RUTGERS HEALTH
Institute for Infectious and Inflammatory Diseases

INSTITUTE FOR INFECTIOUS & INFLAMMATORY DISEASES

FACULTY RESEARCH RETREAT

Topic :

Immunology Across Rutgers

Robeson Campus Center
350 Dr Martin Luther King Jr Blvd, Newark, NJ 07102
Essex Room

Thursday. June 4th, 2026

8:30 AM - 5:00 PM

CO-CHAIR
Jessica Hargarten, PhD
Assistant Professor

CO-CHAIR
Alex Papachristodoulou, PhD
Assistant Professor

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i3D Director:

William C. Gause, Ph.D.

i3D Faculty Research Retreat
"Immunology Across Rutgers"
June 4th, 2026

8:30 am	Breakfast and Registration		
9:00 am	**Opening Remarks** i3D Director	Dr. William Gause, PhD https://njms-web.njms.rutgers.edu/profile/myProfile.php?mbmid=gausewc#tab-pub	Senior Associate Dean for Research; Director, RBHS i3D; Director, CII; Distinguished Professor of Medicine, Department of Medicine
	Opening Remarks Retreat Co-chairs	Drs. Alex Papachristodoulou, PhD and Jessica Hargarten, PhD	
Session I- Cancer Immunology, Chair: Dr. Alex Papachristodoulou & Paul Brennan (Grad Student)			
9:15 am	**Kyle Payne** https://sites.rutgers.edu/payne-group/people/kyle-payne/	BLTP3A restrains lysosomal stress–licensed STING immunity in ovarian cancer	Assistant Professor, Rutgers RWJMS, Department of Medicine, Rutgers Cancer Institute
9:35 am	**Jian Cao** https://cinj.org/caolab	Oncoviral Integrations as Drivers and Therapeutic Vulnerabilities in Cancer	Assistant Professor, Rutgers RWJMS, Department of Medicine, Cancer Institute of New Jersey
9:55 am	**Dongfang Liu** https://njms.rutgers.edu/departments/labs/dongfang/about.php	NK-based immunotherapy (CAR-NK) for treatment of cancer	Professor, Rutgers NJMS, Department of Pathology, Immunology, Laboratory Medicine
10:15 am	**Maria I. Velez Brochero**	*Trainee Abstract Awardee:* Infection-driven neutrophil subset remodeling and local interferon control of antifungal function	Graduate Student, Rivera Lab, i3 track, Rutgers Health SGS
10:30 am	Coffee Break and Trainee Poster Presentation Session #1 (40 minutes)		
Session II- Immunology and the Microbiome, Chair: Dr. Robin Stephens & Rachel Bennett (Grad Student)			
11:10 am	**Donald Nyangahu** https://sites.rutgers.edu/nyangahu-lab/	Gut Microbiota from HIV-Exposed Uninfected Infants Causally Alters Growth, Bone and Immune Development	Assistant Professor, Rutgers RWJMS/CABM, Department of Pharmacology
11:30 am	**Nicholas Bessman** https://bessmanlab.org	Understanding host factors that maintain a healthy microbiome through weaning and beyond	Assistant Professor, Rutgers NJMS, Department of Microbiology, Biochemistry and Molecular Genetics
11:50 am	**Lea Ann Chen** https://rwjms.rutgers.edu/people/lea-ann-chen#:~:text=Lea%20Ann%20Chen%2C%20M.D.%20is,Robert%20Wood%20Johnson%20Medical%20School.	Uncovering the microbial contributors to the development of inflammatory bowel disease	Assistant Professor, Rutgers RWJMS, Department of Medicine, Director Inflammatory Bowel Disease Translational Research
12:10 pm	**Lunch Break: Across-campus Networking Session**		

Session III- Translational Immunology, Chairs: Dr. Dane Parker & Ahri Han (Grad Student)			
1:20 pm	**Bobby Brooke Herrera** https://www.bbherreralab.com/people	Protective and Pathogenic Immunity Across Orthoflavivirus Exposure Histories	Assistant Professor, Rutgers RWJMS, Department of Medicine
1:40 pm	**Darin Wiesner** https://www.wiesnerlab.com	Barrier immunity to inhaled fungi	Assistant Professor, Rutgers NJMS, Department of Medicine
2:00 pm	**Jessica Hargarten** https://www.hargartenlabrutgers.com	Cryptococcosis from Bedside-to-Bench and Back Again: *MTOR* and the Clinical Parabola	Assistant Professor, Rutgers NJMS, Department of Pathology, Immunology, and Laboratory Medicine
2:20 pm	Coffee Break and Trainee Poster Presentation Session #2 (40 minutes)		
Session IV- Charting the Course for AI/ML in Immunology, Chair: Dr. Jessica Hargarten & Roshni Kadam (Grad Student)			
3:00 pm	**Leslie Lenert** https://ifh.rutgers.edu/profile/leslie-a-lenert-md-ms-facmi-facp/	Introduction to the Center for Biomedical Informatics and Health Artificial Intelligence (BMIHAI) at Rutgers Health	Professor, Rutgers RWJMS, Department of Medicine, Founding Director of BMIHAI
3:20 pm	**Priya Kachroo** https://i3d.rutgers.edu/people/priyadarshini-priya-kachroo/	Early-Life Multi-Omic Programming of Immune and Inflammatory Trajectories in Lung Disease	Assistant Professor, Rutgers NJMS, Department of Biomedical Health Informatics, School of Health Professionals
3:40 pm	**Yingda 'Linda' Xie** https://i3d.rutgers.edu/people/yingda-linda-xie-md-public-health-research-division-of-infectious-diseases-department-of-medicine/	Imaging New Frontiers in Tuberculosis: From Point-of-Care Screening to Early Disease Detection	Assistant Professor, Rutgers NJMS, Public Health Research, Division of Infectious Diseases, Department of Medicine, ICPH PHRI
4:00 pm	**Arthur VanValkenburg** https://www.wejlab.org/research-1	Decoding the Adaptive Immune Repertoire: Computational Tools, Limits, and Trust for Disease Research	Supervising Research Scientist W. Evan Johnson Lab, Division of Infectious Disease, Department of Medicine Director, Center for Data Science, Rutgers New Jersey Medical School
4:20 pm	***Post Award Presentation*** 1st Place Award sponsored by Bruker 2nd Place Award sponsored by Transnetyx 3rd Place Award sponsored by 10x Genomics Trainee Abstract Award sponsored by BioLegend		
4:30-5:45 pm	**Happy Hour** (Sponsored by STEMCell)		

