University of Vermont Research Week

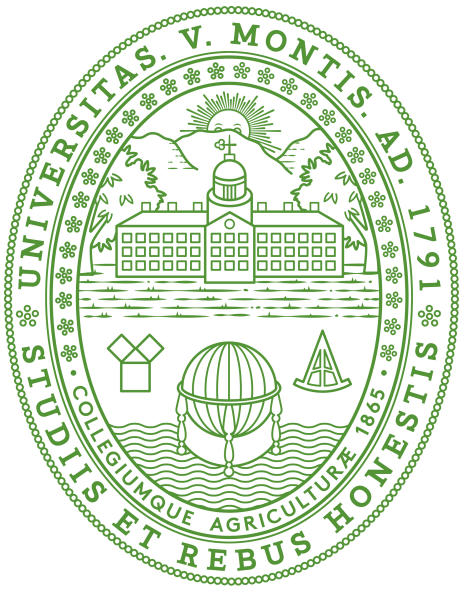
Postdoctoral Research Showcase

Friday, April 21st 2023

2:00 pm — 6:00 pm

MedEd 200 and MedEd Pavilion

Presented by the UVM Postdoc Association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About

UVM Postdoc Association

The mission of the University of Vermont Postdoctoral Association (UVM PDA) is to promote a culture reflecting the University of Vermont Common Ground and six core competencies identified by the National Postdoctoral Association to facilitate professional development, broaden the training experience, and foster a vibrant, open, and collaborative community for all postdoctoral scholars at UVM. We also advocate for postdocs by working with the UVM administration to promote adoption of competitive salary and benefits in line with national guidelines and by connecting with local professional and academic institutes, societies, and organizations.

The primary goals of the UVM PDA and its Executive Committee are to be a common voice for postdoctoral scholars at UVM; build a strong and well-defined postdoctoral community through professional and social networking; provide diverse professional and career development opportunities for postdoctoral scholars; and foster interaction between the UVM PDA, local professional and academic institutes, societies, and organizations.

2023 Postdoctoral Research Showcase

In conjunction with the University of Vermont's Office of the Vice President for Research, the UVM Postdoctoral Association is pleased to host our annual Postdoctoral Research Showcase to highlight the creative and scholarly works of our scholars. The showcase celebrates the professional development, broad training experience, and the vibrant, open, and collaborative community of UVM's postdoctoral scholars.

PDA Executive Committee

Brandon Bensel	Chair	*Molecular Physiology and Biophysics*
Rebekah Honce	Secretary	*Medicine: Immunobiology*
Mikaela Fudolig	Webmaster and PR Officer	*Vermont Complex Systems Center*
Anil Lalwani	Postdoc-at-Large	*Office of Institutional Research and Assessment*
Mojtaba Zeraatpisheh	Postdoc-at-Large	*RESNR and Gund Institute for Environment*
Ajit Kumar Singh	Postdoc-at-Large	*Medicine: Pharmacology*

Useful Information

Postdoctoral Research Showcase Details

Talks will be held at **MedEd 200** of the Medical Education Center. Each speaker will be allotted 10 minutes for their presentation, followed by a 2 minute question-and-answer session. Please hold questions and comments until after the presenter has concluded their talk. Session moderators will hand you a microphone when it is your turn to ask a question. The **Poster Session** will follow from 4:00–6:00 pm in the adjacent **MedEd Pavilion**. Light appetizers and refreshments will be served. The **Spring Postdoc Social** will be held at Zero Gravity, located at 716 Pine Street, Burlington.

Information for Participants

For all scheduled speakers, we request the presenting author to please send their final presentation via file transfer or e-mail at **postdocs@uvm.edu** with the subject line "Research Showcase" no later than 1:30 pm on April 21st. All speakers will use the in-room computer system for presenting. We ask that all poster presenters to please have their poster displayed on their assigned slot no later than 2:00 pm on April 21st.

How to get to MedEd?

The Larner Medical Education Center is located between the Given Building and UVM Medical Center.

- **From Howe Library:** Head southeast on Carrigan Drive, then turn slightly left as you pass Rowell Hall and circle Converse Hall. Climb the stairs and turn right onto Beaumont Avenue. Enter through the double doors next to the Robert Larner, M.D. College of Medicine sign. MedEd 200 is immediately to your left.

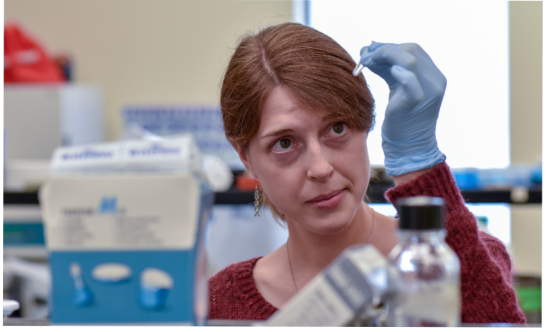
- **From Davis Center:** Exiting on the first floor, walk towards and past the Marsh Life Sciences building. Turn right and walk up a slight incline on Carrigan Drive towards Rowell Hall and the Given Medical Building. Enter through the unlocked double doors in between Rowell and Given. Once inside, turn right through two sets of double doors. You will see the Carpenter Auditorium to your left. Continue straight towards the Given Courtyard, then turn left and follow the signs to the Larner Medical Education Center. MedEd 200 is located to the right up a flight of stairs.

