. Here, we present preliminary results of these aims: (1) empirically, we found higher levels of diseased tissue in larger plants, amplified by fertilizer addition but dampened with microbiome manipulation; (2) clonality enhances pathogen establishment under strong selection and limited migration, by facilitating adaptation to novel hosts and providing a demographic advantage; (3) pathogen persistence in plant litter (in addition to live tissue) does not necessarily increase pathogen spread as compared to a pathogen that cannot persist in litter.

Environment and Priority Effects Jointly Predict Multi-Pathogen Dynamics

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Forecasting disease epidemics may require understanding both abiotic and biotic contributors. Abiotic conditions influence dispersal, emergence, and infection potential, while biotic interactions between pathogen species can alter host susceptibility to subsequent pathogens, creating priority effects. Yet, the relative importance of environmental conditions and priority effects in predicting seasonal disease dynamics remains under explored. To disentangle these drivers and improve ecological forecasts of plant disease risk, we analyzed more than 41,000 plant-level observations of three foliar fungal diseases on the grass species tall fescue in North Carolina, collected from 2017–2024. We built temporally explicit random forest models which for two of our focal diseases accurately (>80%) predicted future disease dynamics from a complex abiotic and biotic predictor space. From these models, we identified key environmental tipping points that intensified annual epidemics. We then supplemented those models with Bayesian hierarchical models and survival analyses, which provided evidence that pathogen-pathogen interactions can be as important as environmental conditions in predicting disease risk. Furthermore, for two of our focal diseases, prior infection by a different pathogen facilitated the subsequent infection and the strength of this facilitation was modulated by environmental context. From this study we draw two major conclusions, one ecological and one methodological. First, knowledge of a host's current disease state may be as important as local environmental conditions for predicting disease dynamics. Second, by integrating complementary modeling approaches, we can develop both predictive forecasts and mechanistic insight into the biotic and abiotic drivers of infectious disease.

Quantifying Seasonal Avian Influenza Virus Transmission Among Dabbling Duck Species at a North American Stopover Site

Presenter: Monica Shah

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Outbreaks of Eurasian-lineage highly pathogenic avian influenza (HPAI) virus H5Nx clade 2.3.4.4b have been ongoing among North American bird populations since early 2022. Waterfowl, specifically dabbling ducks, have long been identified as part of the disease reservoir for avian influenza viruses (AIVs). Because AIVs are often detected in mallards, a species of dabbling duck, they are commonly studied as maintenance hosts, and this research has greatly informed our understanding of avian influenza dynamics in wild birds. However, dabbling ducks display varying life history behaviors and assuming that the ecology of AIVs in mallards extends to other waterfowl species may obscure important species-specific disease dynamics. Frequent detections of AIVs in mallards may be shaped by transmission from other dabbling duck species, and species-specific transmission warrants further investigation. We hypothesize that multiple interacting dabbling duck species are needed to maintain circulation of AIVs. One approach to identifying and quantifying cross-species transmission is to use mathematical models calibrated with species-specific data. We developed a multi-species susceptible, infected, recovered (SIR) model to represent transmission of H5 AIVs within and between seven dabbling duck species and used it to quantify disease dynamics in the Lake Erie Marshes in Northwestern Ohio, which is an important mid-continental migratory stopover site on the Mississippi Flyway. We calibrated our mathematical model using species-specific abundance data and influenza sampling data from the stopover site, allowing us to identify who acquires infection from whom during the spring and fall of 2023 and 2024. We calculated epidemiologically relevant parameters, including R0. This research quantifies transmission dynamics, identifies which duck species contribute to the maintenance community of the currently circulating HPAI H5 viruses, and determines how reservoir dynamics change seasonally. Understanding how cross species transmission contributes to pathogen persistence can inform targeted influenza A virus surveillance efforts and inform control.

The Effect of Dengue Infection and Relative Humidity on the Thermal Preferences of Aedes Albopictus

Presenter: Anna Shattuck

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Each year, mosquito-borne disease impacts more than 700 million people globally, causing over 1 million deaths. With rising global temperatures, mosquitoes have invaded new habitats outside their native ranges, shifting where transmission can occur and exposing new populations to risk. Understanding how ectotherms that vector disease, such as mosquitoes, respond to current and future environmental change has implications for their distributions and the transmission of mosquito-borne pathogens. When confronted with environmental change, ectotherms, can change their behavior to optimize the conditions they experience and fitness outcomes. In this study, we determine if female Aedes albopictus, an invasive species and vector of several arboviruses, are behaviorally optimizing the microclimate they experience while resting in lab conditions. We use a thermal gradient and computer vision to explore thermal preferences of mosquitoes across different humidity conditions. We also determine if thermal preferences of mosquitoes infected with dengue change throughout the infection cycle. If mosquitoes are selecting specific temperatures, this could fundamentally change disease transmission. Models used to predict changes in mosquito-borne disease in the face of climate change that do not account for mosquito behavior are likely over- and under-estimating suitability which could result in the misallocation of finite public health resources. By better understanding how mosquitoes are selecting habitats, we can target control efforts to specific habitats and populations at risk.

Maternal Age Effects on Offspring Virus Susceptibility and Infection Outcomes

Presenter: Clara Shaw

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The maternal environment is increasingly understood to modulate offspring phenotype, including susceptibility to infectious disease and disease outcomes. However, the mechanisms underlying this variation are often poorly understood, and the implications are rarely considered at the population level. In our study using the Caenorhabditis elegans-Orsay virus system, we quantified how the age of C. elegans hermaphrodites impacts offspring susceptibility and infection outcomes as well as virus amplification in populations seeded from early, intermediate, and late offspring. In this system, the +ssRNA virus transmits naturally among hosts via the fecal-oral route in petri dishes filled with nematode growth medium and lawns of bacteria (C. elegans food); the virus infects C. elegans gut cells and modestly reduces reproductive output. We first exposed offspring from young, middle-aged, and old parents to the virus and found that maternal age did not significantly affect offspring susceptibility, but that offspring from younger parents became more heavily infected and shed more virus compared to offspring from older parents. In a second experiment, we quantified the reproductive output of exposed offspring from young, middle-aged, and old parents. We found that exposed offspring from older parents had greater total reproduction than exposed offspring from younger parents. Finally, to explore population-level impacts, we collected ten offspring from young, middle-aged, and old parents, exposed them to the virus, and let populations grow and epidemics take their course. We found that populations derived from younger parents contained less virus than populations derived from older parents. We hypothesize that the more heavily infected early offspring reproduced more slowly due to infection, which could have resulted in smaller populations and smaller epidemics in populations derived from these animals. In our ongoing work, we are exploring the drivers of our findings.

Genetic Drift Acts Strongly on Within-Host Influenza Evolution but not Alone, Motivating Models of Respiratory Virus, Cancer, and Immune Interactions

Presenter: Yike Shi

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Understanding how viral populations evolve within hosts is essential for predicting pathogen adaptation, providing insights into the source of new strains at the population level, and interpreting how acute infections perturb host immunity. Here, we quantify the strength of genetic drift in Influenza A Virus (IAV) using the Beta-with-Spikes approximation applied to longitudinal intrahost Single Nucleotide Variant (iSNV) frequency data. Across natural infections, inferred within-host effective population sizes are small in humans (N_E=49) and swine (N_E=14.4), implying that stochasticity dominates within-host evolutionary dynamics in both host species. However, a small N_E estimation doesn't necessarily imply "drift-only" in the system. Wright-Fisher forward simulations at the inferred N_E recapitulate key aspects of human iSNV frequency changes, yet the swine IAV dataset shows statistical evidence for rejecting the classic Wright-Fisher model as the only process governing within-host iSNV frequency dynamics. These deviations imply other processes such as spatial compartmentalization of viral populations across respiratory tissues and/or skewed viral progeny production may be needed to explain the within-host IAV diversity. Together, these results highlight how early within-host infection and immune dynamics can drive heterogeneity in downstream outcomes. Building on this framework, we present preliminary work on how respiratory viral infections and vaccination might perturb cancer-immune dynamics through inflammatory signaling. Recent studies show that respiratory viral infections can trigger IL-6-mediated reactivation of dormant cancer cells, while augmenting early type-I interferon responses through methods such as mRNA vaccination can sensitize poorly immunogenic tumors to immune checkpoint blockade, facilitating tumor elimination. We outline an integrative approach combining infection, vaccination, cancer, and host genetic data with mechanistic modeling to study how the timing and magnitude of IL-6 and IFN-I responses modulate cancer progression. Together, these projects illustrate how stochastic, structured within-host infection dynamics can scale up to influence immune regulation and disease risk.

Burning Down the Mouse: Effects of Wildfire and Post-Fire Reseeding on Sin Nombre Virus Prevalence in Its Reservoir Host

Presenter: Carleen Silva

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Worldwide, physical habitats and biological communities are being reshaped by wildfire. Such changes have obvious potential to alter pathogen ecology, yet few studies have tested the effects of wildfire – or post-fire mitigation strategies – on pathogen prevalence in wildlife. Here, we quantified the effect of wildfire on the prevalence and intensity of Sin Nombre virus (SNV; Orthohantavirus sinnombreense) infection in western deer mice (Peromyscus sonoriensis) using a matched study design of burned, unburned, and aerially re-seeded sites in northern New Mexico. We screened 413 individual deer mice for SNV via RT-qPCR. Relative deer mouse abundance was significantly higher in reseeded sites compared to unburned sites but did not differ from burned sites; burned and unburned sites did not differ significantly. Similarly, SNV prevalence was significantly higher in reseeded sites than either burned or unburned sites, while prevalence did not differ between burned and unburned sites. Serendipitously, we were able to investigate the impacts of an El Nino Southern Oscillation (ENSO) cycle in a subsample of sites and found that SNV prevalence increased significantly post-ENSO. Sex-specific patterns varied by burn history: SNV prevalence was significantly higher in males than females in unburned areas but did not differ by sex in burned or reseeded sites. Male mice were more likely to be wounded and had higher wound counts than females, especially in reseeded sites. Our findings indicate that post-fire management practices may exacerbate SNV transmission in its reservoir host, an effect that should be considered when implementing such strategies.

A Modeling Framework for Cross-Species Transmission in Co-Roosting Host Communities

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Cross-species transmission can be facilitated by frequent and close contact among wildlife, such as widespread co-roosting behavior. Cross-species transmission is also driven by phylogenetic relatedness between host species, but the degree to which species relatedness drives transmission in the context of closely interacting co-roosting hosts is less understood. We developed a framework for understanding how cross-species transmission is driven by contact and phylogenetic relatedness between two- and three-host species co-roosting communities. Using ordinary differential equation models, we describe the net impact on roost-level infection prevalence from both susceptible–infected–recovered-susceptible and susceptible–infected–latent–infected models. We modeled interspecific transmission as a declining function of phylogenetic relatedness and otherwise parameterized models using co-roosting Neotropical bat systems. We varied both intraspecific transmission rates and phylogenetic relatedness while also factorally manipulating pathogen traits considering model structure. We found that phylogenetic relatedness between co-roosting hosts facilitates pathogen invasion, particularly when infection and immunity or latency periods were short and interspecific transmission was low. Additionally, roost-level prevalence was commonly greatest when species were more closely related. However, we also identified less-frequent instances in parameter space where roost-level prevalence increased when co-roosting species were more distantly related. Our framework can be used for other co-roosting, multi-species systems with pathogens that are directly transmitted and have low virulence. Overall, these generalizable models provide realistic scenarios for understanding community-level infection prevalence in co-roosting hosts and spillover risks.

How Many Drugs are Enough? a Branching Process Model for Evolution of Resistance

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The development of chemotherapeutic drugs such as antibiotics, antiviral drugs, and anticancer agents has revolutionized human and animal health, but the efficacy of these drugs are constantly threatened by evolution. Combination drug therapy, where multiple drugs are administered simultaneously to one individual, is one approach being used to prevent the emergence of drug resistance. However, adding more drugs to a combination is not always possible due to cost and potential side effects. This raises the question of how complex a mixture is necessary. While the precise answer to this question likely depends on numerous system-specific details, here we construct a general model to ask, how many uniquely acting drugs are sufficient to prevent the evolution of resistance within a host, and what are the key parameters for determining this number?

To address these questions, we developed a multi-type branching process model that describes the growth and evolution of pathogens within a host over time (noting that this same model can be applied to cancer). We use the analytical formulation of this process and a simulation-based approach to quantify the probability that resistance emerges over the course of various multi-drug treatment regimens. We define a threshold for what we consider to be “sufficiently effective” in preventing the emergence of resistance, and we use our model to explore parameter space and identify the key parameters that dictate the number of drugs needed to prevent resistance. Our preliminary findings suggest that the number of drugs required to prevent the emergence of resistance varies by system, but some parameters play a greater role in determining this threshold than others. Namely, the mutation rate and the population size at the start of treatment play key roles. Therefore characterizing these values for various systems may be critical to developing evolutionarily robust combination therapies.

