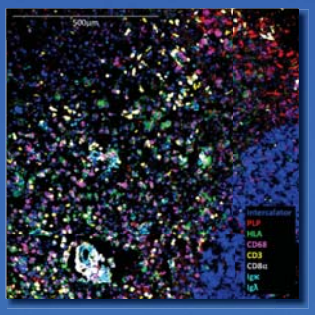

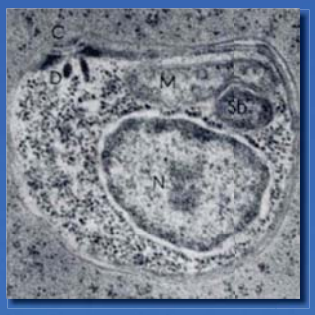

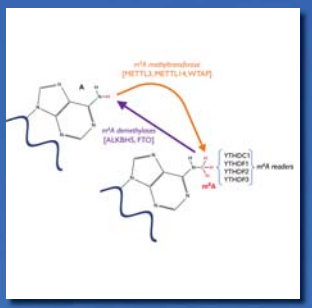

College of Medicine – Tucson
Department of Immunobiology

Sixteenth Annual

Virtual Frontiers in Immunobiology & Immunopathogenesis Symposium

Friday, March 5, 2021

Registration: January 4, 2021 — March 5, 2021
Abstract Submission: January 4, 2021 — February 5, 2021

Plenary Speakers

Jennifer Gommerman, Ph.D. *(Immunologist)*
University of Toronto
Understanding Multiple Sclerosis progression using translational and reverse-translational approaches

Ellen Yeh, M.D, Ph.D. *(Parasitologist)*
Stanford University
Searching away from the streetlight: surprises in the malaria plastid organelle

Ian Mohr, Ph.D. *(Virologist)*
New York University Langone Health
Control of Innate Immunity by rRNA Accumulation & RNA Modification by N⁶-adenosine Methylation Enzymes

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Welcome to the 16th annual Frontiers in Immunobiology & Immunopathogenesis Symposium. We have tried our best to keep the same level of science for you this year, but in an online format through Accelevents (https://www.accelevents.com/e/2021IMBSymposium). Here you can see the schedule, see our sponsors Fisher Scientific and Greiner Bio-One, have others register (in case you want to share with them the great talks or posters that you will see or are seeing), or enter the event (once the event starts of course). Entering the event allows you to see all the event links to the talks, posters, and speed networking that will occur throughout the day. Going to a talk or poster session within Accelevents should look familiar, as we are using Zoom as our base for this platform.

This symposium will feature great scientific talks that will hopefully lead to many thought-provoking moments. The symposium is headlined by our plenary speakers Drs. Ellen Yeh, Jennifer Gommerman, and Ian Mohr. We will also feature trainee talks, two faculty talks, and a much needed talk on science policy from Research!America.

Like last year, there will be posters. This year, we will have two 40-minute sessions instead of one big one at the end. You can use the Accelevents platform to go from poster to poster, jumping in and out as you would at a real poster session. Posters should also be available to download to view independently (as one might look from afar before approaching a poster).

Also like last year, there will be a door prize of an iPad. Going to sponsor sessions will be the only way to be eligible (and the winner needs to be present at the end). Each vendor for each session they present will have a code that you can put into a form with your name, and the winner will be randomly drawn. That means the more you visit the vendors' different sessions, the better your chances!

Unlike last year, we will miss out on some of those organic in-person "learning about each other's science" moments. For that, we have added a "speed networking" session. Here you will be randomly paired with someone for 3 minutes and then moved to the next person, and so on for a 25-minute period. We highly encourage participation as that will make this science-sharing session work the best. We hope this speed networking session will allow you to talk science with someone you had never talked to about it before, as it will be a fun way to build new relations.

If you have any questions on where to go, we encourage you to explore the Accelevents website. If things aren't working once in the event, please click the lounge on the left panel and go to the "help lounge" where we are standing by to help you. While we would rather you use Accelevents for this event, as a last resort the Zoom link for the major talks is https://arizona.zoom.us/j/83057582365 password: 2021, and the chat for assistance there will always be open.

In closing, we truly hope you enjoy the 16th annual Frontiers in Immunobiology & Immunopathogenesis Symposium. We hope you leave inspired and encouraged that we can overcome all sorts of barriers to facilitate the production and discourse of great science.