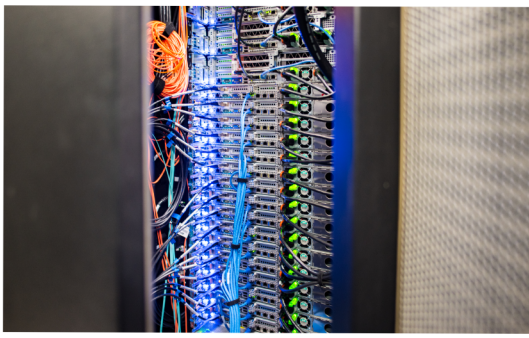
There are elevators located on the first, ground floor of the Larner Medical Education Center upon entering from the Given Building. Also, entering the Medical Education Center from the UVM Medical Center side allows for immediate access to the MedEd 200 lecture hall.

Postdoctoral Research Showcase

Schedule of Events

2:00–4:00 pm	**Oral presentations – MedEd 200**	
2:00–2:05 pm	**Welcome remarks**	
2:05–2:15 pm	**Bianca Possamai, PhD** Rubenstein School of Environment and Natural Resources	Are "lakemounts" biodiversity hotspots?
2:20–2:30 pm	**Peter Knox, PhD** College of Education and Social Services	Exploring educator and school professional perspectives of restorative practices implementation
2:35–2:45 pm	**Colleen Kelly, PhD** Larner College of Medicine	Mechanisms of cardiac myosin replacement
2:50–3:00 pm	**Ashley McCarthy, PhD** College of Agriculture and Life Sciences	Rural residents in the United States more likely to produce their own food during the COVID-19 pandemic
3:00–3:05 pm	**Short recess**	
3:05–3:15 pm	**Kate Hale, PhD** College of Engineering and Mathematical Sciences	The overlooked northeast snowpack
3:20–3:30 pm	**Joe Gunn, PhD** College of Agriculture and Life Sciences	Role of epigenetic modifications in the evolution of insecticide resistance in an invasive crop pest, Colorado Potato Beetles (*Leptinotarsa decemlineata*)
3:35–3:45 pm	**Dhemerson Souza de Lima, PhD** Larner College of Medicine	The role of ER-phagy pathway in influenza virus infection
3:50–4:00 pm	**Sarah Grajdura, PhD** College of Engineering and Mathematical Sciences	Evacuation, accessibility, and equity
4:00–6:00 pm	**Poster session with refreshments – MedEd Pavilion**	
7:00 pm	**Spring Social – Zero Gravity**	





Thank You!

To our participating postdoctoral scholars and their faculty mentors for helping make the 2023 Research Showcase a success. We look forward to learning about your discoveries this year and are eager to welcome you back for the 2024 edition!

List of Posters

1: Benchmarking a resistome pipeline in environmental samples from a dairy farm in Vermont

Felipe Machado de Sant'Anna, Ashma Chakrawarty, and John Barlow, *Department of Animal and Veterinary Studies, College of Agriculture and Life Sciences*

2: Host and viral determinants of arenavirus pathogensis

Rebekah Honce and Jason Botten, *Department of Medicine, Divisons of Immunobiology and Pulmonology and Critical Care, Larner College of Medicine*

3: Early adipose tissue wasting in a novel model of lung cancer cachexia

Deena B. Snoke, Jos A. van der Velden, Jennifer L. Ather, Emma Bellefleur, Sean M. Lenahan, Hailey Sarahusky, Matthew E. Poynter, David J. Seward, and Michael J. Toth, *Department of Medicine, Larner College of Medicine*

4: How do kinesin teams navigate 3D microtubule intersections?

Brandon Bensel, Samantha Previs, Carol Bookwalter, Kathleen Trybus, and David M. Warshaw, *Department of Molecular Physiology and Biophysics, Larner College of Medicine*

5: Characterization and localization within and across breed measures of dominance as observed in inbreeding depression and heterosis

Hafedh Ben Zaabza, Mahesh Neupane, Mohd Jaafar, Srikanth Krishnamoorthy, Stephanie McKay, Asha Miles, Heather J. Huson, Ismo Strandén, Harvey Blackburn, and Curtis P. Van Tassell, *Department of Animal and Veterinary Sciences, College of Agriculture and Life Sciences*

6: The long noncoding RNA, MANCR, is a driver of metastatic triple-negative breast cancer

Janine Warren, Chris J. Pung, Janet L. Stein, Gary S. Stein, and Jane B Lian, *Department of Biochemistry, Larner College of Medicine*

7: Residential segregation and hypertension risk in Black and White Americans

Debora Kamin Mukaz, Andrew D. Sparks, Timothy B. Plante, Suzanne E. Judd, George Howard, Virginia J. Howard, April P. Carson, Lorraine T. Dean, Geoff B. Dougherty, and Mary Cushman, *Department of Medicine, Larner College of Medicine*

8: Structural insights into acetylated histone ligand recognition by PfBDP1

Ajit Kumar Singh, Margaret Phillips, Kiera L. Malone, and Karen C. Glass, *Department of Pharmacology, Larner College of Medicine*

List of Abstracts

Below are participating postdocs by Department and College, with presenting author and page number to aid in locating the complete abstract text. The icon next to the author list in the abstract indicates a P poster presentation or T oral presentation.