Increases in Blastomycosis Incidence in Humans and Dogs by Ecoregion in Minnesota, 1999-2023

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Blastomycosis, an emerging infectious disease caused by inhalation of Blastomyces fungal spores, presents as a respiratory infection but can disseminate, causing severe disease with a mortality rate of 8-10%. Examining incidence changes across ecological regions may yield insights into climate or environmental profiles associated with endemicity and emergence. We analyzed surveillance data reported to Minnesota Department of Health (1999-2023) to assess trends in blastomycosis incidence rates (IRs) in humans and dogs across 7 EPA-defined ecological regions spanning wetlands, plains, and forests. 1,111 human and 2,825 dog cases were reported, and statewide incidence increased 1.6 times for humans and 3.1 times for dogs. The forest regions (N. Central Hardwood Forests and N. Lakes and Forests) comprised 80% of human cases (n=447 and n=443) and 88% of dog cases (n=900 and n=1589). IRs and ratios (IRRs) were highest in 2019-2023 compared to previous years, except N. Glaciated Plains, which has not reported a human case since 2004. Human IRRs (2019-2023 vs. 1999-2003) ranged from 1.7 (95%CI: 1.2-2.0) in N. Lakes and Forests to 9.4 in Lake Agassiz Plain (95%CI: 0.54-164), while dog IRRs ranged from 2.9 in N. Glaciated Plains to 21.0 in N. MN Wetlands. Compared to 2014-2018, recent incidence increased most rapidly for humans in W. Corn Belt Plains and N. Central Hardwood Forests (IRRs 2.7 and 2.4); dog incidence increased most rapidly in N. MN Wetlands (IRR: 2.7) and doubled in 4 regions: N. Central Hardwood Forests, N. Lakes and Forests, Lake Agassiz Plain, and W. Corn Belt Plains (IRRs: 1.9, 2.0, 2.2 and 2.2). These findings show that rising case numbers are a statewide concern for both humans and dogs. While forest regions dominate the epidemiology of blastomycosis in the state, increases across all ecoregions should motivate statewide control measures, such as awareness messaging, to facilitate earlier diagnoses.

Computational Evidence of Population Resilience Mechanisms in Banded Mongoose (Mungos Mungo) in Northern Botswana

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Infectious diseases can have critical impacts on wildlife populations, creating acute declines and threatening the persistence of species. These population impacts can be particularly important for group-living species. Banded mongoose (Mungos mungo) in northern Botswana are infected with a tuberculosis pathogen, Mycobacterium mungi, transmitted through olfactory communication.

In this study, two complementary modeling approaches are used to examine how questions about the influence of Allee effects and fusion events as compensatory behaviors on population persistence can be addressed. Results from the first model, a stochastic, age-structured compartmental model, reveal that Allee effects counterbalance disease-driven population declines and that fusion events further reduce the risk of extinction despite disease transmission risks. While these results provide a broad insight into the roles of density dependence and compensatory social behaviors, they cannot provide insight into heterogeneity and disease dynamics on an individual level.

To address these limitations, the second model – an agent-based model – is used to explicitly represent individual-level social behaviors and disease dynamics both within and between social groups. By comparing the questions and investigations supported by both modeling approaches, this research highlights how variation in modeling techniques and biological scales improves our understanding of population resilience in socially structured wildlife systems.

Estimating Slaughter Surveillance Coverage in the United States

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Detecting infected animals in disease systems like brucellosis or tuberculosis is challenging, especially in low prevalence settings, in part because animals may be cryptically infected. In the United States (US), slaughter surveillance is the primary mechanism for detecting infections like tuberculosis or brucellosis from free or low prevalence areas of the country. Although both beef and dairy herds are captured through slaughter surveillance, the geographic origins of animals at slaughter remain largely unknown. Therefore, it is challenging to evaluate whether current surveillance activities have sufficient geographic coverage to adequately detect cases of tuberculosis and brucellosis. To address this gap, we developed an analytical approach that delineates slaughter plant catchment areas (i.e., slaughter sheds). Our approach uses a spatial shipment kernel to link animal movement networks to slaughter plants. The current approach also allows for a probabilistic determination of whether an animal in each county will be slaughtered at any given slaughter plant in the US. Ultimately, slaughter sheds will help support the surveillance of low prevalence diseases in the US by enabling the development of data-driven strategies to optimize sampling efforts across plants. We expect that this tool will have application for any slaughter surveillance-based program activity.

Land Use Change: Implications for Host-Parasite Dynamics

Presenter: Ipsita Srinivas

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Human-driven changes are reshaping ecosystems worldwide, with profound consequences for the emergence and transmission of infectious diseases. Aquatic ecosystems are especially sensitive to anthropogenic stressors, which often alter community structure and, subsequently, disease dynamics. Deforestation, in particular, can alter water quality through increased allochthonous nutrient inputs, altering resource availability, with cascading effects on food webs and resultant shifts in consumer-host populations. Yet, causally linking these habitat-mediated changes to infectious disease outcomes remains challenging.

This is especially true for macroparasites with complex life cycles (CLC), where environmental drivers often act indirectly by restructuring intermediate host communities, producing unpredictable infection patterns. Furthermore, many CLC parasites rely on understudied aquatic invertebrates as intermediate hosts. Copepods - aquatic crustaceans - exemplify this challenge. These ubiquitous zooplankton serve as the first intermediate host for many macroparasites, yet ecological factors regulating their role in parasite dynamics remain largely overlooked. Given their use as indicators of eutrophication and importance in aquatic food webs, we ask: Can copepods serve as indicators of disease risk in human-modified ecosystems?

We took an exploratory first step at answering this question using Schistocephalus solidus, a helminth with a copepod intermediate host, as a model system. Using field surveys, digital droplet PCR, and a suite of nonparametric approaches, we investigated how deforestation and water-quality variation influence copepod populations and parasite infection across 38 lakes on Vancouver Island, B.C., a region with extensive commercial logging. Copepod densities were linked to increasing forest loss, potentially mediated by nutrient enrichment and shifts toward copepod-dominated communities. Helminth infections, however, were rare and showed weak, variable associations with land-use-driven changes, despite expectations for density-dependent transmission.

These findings reveal a potential decoupling between environmental drivers, host populations, and parasite infection, highlighting both the challenges - and opportunities - of identifying the mechanistic pathways linking land-use change to disease risk.

Spatial Patterns and Environmental Influences of Covid-19 Outbreaks in the United States, Post-Omicron

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The seasonality of many respiratory pathogen outbreaks, such as influenza and respiratory syncytial virus, is driven by climate factors, particularly specific humidity or temperature. COVID-19, a respiratory disease caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has resulted in significant global disease burden, including an estimated over 1 million deaths in the United States (US). While early regression analyses indicated a potential relationship between climate factors and disease transmission, evaluating such relationships early in a pandemic is challenging due the large size of the susceptible population. As COVID-19 shifts into endemic circulation, the shrinking susceptible population enables more robust assessment of climate influences impacting transmission. Here, we analyze US Emergency Department data to quantify state-level geographic variation in COVID-19 outbreak dynamics over three years, from April 2022 through March 2025. The US represents an interesting test case to study the climate-COVID-19 relationship because it spans temperate and tropical climates. We observe that outbreak patterns varied across latitude, with southern states experiencing larger summer peaks and northern states facing more evenly distributed summer to winter outbreaks or larger winter peaks. We find that specific humidity and temperature at the state level are significantly associated with observed differences in ED visits with a COVID-19 diagnosis, even after controlling for state-level variation in vaccination status. Our results indicate that climate contributes to shaping COVID-19 transmission dynamics as the US moves into endemic circulation, similar to other viral respiratory diseases exhibiting seasonal outbreaks. We anticipate these findings will provide a foundation for understanding the factors shaping SARS-CoV-2 transmission as COVID-19 becomes endemic in the US.

The Role of Population Bottlenecks in the Recovery of Small Populations Affected by Disease

Presenter: Alice Stitzer

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Emerging infectious diseases threaten global biodiversity and accelerate declines in wildlife populations. Yet, some populations persist despite severe disease-induced mortality and intense selective pressure. Understanding the mechanisms underlying persistence and species' capacity to adapt to these changes can provide insight into how pathogens drive evolution and regulate populations. In this study, we evaluate how selection pressure, bottleneck size, and immigration shape population recovery dynamics following the invasion of white-nose syndrome, a fungal pathogen that has decimated North American bat populations. We focused primarily on the population dynamics in small colonies of little brown bats (Myotis lucifugus) during the established phase of WNS (year of pathogen arrival > 3). We analyzed 50+ years of census data from 61 hibernacula sites in the northeastern and midwestern regions of the United States. We found that the bottleneck population size was a significant predictor of population growth, with growth rates increasing as the population bottleneck size decreased. Our analyses indicate that on average, small colonies (N<1,000) continued to experience negative population growth in the established phase of WNS (Œª = 0.98), whereas large colonies (N>1,000) experienced positive population growth (Œª = 1.05). Our data suggest that small colonies potentially lack adaptive traits that may have evolved in large colonies, thus leading to lagging population recovery in the established phase of white-nose syndrome. Elucidating these dynamics reveals the potential mechanisms for the persistence of small bat colonies and provides insight into how to best manage infectious diseases in wildlife populations.

Cuticular Microbiota Limit Pathogen Virulence Evolution in Drosophila Melanogaster

Presenter: Bengisu S. Subasi

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Pathogen virulence, the ability of a pathogen to reduce host fitness, is a fundamental aspect of infectious disease dynamics. Virulence is shaped by complex host-pathogen interactions, and host-associated microbiota can also mediate these interactions and influence virulence evolution. While some studies have examined the role of gut microbiota in pathogen virulence evolution, the role of cuticular microbiota remains largely unexplored.

Here, we investigated whether co-infection with cuticular microbiota affects pathogen virulence evolution in Drosophila melanogaster. We experimentally evolved an opportunistic pathogen, Providencia burhodogranariea, for increased virulence either alone or by coinjecting one of two common cuticular microbiota, Lactiplantibacillus plantarum and Acetobacter pasteurianus. Virulence increased across all treatments but evolved to significantly higher levels in the pathogen-alone condition. Using a virulence decomposition framework with evolved pathogens, we identified the pathogen traits underlying these virulence differences. Analyses revealed that microbiota limited the evolution of pathogen exploitation (infection intensity) but did not prevent the evolution of per parasite pathogenicity, the amount of damage caused by each individual pathogen to its host. This suggests that while microbiota can limit bacterial growth, they do not necessarily restrict the emergence of more harmful pathogen traits. To investigate the genetic basis of these phenotypic responses in evolved pathogens, we conducted whole-genome sequencing of both ancestral and evolved populations. Ongoing genomic analyses aim to identify mutations associated with pathogen virulence factors that are under selection through interactions with cuticular microbiota, potentially underlying microbiota-mediated limits on pathogen exploitation.

Our findings highlight the complex role of microbiota in shaping pathogen evolution and suggest that cuticular microbes may significantly influence pathogen virulence in host-pathogen systems.

Inferring Anatidae Connectivity from Occurrence Data Using Seasonal Migration Networks to Inform 2.3.4.4b H5nx Spread

Presenter: Sachin Subedi

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Migration is often inferred from sparse tracking data, uneven surveillance, or indirect ecological signals, which constrains robust quantification of population connectivity and the strength of exchange among locations. Here, we present Anatidae-focused migration-network framework that reconstructs movement corridors and hubs from widely available occurrence data, and demonstrates how these inferred networks can be used to used to interpret pathogen spread linked to migration. We build seasonal migration networks for Anatidae birds from citizen-science observations (e.g., eBird) by overlaying a spatial grid, summarizing community composition within grid cells, and connecting cells using a sparse k-nearest-neighbor graph. Candidate corridors are weighted using distance, community similarity (Jaccard index), and a directional orientation term that emphasizes north-south alignment. The primary corridor weight is W=“Angle”×“Jaccard”/“Distance” , with a sensitivity analysis using W=“Jaccard”/“Distance” . Directionality is imposed by migration season (spring: south to north and fall: north to south), and cell-level corridors are aggregated into region-to-region connectivity matrices (e.g., SUMW, EDGE_COUNT) that serve as quantitative predictors of downstream analysis. Applied across Europe, the inferred Anatidae network reveals consistent large-scale structure. Central-Western Europe acts as a connectivity hub with dense internal corridors, while Northern Europe forms a dominant latitudinal backbone with high-betweenness nodes, and these patterns persist under alternative weighting choices. In a downstream HPAI H5Nx phylodynamic analyses, Anatidae-derived connectivity is strongly supported as a predictor of inferred between-region transition rates, outperforming many environmental covariates and remaining robust across sensitivity analyses. Overall, Anatidae migration networks reconstructed from occurrence data provide an interpretable, scalable approach for quantifying migratory connectivity, identifying hubs and corridors, and generating actionable movement predictors for ecological and epidemiological inference.