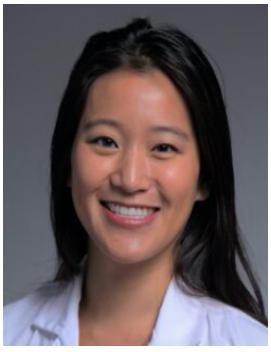
Guest Speakers

Nicholas J. Bessman, PhD

Dr. Bessman completed a PhD in Biochemistry and Biophysics at the University of Pennsylvania, where he studied the activation mechanism of the Epidermal Growth Factor Receptor (EGFR). As a post-doctoral researcher, he worked with Dr. Gregory Sonnenberg in the Jill Roberts Institute for IBD Research at Weill Cornell Medical College, where he became fascinated with the interplay between iron, the immune system, and intestinal bacteria. In 2021 Dr. Bessman started an independent lab at Rutgers-New Jersey Medical School in the Center for Immunity and Inflammation. The Bessman lab continues to explore the relationship between iron, the immune system, and bacteria in settings of health and disease, with support from an NIH/NIAID DP2 New Innovator Award and a K01 award from NIDDK. The goal of the Bessman lab is to discover new therapeutic strategies for the treatment of IBD and cancer.

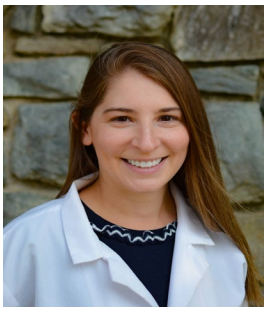
Jian Cao, PhD

Jian Cao, Ph.D. is an Assistant Professor at Rutgers Cancer Institute and Robert Wood Johnson Medical School. He received his Ph.D. from the Chinese Academy of Sciences and completed his postdoctoral training with Dr. Qin Yan at Yale University. Since joining Rutgers Cancer Institute in 2019, his research has focused on cancer epigenetics, tumor-intrinsic immunity, and virus-associated cancers. His laboratory investigates how oncogenic viruses, such as hepatitis B virus and human papillomavirus, contribute to cancer through viral integration, chromatin dysregulation, and persistent viral oncogene expression. Dr. Cao's work also explores therapeutic strategies for HPV-associated cancers, including TCR-engineered T cell therapy and epigenetic approaches to suppress HPV E6 and E7 oncogene transcription.



Lea Ann Chen, MD

Lea Ann Chen, MD, AGAF, FACG is the Director of Inflammatory Bowel Disease Translational Research at Rutgers Robert Wood Johnson Medical School in New Brunswick, NJ. She completed her medical degree at Washington University School of Medicine in St. Louis, her internal medicine training at Mount Sinai Hospital in New York City, and her gastroenterology fellowship in the physician-scientist track of Johns Hopkins School of Medicine. Clinically, Dr. Chen specializes in the care of patients with IBD and complicated C. difficile infections, and she has a special interest in working with underserved populations. Dr. Chen's research is focused on understanding longitudinal microbiome dynamics in the pathogenesis and behavior of IBD and its implications for clinical care. Her research has been funded by the National Institute of Health, the American Gastroenterological Association, the Crohn's and Colitis Foundation, the American College of Gastroenterology, and multiple private and industry sponsors.



Jessica C. Hargarten, PhD

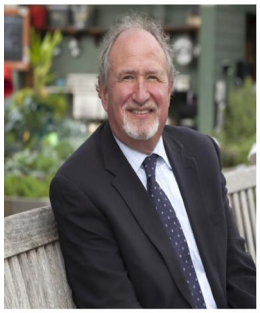
Dr. Jessica C. Hargarten received her B.S. from the University of California, Davis and her Ph.D. from the University of Nebraska-Lincoln. She did her postdoctoral training at the National Institute of Allergy and Infectious Diseases (NIAID) and the NIH Clinical Center under the mentorship of Dr. Peter R. Williamson, MD/PhD in the Translational Mycology Section where she began to uncover the genetic and immunologic factors underlying human susceptibility to invasive fungal disease. Her work also identified the predominant pathway underlying a post-fungal infection inflammatory syndrome and a new treatment modality for cryptococcal- post-infectious inflammatory response syndrome in patients. After her training, she moved to Rutgers where she is an Assistant Professor in the Department of Pathology, Immunology, and Laboratory Medicine and member of the Center for Immunity and Inflammation. Dr. Hargarten's long-term research goal is to define and interrogate human genetic, immunologic, and lifestyle factors that skew immune responses towards severe disease following fungal infections in previously healthy populations in order to inform precision medicine approaches to care and treatment. Her lab uses relevant in vivo and in vitro models of disease and clinical samples to further determine the roles of these genes (particularly in the MTOR pathway) in immunity and susceptibility to *Cryptococcus*-induced disease. Her research is currently supported by extramural funding from NIAID.