Characterization and localization within and across breed measures of dominance as observed in inbreeding depression and heterosis

***Hafedh Ben Zaabza*, Mahesh Neupane, Mohd Jaafar, Srikanth Krishnamoorthy, Stephanie McKay, Asha Miles, Heather J. Huson, Ismo Strandén, Harvey Blackburn, and Curtis P. Van Tassell** P

Department of Animal and Veterinary Sciences, College of Agriculture and Life Scinces

The global application of genomic selection in dairy cattle has raised interest in characterizing dominance effects for a better understanding of the genetic architecture of inbreeding depression. We believe that a richer understanding of additive, dominance, and runs of homozygosity (ROH) effects in purebred and crossbred dairy cattle will help to understand the impact of these factors on inbreeding depression and heterosis. To identify and localize genomic regions associated with additive, dominance, and ROH effects we performed a single-SNP genome-wide association study (GWAS) analysis, where SNPs were fit as fixed effects for the additive, dominance, and ROH effects one locus at a time. The current analysis has been performed using 125,000 genotyped US Holstein cows born between 2015 and 2020 genotyped on 79,294 SNP markers. We have analyzed only milk yield to date but will analyze production, fertility, and health traits. We found that the regions with the most notable effects were located on chromosomes 14 between 0 and 2Mb and on chromosome 6 between 20 and 30Mb. Dominance effects had less pronounced -log10(P) peaks compared to additive effects, and only a few significant dominance effects were detected. The most notable dominance effect was observed on chromosome 5. Similarly, the effects of ROH revealed less prominent -log10(P) peaks than the additive effects, although higher than dominance effects. Indeed, some narrow ROH peaks occurred on chromosome 14.

How do kinesin teams navigate 3D microtubule intersections?

***Brandon Bensel*, Samantha Previs, Carol Bookwalter, Kathleen Trybus, and David M. Warshaw** P

Department of Molecular Physiology and Biophysics, Larner College of Medicine

Exocytic vesicular cargoes, driven by kinesin motor ensembles, reach their destination by navigating the cell's 3D multi-intersectional microtubule (MT) cytoskeleton. Using reductionist approaches, we investigate how kinesin-1 motor ensembles maneuver cargo through MT-MT intersections *in vitro*. 350-nm fluid-like liposomes, a biologically relevant cargo that allows surface diffusion of motors, were incubated with truncated kinesin-1 (K543) at varying stoichiometries. Kinesin-cargo complexes (5-20 motors per liposome) have track-limited run lengths, implying multiple simultaneously engaged motors. When kinesin-liposome complexes encounter an obstructing, intersecting MT in 2D, liposomes with fewer motors (i.e., 5) prefer going straight (56%) to turning (33%), yet liposomes with more motors (i.e., 10-20) go straight (48%) and turn (47%) equally. Interestingly, liposome pause frequency and duration at intersections scale with motor number, indicating motor teams engaged with each of the intersecting MTs enter a tug-of-war. With less motors the tug-of-war outcome favors going straight because less free motors can engage the intersecting MT. Whereas with more motors, the tug-of-war is between teams with equivalent motor number, leading to no directional preference. To better model the cells' MT cytoskeleton, 3D intersections were created by suspending MTs between 0.7-3micron pedestal beads. Super-resolution fluorescence microscopy allowed the spatial relationship between liposomes and intersecting MTs to be precisely defined. While approaching the intersection, liposomes can move in a helical trajectory that tracks the *in vitro* MT protofilament supertwist (5 microns). Upon reaching the intersection, liposomes pause and deform the intersecting MTs as competing motor teams undergo a tug-of-war. After the tug-of-war resolves, liposomes transported by 10 kinesins prefer going straight (58%) to turning (29%), which differs from the 2D intersection outcomes. *In silico* modeling of both 2D and 3D intersection outcomes will provide insight into the underlying biophysical mechanism(s) governing kinesin-cargo transport *in vivo*.

Evacuation, accessibility, and equity

Sarah Grajdura* and *Dana Rowangould

Department of Civil and Environmental Engineering, College of Engineering and Mathematical Sciences

"The concept of equity in relation to evacuation modeling and natural disaster planning has received much attention recently, and first came to light after Hurricane Katrina, when there were grave racial inequities among evacuee outcomes and experiences. Despite equity being an important consideration to ensure safety during evacuation for all communities and people, the current literature mainly relies on measuring evacuation travel time and comparing these times across different evacuating groups, or looks to see if evacuation plans consider specific marginalized groups. Travel time is not a perfect measure of evacuation safety, equity, nor does it account for the quality of evacuations people experience. There is a need for metrics that measure these experiences, allowing for comparison across evacuation routes and improved pre-disaster planning. The concept of accessibility, or access to desired locations, is uniquely positioned to handle this task. In the evacuation context, desired locations can be considered as safe destinations where evacuees terminate their evacuation. Accessibility measures can take into consideration those people without access to cars, which much of the current evacuation literature focuses on. Moving from the idea of mobility in evacuation to accessibility in evacuation also incorporates land use changes that can bring safe locations closer together. In this paper, we consider the accessibility of evacuation routes and their associated metrics as a better way to develop and assess evacuation plans. Our research questions include the following:

1. How is accessibility currently addressed in the disaster and evacuation literature?
2. What are the benefits of incorporating accessibility metrics into evacuation planning?
3. What accessibility metrics can be translated to the evacuation context?