Quantifying the Magnitude of Short and Long-Term Immunity Following Sars-Cov-2 Ancestral Booster Vaccination

Presenter: Rahul Subramanian

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Background and Aims of Study Understanding how prior exposures shape susceptibility to new variants has implications for public health responses to rapidly evolving viruses. Booster vaccination with the ancestral strain of SARS-Cov-2 can broaden protection by increasing antibody titers to new strains. However, it is unclear how long increases in titer last, how they differ in magnitude across strains and individuals, and how increases compare between binding and neutralizing titers. Here, we quantified the magnitude, duration, and breadth of immunity following 2-3 doses of ancestral mRNA vaccination.

Methods and Results We fitted stochastic mathematical models to neutralization titers from samples from two longitudinal cohorts of healthcare workers in Israel and the United States. One cohort consisted of many individuals with one sampling timepoint per dose, with a small subset sampled at multiple timepoints. The second cohort, for which both binding and neutralization titers were measured, mostly comprised individuals sampled at multiple timepoints per dose. Models were fit separately to each cohort to characterize heterogeneity and jointly to capture overall trends following each dose.

Our analyses indicated that the increase in binding titers after a second vaccine dose is broader and more durable than the corresponding increase in neutralizing titers, which decreases as a function of antigenic distance. A third ancestral vaccine dose broadens the immune response in the short-term with long-term variation across individuals shaped by demographic factors including gender and age.

Implications Our results provide insights on the durability of vaccine-induced cross-immunity, the extent to which that immunity decreases with antigenic distance, and the implications of repeated vaccination in the presence of viral evolution. We use these results to construct a multi-pathogen conceptual framework for immune imprinting. This framework can be directly extended to model the impact of different vaccination schedules and vaccine composition on disease burden.

Joint Impacts of Temperature and Water on Within-Host Dynamics and the Heterogeneity of Infection Intensity

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Climate change and emerging infectious diseases are primary drivers of global biodiversity loss. While the impacts of temperature on disease have been studied extensively, emerging evidence suggests that water availability, including precipitation and humidity, interacts with temperature to jointly shape pathogen-host dynamics. Both factors modulate host and pathogen life histories, yet few mechanistic models incorporate their joint effects or account for the interplay between within-host processes and between-host transmission. In this study, we developed a metabolic-theory-based model that integrates both thermal and water dependencies on infection intensity heterogeneity and within-host disease progression. We applied this framework to the Batrachochytrium dendrobatidis (Bd) system in the endangered California red-legged frog (Rana draytonii), a species currently threatened by rapid climatic shifts and fungal disease. Our model reveals three critical insights: (1) environmental conditions drive shifts in pathogen aggregation levels and host population dynamics; (2) thermal optimal mismatches between host and pathogen performance curves are primary drivers of outbreaks under specific environmental conditions; and (3) fluctuations in environmental variation versus shifts in environmental means exert distinct, non-linear effects on disease risk. These results underscore the necessity of an integrative modeling approach that accounts for the joint effects of temperature and water on both host and pathogen across scales. Our findings provide a predictive tool for conservation efforts in species vulnerable to the synergistic threats of climate change and disease.

Zika Virus in the Americas: A Decade of Surveillance, Gaps, and Future Public Health Response

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A decade after the 2016-17 Zika epidemic questions remain about how viral lineage diversification, geographic structure, and post-epidemic decline have shaped Zika's evolutionary trajectory in the Americas. Most previous phylogenetic studies have examined narrow spatial or temporal subsets of data, leaving continental-scale evolutionary and ecological patterns unresolved. We hypothesized that Zika's spread involved multiple lineage-specific expansion events originating from Brazil, each following distinct ecological and transmission pathways across the Americas. To test this, we compiled 756 near-complete Zika genome sequences from GenBank and GISAID, and paired them with case data reported to PAHO spanning 2015–2025. We quantified spatial and temporal gaps in genomic surveillance and reconstructed viral diffusion and demographic change using BEASTX and BEAST2, we reconstructed viral diffusion across space and time and estimated changes in the viral effective population size with an HMCSkygrid model. Effective population size dynamics revealed three major expansion phases: March 2014, September 2015, and September 2017. Phylogenetic inference identified four robust clades corresponding to distinct transmission clusters. Phylogeographic and BDSKY analyses indicated Brazil as the primary source population for subsequent continental spread, with each clade exhibiting unique dispersal routes and persistence patterns. Despite extensive epidemic transmission, genomic sampling declined sharply after 2018, limiting resolution of post-epidemic evolutionary processes. Together, these results reconstruct Zika's evolutionary and ecological landscape across the Americas, revealing lineage-specific spatial diffusion and demographic history. The work underscores how discontinuous molecular surveillance constrains inference about arboviral evolution and maintenance. Sustained, geographically inclusive genomic monitoring is essential to capture ongoing viral adaptation and anticipate future shifts in arbovirus ecology and epidemic potential.

Feeding Disease: Threshold Conditions for Bird Feeder-Mediated Epidemics

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Infectious diseases often spread through both direct contacts and environmentally mediated pathways, and the extent to which pathogens rely on each route shapes how they can be effectively managed. Mycoplasmal conjunctivitis in house finches is caused by Mycoplasma gallisepticum (MG), a host□dependent bacterium historically assumed to transmit mainly through direct contact because of its poor survival on environmental fomites and its specific nutritional requirements. However, recent work demonstrates that MG can persist on bird feeder surfaces far longer than expected, particularly at low ambient temperatures, reopening questions about the epidemiological relevance of indirect transmission in the wild. To address this question, we quantified MG decay rates on feeder surfaces across regionally realistic temperatures and incorporated these empirical data into an environmental□reservoir transmission model. We extended the Environmental Infection Transmission System (EITS) modelling framework to include three infectious compartments to capture deposition rates onto feeder surfaces that change over the course of infection, and included cleaning parameters to explore the impact of feeder surface cleaning interventions. This framework does not include direct transmission, since the goal of the study was to isolate the contribution of the indirect transmission pathway. We found experimentally that decay rates on feeder surfaces vary substantially across a natural temperature gradient, with cold conditions extending bacterial viability. Model outputs that include decay rates based on these experiments show that feeder□mediated transmission alone can generate epidemics under realistic ecological conditions and that typical cleaning interventions are unlikely to fully mitigate this risk. Unexpectedly, the model predicted that epidemics could occur not only at cold temperatures when decay rates are slow, but even at decay rates expected at temperatures common in spring or early summer. These findings underscore the importance of environmental pathways in wildlife disease dynamics and the need to consider these pathways when designing management strategies.

Real-Time County-Level Effective Reproductive Number (Rt) Estimates for Seasonal Respiratory Epidemics Using Hierarchical Generalized Additive Models

Presenter: Zachary Susswein

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Real-time estimates of the effective reproductive number (Rt) must be timely, local, and accurate to best inform decision-making and epidemic situational awareness. To estimate state-level Rt, CDC uses EpiNow2, a semi-mechanistic Bayesian model, and releases estimates for COVID-19, influenza, and RSV weekly. To scale tractably from approximately 150 state-level Rt estimates to approximately 9000 county-level Rt estimates, we developed a hierarchical generalized additive modeling (HGAM) approach and retrospectively evaluated predictive performance across the 2024-2025 respiratory virus season.

To evaluate HGAMs, we used real-time data snapshots to estimate Rt from projected emergency department (ED) visits for COVID-19, influenza, and RSV from November 2024 to March 2025 in 48 states and DC with data from the National Syndromic Surveillance Program. HGAMs incorporated smooth state- and county-level trends in ED visits, a location-specific nowcast correction for routine reporting delays, explicit spatial structure, and automated quality control for incidental reporting anomalies. Rt estimates were generated from posterior samples of nowcasted and forecasted incident ED visits, which were shifted in time to approximate incident infections. We scored real-time HGAM predictions against final ED visit data and evaluated performance relative to EpiNow2 estimates using the continuous ranked probability skill score (CRPSS) at the county and state levels; the county-level baseline was defined by population-scaled state-level EpiNow2 estimates.

HGAMs produced estimates for 9000 counties in the same runtime that EpiNow2 requires for 150 state-level fits (about 19 node-hours). HGAMs matched or improved on EpiNow2's state-level performance (18%, 37%, and –4% average improvement in one-week-ahead forecast CRPSS for COVID-19, influenza, and RSV, respectively), and improved on county-level performance (4%, 31%, and 11% average improvement), indicating that county-level data added predictive value. These results suggest HGAMs can produce timely estimates at fine spatial scales while improving predictive accuracy over current estimation procedures.

Picking a Fight: Investigating Aggression-Immune Trade-Offs in the Jamaican Field Cricket (Gryllus Assimilis)

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Life-history theory posits that organisms distribute limited resources among growth, maintenance, and reproduction. Male aggression may determine access to females and hence reproductive success, whereas immunity contributes to maintenance, ensuring survival and future mating. We hypothesize that there is a trade-off between investment in aggression and immunity. This trade-off could be realized through one of two non-mutually exclusive routes, with immune investment determined by either an intrinsic difference in male investment in these traits, or through direct costs of competitive interactions. This study investigates the nuances of the aggression-immunity trade-off in male field crickets, Gryllus assimilis, to determine, (i) whether the outcome of aggressive interactions is associated with baseline immunity, and (ii) how engaging in aggression affects future immunity. To investigate intrinsic costs of investing in aggression, I quantified male aggression and combined assays of cellular and humoral immunity to assess whether dominant males had lower baseline immunity compared with subordinate males. I found that baseline immunity does not predict fight outcome, where there was no significant difference between dominant and subordinate male immunity prior to fight engagement. In a separate experiment, males were subjected to three rounds of fights against a competitor. This provided a spectrum of fighting outcomes from which I can then assess the energetic trade-off of aggression and immunity across dominance hierarchies. Following fight rounds, hemolymph was collected and cricket immunity will be assessed using a suite of immune assays. I predict that males engaged in fights will have decreased immunity relative to control males, with the reduction more pronounced in dominant males. This work will provide an integrative assessment of the trade-off between aggression and immunity, contributing to our understanding of factors maintaining variation in immunity.

The Macroecology of Viral Coinfection

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Coinfection is common in wild animals, and can have profound consequences for disease outcomes and transmission. However, most research on coinfection is based on laboratory experiments or a few well-studied wildlife systems. Here, we use the testing data from the PREDICT project – the largest standardized wildlife disease surveillance project ever conducted – to describe patterns of viral coinfection, and evaluate their association with host, virus, and methodological factors. We find that coinfection is rare (detected in just 223 of 65,662 animals) but still more common than expected by chance – especially coinfections involving coronaviruses, paramyxoviruses, and influenza A virus. We further find that coinfection is associated with host age, but bats and rodents exhibit opposing relationships. Additionally, we find that host social structure could drive coinfection patterns, but our results show divergent effects between natural and un-natural settings. Specifically, we find that cave-roosting bats do not have a significantly higher rate of coinfection, but wild animals in captivity do – highlighting potential risks to wildlife and human health from the wildlife trade. Finally, coinfection patterns in the PREDICT data appear shaped by sampling and testing biases of the project. Future work could build on initial steps here by designing surveillance to more explicitly search for and report coinfection.

Modelling the Influence of Spatial Coupling on Pathogen Dynamics Between Natural and Anthropogenic Roosting Molossid Bats

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Among mammals with fission–fusion dynamics, bats have diverse roosting strategies. Different species show varying fidelity to specific roost types, and why they choose and change roosts is highly dependent on roost permanence, microclimate, social structure, and physiological requirements. Molossid bats show high plasticity to roost microclimate and structure, often using natural tree roosts and anthropogenic structures, which have highly contrasting attributes. While this can allow molossids to persist in heterogeneous environments, movement between natural and urban roost subpopulations (i.e., coupling) can influence pathogen dynamics and spillover events, as urban subpopulations have frequent human contact. We developed a susceptible–infected–recovered model, based on spatial coupling, to investigate how bat movement between tree and building roosts influences pathogen dynamics. Our model assumes different subpopulation sizes, driven by lower carrying capacity of tree roosts, and that time spent in the other subpopulation, as a function of movement rates between roost types, depends on bat density. We loosely parameterized our model around Molossus species that inhabit both roost types and assessed sensitivity to pathogen traits. In this system, movement sustains infection in both roosts. However, infection is more prevalent in the building due to its higher carrying capacity. A sensitivity analysis shows that pathogen prevalence in the building increases with higher return rate ($\tau = 0.9$). In contrast, the increased prevalence in the tree roost is obtained at lower return rates. Our modeling framework, which accounts for movement between subpopulations with variable roosting attributes, may better reflect high–risk human–wildlife interfaces. Ongoing efforts to quantify roost preference in molossid bats and effects on pathogen dynamics are fundamental to validating our model predictions. Although movement between two bat roost types is a simplistic approach, it provides novel insights into understanding differential movement and pathogen dynamics in wild bats.