Bobby Brooke Herrera, PhD

Dr. Bobby Brooke Herrera is a scientist-entrepreneur whose research focuses on the immune mechanisms that govern protection, pathology, and long-term immunity during viral infections. He earned his PhD in Biological Sciences in Public Health from Harvard University and completed postdoctoral training at Harvard Medical School. Now a faculty member at Rutgers Robert Wood Johnson Medical School, Dr. Herrera leads a multidisciplinary research program investigating how T cells and B cells shape outcomes following infection and vaccination. His laboratory integrates epidemiology, immunology, virology, and translational models to better understand why some hosts develop severe disease while others generate durable protective immunity, with the ultimate goal of informing next-generation vaccines and immunotherapies against emerging infectious threats.

Priya Kachroo, PhD

Dr. Kachroo is an Assistant Professor in the Department of Biomedical Informatics at the Rutgers School of Health Professions and a core member of i3D. Her research focuses on discovering clinically relevant multi-omic biomarkers and biological drivers for lung and inflammatory diseases across life course, using machine learning and network biology methods. As a PI, Dr. Kachroo is a recipient of the K99/R00 award from NIH National Institute of Heart, Lung and Blood Disorders, and a Rutgers Pilot Grant from The Center for Biomedical Informatics and Health AI. Additionally, she has authored 40 peer-reviewed publications with first author papers in prestigious national and international journals including European Respiratory Journal, Nature Medicine, Scientific Reports, and eBioMedicine.



Leslie Lenert, MD

Leslie Lenert, MD, MS, FACMI, FACP is the founding director of the Center for Biomedical Informatics and Health Artificial Intelligence (BMIHAI) at Rutgers Health. He holds degrees from the University of California, Riverside, the University of California, Los Angeles, School of Medicine and Stanford University. Trained in Internal Medicine, Clinical Pharmacology and Medical Informatics, Dr. Lenert is an internationally recognized leader in health informatics. During his long career, he has held numerous leadership positions in this field, including Founding Director of the National Center for Public Health Informatics at the Centers for Disease Control and Prevention and Associate Provost for Data Science and Informatics and Distinguished Professor of Internal Medicine at the Medical University of South Carolina. At Rutgers, Dr. Lenert is leading a new Center, BMIHAI, focused on advancing health, science, and education through the application of artificial intelligence supported by informatics infrastructure. Dr. Lenert has published over 250 original articles and book chapters, is a Fellow of the American College of Medical Informatics and the American College of Physicians, and is an Associate Editor of the Journal of the American Medical Informatics Association.

Dongfang Liu, PhD

Dongfang Liu, Ph.D., is a tenured Professor at the Department of Pathology, Immunology, and Laboratory Medicine in Rutgers University - New Jersey Medical School (NJMS) and CII. He also serves as the Scientific Director of the Cellular Imaging & Histology Core at Rutgers-NJMS. In 2012, Dr. Liu was recruited to Baylor College of Medicine as a tenure-track Assistant Professor in the Departments of Pediatrics, and Pathology & Immunology. In 2015, he joined the Houston Methodist Research Institute (HMRI, affiliated with Weill Cornell Medical College (WCMC)/Cornell University) as a tenure-track Assistant Professor. He was promoted to Associate Professor in 2018 in HMRI. Dr. Liu earned his Ph.D. in immunology from 2001 to 2005 in Huazhong University of Science and Technology (HUST), with a focus on natural killer (NK) biology and immunology, his M.D. training in medicine in Wuhan University School of Medicine in 2001. After completing his Ph.D. training in HUST, he joined the National Institutes of Health (NIH) for his postdoctoral training from 2005 to 2011, specializing in the immunobiology of NK cells and immunological synapse. After completing his postdoctoral training at NIH, he joined the Ragon Institute of MGH, MIT, and Harvard in 2011 as a Senior Research Scientist, focusing on HIV-specific immune cell dysfunction and immunological synapse. Dr. Liu's current research focuses on the immunobiology of NK cells, Chimeric Antigen Receptor (CAR)-NK cells, and immunological synapse biology and application. With over 20 years of experience in NK cell research and > 10 patent applications, Dr. Liu has published extensively in top-tier journals, including Nature Immunology, Immunity, Nature Communications, JACI, and the Proceedings of the National Academy of Sciences (PNAS). He serves on several editorial boards and acts as a reviewer for numerous journals and grant agencies, including the NIH and DOD. Dr. Liu holds multiple federal research grants to study the basic mechanisms of NK cell biology and CAR-NK.