Role of epigenetic modifications in the evolution of insecticide resistance in an invasive crop pest, Colorado Potato Beetles (*Leptinotarsa decemlineata*)

Joe Gunn* and *Yolanda Chen

Department of Plant and Soil Science, College of Agriculture and Life Sciences

Human-driven global change poses complex environmental and societal challenges which will require integration of basic science and applied strategies to develop lasting solutions. A relatively recent but urgent consequence of human activity is biological invasion-colonization of pristine ecosystems by non-native species due to deliberate or accidental movement of organisms. Invasive species can disrupt critical ecological processes by outcompeting or preying on native species, potentially leading to loss of local populations or even ecosystem collapse. In economically important agroecosystems, invasive species may threaten valuable food crops and overall food sustainability. The Colorado Potato Beetle (*Leptinotarsa decemlineata*; CPB) is among the most pervasive and destructive invasive crop pests, annually causing billions of dollars in yield losses across all major potato (*Solanum tuberosum*) varieties. Industry professionals have tried to control CPB outbreaks with chemical insecticides. Despite persistent efforts, CPB have rapidly evolved strong resistance (the ability to withstand exposure) to over 50 novel chemical combinations. Some studies have revealed that preexisting or newly emergent genetic variation (differences in the DNA code) is at least partly responsible for insecticide resistance. However, genetics cannot fully explain why resistance evolves so quickly and universally. Our lab aims to identify the underlying eco-evolutionary mechanisms facilitating establishment and spread of CPB and other agricultural insect pests, with the ultimate goal of developing innovative approaches for mitigation and pest removal. We are interested in whether insecticide resistance in CPB is induced by the stress of chemical exposure itself through the process of epigenetic modification, or changes to the structure and function of DNA without changes to the DNA code itself. Through a multigenerational experiment, we will assess whether the exposure stress response is inherited by future, unexposed generations. We hope our findings will help circumvent the expensive need to develop new insecticides and inform practice in agroecological sustainability.

The overlooked northeast snowpack

Kate Hale*, *Anna Grunes*, *Beverley Wemple*, *and Arne Bomblies

College of Engineering and Mathematical Sciences

Across the northeastern United States, the effect of snowfall and the regional snowpack on the surrounding environmental system remains relatively understudied, yet these are critical components of the hydrologic cycle. The most recent region-wide analyses of snow and winter-season climate in the northeast extend to the early 2000s. Further, these previous analyses capture only trends in temperature, snowfall depth and fraction, and snow-covered days, with low spatial coverage. Yet the northeastern snowpack likely plays a first principle role in delaying surface water inputs (i.e., SWI, the daily sum of rainfall and snowmelt) to the terrestrial system by storing water until periods of intermittent snowmelt. Both snow water equivalent (SWE) and snowpack water storage trends have largely been overlooked in the northeast, in part due to scarce observations. The amount of water in the snowpack and the timing of snowmelt are known to strongly influence downstream runoff (timing and volume), spring nutrient fluxes, flooding and drought. In response, this work leverages both longstanding datasets and those recently developed by the University of Vermont (Summit-to-Shore Cold Region Observation Network) aimed at characterizing the regional snowpack. Early analyses confirm that the snow-on season is shrinking in time with unknown effects on downstream dependents.

Host and viral determinants of arenavirus pathogenesis

***Rebekah Honce* and Jason Botten**

Department of Medicine, Divisions of Immunobiology and Pulmonology and Critical Care, Larner College of Medicine

Zoonotic spillover from wild animals to humans is a major threat to global health. Just in the 21st century, viral spillovers from animal reservoirs have caused numerous outbreaks of devastating disease ranging from localized epidemics, like Ebola, Nipah, and Zika viruses, to full-fledged pandemics caused by influenza and coronavirus species. These and other viruses of pandemic potential—including mammarenaviruses—are priority pathogens for continued research. The mammarenavirus genus comprises agents of hemorrhagic fever, encephalitis, meningitis, and can act as teratogens; however, they range widely in their pathogenesis depending on host species. Rodents present with asymptomatic yet persistent infection while humans are acutely infected with often severe or deadly outcomes. We believe this dichotomy in disease progression has both host species and viral determinants. Our hypothesis is a unique class of viral particles—termed interfering particles—serve to protect rodent fitness and ensure persistency. However, empirically testing this hypothesis has been impossible due to inability to separate interfering particles from traditional infectious particles. We recently discovered a unique property of the mammarenavirus matrix protein which, when rendered unphosphorylatable in its late domain, abrogates interfering particle production. Pairing this groundbreaking finding with classic reverse genetics in the lymphocytic choriomeningitis virus model produces a viral population lacking interfering activity, a key tool in discerning the contribution of interfering particles to pathogenesis. We are working to apply these tools to distinguish particle- and species-specific responses to LCMV infection. Using representative rodent and human cell lines, we have revealed the apparent necessity of interfering particles in maintaining persistency. On-going *in vivo* studies are monitoring murine fitness, including growth, fecundity, and lifespan, to assess the role of interfering particles in the natural host. Future studies will untangle how interfering particles shape host immunity and identify key host factors required for the observed relationships.