Lagged Temperature Effects on Seasonal Mosquito Dynamics

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Mosquito life-history traits are influenced by temperature across all life stages. We consider a mosquito population modeling framework that allows for fixed delays in temperature-dependent birth, development, and mortality rates as a potential representation of lagged biological responses. By examining different combinations of delayed traits, we evaluate whether past environmental conditions help explain observed mosquito population dynamics. The model is informed by mosquito surveillance data and assessed using sensitivity and identifiability analyses.

Ecological Interactions in Malaria Coinfections

Presenter: Luna Taguchi

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Malaria infections can be caused by four different species of Plasmodium parasites. These species, which preferentially infect different ages of host red blood cells (RBCs), can often coinfect a host, with outcomes that depend on the specific species pair, and importantly, arrival order. Infection by the most common human malaria parasite, P. falciparum, which infects RBCs of all ages, leads to anemia and subsequent production of new RBCs by the host, an effect which is predicted to facilitate infection by P. vivax, which preferentially infects these young RBCs (reticulocytes). This prediction was supported by results amouse model system using two Plasmodium species with resource preferences that mimic the human-infecting ones. Specifically, the burden of P. yoelii, the reticulocyte specialist, increased when there was an established infection by the generalist P. chabaudi. This study looked at summary metrics for infections (e.g., cumulative parasite densities) and showed that at a broad scale, changes in resource availability were more important than changes in immunity for altering outcomes in coinfections. This leaves open the question of how these factors – and their relative importance – change over the course of an infection. In this project, I extend a previously published quantitative framework of cell-to-cell parasite propagation to explicitly allow for coinfection by two parasite species. Using this model, I dissect the temporal dynamics of resources and immunity in several infection treatment groups: single infection of P. yoelii, P. yoelii infection after phenylhydrazine treatment to kill RBCs, mixed species coinfection between P. chabaudi and P. yoelii, and P. yoelii infection followed by treated or untreated P. chabaudi infection. Understanding the temporal dynamics of resources and immunity could inform us on the role of arrival order and timing on coinfection outcomes.

Prior Pathogen Exposure Induces Higher Heterogeneity in Future Susceptibility Among Male Compared to Female Songbirds

Presenter: Katherine Talbott

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Individuals frequently encounter the same pathogens repeatedly. Combined with incomplete immunity, this often yields multiple infections in a host's lifetime. Previous work shows prior exposure to a pathogen increases population-level heterogeneity in susceptibility to future infection (the probability of infection given exposure), as many, but not all, individuals gain some immune protection. Critically, predictable differences in responses to initial pathogen exposure, for example sex-biased immune protection, could affect the process by which heterogeneity in susceptibility is generated. Here we asked whether accounting for host sex might reveal such differences in the relationship between prior exposure and heterogeneity in susceptibility to a future exposure. To address this question, we inoculated wild-caught, pathogen-naive house finches (Haemorhous mexicanus) sequentially with Mycoplasma gallisepticum (MG), a conjunctivitis-causing bacterium, allowing time for recovery between inoculations. During secondary inoculation, finches received one of four MG doses, allowing us to quantify heterogeneity in susceptibility using a dose-response approach. While prior MG exposure increased heterogeneity in susceptibility to a second inoculation across both sexes, this effect was more dramatic for males. These results indicate that among males, both the proportion of highly protected and highly susceptible individuals increased after initial inoculation. In contrast, among females, only the proportion of highly protected individuals increased after initial inoculation. These results raise a novel possibility: that males are less consistent than females in balancing opposing impacts of initial infection, specifically immune protection vs. resource depletion, which would reduce susceptibility among some, but increase susceptibility among others. Testing this hypothesis, and uncovering how such differences may arise mechanistically, would help predict whether such differences are likely to be widespread across taxa. Regardless of mechanisms, however, accounting for such sex differences in the relationship between prior pathogen exposure and heterogeneity in susceptibility to subsequent exposures may improve transmission models, especially when such models include demographic feedbacks.

Social and Ecological Traits Along with Network Structure Predict Viral Exposure in a Rural Human Population

Presenter: Itamar Talpaz

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Individual-level heterogeneity in exposure is fundamental to infectious disease dynamics, yet quantifying its drivers across multiple pathogens remains challenging, particularly in rural, low-income populations. In humans, demographic factors (e.g., age, household size) and social connectivity shape infection risk, but their interaction with pathogen traits remains unclear. Moreover, the structure of "who infect whom" networks provides information not captured by human or pathogen factors, yet network properties are rarely integrated into infection models.

Here, we use a unique bipartite human–virus network derived from serological evidence, describing the past exposure of 156 individuals to 61 viruses in rural northern Madagascar, a disease hotspot. The data includes demographic factors, connectivity (from GPS tracking), and viral traits (e.g., transmission mode, virion structure). We then use an XGBoost classifier to quantify the contribution of these factors to predicting exposure, incorporating also node degree as a structural predictor.

Our model outperformed random prediction (PR-AUC = 0.326, 6.63-fold improvement). Importance analyses identified virus degree (number of humans exposed), proximity to infected households, and human degree (number of viruses detected) as the strongest predictors. Since degree outweighed most factors, we further analyzed virus-specific models using only socio-demographics and co-exposure as predictors. Virus-specific models generally outperformed random (mean PR-AUC = 0.285), with the highest improvements observed for HSV-1 and Orf virus (fold increase of 2.00 and 1.70). The importance of human traits and co-exposure patterns varied among viruses. For example, economic factors and close contact explained HSV-1 exposure, whereas co-exposure with HRSV and HCMV explained Orf exposure.

Our work uncovers crucial factors affecting our ability to predict exposures in low-income human populations. While structure is a dominant factor in predicting viral exposure networks, host and pathogen traits still remain important from a single-virus perspective. This highlights the value of integrating both traits and structure in infection risk prediction attempts.

Cross-Species Transmission of Avian Influenza Between Wild Birds and Feral Pigs in Dynamic Environmental Systems

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Recent outbreaks of highly pathogenic influenza A (i.e. avian influenza) have severely impacted the poultry and dairy industry and resulted in human infections. However, avian species are not the only susceptible hosts to the influenza A viruses (IAVs). The 2009 H1N1 pandemic, caused by a reassortant swine IAVs, underscored the critical role of swine populations as mixing vessel reservoirs for IAVs and their potential to facilitate spillover events into human populations. While sporadic surveillance has provided limited evidence of avian-origin influenza virus infections in free-ranging wild pigs in the U.S., their extensive population and widespread distribution suggest they may represent an overlooked component of influenza ecology. There is a current gap in understanding where cross-species transmission may likely occur. In this study, we used a spatially explicit multi-species modeling framework for quantifying the risk of environmentally mediated avian influenza in the United States, considering imperfect detection and varying levels of surveillance efforts. Surveillance data for both wild birds and feral pigs were integrated at the watershed scale and linked to environmental metrics including surface water quantity, wetland availability and accessibility, hydrological connectivity, land-cover composition, and climatic conditions influencing viral persistence and host exposure. Our results show that the spatial and seasonal variability of environmentally mediated AIV presence is high, and that increased probabilities are linked to watersheds with dynamic surface water regimes, large wetland availability, and significant seasonal variation in habitat accessibility. The risk of cross-species transmission was consistently found to be higher in watersheds where feral pigs and wild birds use the same habitat. These findings highlight the significance of including multi-host surveillance data and seasonal environmental dynamics in national avian influenza monitoring frameworks. They also offer recommendations for focused surveillance that aims to identify environmentally mediated spillover risk early.

Using Phylogenetics to Predict Bat Species' Adaptability to White-Nose Syndrome

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Global change, including emerging zoonotic diseases, is forcing species to adapt or face extinction, making it critical to understand their physiological capacity to respond. Because evolution leaves a strong phylogenetic signal on species‚Äô traits, integrating physiological, behavioral, and morphological data within a phylogenetic framework can improve predictions of adaptive capacity by linking present responses to evolutionary history. Our research applies phylogenetic comparative methods to test the macroevolutionary predictability of hibernating bats‚Äô responses to novel threats, focusing on White-nose syndrome caused by the fungus Pseudogymnoascus destructans. Using cross-validated models informed by empirical data from known populations, we find strong phylogenetic signal in species‚Äô responses to infection, reflected in the fungal loads they can sustain. This work addresses a key gap in predicting pathogen vulnerability in New World bats and will extend to forecasting risk in currently uninfected species.

Coexistence, not Extinction: Tombusvirus Lycopersici and Its Defective Interfering Rna Di72 Form a Stable Equilibrium in Planta

Presenter: Anthony Taylor

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Defective Interfering (DI) RNAs are truncated viral genomes that arise during active infection and require co-infection with a functional wild-type virus to replicate, interfering with typical disease progression and transmission. Lacking most coding capacity, they exploit viral and host replication machinery and can replicate to high titer during infection. Evolutionary theory predicts that populations of “cooperative” wild-type genomes, which encode for proteins that are ultimately used as shared resources by all genomes, are vulnerable to invasion by these “defector” DIs that exploit the shared resources without contributing. DI RNAs, however, often seem to coexist with viral genomes. We suggest that this is possible because viral proteins likely provide synergistic (non-linear) benefits, like the majority of biological molecules, rather than additive (linear) benefits. Based on modelling data, non-linear dynamics can lead to a polymorphic equilibrium between cooperators and defectors under certain conditions. Here, we show a stable equilibrium between a plant virus and its prototypical DI RNA, using tomato bushy stunt virus (TBSV), its prototypical DI RNA DI72, and Nicotiana benthamiana plants. We infected plants via agroinfiltration of TBSV and DI72 infectious clones mixed in different ratios and sampled systemically infected tissues daily, using qPCR to determine viral and DI RNA quantities and the resulting ratio of DI72:TBSV RNA in the infected plants over time. Our results demonstrate that the ratio settles at an equilibrium around 7 days post inoculation irrespective of the starting ratio: hence, TBSV and its prototypical DI coexist at a stable polymorphic equilibrium.

A Comparative Transcriptomics Approach to Elucidate Differences in Chagas Disease Vector Capacity Among Rhodnius Species

Presenter: Ibukunoluwa Tella

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Chagas disease is caused by the parasite Trypanosoma cruzi, which is primarily transmitted by blood-feeding insect vectors known as kissing bugs. Within the kissing bug genus Rhodnius, two sister species (R. prolixus and R. robustus) exhibit clear differences in ecological behavior and vector capacity despite being separated by less than 1.5 million year of divergence. R. prolixus readily colonizes human dwellings due to its adaptation to drier, warm microclimates, making it a major vector of Chagas disease. In contrast, R. robustus sporadically colonizes human dwellings, and prefers cooler, moist microclimates, and is not considered a major Chagas disease vector. We hypothesize that physiological differences associated with vector capacity are encoded in the genomes of the two species that can be detected at the transcriptomic level.

To test this hypothesis, we generated and analyzed a whole organism RNA-seq dataset (5 replicates per condition) comprised of mild and moderate dehydration stress treatments for both species. Genome-wide analysis of gene expression profilers under these conditions revealed hundreds of genes that differ in expression between these two species. Genes upregulated in vector R. prolixus relative to the non-vector R. robustus are enriched in adaptive immune response, response to bacteria, and histamine binding. In contrast, genes upregulated in the non-vector R. robustus relative to the vector R. prolixus are enriched in cuticle structure, chitin structure and binding, extracellular matrix, and reproductive processes. These results provide important insights into the molecular processes involved in kissing bug vector capacity and can potentially inform future mitigation strategies.