Donald Nyangahu, PhD

Dr. Donald Nyangahu completed his PhD in Immunology at the University of Cape Town, where he studied the influence of maternal gut microbiota during pregnancy and nursing in shaping offspring immunity. He then pursued postdoctoral training at the University of Washington and the Seattle Children's Research Institute, investigating the relationship between early-life gut microbiota in HIV-exposed uninfected (iHEU) infants and immune responses to the BCG vaccine. Dr. Nyangahu joined the faculty at Center for Advanced Biotechnology and Medicine in September 2024, where his lab studies the gut microbiome of iHEU infants and its influence on immunity, vaccine response, and growth.

A major focus of the Nyangahu Lab is infants who are exposed to HIV but remain uninfected, a population known to experience higher risks of illness, immune dysfunction, impaired growth, neurodevelopmental delays, and mortality despite being HIV uninfected themselves. His lab is currently evaluating whether disruptions in early-life microbial communities causally contribute to these adverse outcomes. Through this work, Dr. Nyangahu aims to identify critical microbial drivers and developmental windows that could support microbiota-targeted interventions to promote healthier child development.

Kyle K. Payne, PhD

Kyle K. Payne, PhD, is an Assistant Professor in the Department of Medicine at Rutgers Robert Wood Johnson Medical School and a resident member of the Rutgers Cancer Institute of New Jersey, where he serves as Co-Leader of the Cancer Metabolism and Immunology Program. Dr. Payne received his bachelor's degree in Biology from Indiana University and his PhD in Tumor Immunology from Virginia Commonwealth University under the mentorship of Dr. Masoud Manjili. He completed postdoctoral training at the University of Pennsylvania and Moffitt Cancer Center, where he investigated mechanisms of immune suppression and checkpoint dysregulation in the tumor microenvironment. Since joining Rutgers Cancer Institute, Dr. Payne has established an independent research program focused on how tumor-intrinsic stress-response pathways reshape antitumor immunity, with a particular emphasis on ovarian cancer. His laboratory studies how stress signals in the tumor microenvironment alter T cell function, lipid trafficking, antigen presentation, and immune cell fate. The long-term goal of his work is to define new mechanisms of immune resistance and translate these discoveries into more effective immunotherapies for patients with gynecologic malignancies. Dr. Payne's work has been supported by the National Cancer Institute, the V Foundation for Cancer Research, the American Cancer Society, the Ovarian Cancer Research Alliance, the Pershing Square Sohn Cancer Research Alliance, and other organizations. His research has contributed to publications in leading journals including Science, Nature, Immunity, and Cancer Cell.

Arthur VanValkenburg, PhD

Arthur VanValkenburg, Ph.D., is a Supervising Research Scientist at Rutgers University specializing in tuberculosis, with a focus on the interactions between malnutrition, treatment, and the host immune response. He completed his postdoctoral training at Boston University with Dr. W. Evan Johnson, characterizing immune signaling differences between malnourished and well-nourished individuals with latent tuberculosis infection.

Dr. VanValkenburg earned his Ph.D. from the University of Alabama at Birmingham, where he investigated the roles of CD19 and HSH2 in regulating class-switched antibody production in B cells.

Darin Wiesner, PhD

Dr. Wiesner performed his doctoral training at the University of Minnesota in the Microbiology, Immunology & Cancer Biology graduate program. His PhD dissertation focused on the induction, suppression, and detrimental consequences of helper T cell responses to pulmonary fungal infections. During his postdoctoral fellowship at the University of Wisconsin Madison, he expanded this interest in T cells and fungi to examine how proteolytic allergen damage to the airways is sensed and responded to by lung epithelial cells to drive allergic T cell sensitization and asthma. Dr. Wiesner joined faculty at Rutgers-NJMS in the Fall of 2021 where his lab investigates how stromal tissues in the lung impact T cell responses to fungal pathogens and allergens.

Yingda "Linda" Xie, MD

Yingda (Linda) Xie is an infectious diseases physician-scientist with an interest to find tuberculosis when it least wants to be found. Linda's research team conducts clinical and translational studies in tuberculosis diagnostics, biomarkers, and AI-interpreted clinical imaging for difficult-to-detect tuberculosis. Their interests include detecting and treating TB at an early stage before it spreads or progresses to disease, multiplexing TB detection with other respiratory diseases, and applying clinical imaging ranging from point-of-care ultrasound to PET/CT scans to predict TB disease status and treatment response.

Trainee Abstract Awardee:

Maria I. Velez Brochero

Maria Velez-Brochero is a 4th-year Ph.D. candidate at Rutgers School of Graduate Studies and a member of Dr. Amariliz Rivera's lab in the Center for Immunity and Inflammation at Rutgers Health. Her research focuses on neutrophil heterogeneity and interferon-mediated regulation of antifungal immunity during pulmonary Aspergillus fumigatus infection.