Residential segregation and hypertension risk in Black and White Americans

Debora Kamin Mukaz*, *Andrew D. Sparks*, *Timothy B. Plante*, *Suzanne E. Judd*, *George Howard*, *Virginia J. Howard*, *April P. Carson*, *Lorraine T. Dean*, *Geoff B. Dougherty*, *and Mary Cushman P

Department of Medicine, Larner College of Medicine

Introduction: Black adults experience the highest hypertension burden of any American group. Evidence indicates social factors adversely affecting Black people explain some of the excess hypertension burden. It's unclear whether residential segregation, a key cause of health inequities, has a differential impact on Black and White people. Hypothesis: The magnitude of the association of residential segregation and risk of incident hypertension will be greater in Black than White people.
Methods: Our sample included 6,143 Black and White Reasons for Geographic And Racial Differences in Stroke (REGARDS) study participants without prevalent hypertension (2003-7), and with a follow-up visit 9.3 years later. Baseline county-level segregation was measured with the (1) dissimilarity index (DI, the difference in race distribution of census tracts relative to their county), (2) isolation index (ISI, the degree to which Black people are exposed only to one another in a county), and (3) interaction index (ITI, the degree to which Black people are exposed to White people in a county). Modified Poisson regression estimated the risk ratios (RR) of incident hypertension per SD increment of baseline residential segregation.
Results: The mean (SD) age was 61(8) years for Black people and 62(8) years for White people. Hypertension incidence was 46% for Black people and 33% for White people. There was no association of any of the three measures of residential segregation (DI, ISI and ITI) with incident hypertension, with RRs all around 1.0.
Conclusions: Three measures of residential segregation were not associated with incident hypertension risk in Black and White participants of the REGARDS cohort. Findings differ from a previous study that reported that a measure of racial clustering was associated with higher risk of hypertension in Black people. Taken together, findings suggest that, in Black people, different domains of residential segregation capture factors related differently to hypertension development.

Mechanisms of cardiac myosin replacement

Colleen M Kelly*, *Molly Coseno*, *Jody L. Martin*, *and Michael J. Previs

Department of Molecular Physiology and Biophysics, Larner College of Medicine

The heart contracts continually throughout one's lifetime through antiparallel sliding of actin-based thin filaments along myosin-based thick filaments, organized within muscle sarcomeres. A recent biochemical study from our lab demonstrated that individual myosin are randomly replaced in existing thick filaments on the order of days in adult mouse hearts. Here, we hypothesize that myosin replacement involves dynamic exchange of single molecules into thick filaments in vivo. To test this, we generated an adeno-associated virus that replaced 27±7% of the endogenous regulatory light chain (RLC) on myosin molecules with a fluorescent GFP-RLC. We then visualized myosin within intact hearts using two-photon microscopy. At high magnification, individual sarcomeres were observed with GFP-RLC incorporated into thick filaments. Next, we measured the movement of fluorescently-labeled myosin within the heart by irreversibly photobleaching limited areas of the cells and quantifying fluorescence recovery after photobleaching (FRAP). Rapid FRAP occurred after photobleaching small portions of single sarcomeres at rates orders of magnitude faster than protein synthesis. To determine whether the mechanism of this exchange may involve the folding of monomeric myosin, GFP-labeled myosin molecules were extracted from the transfected hearts and their Stokes radii were measured over a range of ionic strengths using microfluidic diffusional sizing. At low ionic strengths (150 mM KCl), filament formation was favored, but soluble GFP-labeled myosin demonstrated radius of 12.6 ± 1.1 nm. Similar radii have been reported for smooth muscle myosin monomers in folded conformation. Together, these data suggest that cardiac thick filaments are dynamic, exchanging myosin between a filamentous and cytosolic pool, where they adopt a folded conformation. This rapid incorporation and release of myosin molecules supports protein replacement while maintaining the structural integrity that is essential to support contractility.

Exploring educator and school professional perspectives of restorative practices implementation

Peter Knox*, *Bernice Garnett*, *Colby Kervick*, *Amanda Simpfenderfer*, *Lance Smith*, *and Mika A. Moore

College of Education and Social Sciences

Restorative practices (RP) have been identified as an effective alternative to traditional, punitive school disciplinary practices. Sustainable wholeschool approaches to RP implementation require substantial adult buy-in, time, leadership support, and resources. However, limited studies have examined the implementation of RP from the unique perspectives of different groups of school professionals (e.g., teachers, paraprofessionals, and non-classroom staff) and their perceptions of RP implementation climate (i.e., support, efficacy, use). Even fewer studies have investigated such differences in perceptions of RP support, efficacy, and utilization among different groups of school professionals at varying school levels (e.g., elementary, middle, and high school). We applied an exploratory, descriptive study design in which we utilized quantitative analysis to better understand the implementation of restorative practices among varying school roles and at differing school levels. Data from this study is derived from a district-wide survey of RP implementation among school adults (N=392) administered in 2019 in a midsize urban school district in the Northeast engaged in district-wide RP. Results indicate differential perceptions of RP implementation by professional role, where paraprofessionals have similar levels of RP use and support in comparison to classroom teachers but indicate the lowest level of RP efficacy. Additionally, non-classroom staff reported the highest levels of RP support in comparison to paraprofessionals and teachers. Across school levels and each implementation climate domain (support, efficacy, and use), elementary school staff reported the highest or most positive perceptions of RP implementation climate compared to middle and high school staff. Implications for the implementation of RP amongst various school roles and within diverse school contexts and levels are discussed.