Pathogen Invasion and Establishment Modifies the Effects of an Environmental Driver of Disease

Presenter: Ellie Timmins

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Climate is a key factor that drives disease emergence, establishment, and impacts. However, in newly emerged pathogens, the effects of climatic variables may change as hosts and pathogens co-evolve. Using over a decade of climate and infection data from the emerging disease of bats, white-nose syndrome, we find that humidity mediates fungal growth, tissue invasion, and host survival, but effects shift across invasion phases and interact with temperature. During pathogen invasion, warmer temperatures and drier conditions increased fungal loads, whereas tissue invasion appeared unaffected by environmental conditions. However, as the pathogen established, the influence of both temperature and humidity on fungal loads diminished, but dry conditions increased the degree of tissue invasion, except when fungal loads were low. Correspondingly, dry conditions also decreased survival. Over time, changes in the pathogen or host may have magnified the importance of humidity, likely because white-nose syndrome kills hosts through excess evaporative water loss, targeting environmental moisture as an important gradient by which evolution could occur. Collectively, these findings demonstrate that environmental drivers of disease are not static, but can shift as pathogens invade and establish, with important implications for understanding and predicting disease outcomes.

Social Resurrection: Social Interactions and Restoration of Disturbed Bumble Bees Microbiota

Presenter: Ravi Timsina

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Eusociality represents a major evolutionary transition. Eusociality, and social living more generally, have several associated benefits but also counter costs, affecting their evolution. The ecological dominance of eusocial insects suggests advantages of group living, including reduced predation risk, better resource utilization, and increased tolerance of adverse conditions. Conversely, costs include greater likelihood of pathogen transmission due to individual proximity and high relatedness. However, little attention has been given to the transfer of beneficial microbes among group individuals as an additional benefit of sociality, including those that help defend against disease. Both intrinsic, including host immunity, and extrinsic factors, including infection and antibiotic exposure, can disrupt the structure and functioning of a beneficial microbiota, leading to dysbiosis. We hypothesize that sociality can maintain a healthy gut microbiota, with social interactions facilitating the spread of beneficial microbes or resurrecting beneficial microbial communities following dysbiosis. Using the bumble bee Bombus impatiens, we test this hypothesis by disturbing a focal individual's gut microbiota through a stimulation of host immunity or antibiotic treatment. Subsequently we expose these focal individuals to solitary or social settings, before assessing gut microbiota structure and health effects. We show that in solitary situations, dysbiosis of benefical gut communities is persistent. However, dysbiotic gut microbial communities are resurrected by social interactions, and predict that this will be accompanied by associated health benefits. This work furthers our understanding of host-microbiota relationships, including how social transmission of beneficial microbes may favor the evolution of social living.

Filtering Disease: Do Eastern Oysters Exhibit a Dilution Effect for Hematodinium Perezi in Blue Crabs?

Presenter: Megan Tomamichel

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Disease dynamics are shaped by interactions between hosts and pathogens and by the broader ecological community. A central question in disease ecology is whether increased community complexity reduces infection risk through the dilution effect or instead amplifies disease impacts. Filter-feeding organisms such as Eastern oysters (Crassostrea virginica) may play a key role in aquatic disease dynamics by removing pathogens from the water column and altering local environmental conditions. The parasitic dinoflagellate Hematodinium perezi causes substantial mortality in juvenile blue crabs (Callinectes sapidus). We tested whether oyster presence and density reduce transmission of H. perezi to juvenile blue crabs using complementary field and laboratory approaches. Two field experiments were conducted in the waters along the Eastern Shore of Virginia, USA, a region of naturally high disease prevalence. In the first experiment, uninfected juvenile crabs were deployed across treatments with high oyster density (162 oysters m,Åª¬≤), low density (81 oysters m,Åª¬≤), and no-oyster controls. The second experiment assessed the ability of natural oyster reefs to reduce H. perezi transmission by deploying uninfected juvenile blue crabs within 2m of an established natural oyster reef and along a mud flat as a control. In parallel, laboratory transmission trials manipulated oyster density (0.7 oysters L,Åª¬π, 0.35 oysters L,Åª¬π, and zero oysters). Field experiments revealed no significant differences in disease prevalence among oyster density treatments. However, the natural reef experiment coincided with low transmission (12% overall prevalence), limiting inference regarding reef effects. In contrast, laboratory experiments demonstrated strong density-dependent reductions in infection, with zero prevalence in high-density oyster treatments, 10,Äì16% prevalence in low-density oyster treatments, and 21,Äì66% prevalence in no-oyster controls. Together, these results suggest that oysters can suppress H. perezi transmission under some conditions consistent with a dilution mechanism, but that environmental complexity in the field may modulate or overwhelm this effect.

The Role of Livestock in Shaping Rift Valley Fever Dynamics

Presenter: Beth Tuschhoff

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Rift Valley fever (RVF) is an emerging zoonotic disease that can have detrimental consequences for livestock and human health. It is often characterized by infrequent major epidemics followed by long interepidemic periods with low-level virus circulation. Mechanistically, major epidemics are thought to be triggered when large rainfall events result in mass mosquito emergence and population expansion. However, because RVF transmission into humans relies on infection and multiplication within livestock, the dynamics of immunity within livestock populations may also play an important role. We investigated if and when livestock population dynamics influence the occurrence of epidemics by studying compartmental models in which livestock birth rate responds to the availability of green vegetation (e.g., NDVI). Our analyses demonstrate that livestock population dynamics contribute to the origin and timing of RVF epidemics. We additionally demonstrate that RVF dynamics in livestock depend on life history traits, such as gestational period and lifespan, or management practices that affect such traits, indicating that livestock herd composition and practices may impact RVF dynamics. While mosquitoes play an important role in RVF persistence and epidemic dynamics, we show that it is also important to consider livestock.

Take the Ibex by the Horns: A Mechanistic Basis for Sarcoptic Mange Dynamics in Iberian Ibex Populations

Presenter: Marta Valldeperes

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The increasing studies on wildlife diseases have been shifting interest towards wildlife conservation focusing on intervention and management actions to minimize epizootic's consequences in host populations. Descriptions of mechanistic processes driving wildlife diseases systems are of significant value for understanding host-pathogen dynamics and assessing management strategies. However, this framework based on modelling-before-acting is not yet deeply rooted in the wildlife community. Here, we propose a mathematical model for the well-studied and challenging case of the Iberian ibex (Capra pyrenaica) and sarcoptic mange (caused by Sarcoptes scabiei) to inform and guide species disease management and research. Using an extensive body of published literature and field expertise, we developed a mechanistic model characterizing important properties of host-pathogen interactions for ibex-mange. We created a state-based deterministic model segregating ibex by sex and using their seasonal behavior to shape transmission events. We performed two different sensitivity analysis to assess the relative importance of parameters included in the model: partial rank correlation coefficient and extended Fourier amplitude sensitivity test. The resulting five-year model showed an infection peak at two years after mange detection with 42.0% of individuals affected, and a total population decline of 86.2% by five years. These epidemiological outcomes are comparable to field observations. Sensitivity analysis demonstrated strong monotonic relationship for most parameters, and that output variability arose almost entirely from interactions among parameters. Our model represents a fair mechanistic description of sarcoptic mange in Iberian ibex, including seasonal mating behaviors. This research forms a foundation for quantitatively assessing strategies for management actions against sarcoptic mange in Iberian ibex, and can potentially be translated to other mountain ungulate species. We illustrated modelling feasibility with parameter uncertainty requiring little modelling experience willing to inspire and motivate wildlife managers and researchers to endeavor this line of work.

A Preliminary Assessment of Population Genetic Structure of Rabies Reservoir, Desmodus Rotundus, in Colombia

Presenter: Paige Van de Vuurst

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Rabies virus (RABV) is a neglected tropical pathogen in Latin America predominantly transmitted to mammals by the common vampire bat (Desmodus rotundus). Transmission of RABV among D. rotundus individuals and colonies is a function of individual dispersal between colonies, patterns of which can be inferred from population genetic structure. Nevertheless, a baseline assessment of population genetic structure among D. rotundus individuals has been lacking for some areas of South America, including Colombia, where RABV has impacted some areas more heavily than others. To assess individual dispersal and hence population structure of D. rotundus across heterogenous landscapes in Colombia, we conducted a cross-elevational assessment of population genetic variation using nuclear microsatellite DNA markers. We quantified genetic variance and geographic distribution of genetically clustered D. rotundus individuals across the landscape of Colombia with reference to a comparator group of individuals from Mexico. Our results indicate that D. rotundus is mobile within the region, potentially contributing to RABV transmission among colonies. Our results also support previous hypotheses ecological resistance-mediated patterns of dispersal for D. rotundus, and inform future research on the role of genetic connectivity in RABV transmission among bat colonies.

Parasite-Induced Hormonal Manipulation Associated with Severe Reproductive Costs in a Wild Male Primate

Presenter: Medhavi Verma

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Parasitism is a ubiquitous life history strategy and a major driver of host evolution. Yet, remarkable heterogeneity across parasite-host systems has led to gaps in our understanding of the more cryptic dimensions of these relationships, such as parasite manipulation. Extreme examples of parasite manipulation of host behavior to promote host death, and therefore transmission, have been well characterized. However, parasites can also manipulate hosts in more subtle ways that benefit their own fitness and may still impact host fitness. Experimental research has shown, for example, that the larval parasite Taenia crassiceps promotes aromatization of host testosterone to estradiol, which enhances its own growth while also diminishing male host reproductive success. The observation of this strategy in nature has been stymied by the challenges of quantifying fitness while integrating hormonal and health data in wild populations. Here, we harnessed longitudinal and cross-sectional data on wild geladas (Theropithecus gelada) infected with the larval tapeworm Taenia serialis to determine if similar mechanisms are at play in other Taenia species and in naturalistic settings. We demonstrated that infected male geladas had 65% higher plasma estradiol ($p < 0.001$, $n = 36$) and a 151% greater risk of losing reproductive access than uninfected males ($p < 0.01$, $n = 103$), translating into ~1.5 fewer lifetime offspring for these males. Contrary to expectations, males maintained plasma testosterone levels ($p = 0.765$, $n = 36$) and showed increased fecal androgen metabolites ($p < 0.01$, $n = 185$). This points to compensatory mechanisms that may have developed in the evolutionary arms race between parasite and host.

Urbanization and Vector-Borne Parasitism in Overwintering Sparrow Assemblages

Presenter: Taylor Verrett

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Affiliation: University of Oklahoma

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Urban habitat use can alter disease dynamics in wildlife by influencing contact with parasites and susceptibility to infection. Land-use changes associated with urbanization may structure parasite transmission by altering the distribution of arthropod vectors and/or by moderating host immunity (e.g., increased susceptibility due to urban stressors or decreased susceptibility due to abundant anthropogenic resources). We investigated how urbanization drives patterns of vector-borne parasite infection in migratory birds by collecting infection data from overwintering sparrow assemblages across rural, suburban, and urban habitats in central Oklahoma, with an emphasis on locally common Dark-eyed Juncos and Harris's Sparrows. We sampled birds during both winter and pre-migration spring, when infection patterns are expected to be governed by distinct seasonal processes (pre-migration immunosuppression and active vector transmission). We use PCR and serology to test birds for West Nile virus (WNV) infection as well as microscopy and PCR to test for haemosporidian infections (e.g., avian malaria). Using generalized linear mixed effect models, we tested how urbanization (quantified using the Global Human Modification index) affects parasitism across seasons, predicting that infection prevalence and intensity will be higher in urbanized sites because of habitat-related stressors, especially before spring migration. Between 2022 and 2024, we found haemosporidian infection dynamics were affected by both land-use and season. Infection prevalence was higher closer to spring migration and in urban and suburban habitats, but birds wintering in suburban habitats had less intense infections prior to migration. Our ongoing research contributes an additional year of sampling in 2025, WNV diagnostics, and the quantification of seasonal vector activity across sampling sites using carbon dioxide traps. This study provides insights on how vector-borne disease dynamics may respond to urbanization in tandem with seasonal stressors in songbirds, which is timely given the rapid expansion of urbanized landscapes and high dispersal potential of migratory birds.

Coccidioidomycosis Epidemiology and Seasonality, Utah, 2009-2023

Presenter: Gabriella Veytsel

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Coccidiomycosis, or Valley fever, is a respiratory illness caused by inhaling spores of the fungus Coccidioides immitis. While 20,000 cases of Valley fever are reported annually in the United States, the true case burden is estimated to be 10-18 higher. Understanding the incidence and geographic distribution of coccidiomycosis cases is urgently needed to inform public health. Although the range of C. immitis is constrained by environmental factors, the distribution and seasonality of the disease are poorly understood in moderately endemic areas such as Utah. The most recent study in Utah described cases reported through 2015; however, environmental and anthropogenic changes are rapidly increasing the host range of C. immitis and human exposure. In this study, we characterize the epidemiology of Coccidiomycosis in Utah between 2009-2023 and describe trends at the state and county levels. Time series models were used to assess seasonality and included air temperature and precipitation. A total of 1,302 coccidioidomycosis cases were reported to the Utah Department of Health and Human Services during 2009-2023, including 442 associated hospitalizations (34%) and 16 deaths (1.2%). Among cases, 687 individuals were aged 65 years or older (52.8%) and 719 were immunocompromised (55.2%). Washington County in southern Utah, where St. George has become the fastest-growing metropolitan area in the U.S., reported the highest number of cases (n=547). The highest county-level incidence occurred in Daggett County (80.74 cases per 100,000), the least populous county in Utah located in the northeastern corner of the state, representing approximately 27 times the cumulative statewide incidence. Most cases were reported in summer (n=547), with the fewest in winter (n=435). Time-series decomposition suggested seasonality in cases, however precipitation and temperature were not significantly associated with case counts. Improved awareness, reporting, and clinical testing are essential to improve our understanding of Valley Fever and improve patient outcomes.