Talk

Understanding host factors that maintain a healthy microbiome through weaning and beyond

Dr. Nicholas J. Bessman, PhD
Assistant Professor
Rutgers NJMS, Department of Microbiology, Biochemistry and Molecular Genetics

Bifidobacterium is a genus of probiotic commensal bacteria exhibiting various health-promoting effects in humans. As a dominant genus in the gut of breast-fed infants, Bifidobacterium is critical for intestinal barrier function, infection prevention, and anti-inflammatory and anti-cancer responses. Despite its prominent role in long-term health, Bifidobacterium is replaced by diverse microbiome communities after weaning in many individuals. Efforts to reintroduce Bifidobacterium in adults frequently fail for unclear reasons. Thus, uncovering the factors impacting intestinal persistence and probiotic function of Bifidobacterium is necessary to develop new strategies to maintain this beneficial microbe throughout weaning and later life, to prevent inflammatory and infectious disease. To this end, we have begun to evaluate host factors of Bifidobacteria persistence. In ongoing work in the lab, we are studying dietary and bacterial factors that regulate Bifidobacteria persistence and mammalian health.

Talk

Oncoviral Integrations as Drivers and Therapeutic Vulnerabilities in Cancer

Dr. Jian Cao, PhD
Assistant Professor
Rutgers RWJMS, Department of Medicine, Cancer Institute of New Jersey

Seven well-established human oncoviruses collectively contribute to approximately 10-15% of human cancers, with hepatitis B virus (HBV) and human papillomavirus (HPV) representing two of the most important cancer-associated viruses worldwide. Although integration is not required for the normal life cycle of either HBV or HPV, viral integrations are found in the vast majority of HBV- and HPV-associated tumors, suggesting important roles in cancer development. We and others have found that HBV integrations are enriched in hotspot genes in tumors and can induce chromosomal translocations. By investigating the mechanisms and consequences of these events, we identified novel oncogenic mechanisms through which HBV integration contributes to hepatocellular carcinoma. In contrast, HPV integrations in tumors often form complex virus-host genomic structures that sustain E6 and E7 oncogene expression, with less recurrence in specific host genes. This persistent viral oncogene expression not only drives tumor maintenance but also creates therapeutic opportunities. Because HPV E6 and E7 are viral, tumor-specific antigens required for malignant survival, they represent attractive targets for TCR-engineered T cell therapy. In parallel, the chromatin dependencies that sustain E6/E7 transcription create opportunities for epigenetic therapeutic strategies. Together, these studies illustrate how defining the mechanisms and consequences of viral integration can reveal principles of virus-induced carcinogenesis and create opportunities for targeted treatment.

Talk

Uncovering the microbial contributors to the development of inflammatory bowel disease

Dr. Lea Ann Chen, MD
Assistant Professor; Director of Inflammatory Bowel Disease Translational Research
Rutgers RWJMS, Department of Medicine

Host genetics has long been recognized as a key determinant of inflammatory bowel disease (IBD) susceptibility. However, growing epidemiologic and mechanistic data indicate that environmental exposures—particularly those that shape the gut microbiome—play a central role in disease initiation and progression. Our laboratory seeks to define the specific microbial taxa and functions that contribute to disease pathogenesis, as well as those that confer protection. To do so, we focus on individuals who are discordant for genetic risk and disease status (i.e., those who develop IBD despite low genetic susceptibility and, conversely, those who remain disease-free despite high genetic risk.) Utilizing study designs leveraging genotype-phenotype discrepancy , we have identified microbiome features, functional pathways, and associated fecal metabolites linked to IBD risk, highlighting candidate microbial drivers of disease development.

Talk

Cryptococcosis from Bedside-to-Bench and Back Again: Probing the breadth of the Clinical Parabola

Dr. Jessica Hargarten, PhD
Assistant Professor
Rutgers NJMS, Department of Pathology, Immunology, and Laboratory Medicine

The Hargarten Lab is interested in understanding why some people develop severe disease when they encounter fungi, and others don't, through studying human infections with Cryptococcus. Cryptococcosis primarily affects individuals with advanced immunosuppression, including those with HIV/AIDS, solid organ transplants, or prolonged corticosteroid exposure; however, little is known about why otherwise healthy persons develop severe disease. In the present studies, the largest cohort of previously healthy cryptococcosis patients were investigated to determine underlying immune deficiencies leading to susceptibility during primary infection and exuberant neuroinflammation during the post-infection period. Our goal is to utilize this information to inform patient risk stratification and develop precision medicine approaches to restore host immunity and minimize post-infectious inflammation. Through whole-exome sequencing analysis of this patient cohort, we recently identified clusters of potentially deleterious genetic defects in patients that fall within biological and immunological pathways previously unexplored in the context of fungal disease, including MTOR signaling. Ongoing experiments, utilizing MTOR-flox mice and human cells, aim to further elucidate MTOR's role in immunity and the unique susceptibility to this important fungal pathogen. Additionally, through transcriptional analysis of patient cerebral spinal fluid, we have identified the predominant pathway underlying post-infection neuroinflammation in this cohort, which can be successfully inhibited to improve clinical response.