Sincerely,

Michael, Justin, and the 2021 Symposium Committee Team

Agenda - Frontiers in Immunobiology & Immunopathogenesis Symposium

Morning Activities

8:00 - 8:15 AM **Welcome Announcements**
Janko Nikolich-Žugich, MD, PhD
Professor and Department Head, Immunobiology
Co-Director, Arizona Center on Aging

Michael Abecassis, MD, MBA
Dean, University of Arizona College of Medicine-Tucson

Michael D. L. Johnson, PhD
Assistant Professor, Immunobiology

Session I
Moderator: Henrik O'Brien

8:15 - 9:05 AM **Plenary Lecture**, ***Ellen Yeh, PhD***
Stanford University
"Searching Away From the Streetlight: Surprises in the Malaria Plastid Organelle"

9:10 - 9:20 AM *Emily Merritt*
"Are T Cells Recognizing Toxoplasma Injected Neurons"

9:25 - 9:35 AM *Melissa Moy*
"UL136-33kDa Accumulation Drives Increased Expression of Viral Genes Required for Human Cytomegalovirus Reactivation from Latency"

9:40 - 9:50 AM *Yuecheng Xi*
"Human Cytomegalovirus uses a Host Stress Response to Balance the Elongation of Saturated/Monounsaturated and Polyunsaturated Very Long Chain Fatty Acids"

9:55 - 10:05 AM ***A Word From Our Sponsors***

Session II
Moderator: Danielle Becktel

10:05 - 10:15 AM *Sandip Ashok Sonar, PhD*
"Cell-intrinsic and -extrinsic Age-related changes influence the Peripheral Maintenance of Naive T Cells"

10:20 - 10:40 AM *Karen Taraszka Hastings, MD, PhD*
"GILT and MHC Class II in Melanoma: Impact on Immune Recognition"

10:45 - 11:35 AM **Plenary Lecture**, ***Jennifer L. Gommerman, PhD***
University of Toronto
"Understanding Multiple Sclerosis Progression using Translational and Reverse-translational Approaches"

11:40 - 12:20 PM *Poster Session I/Sponsors*

12:25 - 1:25 PM ***Lunch sessions with Plenary***

Session III
Moderator: Tyler Ripperger

1:30 - 1:50 PM *Felicia Goodrum, PhD*
"Sensing and Responding to Host Signals in Regulating Latency and Reactivation"

1:55 - 2:05 PM *Sanna Loppi, PhD*
"Metabolic Reprogramming of the Brain as a New Treatment Approach for Post-Stroke Rehabilitation"

2:10 - 2:30 PM *Mary Woolley*
"Research!America"

2:35 - 2:45 PM ***A Word From Our Sponsors***

2:50 - 3:00 PM *Anne Macy, BS*
"Role of GILT and MHC Class II in Melanoma Cells on Regulating the Anti-tumor Immune Response"

3:05 - 3:55 PM **Plenary Lecture**, ***Ian J. Mohr, PhD***
New York University Langone Health
"Control of Innate Immunity by rRNA Accumulation and RNA Modification by N6- adenosine Methylation Enzymes"

4:00 - 4:10 PM ***A Word From Our Sponsors***

Afternoon Activities

4:15 - 4:40 PM *Speed Networking*

4:40 - 5:20 PM *Poster Session II/Sponsors*

5:25 PM *Poster Awards*

Plenary Lecture

Searching Away From the Streetlight: Surprises in the Malaria Plastid Organelle

Ellen Yeh, PhD

Associate Professor of Biochemistry and of Pathology Stanford University

Plasmodium parasites that cause malaria evolved from photosynthetic algae in the ocean. Despite the drastic change in environment and lifestyle, malaria parasites retained a non-photosynthetic plastid called the apicoplast, which is essential for its infection of humans. From this obscure origin and a twisted evolutionary path, our study of apicoplast biology has been full of surprises including metabolic devolution and hybrid endosymbiotic-endomembrane pathways, highlighting the opportunities in exploring non-model biology.