Human Behavioral Dynamics and Vector Awareness Shape Aedes-Borne Disease Transmission: An Evolutionary Game Theory Approach

Presenter: Santiago Villamil-Chacón

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Aedes-borne diseases like Dengue threaten nearly half the global population, and vector control remains the primary tool to reduce transmission. Public health agencies promote strategies targeting water storage practices to reduce mosquito breeding sites. These strategies likely trigger adaptive responses driven by disease awareness and vector abundance. However, because vector population dynamics change much more slowly than disease dynamics, it remains unclear whether these non-pharmaceutical interventions are effective. We developed a coupled transmission model for vectors and humans incorporating adaptive human behavior using evolutionary game theory. Individuals adopt cooperative vector control practices or defect according to replicator dynamics. Two awareness types modify the payoff matrix: disease awareness (proportional to the fraction of infected individuals) and vector awareness (proportional to mosquito abundance). We explored four game structures (Prisoner's Dilemma, Stag Hunt, Snowdrift, Harmony) and incorporated seasonal variability using temperature-dependent parameters from ERA5 daily temperature data in Thailand and Colombia. We find steady states are more sensitive to vector awareness than disease awareness, likely due to different timescales between epidemiological and vector dynamics. When disease awareness is maximum, oscillatory equilibria emerge promoting cooperation and larger parameter regions yielding low case counts across all games. The Prisoner's Dilemma simulates the highest disease incidence for any combination of awareness levels. Seasonal transmission shows higher disease incidence at lower elevations, promoting cooperation. We find less seasonal amplitude variability in incidence across latitudinal gradients. We conclude that vector awareness critically shapes cooperative behavior and transmission control more than disease awareness alone. As disease dynamics occur faster we hypothesize disease awareness is less effective promoting cooperation and vector control. These findings suggest public health campaigns should shift from outbreak-responsive interventions to year-round water management practices.

Seasonality of Sarbecovirus Seroprevalence in Cambodian Horseshoe Bats

Presenter: Charlie Voirin

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Bats are reservoirs for many highly virulent viral zoonoses such as coronaviruses, henipaviruses, and filoviruses, and there is evidence that these viruses shed into the environment seasonally in times of acute nutrient and reproductive stress. Horseshoe bats (Rhinolophus spp.) in Southeast Asia are thought to be the specific reservoir for the sarbecovirus subgenus of Betacoronaviruses which show the highest sequence homology to SARS-CoV and SARS-CoV-2. Despite this clear importance, very little is known about the seasonal infection dynamics of Sarbecoviruses within wild bats in this region; studying these bats in the wild thus provides an opportunity for both public health surveillance and inference into enzootic Sarbecovirus transmission and shedding. To this end, we collected blood samples and fecal swabs from bats in Cambodia every other month from 2021 to 2022, and again from 2024 to 2026. Subsequently, all blood samples were assayed on the Luminex platform to detect seropositivity to a panel of Sarbecovirus spike proteins. Over 500 bats from 4 different species of Rhinolophus were sampled over the duration of this project. We found that Sarbecovirus seroprevalence ranged from 50-90%, depending on species of bat and season of sampling. Seroprevalence increased across all species in the dry season (December to April), potentially indicating increased transmission due to reduced immunocompetence caused by resource limitations. This work highlights the high seroprevalence of Sarbecoviruses in this system as well as the importance of long-term surveillance projects. In the future, we aim to incorporate paired measures of viral prevalence and develop a mechanistic model of bat Sarbecovirus transmission, to gain a better understanding of how season and location may impact infection dynamics and thereby spillover risk.

How are Endangered Frog Populations Recovering from Chytridiomycosis?

Presenter: Jason Walsman

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Emerging infectious diseases threaten diverse host species but, fortunately, rapid evolution of hosts can help mitigate these threats through evolutionary rescue. Unfortunately, evolutionary rescue from an infectious disease requires understanding the evolving mechanism of host defense to guide management actions and improve predictions for the rate of recovery. The evolving mechanism of host defense can be identified through extensive common garden testing of host lines sourced from naïve and recovering populations, but these data can be hard to collect, particularly for an endangered host species. These problems are exemplified by a devastating fungal pathogen, Batrachochytrium dendrobatidis (Bd) that has driven declines and extinctions in numerous amphibian species worldwide. Endangered Mountain Yellow-Legged frog populations are variously extirpated, sparse, or recovering from Bd with some evidence for frog immune evolution but of unknown mechanism. A solution is found in new theory for dynamic mean and standard deviation of individual frog infection loads that gives strong, qualitatively distinct predictions for how different immune mechanisms affect this mean and standard deviation. We fitted a stochastic version of this model to a substantial but noisy field dataset from Mountain Yellow-Legged frogs (>500 abundance and >3900 infection load measurements across nine populations) and competed hypotheses for frog recovery. We found strong, quantitative support for the hypothesis that frogs are evolving resistance to pathogen growth that turns on late in infection but does not have immune memory. This hypothesis resoundingly beat the others, e.g., tolerance mechanisms such as tissue repair or acquired resistance mechanisms such as antibodies. These findings inform efforts to manage and predict frog recoveries, unfortunately contraindicating immune priming of captive bred frogs, an ongoing intervention for Mountain Yellow-Legged frogs that relies on the presence of immune memory. More broadly, this approach provides powerful ways to improve our inferences about host-pathogen dynamics from field data.

Surviving Maternal Infection During Lactation: Post-Infection Energetic Deficit Explains Increased Mortality – a Modeling Study

Presenter: Jasmine Wang

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Lactation is among the most physiologically and energetically demanding life stages in mammals. Compared to pregnancy, the drastic metabolic and immunological changes in lactating mothers are poorly understood. These adaptations potentially come with trade-offs that impact maternal resilience upon perturbations such as infection.

Informed by experimental data showing significant weight loss and increased mortality in lactating mice after resolution of maternal Yersinia pseudotuberculosis (Yptb) infection, we built an ordinary differential equation-based bioenergetic model incorporating the dynamic energy budget theory to simulate maternal energy utilization in lactation, maintenance, and immunity. We aimed to explain subsequent maternal and offspring survival.

Simulations showed that lactating mice had significantly decreased maximal spleen Yptb loads compared to nulliparous controls (mean=4.9e+5 vs. 1.5e+6 CFU/g spleen, respectively) and cleared the infection faster (Day 9 vs. 12 post-infection) by mounting faster and more robust immune response (peak energy expenditure in immunity=11.5 vs. 10.3kJ/day). The increased immune response by lactating, infected mice induced more severe anorexia (~75% decrease in daily food intake compared to healthy lactating mice), while nulliparous infected mice only decreased food intake by 40% compared to their healthy counterparts. This energy intake deficiency, combined with increasing milk demands by pups, led to significant reductions in body reserve biomass and decreased maternal survival, even after bacterial load was controlled. Litter mass of these lactating, infected mice also stayed significantly lower than those of healthy controls. Each of these predictions was consistent with experimental data.

Further explorations of parameter space revealed differential optimal energy allocation strategies for prioritizing maternal or offspring survival during energetic deficiency. Our model showed new potential for utilizing conceptual bioenergetic frameworks to evaluate energy utilization optima and life history trade-offs during lactation upon perturbations. Such models may prove informative for understanding infectious disease dynamics under the simultaneous energetic challenges of reproduction and immune defense.

Estimating Vaccination- And Infection-Induced Protection Accounting for Heterogeneous Exposure Histories

Presenter: Yintong Rita Wang

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Estimating protection against influenza infection is challenging because immune protection is not directly observable and depends on individual exposure histories, with each exposure modifying responses to subsequent ones. However, most methods for estimating vaccine protection from observational data do not explicitly model past exposures or how immune effects interact or wane over time. To overcome those limitations, we developed a stochastic mechanistic model that uses longitudinal data on PCR-confirmed infections, vaccinations, and antibody titers to separately estimate protection induced by vaccination and infection while accounting for interactions between exposures. The model decomposes protection into titer-mediated and non-titer-mediated components with boosting and waning dynamics. Modeling antibody titer dynamics enables inference of unobserved infections. Experiments with synthetic data show that parameters of interest can be estimated through a partially observed Markov process framework (panelPomp). We will apply this model to longitudinal household data from the Household Influenza Vaccine Evaluation (HIVE) study. Models such as this could serve as a robust method for estimating vaccine effectiveness given heterogeneous population immunity.

Within-Host Interactions Affect Both Parasite Density and Fecundity with Compounding Effects on Transmission Potential

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Coinfection can have profound effects on parasite fitness. To understand the consequences of coinfection for disease transmission, prior work has largely focused on how within-host parasite interactions shape parasite density. Yet simultaneous effects of these interactions on parasite traits, like fecundity, may exacerbate or weaken the effects of coinfection on disease transmission. Here, we conducted a systematic meta-analysis of 124 experimental coinfection studies involving helminths interacting with other helminth or non-helminth parasites. We used these data to test whether coinfection shapes parasite fecundity and density in similar ways, and to identify ecological mechanisms governing these effects. Overall, coinfection was associated with reductions in both parasite fecundity and density, and the ecological principles used to predict density effects in prior work also applied to fecundity. Negative effects were explained by: (1) infection order (priority effects) and (2) niche overlap between coinfecting parasites (i.e., shared space use, resource use, or host immune responses). Resource competition, especially for blood, was associated with particularly strong, negative effects of coinfection on parasite fecundity. Importantly, coinfection was associated with similar effects on density and fecundity across studies, and this relationship was stronger for parasites with greater niche overlap. Combining density and fecundity to approximate the compound effects of coinfection on transmission potential, we found that simultaneous negative effects of coinfection on density and fecundity nearly doubled the attenuating effects of density alone. Although often overlooked, effects of coinfection on parasite traits are similarly important to effects on density, and ignoring them risks missing key consequences of coinfection for disease dynamics.

Co-Occurrence of Endemic, Expanding, and Invasive Tick Species Across an Urban Gradient

Presenter: Fu Wen

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Urban landscapes increasingly support multiple human-biting tick species associated with distinct health risks, including Lyme disease caused by Borrelia burgdorferi and vectored by Ixodes scapularis, and alpha-gal syndrome linked to Amblyomma americanum. However, how these vector species assemble and co-occur along gradients of urban intensity and through time, and whether there are direct or indirect (via host) interactions among them remain poorly understood. Here, we examined co-occurrence patterns of nymphal I. scapularis (native, endemic), A. americanum (native, expanding), and Haemaphysalis longicornis (non-native, invasive) across New York City–Long Island (NYC–LI) using standardized drag sampling conducted from 2023 to 2025. We collected >22,000 nymphal ticks across the study period, with the most extensive spatial coverage in 2023. To account for unequal sampling intensity across years, we implemented complementary spatial and temporal analyses within a co-occurrence–based species distribution framework. Spatial co-occurrence was assessed using 2023 data which captured a more extensive gradient of housing density, landscape connectivity, and ecoregions, while temporal dynamics were evaluated using 45 parks sampled consistently from 2023–2025. In spatial analyses, I. scapularis and A. americanum co-occurred more frequently than expected in low housing-density, high-connectivity parks, particularly within the Pine Barrens ecozone, whereas H. longicornis occurrence showed weak association with either native species and was more common in highly urbanized or low-connected contexts. Conditional probabilities indicated declining A. americanum occurrence given I. scapularis presence with increasing urbanization. Temporal analyses revealed post-2023 declines in I. scapularis and A. americanum nymph density, while H. longicornis remained comparatively stable. Together, these findings demonstrate that urbanization structures multi-species tick assemblages and motivate the development of a combined indicator for mapping tick species richness and co-occurring risk across urban regions.