Talk

Protective and Pathogenic Immunity Across Orthoflavivirus Exposure Histories

Dr. Bobby Brooke Herrera, PhD
Assistant Professor
Rutgers RWJMS, Department of Medicine

Orthoflaviviruses, including yellow fever virus (YFV), dengue virus (DENV), and Zika virus (ZIKV), co-circulate across large regions of the world, where sequential viral exposures generate complex immune landscapes that can profoundly alter susceptibility to subsequent infection and disease outcomes. Yet the mechanisms through which cumulative orthoflavivirus immune histories shape protection versus pathology remain incompletely understood. Our work has focused on defining how heterologous immunity modulates viral control, antibody-dependent enhancement (ADE), and T cell-mediated cross-protection across sequential orthoflavivirus exposures. Using integrated seroepidemiological studies, functional immunological assays, and murine challenge models, we demonstrate that isolated YFV immunity alone produces limited enhancement phenotypes, whereas cumulative exposure histories involving DENV and ZIKV generate increasingly complex and concentration-dependent ADE profiles. In Fcγ receptor-bearing cells, plasma from individuals

with multiple orthoflavivirus exposures exhibited broad enhancement activity against heterologous viruses, while passive transfer studies in IFNAR1$^{-/-}$ mice revealed exposure-dependent modulation of viremia, disease severity, and survival following ZIKV and DENV challenge. Importantly, enhancement phenotypes were highly dose-dependent, identifying immunological "risk windows" shaped by antibody concentration and prior exposure composition. In parallel, our mechanistic studies demonstrate that YFV-17D immunity can also mediate potent heterologous protection against DENV-2 infection through cross-reactive T cell responses rather than neutralizing antibodies. YFV-17D-elicited CD4^{+} and CD8^{+} T cells recognized conserved DENV non-structural proteins, exhibited cytotoxic activity against DENV antigen-pulsed targets, and significantly reduced viremia, weight loss, and disease severity following challenge. Together, these findings support a model in which sequential orthoflavivirus exposures generate competing immunological forces, where cross-reactive antibodies may enhance infection under defined conditions while heterologous T cell immunity can simultaneously mediate protection. These studies provide mechanistic insight into the immunological architecture underlying orthoflavivirus endemicity, outbreak severity, and vaccine responses, with important implications for next-generation flavivirus vaccine design and global immunization strategies.

Talk

Early-Life Multi-Omic Programming of Immune and Inflammatory Trajectories in Lung Disease

Dr. Priya Kachroo, PhD
Assistant Professor
Rutgers NJMS, Department of Biomedical Health Informatics, School of Health Professions

Understanding how immune and inflammatory diseases originate across the life course requires integrating molecular, environmental, and clinical data. Our work applies machine learning and multi-omic approaches including genomics, epigenomics, transcriptomics, and metabolomics to uncover biomarkers and mechanisms that shape respiratory health from early life through adulthood. Leveraging population cohorts, clinical trials, and electronic health records, we investigate how early-life exposures particularly in utero environmental insults such as tobacco smoke reprogram the regulatory epigenome and influence immune-related pathways involved in lung development, inflammation, and disease susceptibility. Multi-omic integration frameworks reveal coordinated molecular signatures linking oxidative stress, lipid metabolism, and immune response pathways that persist across the life course. We further demonstrate the translational potential of these approaches by identifying clinically relevant metabolomic signatures associated with asthma heterogeneity and treatment response, bridging molecular insights with real-world patient outcomes. Together, this work highlights how integrating multi-scale data can uncover biologically meaningful immune trajectories, enabling earlier risk stratification and advancing precision medicine strategies for inflammatory lung diseases.

Talk

Introduction to the Center for Biomedical Informatics and Health Artificial Intelligence (BMIHAI) at Rutgers Health

Dr. Leslie Lenert, MD, MS, FACMI, FACP
Professor; Founding Director of BMIHAI
Rutgers RWJMS, Department of Medicine

The Center for Biomedical Informatics and Health AI was established to serve as the catalyst for a transformative effort that establishes Rutgers as a national and international leader in computational medicine and health AI. The overarching goal is to bring together substantial existing, but currently siloed, strengths in the broad area of biomedical informatics, including bioinformatics, clinical informatics, clinical research informatics, public health informatics, translational bioinformatics, etc., and substantially expanding them, especially in the area of health AI, making them collectively much more than the sum of their parts. Dr. Lenert joined BMIHAI as its Founding Director in November of 2025. In this talk he

will detail the progress of the Center since its initial funding as a Roadmaps initiative and its future plans for transformation of science and education in Rutgers Health.

Talk

NK-based immunotherapy (CAR-NK) for treatment of cancer

Dr. Dongfang Liu, PhD
Professor
Rutgers NJMS, Department of Pathology, Immunology, and Laboratory Medicine

Natural killer (NK) cells provide a promising platform for "off-the-shelf" cancer immunotherapy because of their intrinsic antitumor activity, favorable safety profile, and compatibility with allogeneic cell therapy. My recent work has focused on overcoming key barriers in CAR-NK translation, including efficient NK and CAR-NK cell expansion, solid-tumor targeting, NK and CAR-NK product potency prediction. At Rutgers-NJMS, my laboratory developed a 721.221-mIL21 feeder-cell platform for robust NK and CAR-NK expansion, supporting scalable production with strong function, purity, consistency, and reduced cost.

Using this platform, we developed CD147-CAR-NK cells for hepatocellular carcinoma and other CD147-positive solid tumors, demonstrating potent antitumor activity and encouraging safety in preclinical models. In parallel, we established "immunological synapse quality" as a functional biomarker and combined high-resolution imaging with machine learning to predict CAR immune-cell efficacy. Together, these studies integrate NK cell biology, CAR-NK engineering, scalable manufacturing, and AI-enabled potency prediction, providing a translational foundation for next-generation CAR-NK therapies for cancer.