Benchmarking a resistome pipeline in environmental samples from a dairy farm in Vermont

Felipe Machado de Sant'Anna*, *Ashma Chakrawarty*, *and John Barlow P

Animal and Veterinary Sciences, College of Agriculture and Life Sciences

Antimicrobial resistance (AMR) is a major concern for public health and food safety issues. Bacteria can harbor antimicrobial resistance genes (ARG) that can be spread conferring multirresistance to many commonly used and novel drugs and may be carried out by all food-producing animals. Recent advances in next generation sequencing (NGS), such as metagenome/resistome sequencing, allow for a more comprehensive and deeper understanding of the microbiota from food producing plants, such as dairy farms. Assessing the detection of AMR genes in environmental samples is of utmost importance for developing ways of mitigating the transmission and prevalence of these genes throughout the food chain. The objective of this study was to benchmark and validate the resistome of environmental samples collected from a dairy farm in Vermont. Samples were obtained from a local dairy farm. DNA was extracted then submitted to quality control, submitted to library prep, and later sequenced in Illumina MiSeq® . Raw data was trimmed and demultiplexed into FASTQ files and then submitted to quality control using the FastQC software. For downstream analysis aiming AMR genes, FASTQ files were submitted to a customized bioinformatic pipeline called Amr++ using the MEGARes database for antimicrobial drugs A total of 33 AMR genes were accounted for the drinking water samples; 28 AMR genes for manure; 75 AMR genes for the milking line filter and 27 AMR genes for cow feeding. The most prevalent hits were accounted for Aminoglycosides, MLS, Oxazolidinone, Tetracyclines and Elfamycins. The filter sample showed higher counts when compared to the feeding, water, and manure samples ($p<0.05$) for the Dunn's multiple comparison test. It can be concluded that these methods are adequate for assessing AMR genes in different samples (environmental and food samples). Further studies are needed to evaluate interactions between taxonomical values and antimicrobial resistance genes in environmental matrices.

Rural residents in the United States more likely to produce their own food during the COVID-19 pandemic

Ashley C. McCarthy*, *Francesco Acciai*, *Emily Belarmino*, *Joelle Robinson-Oghogho*, *and Meredith T. Niles

Department of Nutrition and Food Sciences, College of Agriculture and Life Sciences

Many rural communities in the United States face reduced access to traditional grocery stores and the COVID-19 pandemic likely exacerbated food access challenges in rural communities. Home food production (HFP) (e.g., gardening, hunting, fishing) and local food sources (e.g., farmers markets, Community Supported Agriculture) are two alternatives that can be important sources of food for people living in rural communities and areas with limited access to traditional food retailers. Previous research suggests that HFP increased in high-income countries during the pandemic, but little evidence exists on whether this occurred equally across rural and urban locations. We used data from two waves of a national survey (n = 3,196) conducted during the COVID-19 pandemic, in July-August 2020 and April-May 2021, which also asked retrospective questions relative to the year preceding the onset of the pandemic. We used multivariate logistic regression models to examine differences in use of local foods and HFP between rural and urban areas. In the year before the pandemic, rural respondents were more likely to obtain food through local sources (OR 1.32; 95% CI: 1.03 - 1.68; p = 0.028) and through HFP (OR 1.78; 95% CI: 1.36 - 2.32; p < 0.000) than urban respondents. During the first 14 months of the pandemic, the rural-urban gap in obtaining food through HFP slightly increased (OR 2.08; 95% CI: 1.54 - 2.82; p < 0.000), while the urban-rural gap in the use of local foods disappeared. Additionally, when asked which strategies they used to afford food during the pandemic, rural respondents were more likely to report relying on hunting, fishing, or foraging (OR 2.07; 95% CI: 1.51 - 2.84; p < 0.000) and growing their own food (OR 1.63; 95% CI: 1.12 - 2.39; p = 0.011) than urban respondents. Future research should explore the effect of HFP on food security and diet quality.

Are "lakemounts" biodiversity hotspots?