Disease-Associated Mortality Reduces Yukon River Chinook Salmon Escapement: A Novel Method for Quantifying Parasite Suppression of Host Populations

Presenter: Mark Wilber

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Parasites can suppress host populations through parasite-induced mortality. However, we have few existing tools for quantifying the magnitude of parasite-induced mortality in wild populations. This is especially true for many “misfit” ’ parasites that do not fit into standard classifications (e.g., fungal-like parasites and myxozoans). As such, we are limited in our ability to include the effects of parasites in fish and wildlife management strategies. Chinook salmon (Oncorhynchus tshawytscha) are a species of immense cultural and ecological significance and populations are declining across much of their range. In the Yukon River, Alaska, USA, episodic outbreaks of the ichthyosporean parasite Ichthyophonus have been linked to declines, but population-level effects of Ichthyophonus on Yukon Chinook remain largely unknown. We developed a novel model that leverages changes in parasite intensity distributions to quantify the magnitude of disease-induced mortality occurring in host populations. We used it to address two questions: i) Is parasite-induced mortality occurring in Chinook? ii) What are the drivers of spatio-temporal variability in parasite-induced mortality? Using three years of surveys along the Yukon River, we quantified the magnitude and variability in Ichthyophonus-induced mortality in Chinook. We found evidence that Ichthyophonus was responsible for between 8%-16% mortality of the migrating Chinook population and could account for nearly 40% of natural mortality in Chinook. We also found that variability in mortality among years could largely be explained by differences in parasite acquisition in the marine environment rather than differences in in-river infection dynamics. Our model was developed as part of a project to estimate the proportion of fish at risk for mortality to inform annual management on the Yukon River. Moreover, the model is broadly applicable to other fungal-like ‘misfit’ parasites of conservation concern, where improved estimates of parasite-induced mortality could be used to predict parasite suppression of host populations.

Novel Management of Haemaphysalis Longicornis Using Baling:

Presenter: Syd Wilson

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In recent years Haemaphysalis longicornis (a.k.a. Asian Longhorned Tick or ALT) has been introduced into the United States, expanding rapidly and continuing to thrive with minimal success in control. Current measures for management are lacking, largely focused on other tick species with differing biology and show low effectiveness against ALT. We attempt to exploit the biology of this specific tick with paired laboratory and field experiments that utilize the fermentation process of forage baling to provide tick management. In the baling process, forage is cut and dried, initially reducing tick refugia and increasing solarization. We anticipate substantial tick mortality during rapid fermentation following bale formation, with high peaks in temperature and acidity that, with current literature values, indicate we may see substantial tick mortality. Initial field results promise high mortality for all in field specimens, though lab results give a conflicting story, indicating the microenvironment within the bale may be more complicated than initially thought. We conclude initially that mowing and baling impacted pastures may improve ALT control.

Sources of Stochasticity Shaping Within-Host Viral Evolution in Acute Respiratory Infections

Presenter: Wenfei Xiao

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The ecological and evolutionary dynamics of populations, including infectious diseases, are known to be jointly shaped by deterministic and stochastic processes (Coulson et al., 2004). The role of noise in population-level infectious disease dynamics has been rigorously explored in the last two decades. At the within-host scale, however, most models for viral dynamics remain deterministic in their formulation. While this may be reasonable for understanding within-host viral population dynamics, recent studies have shown that viral allele frequencies can change dramatically over the time course of days. These findings have led to a conclusion that within-host viral evolution is strongly impacted by stochastic processes (McCrone et al., 2018). Here, we use stochastic mechanistic models to explore the role of noise in shaping observed patterns of virus evolution in acute respiratory infections, with a focus on influenza A virus. We first summarize ways in which environmental stochasticity can be biologically realized in these acute infections. We then examine a within-host model incorporating both target cell depletion and an innate immune response and consider environmental stochasticity acting on various parameters, including the viral infectivity rate and the viral clearance rate. We further consider correlations between stochastic effects that two viral variants may experience due to their spatial localization. We find that a model incorporating environmental stochasticity and some degree of correlation between stochastic effects can reproduce key features of allele frequency changes observed in longitudinally sampled infected individuals. Our results underscore the importance of environmental stochasticity in not only driving infectious disease population dynamics but also viral evolutionary dynamics at the within-host scale.

Evidence of Enteric Pathogens and Their Antibiotic Resistance Genes Escaping Wastewater Treatment Plants in Riverine Microbial Communities

Presenter: Olivia Yancey

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Wastewater treatment plant (WWTP) discharge acts as an important junction where human-associated pathogens, antibiotic resistance genes (ARGs), and environmental communities mix. WWTP effluent continuously introduces allochthonous microbes to aquatic ecosystems enriched in mobile ARGs relative to less anthropogenically-disturbed communities, creating infinite opportunity for persistence of resistant pathogens and horizontal transfer of ARGs into native microbial communities. Riverine environments are also a key point of convergence for wildlife and humans, who can be exposed during recreational activities or insufficient drinking water treatment. Here we surveyed cefotaxime-resistant Escherichia coli and vancomycin or erythromycin- resistant Enterococcus spp. in the influent, effluent, and receiving environments of a cross section of WWTPs across Virginia during spring, summer and fall. Antibiotic-resistant E. coli and Enterococcus CFU counts ranged from 0-21 CFU/mL in effluent wastewater and 0-130 CFU/mL in downstream surface water. Across sampling events and at most sites, the percent of positive cefotaxime-resistant E. coli and vancomycin or erythromycin- resistant Enterococcus was higher in downstream surface water compared to upstream. These results suggest that the mixing of WWTP effluent tends to amplify antibiotic resistance. Elevated resistance was observed in both Gram-negative and Gram-positive human enteric genera, suggesting this phenomenon may be common across multiple microbial species. WWTP size and performance could provide an avenue to reduce inputs of ARB and ARGs to aquatic environments. For example, 7.9% of E. coli in a small poor-performing WWTP's effluent grew on media containing cefotaxime, in comparison to 0% from large high-performing urban WWTPs. Additional analyses (i.e., metagenomics, microbial source tracking, heavy metals analysis, antibiotic analysis) are underway to further understand sources and drivers of clinically-relevant antibiotic resistance in surface waters. This research will advance understanding of ecology and evolution of ARB and ARGs in riverine environments and possible means to reduce their spread.

Hidden Reservoirs of Xylella Fastidiosa: Prevalence in Wild Hosts Surrounding Grapevine Regions in the Eastern Usa

Presenter: Yang Jingjing

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Xylella fastidiosa is a devastating xylem-limited, insect-transmitted bacterial pathogen with a global distribution and a host range exceeding 720 plant species. Its increasing emergence in southern Europe, which threatens diverse agricultural sectors, is largely attributed to the repeated introductions of contaminated plant materials from the Americas. While its impact on commercial crops like grapevines, peaches, plums and citrus is well-characterized, the prevalence of the pathogen in surrounding native flora, such as forest trees and wild understory plants, poses a continuous risk of spillover. Identifying these “hidden” wild reservoirs is critical to predict the risk of emergence of new Xylella fastidiosa-caused crop diseases and develop appropriate biosecurity policies and management practices. In this study, we assessed the prevalence and genetic diversity of X. fastidiosa across wild plant communities adjacent to vineyards and orchards in 6 states throughout the Eastern USA. A total of 126 samples with symptoms indicative of X. fastidiosa infection were collected through fieldwork in Virginia and by collaborations at regional extension centers. Pathogen detection and characterization were performed using real-time qPCR, metagenomic sequencing, and culturing followed by genome sequencing. Our results reveal an unexpectedly high prevalence of X. fastidiosa across the surveyed geographic range, with a 95% infection rate among collected samples as determined by qPCR. Notably, we identified poison ivy (Toxicodendron radicans) growing adjacent to a vineyard as a novel host for X. fastidiosa subsp. multiplex. The high infection rate and the identification of new species as reservoirs suggest substantial inoculum pressure on vineyards. These results suggest the need for integrated commercial crop management and the strategic implementation of buffer zones to minimize spillovers. Improved understanding of wild reservoirs is essential for refining vector control strategies and mitigating the biosecurity risks posed to grapevine production worldwide.

Epidemiology and Control of H5 Avian Influenza in a Conserved Pelican Population

Presenter: Qiqi Yang

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The ongoing epizootic of highly pathogenic avian influenza (HPAI) continues to cause massive deaths in wildlife, in addition to large-scale culling of livestock and occasional human infections. Fundamental understanding of its disease ecology in natural populations is urgently needed. This knowledge has been hindered by the difficulty of acquiring relevant data in migratory wild bird populations. Here, using data collected from a conserved population of Dalmatian pelicans (Pelecanus crispus) in Greece, we recover the epidemiological and evolutionary history of one of the largest HPAI wildlife mortality event, using a combination of mathematical modelling and phylogenetic analyses. The results show that this devastating outbreak was likely seeded by a single introduction two weeks before the first death was observed; and the outbreak is highly linked with other outbreaks in the same species in other countries (Albania and Romania), sharing the same evolutionary source. Additionally, by estimating the epidemiological features of this ‘natural experiment’ of two outbreaks in the same population, we show that the viral fitness of clade 2.3.4.4b increased in 2022 with higher transmissibility and longer viral shedding. This demonstrates that virus fitness difference is a key factor to the expanded epizootic in 2022, complementing evidence from virus challenge experiments in the lab. In 2022, carcasses were removed with the hope of reducing infections. Surprisingly, it is shown to have little impact on mitigating the mortality, based upon the well-calibrated model. This provides first field evidence on highly debated HPAI management strategies in wildlife populations. The model also predicts that current H5 vaccines relying on capture and injection to deliver cannot establish herd immunity in a wildlife population, underlining the importance of novel HPAI vaccine development for wildlife.

Heat-Sensitive Pathogens in a Warming Word: Effect of Thermal Fluctuations, and Potential for Adaptation.

Presenter: Yang Yang

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Affiliation: University of Maryland; College Park, MD; United States

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Warming temperatures and more frequent heat-wave events are changing disease dynamics. While warming is often associated with increased severity and spread, there is growing that evidence for some pathogens, high heat can lead to reduced disease severity and transmission. However, predicting the impacts of heat-waves on the dynamics of heat-sensitive pathogens requires knowledges in two areas: 1) Do pathogens have the capacity to evolve increased heat-tolerance? And 2) What role do fluctuations in temperature have on disease severity and transmission? To address the first question, we quantified thermal performance of 8 strains of a heat-sensitive fungal pathogen (Microbotryum lychnidis-dioicae) from wild plant populations (Silene latifolia) distributed across an elevational gradient. While pathogen strains differed significantly in their infection ability at high temperatures, indicating evolutionary potential for thermal adaptation, no significant signature local adaptation to elevation of origin was found: strains originating from high temperature environments did not have higher thermal tolerance than strains from low temperature environments. To answer the second question, we used growth chambers to investigate how variations in day and nighttime temperatures influenced transmission potential. High daytime temperatures consistently triggered temporary curing of infected hosts, while cooler nighttime temperatures slowed this process. Together, these results suggest that increasing summer heat-wave events will likely reduce disease transmission and potentially extirpate disease from warmer habitats, with little chance of “evolutionary rescue.”

Plastic Pollution Amplifies Schistosomiasis Risk by Altering Snail Host Life-History

Presenter: Ao Yu

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Plastic pollution is increasingly recognized as an ecological driver of mosquito-borne disease by creating productive freshwater breeding habitat, yet its effects on other medically important freshwater disease vectors remain poorly understood. In particular, how plastic pollution influences the population dynamics of freshwater snail hosts critical to schistosomiasis transmission is largely unknown. In Bulinus truncatus, the obligate host of urogenital schistosomiasis, plastic pollution could alter key life-history processes through biofilm-derived nutritional subsidies, habitat modification, and physiological stress. We performed two laboratory experiments that investigated the effects of macro- and microplastics, individually and jointly, on Bulinus truncatus' life history traits (survival, growth, egg mass production, hatching) by using environmentally realistic sizes, polymers, concentrations, and biofouling status. To assess the overall impact of plastic pollution on snail demography, we derived a measure of reproductive output under each treatment, i.e., the expected number of cumulative viable offspring produced over the experiment. We found that macroplastic boosted somatic growth, egg mass production, and hatching, consistently playing the most critical role in the expected reproductive output increase. Microplastics reduced hatching success but improved survival and growth, resulting in a marginal population decline. Combined micro-macro plastic exposure generated the positive but attenuated gains, driven by biofilm-derived nutritional subsidies that elevated survival, growth, and egg mass production while mitigating microplastic-induced hatching costs. Our findings show that plastic pollution can potentially boost Bulinus truncatus population growth, which has implications for cercarial shedding and transmission risks. These results provide mechanistic insights into how plastic pollution may influence Bulinus population dynamics and underscore the importance of integrating environmental plastic debris management into schistosomiasis control.