Talk

Gut Microbiota from HIV-Exposed Uninfected Infants Causally Alters Growth, Bone and Immune Development

Dr. Donald Nyangahu, PhD
Assistant Professor
Rutgers RWJMS/CABM, Department of Pharmacology

Combination antiretroviral therapy (cART) has led to a decline in vertical HIV transmission and a growing population of infants who are exposed to HIV but uninfected (iHEU). Despite being uninfected, iHEU exhibit higher mortality risk, impaired growth, bone development, suboptimal responses to some vaccines, and neurodevelopmental delays compared to infants who are HIV-unexposed and uninfected (iHUU). The mechanism(s) underlying these adverse outcomes remain poorly understood. We hypothesized that differences in the very early-life gut microbiota of iHEU contribute directly to these developmental phenotypes. To test this, we performed fecal microbiota transplantation experiments using stool collected from iHEU and iHUU neonates during the first week of life (days 4-7). Neonatal germ-free mice were transplanted with neonatal donor stool and assessed for growth, immune, brain and bone phenotypes at weaning. We also evaluated vaccine response using BCG, a TH1 inducing vaccine. We find that early-life HEU gut microbiota can causally drive adverse developmental outcomes, highlighting the importance of the pioneer microbiome in shaping child health.

Talk

BLTP3A restrains lysosomal stress–licensed STING immunity in ovarian cancer

Dr. Kyle Payne, PhD

Assistant Professor
Rutgers RWJMS, Department of Medicine, Rutgers Cancer Institute

High-grade serous ovarian cancer remains one of the most lethal gynecologic malignancies, despite the fact that many tumors contain T cells capable of recognizing cancer-associated antigens. This paradox suggests that ovarian tumors do not simply evade immunity by excluding T cells, but by actively shaping whether those T cells become protective.
Our work identifies BLTP3A, a bridge-like lipid transfer protein, as a tumor-intrinsic regulator of this process. We discovered that a germline nonsynonymous variant in BLTP3A — rs13205210, encoding M1098T — is associated with markedly improved survival in patients with high-grade serous ovarian cancer. Tumors harboring this variant show increased cytotoxic T cell infiltration, suggesting that impaired BLTP3A function may create a more immune-permissive tumor microenvironment. Using syngeneic ovarian cancer models, we find that tumor-intrinsic Bltp3a deficiency recapitulates this protective phenotype, prolonging survival through a $CD8^+$ T cell–dependent mechanism. Rather than acting directly on T cells alone, BLTP3A loss rewires tumor stress signaling and promotes inflammatory remodeling of the tumor myeloid compartment, including the emergence of a $CXCL9^+$ macrophage state required for optimal antitumor immunity. Mechanistically, our data suggest that BLTP3A links endolysosomal trafficking to innate immune signaling. Loss of BLTP3A alters STING compartmentalization under lysosomal stress, sustains TBK1/IRF3 activation, and amplifies interferon-stimulated gene programs. Together, these findings define BLTP3A as a stress-responsive brake on tumor-intrinsic inflammation and reveal a previously unrecognized endolysosomal–innate immune axis that may be leveraged to enhance protective T cell immunity in ovarian cancer.

Talk

Decoding the Adaptive Immune Repertoire: Computational Tools, Limits, and Trust for Disease Research

Dr. Arthur VanValkenburg, PhD
Supervising Research Scientist; Director, Center for Data Science
Rutgers New Jersey Medical School

The adaptive branch of the immune system enables defense against pathogens by generating diverse T cell receptor (TCR) and B cell receptor (BCR) repertoires through clonal expansion, selection, V(D)J recombination, class-switch recombination and somatic hypermutation (B cells). These processes produce expansive receptor repertoires; however, the sheer number of BCR/TCRs generated in response to infection has made identification of infection and disease-relevant clones difficult. Recent advances in repertoire sequencing and analysis have enabled important insights across infection, disease, and clinical outcomes. Here we present the available computational tools and methods, summarize recent benchmark evidence on their accuracy and limits, and offer a defensible analysis stack to help immunology labs better understand adaptive immune function in modulating infection and disease outcomes.

Talk

Barrier immunity to inhaled fungi

Dr. Darin Wiesner, PhD
Assistant Professor
Rutgers NJMS, Department of Medicine

The lung mucosa serves as a critical barrier to inhaled pathogens, including *Coccidioides*, the causative agent of Valley Fever, yet infection outcomes range widely from asymptomatic disease to severe pulmonary illness requiring prolonged antifungal therapy and, in some cases, fatal dissemination. Because exposure is common in endemic regions while only a subset of individuals develop severe disease, host–pathogen interactions during the earliest stages of infection are likely key determinants of outcome. *Coccidioides* spores are particularly vulnerable to host defenses before they transition into spherules, underscoring the importance of immune responses within the first 24 hours after inhalation. To define these

early events, we investigated lung barrier immunity, which integrates structural and immune components including epithelial cells lining the conducting airways and alveoli, as well as alveolar macrophages in the terminal airspace. Although many cellular and molecular pathways involved in host defense are increasingly understood, the spatial coordination of these responses at sites of initial spore deposition remains unclear. To address this gap, we developed an experimental pipeline combining precision-cut lung slices (PCLS), tissue optical clearing, immunostaining, spinning disk microscopy, and machine-learning analysis to quantify spatial relationships and dynamic changes within the tissue-immune environment. Our findings reveal marked heterogeneity within the airway microenvironment and provide a spatial framework that links prior observations of epithelial sensing in both bronchioles and alveoli. Ongoing studies are focused on defining the distinct roles of club cells and type II alveolar epithelial cells in coordinating neutrophil recruitment through specific vascular portals, further advancing our understanding of lung barrier immunity to fungal pathogens.