Bianca Possamai*, *J Ellen Marsden*, *and Jason D Stockwell

Rubenstein School of Environment and Natural Resources

Seamounts modify water flow and create nutrient-enriched upwelling zones that support increased productivity and biodiversity. However, similar systems are largely unstudied in lakes. We hypothesized that steep reefs in deep lakes ("lakemounts") act as seamounts. In a preliminary study, we monitored water temperature and compared fish and benthic invertebrate diversity nearshore (NS) and around a lakemount (LM) in Lake Champlain, US. In a 20-day period, the thermocline oscillated around 15 m depth. We observed two seiche events that upwelled cold water, both with 4 days duration. Temperature was positively related to NE winds ($t=1.95$, $p=0.05$) and negatively related to SSW winds ($t=-5.14$, $p<0.001$), indicating formation of a wind-driven seiche. Taxonomic richness was higher at the NS than LM site (12 vs 11 fish species, and 25 vs 20 benthic taxa, respectively). Shannon-Weiner diversity (H) and Evenness (evar) indices showed that NS benthos had higher diversity and evenness compared to the LM benthic community (H=2.2 vs 1.7; evar=0.7 vs 0.6; NS vs LM, respectively), while the fish diversity and evenness were higher in the LM (H=1.5 vs 1.8; evar 0.6 vs 0.7; NS vs LM, respectively). Salmonids were present only at the LM and insects were exclusively in the NS, while other taxonomic groups were similar between the habitats. Zooplankton samples remain to be processed. Our early results suggest the diversity of benthic invertebrates and fishes were comparable between lakemount and nearshore habitats, suggesting lakemounts may act as a biological hotspot in the offshore habitat.

Structural insights into acetylated histone ligand recognition by PfBDP1

Ajit Kumar Singh*, *Margaret Phillips*, *Kiera L. Malone*, *and Karen C. Glass P

Department of Pharmacology, Larner College of Medicine

Plasmodium falciparum is a unicellular protozoan parasite that is commonly known to cause malaria in humans. According to a WHO report in 2019 there were 409,000 malaria-related deaths reported worldwide, and the most affected age group was of children under 5 years of age. A recent spike in instances may be attributed to drug-resistance in *P. falciparum*, thus we need a better understanding of the parasite's life cycle to produce more effective antimalarial drugs. The *P. falciparum* genome encodes for ten bromodomain-containing proteins. *In vivo* knockdown experiments demonstrate that *P. falciparum* bromodomain protein 1 (PfBDP1) regulates the expression of invasion-related genes by tethering a transcriptional activator complex to acetylated histones. However, the molecular mechanisms driving chromatin binding and recognition by PfBDP1 are currently unknown. PfBDP1 contains a unique combination of seven ankyrin repeats (Ank) domain followed by a bromodomain (BRD). Bromodomains (BRDs) are evolutionary conserved protein-protein interaction modules (110 amino acids long) that recognize acetylated lysine (Kac) on histones and other proteins. Here, we have determined the crystal structure of PfBDP1-BRD at 2.0 Å, and our results shows that it has a conserved bromodomain fold, and an acetylation binding pocket comprised of four alpha helices. However, comparing the Kac binding pocket to human bromodomains reveals the PfBDP1-BRD has a unique binding mechanism that might be leveraged for the design novel therapeutic treatments. As previously reported, PfBDP1 has been shown to interact with acetylated histone H3, but our *in vitro* binding experiments using isothermal titration calorimetry (ITC) and nuclear magnetic resonance (NMR) have revealed that PfBDP1-BRD preferentially binds to tetra-acetylated histone H4. This suggests that PfBDP1 may have additional, yet unidentified roles in the *P. falciparum* life cycle.

Early adipose tissue wasting in a novel model of lung cancer cachexia

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Lung cancer is the leading cause of cancer-related deaths. Up to 75% of lung cancer patients exhibit cancer cachexia (CC), a syndrome of skeletal muscle and fat tissue wasting. No effective therapies for CC have been identified, in part because pathoetiological mechanisms contributing to its development are difficult to capture in currently available, rapidly progressing preclinical models. Towards development of a more clinically relevant mouse model of CC, we found that mice with lung epithelial cell specific KrasG12D induction (club cells) were characterized by 15% body weight loss over 12 weeks, yielding a rate of body weight loss (1.9%/week) that corresponds favorably with human CC patients (1%/week) and is much slower than other currently used models (5-10%/week). Body weight loss was accompanied by 30% and 18% reductions in gastrocnemius and soleus muscle mass, respectively, and marked depletion of adipose tissue mass. Six weeks post-induction, when body weight loss has occurred, but animals are still pre-cachectic (<5% body weight loss), we observed substantial fat pad loss, including 50% reduction in inguinal and perigonadal adipocyte cross-sectional area, but no loss of gastrocnemius or soleus muscle mass or fiber size. Additionally, we found that conditioned media from organoids developed from murine KrasG12D lung tumors elicited glycerol release from cultured adipocytes but less pronounced effects on cultured myotubes. These findings suggest that lung epithelial-specific, inducible KrasG12D mice better parallel the time course of CC development and progression in humans compared to currently available lung cancer models and highlight fat loss as an early pathological event in CC that may be mediated by tumor-derived factors.

The role of ER-phagy pathway in influenza virus infection

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Rationale: Influenza is a major respiratory pathogen in the world that causes severe respiratory disease in susceptible population. Influenza exclusively infcets and replicates in lung epithelial cells. It utilizes various intra-cellular pathways including endoplasmic reticulum (ER) based pathways. ER-phagy is a specialized pathway to recycle the damaged ER. Deregulation in ER-phagy pathways are reported with the infectious agents such as Ebola, Zika, and Dengue. However, it is not clear whether influenza utilizes ER-phagy pathway to propagate and alterations in ER-phagy leads to inflammatory response is unknown. Our objective was to determine the role of ER-phagy in influenza propagation and inflammatory response.