Heterogeneity of Airborne Virus Transmission in the Built Environment

Presenter: Yizhi Zhang

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The COVID-19 pandemic accelerated recognition of airborne transmission of infectious diseases. Despite improved mechanistic understanding, our ability to predict the risk of infection in a given scenario remains limited owing to high heterogeneity in factors involved in disease transmission. The goal of this work is to quantify variability in factors that control risk of airborne virus transmission in the built environment. Using SARS-CoV-2 as a model, we conducted a narrative review of selected literature on transmission via inhalable respiratory particles (<100 μm). We divided transmission into three key processes: emission of virus in respiratory particles from an infected individual (the source) into the air; transport and decay of virus in the environment; and deposition and infection in a susceptible new host. Among the source-related factors, we found large variabilities spanning 7 or more orders of magnitude. For example, the rate of bioaerosol emission from an infected individual ranges from ~1 to > 10□ particles/s, depending in part on respiratory activity types and individual physiological factors. Unexplained inter-individual variations, such as those defining “superemitters”, introduce additional uncertainties. We also found considerable variability in the physical and biological decay of virus-laden particles, as they move from the source to a susceptible new host. Studies report that the air exchange rate, which controls physical loss of particles by ventilation, ranges from ~0.3 to > 20 air changes per hour in typical residences. Lastly, upon inhalation, the quantity and site of aerosol deposition vary with the physiological state of the susceptible new host. The new host’s immunological status further influences whether infection is established. Taken together, even with full information on individual physiological and environmental conditions, predicting overall risk of infection remains highly challenging due to the combined effects of variability in key determinants.

Changes in Individual Susceptibility Across Reinfection Histories Shapes Epidemic Dynamics

Presenter: Kejia Zhang

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Epidemics unfold in heterogeneous populations. Individuals differ in susceptibility due to inherent attributes and behavioral responses that change with infection histories. Previous studies of outbreak intensity have shown that heterogeneity in susceptibility can reduce epidemic size compared to homogeneous models. Moreover, real-time changes in behaviour can lead to transient reductions in susceptibility driving reductions in epidemic intensity, transient oscillations, and/or epidemic plateaus. Integrating susceptibility into infectious disease models typically focuses on dynamics occurring within a single outbreak. For diseases where immunity is not lifelong, we expect that heterogeneity may have additional impacts on endemic dynamics as recovered individuals lose immunity and become susceptible (or partially susceptible) again. Here, we develop a unified framework to explore how behavior shaped by infection history influences population susceptibility and disease dynamics. To do so, we introduce a resusceptibility mapping that explicitly characterizes how susceptibility changes following waning immunity, integrating heterogeneous susceptibility with Erlang-structured waning immunity. This approach captures how susceptibility cohorts shift over time as immunity wanes and behaviors adapt, offering a structured way to interpret the population-level consequences of infection history and behavioral change. Our framework highlights how shifts in susceptibility and waning immunity create conditions under which behavior during reinfection can further shape epidemic outcomes, including shifts from oscillatory to stable endemic states. We also share perspectives on how these shifts in long-term dynamics are influenced in cases where both susceptibility and transmissibility covary - during and between outbreaks.

Characterize Molecular and Antigenic Evolution of Avian Influenza Virus H5 2.3.4.4b in North America

Presenter: Xinyi Zhou

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Since the 2021 emergence of H5 clade 2.3.4.4b in North America, intensive surveillance has generated plenty of antigenic data. However, these experimental results have yet to be systematically analyzed in a quantitative framework. In this study, we combined Hemagglutination Inhibition (HI) assay data consisting of 278 test antigens collected from Feb 2022 until Feb 2025 with publicly available HA sequences to characterize the virus's molecular and antigenic trajectories over the past four years. Antigenic cartography revealed that 2.3.4.4b antigens do not cluster chronologically, a finding consistent with the non-linear antigenic evolution recently observed in the H5 subtype. We estimated a substitution rate of 4.992 x10^(-3) substitutions/site/year and an antigenic drift rate of 1.27 units/year, which are similar with those of human seasonal influenza virus. While we detected a moderate correlation between genetic and antigenic distances, the other possible contributing factors have not been fully explored. These results underscore the urgent need to identify the underlying ecological and biological drivers of phenotypic evolution in avian influenza to better inform zoonotic risk assessment and vaccine strain selection.

Adaptation of Malaria Parasites Through De Novo Copy Number Variations Studied Through Long-Read Sequencing

Presenter: Julia Zulawinska

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Plasmodium falciparum is a protozoan parasite largely responsible for human malaria deaths. Despite continuous attempts to find a reliable antimalarial treatment, the parasite easily develops resistance to newly introduced drugs. Changes in gene copy number are an important adaptive strategy for these parasites, contributing directly to drug resistance and fitness. Apart from “common” CNVs that occur widely in parasite populations under drug selection, our group has observed distinct CNVs at various locations across individual parasite genomes. We hypothesize that these relatively rare “de novo” CNVs prepare the parasite for future stressors and may be an important source of genetic diversity. To study de novo CNVs, we propose a bulk ONT long-read sequencing approach followed by an automated CNV calling and a manual single-read visualization. Because long reads often cover entire duplicated regions (>50kb or tens of genes), we can assess CNV boundary sequences to uncover mechanisms of generation and change over time. Here, we evaluate the basal rate of de novo CNVs in parasites grown in standard media and assess how exposing the parasites to different types of sublethal stress increases the de novo CNV rate. Through these investigations, we have uncovered a positive relationship between CNV frequency and replication stress, and a pattern of AT-richness at CNV boundaries. This provides invaluable information as we seek to understand how the Plasmodium genome adapts and evolves to confer new phenotypes. The long-read sequencing approach can be employed for any organism, including cancers and other microorganisms, to facilitate investigations of CNV emergence and analysis of complex structural variations.

Context-Aware Machine Learning for Differential Classification of Dengue, Zika, and Chikungunya in National Surveillance Data

Presenter: Carol de Souza Moreira

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Accurate classification of dengue, Zika, and chikungunya in surveillance systems remains a major challenge in regions where these arboviruses co-circulate and laboratory confirmation is incomplete. Rule-based case definitions and clinical diagnoses often fail to account for epidemiological context, leading to systematic misclassification and biased estimates of disease burden. Using Brazil's national surveillance system (SINAN) as a case study, we developed probabilistic multi-class classification models for dengue, Zika, and chikungunya that output diagnostic probabilities rather than binary labels. Clinical features such as demographics, symptoms, and laboratory results are combined with contextual predictors, including recent incidence, reconstructed susceptibility, force of infection, spatiotemporal clustering, and climate variables. Model development employes a variety of machine learning approaches and was extended to Bayesian additive regression trees to capture nonlinear interactions while quantifying uncertainty. Laboratory-confirmed cases were used as reference observations for supervised learning, while uncertain and clinically diagnosed cases were incorporated using label-noise-robust methods and explicit modeling of misclassification probabilities. Model performance was evaluated using discrimination metrics (AUC, F1), calibration metrics (Brier score and expected calibration error), and epidemiologically relevant predictive values under realistic prevalence scenarios. Cross-validation and temporal–spatial holdout validation assessed transferability across regions and epidemic phases. Interpretability analyses quantified the contributions of clinical and contextual predictors, enabling translation of model outputs into public-health-relevant insights. This work demonstrated that incorporating epidemiological context into machine-learning models substantially improves diagnostic classification in arboviral surveillance systems. The proposed approach provides probabilistic, context-dependent diagnostic predictions, offering a scalable methodology for improving burden estimation and informing outbreak response for co-circulating arboviruses and other febrile diseases.

Cascading Effects of Functional Connectivity on Tick Hazard and Host Pathogen Infection Status in a Highly Urban Environment

Presenter: Marie Lilly

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Tick-borne hazards are increasing in urban areas yet it is unclear how urban landscape structure and host communities influence emergence. Blacklegged ticks transmit multiple pathogens of human health concern, including Borrelia burgdorferi (Lyme disease agent) and Babesia microti (babesiosis agent). White-footed mice (hereafter 'mice') are both the dominant host for juvenile blacklegged ticks and for B. burgdorferi and Ba. microti. Small less connected habitat patches tend to enhance mouse population density and therefore the dilution effect predicts a negative relationship between connectivity and tick-borne hazards. However, we previously demonstrated a positive effect of functional connectivity on occupancy of blacklegged tick reproductive hosts, the white-tailed deer, and of deer occupancy on density of nymphs and density of pathogen infected nymphs. Here we describe how these links are mediated by pathogen host communities. We used structural equation models to identify causal pathways between urban landscape structure, tick hazard, host traits, host community, and host hazard (host infection status and tick burden). We surveyed host-seeking nymphal blacklegged ticks and live-trapped mice and meso-mammals at 12 highly urban greenspaces in New York City, NY (2023-2024) with varying levels of functional connectivity. In contrast with predictions of the dilution effect, increased functional connectivity strongly increased density of nymphal blacklegged ticks, the density of B. burgdorferi infected ticks, and the probability of mouse B. burgdorferi and B. microti infection. Host infection with B. burgdorferi additionally increased the likelihood of its coinfection with Ba. microti, consistent with previous findings that B. burgdorferi facilitates Ba. microti infection. Host traits additionally influenced both mouse tick burden and infection status. Meso-mammal community parameters were not significantly associated with mouse infection. Through this study, we novelly identify causal pathways by which functional connectivity increases tick and host hazard in a highly urban landscape.

Isolation of a Reassortant Jamestown Canyon Virus, Flanders Hepavirus and Various Insect-Specific Viruses Across Virginia.

Presenter: Krisangel Lopez

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Arthropod-borne pathogens are among the leading causes of morbidity and mortality worldwide. As we start to experience the effects of climate change and the range expansion of viable disease vectors, establishing a known baseline of vectors and pathogens is integral in developing proper management strategies for disease outbreaks. The state of Virginia has a diverse ecological landscape which, spans from coastal swamps to mountainous ranges. This diverse landscape enables us to test how differences in landscape features may influence vectored pathogen dispersal. We surveyed three sites across Virginia: including the Coastal Plain (swamp), Piedmont (savannah), and Blue Ridge Mountains (primary forest) for one week every month from May until October of 2022. Mosquitoes were collected using CO2 baited CDC light- and gravid- traps, and were sorted into pools by trap type, date, and species. A total of 7899 mosquitoes were collected and sorted into 974 pools. Pools were screened for viruses via cytopathic effect assays in three cell lines (Vero-76, BHK-21, and C7/10) at three different incubating temperatures (37□ C, 30□ C, and 28□ C, respectively). We used a diagnostic PCR with pan-Flavi-, pan-Bunya-, pan-Alpha- virus primers to identify virus families, and amplicons were sequenced to identify pathogens. We isolated three vertebrate viruses including Jamestown Canyon virus, Flanders Hapavirus, and a novel Rhabodovirus. In addition, we have isolated 58 insect-specific viruses including multiple Culex Flaviviruses. Several of the viruses that failed initial identification methods were sequenced and identified using next-generation sequencing. We will report on the phylogenetic characteristics and host-pathogen associations observed during our state-wide vector surveys. This study will shed light on the immense unknown viral diversity across the state and can aid public health officials in developing risk assessments for Virginia and neighboring states.

Evolution of Cell-Fate Regulation and Phenotypic Plasticity for Bacteriophage in Fluctuating Environments

Presenter: Tapan Goel

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Temperate phages have two alternative life cycles ‚Äö√Ñ√¨ lysis, which involves the synthesis and release of viral progeny at the expense of host cell lysis, and lysogeny, which involves the integration of the viral genome with that of the host and vertical viral transmission through host replication. The probability of lysis or lysogeny depends on host, viral, and environmental factors - including multiplicity of infection (MOI). For example, classic work on phage lambda shows that lysis is more typical in singly-infected cells and lysogeny becomes more likely as MOI increases. However, the functional relationship between the MOI and the propensity for lysogeny may depend on the phage-bacteria system. To examine the drivers of these functional relationships, over the near- and long-term, we explore the eco-evolutionary dynamics of temperate viruses in periodic environments with varying levels of host availability and viral mortality. We use a non-linear coupled differential equation model to simulate periodically-forced dynamics that separate a growth phase and a filtration phase in which a fraction of virus particles and lysogens survive. Using this model we show how conflicting selection pressures can favor lysis in the short-term and lysogeny in the long-term. In doing so, we identify a range of conditions in which fixed temperate strategies can outperform obligately lytic or lysogenic strategies. We also demonstrate that temperate strategies can mitigate against the potential local extinction of viruses in stochastically fluctuating environments. Finally, we investigate the evolution of phenotypic plasticity and explore how different forms of environmental fluctuations select for different functional responses between MOI and propensity for lysogeny.

Post Job Opportunities Here

Presenter: Job Board

Coauthors: Contact Job Board

Affiliation: EEID

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