Talk

Imaging New Frontiers in Tuberculosis: From Point-of-Care Screening to Early Disease Detection

Dr. Yingda “Linda” Xie, MD
Assistant Professor
Rutgers NJMS, Division of Infectious Diseases, Department of Medicine

Tuberculosis exists across a broad spectrum, from asymptomatic and paucibacillary disease to clinically apparent illness, yet current diagnostic approaches often detect disease only after substantial pathology has developed. This talk will discuss how imaging can help reveal earlier and less clinically obvious forms of TB, with a focus on two emerging approaches: point-of-care ultrasound for scalable community-based screening, and chest X-ray/CT imaging to better characterize early TB pathology and progression risk. Using examples from ongoing studies in TB patients and household contacts, the talk will highlight how portable and field-adapted imaging tools may complement sputum-based testing, improve active case finding, and support more nuanced evaluation of disease burden and treatment-relevant pathology. The discussion will also consider how imaging signatures, when integrated with clinical and microbiologic data, may help identify individuals who are missed by conventional diagnostics or who are at increased risk of progression. Together, these approaches point toward a more staged and precise framework for TB diagnosis and treatment evaluation, with translation into real-world settings.

POSTERS

1. Eden Hirsch - NK Cell Regulation of ICOShi Tfh Cells during Acute Viral Infection
2. Ensueno Saenz Altamirano - SARS-CoV-2 NSP14 Induces Internal m7G RNA Modifications and Rewires Host Splicing
3. Yen-fei Wu - The function and regulation of viperin-generated antiviral nucleoside analog ddhC during influenza infection
4. Chien-hsin Huang - Uncovering the Role of Viperin-Derived ddhC in Influenza Pathogenesis
5. Nicole Schwardt - Determining the role of SLC7A2 in the development and function of alveolar macrophages
6. Anjali Gupta - Identification and functional characterization of internal m^7G epitranscriptomic modifications in positive-sense RNA virus genomes
7. Alcina Alex Rodrigues - Role of methionine metabolism in NK cell function
8. Joaquin Moreno Contreras - Lung Fibroblasts Promote Early Neutrophilic Detrimental Inflammation During Viral Infections via a TRIM6-PI3K-CXCL1 Pathway
9. Cole Santucci - The regulation of liver cNKs and ILC1s by lysophosphatidic acid (LPA)
10. Yoatzin Penaflor-Tellez - The ubiquitination landscape during Ebola virus infection reveals cellular targets of immune dysregulation
11. Padmanava Behera - Mannose Receptor Type C1 (CD206) Promotes Ebola Virus Entry by Interacting With GP
12. Afia Nkansah - Staphylococcus aureus-induced metabolic reprogramming of innate immunity during tissue repair following thermal injury
13. Ahri Han - Investigating Mycobacterium tuberculosis-induced changes to macrophage migration
14. Eric Tang - Ketogenic diet improves airway clearance of Klebsiella pneumoniae by neutrophils
15. Neil Reddy - Extracellular Matrix Stiffening Activates IL-33/ST2 Signaling to Drive Lymphatic Endothelial Dysfunction in Lymphedema
16. Ting-yu Chu - Investigating lipid-laden phenotypes of tumor-associated macrophages causing KRAS inhibitor therapy resistance in pancreatic ductal adenocarcinoma
17. Naoya Tatsumi - Sequential priming by distinct dendritic cell subsets shapes effector CD4 T cell fate
18. Samhita Bapat - Stat3 regulates late-phase innate immune response during tissue repair
19. Marissa Schroeter - The serotonin receptor 5'HTR2c regulates alveolar macrophage responses post-helminth infection
20. Grace Smithwick - Extracellular Matrix Stiffening Activates IL-33/ST2 Signaling to Drive Lymphatic Endothelial Dysfunction in Lymphedema
21. Isha Pandey - Depletion of alveolar macrophages increases disease severity during SARS-CoV-2 infection in mice
22. Roshni Nagesh Kadam - Characterization of immunogens in a heat-inactivated whole cell based fungal vaccine

23. Joycelyn Radeny - No title listed

24. Shruti Chatterjee - Impact of Spike Mutations on MERS-CoV Fitness, Stability, and Transmission

25. Arman Sawhney - Investigating the regulatory mechanisms of helminth-mediated neuroinflammation

26. Amirhossein Abazarikia - Effects of Tirzepatide, a Dual GLP-1/GIP Receptor Agonist, on Ovarian Follicles in Mice

27. Trevor Frederick - Investigating the Use of IFNλ as an Anticancer Therapeutic in Colorectal Cancer

28. Nadia Domingo - Contributions of Microglia Cytokines to Cerebral Thrombosis in Experimental Models of Cerebral Malaria

29. Jisun Kim - The electron transport chain in Staphylococcus aureus impacts antibiotic tolerance through membrane charge remodeling

30. Paul Brennan - Early Innate Immune Cell Responses to Inhaled Coccidioides Spores in the Lung

Notes