Methods: Human bronchial epithelial cells (HBEs) and C57BL/6JN mice were infected with H1N1 PR8. Multiple ER-phagy receptors (e.g., FAM134B, SEC62, RTN3, CCPG1 etc) expression were measured by RT-qPCR and western blot analysis and the flux of ER-phagy pathway was measured by immunoprecipatation and immunofluorescence. The knockdown (siRNA) and overexpression methodology was used to alter specific ER-phagy receptors and Viral propagation was measured by plaque assay, inflammatory response was measured by ELISA.

Results: Our data report for the first time, influenza virus upregulated the levels of two ER-phagy receptors, FAM134B and SEC62 in HBEs and mice. These receptors shows interaction with LC3B with increased the punctas *in vitro*, *in vivo* model. FAM134B and SEC62 knockdown increased the virus propagation and decreased type I and III interferon. However, FAM134B and SEC62 overexpression decreased the viral burden and increased type I and III interferon.

Conclusion: These results indicate that FAM134B and SEC62 are associated for effective "control" of influenza propagation affecting the axis of type I and III interferon. Therefore, our data support important role of FAM134B and SEC62 against influenza infection.

The long noncoding RNA, MANCR, is a driver of metastatic triple-negative breast cancer

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Metastatic breast cancer (BC) remains a prominent cause of death worldwide, despite many advances in cancer treatment over the decades. Early diagnosis in combination with modern treatment regimens for breast cancer has led to a high disease-free survival rate. However, patient survival decreases significantly after BC has metastasized, and this occurs more frequently in the Triple Negative Breast Cancer (TNBC) patient group. Among the recent class of epigenetic regulators of the genome are the long non-coding RNAs that function in the nucleus to support stability of the cells and maintain chromatin interactions. Our laboratory discovered the mitotically associated long noncoding RNA MANCR (LINC00704) to be highly upregulated in human BC tumors and this is indicative of a very poor survival rate. Using the MDA-MB-231 TNBC cells, we knocked down MANCR with GapmeRs and found that the cells have a poor survival after only 24 hours. Clearly this shows that the TNBC cells are dependent on MANCR for survival. Furthermore, loss of MANCR promotes DNA damage and decreases cell proliferation *in vitro*. MANCR knockdown also drives differential gene expression of genes important for cell-cycle regulation. TNBC cells were inoculated the 4th mammary fat pad and formed a tumor over 3 weeks, and then the animals were treated with 2 nmol/g of a non-targeting control GapmeR or a GapmeR designed to target MANCR *in vivo*. These *in vivo* studies revealed that targeting MANCR in animals with existing tumors drastically inhibited tumor growth over time and end-point tumor mass. These data suggest that established "MANCR-high" TNBC tumors require MANCR to grow quickly and promote disease progression. Current studies use ChIRP (identifies chromatin interaction) to identify the regions of the genome MANCR interacts with.

Spring Social

Come for the scholarship, stay for the community

Join the Postdoc Association for our Spring Social! Our social will be hosted by Zero Gravity Craft Brewing and will immediately follow the conclusion of the Research Showcase. Carpooling is encouraged, and please use a designated driver. Be sure to watch your email, our Slack channel uvm-pda.slack.com and Twitter @UVMpostdocs for future announcements of social and professional development events hosted by the UVM PDA.

Directions to Zero Gravity: Start by heading south on South Prospect Street toward Main Street. Turn righht at the first cross street onto Main Street and continue for 1 mile before turning left onto South Willard Street. At the traffic circle, continue straight onto Locust Street for a half mile then turn left onto Pine Street. Zero Gravity Craft Brewing will be on your left at 716 Pine St, Burlington, VT 05401.

Thank You!

The UVM Postdoctoral Research Showcase is proud to be part of the University-wide Research Week and to celebrate the research, scholarship, and creative works of our postdoctoral scholars. Thank you to all participating postdocs and their faculty advisors. Special thanks to the Office of the Vice President for Research for coordinating the week's events.

Special Thanks

Cynthia Forehand, PhD, Dean of the Graduate College

Kirk Dombrowski, PhD, Vice President for Research and Gund Internal Steering Committee

Dan Harvey, Assistant Dean, Graduate College and Director of Operations, Office of the Vice President for Research

Christopher Berger, PhD, Associate Dean of Graduate Education and Postdoctoral Training

Erin Montgomery, for assistance in UVM PDA affairs and Showcase organizing

Office of Medical Communications at the Larner College of Medicine for use of posterboards

Get Involved

The UVM Postdoc Association is always looking for motivated postdocs to join our ranks to improve the postdoc experience at UVM. Check our Slack channel uvm-pda.slack.com and Twitter @UVMpostdocs for the latest events and announcements and for other ways to get invovled.

Want to join the Executive Committee? Elections will occur in early May, and self-nominations are encouraged! Please inquire at **postdocs@uvm.edu** or visit us at www.uvm.edu/postdocs for more information.

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