Plenary Lecture

Understanding Multiple Sclerosis Progression Using Translational and Reverse-Translational Approaches

Jennifer L. Gommerman, PhD

Professor & Associate Chair, Graduate Studies
Department of Immunology
University of Toronto

Evidence from animal models of Multiple Sclerosis (MS) as well as genome-wide association studies and clinical trials in relapsing-remitting MS all point to lymphocytes as being critical mediators of MS pathogenesis. Indeed activated myelin-reactive T lymphocytes are sufficient to passively transfer Experimental Autoimmune Encephalomyelitis (EAE) to naïve mice. We have previously shown that pathogenic encephalogenic T lymphocytes populate the central nervous system (CNS), particularly the sub-arachnoid space of the leptomeninges, during passive EAE. Herein we propose a method for modeling the progressive phase of MS in mice, and we examine how some aspects of this meningeal-resident inflammatory process is recapitulated in human MS tissue. Moreover, taking cues from recent clinical trial data, we find that there are nuanced roles for B lymphocytes in MS/EAE, and that at least some of the B cells that enter the CNS during episodes of neuroinflammation show evidence of microbiota-reactivity. Collectively, our results shed new light on pro- and anti-inflammatory roles for lymphocytes in MS/EAE, and underscore the role of the microbiota in shaping neuroinflammatory processes.

Plenary Lecture

Control of Innate Immunity by rRNA Accumulation and RNA Modification by N6-adenosine Methylation Enzymes

Ian J. Mohr, PhD

Director, Infectious Disease & Basic Microbiological Mechanisms Training Program, New York University Langone Health

Unlike viruses that globally suppress cellular protein synthesis to antagonize innate defenses, host gene expression proceeds during human cytomegalovirus (HCMV) reproduction. Among the numerous cellular genes whose expression is stimulated upon HCMV infection are those involved in ribosome biogenesis and the chemical modification of RNA by N6-adenosine methylation. Studies investigating how these host processes impact innate immune responses to control HCMV productive replication will be presented.

Are T Cells Recognizing Toxoplasma Injected Neurons

***Emily F Merritt*[1], *Hannah J Johnson*[2], *Zhee Sheen Wong, PhD*[5], *Adam Buntzman, PhD*[3], *Austin C Conklin*[4], *Carla M Cabral*[3], *Casey Romanoski, PhD*[4], *John P Boyle, PhD*[5], *and Anita A Koshy, MD*[1,3]**

[1]Department of Immunology, [2]Neuroscience Graduate Interdisciplinary Program, [3]BIO5 Institute, [4]Department of Cellular and Molecular Medicine, University of Arizona, Tucson, AZ, [5]Department of Biological Sciences, Dietrich School of Arts and Sciences, University of Pittsburgh

Toxoplasma gondii is an intracellular parasite that persistently infects the CNS of up to 1/3 of the world's population. Given that host cell-Toxoplasma interactions govern parasite survival and that Toxoplasma persists in neurons, we focus on understanding the Toxoplasma-neuron interaction. To accomplish this goal, we use a unique mouse model system that allows us to identify and track neurons that have been injected with parasite protein. By coupling laser capture microdissection and RNAseq, we were able to transcriptionally profile these Toxoplasma-injected neurons (TINs) compared to neighboring, uninjected neurons, which we call bystander neurons. To our surprise, the TINs transciptomes had an increase in T cell transcripts compared to the bystanders transcriptome, suggesting that T cells were recognizing TINs as infected cells. The idea of T cells recognizing infected neurons is remarkable because, until recently, neurons were considered one of the few cell types that did not express antigen-loaded major histocompatability complex I (MHCI), the key molecule by which T cells identify infected cells. Thus, these data led us to ask "Are T cells recognizing TINs through a T cell-MHCI interaction?" We approached this question by visualizing T cells in the brain: using immunofluorescent staining, confocal imaging, and three dimensional rendering of brain sections. Our preliminary data suggest that, at early time points of infection, T cells are more often in close proximity to TINs compared to bystanders, suggesting a direct interaction could be taking place and T cells may be able to recognize infected cells. Our current work focuses on using the OT-1/OVA model antigen system in neuronal cultures to determine: i) if T cells are recognizing TINs via loaded MHC-I and ii) what the outcome of this interaction is.

UL136-33kDa Accumulation Drives Increased Expression of Viral Genes Required for Human Cytomegalovirus Reactivation from Latency

***Melissa Moy*[1], *Sebastian Zeltzer, PhD*[2], *Katie Caviness, PhD*[4], *Jason Buehler, PhD*[5], *Luwanika Mlera, PhD*[2], *Louis Cicchini, PhD*[6], *and Felicia Goodrum, PhD*[2,3]**

[1]Cancer Biology Graduate Interdisciplinary Program, [2]Bio5 Institute, [3]Department of Immunobiology, University of Arizona, Tucson, AZ, [4]Genomics, National Biodefense Analysis and Countermeasures Center (NBACC), Fort Detrick, MD, [5]Imanis Life Sciences, Rochester, MN, [6]Cytiva, Denver, CO

Human cytomegalovirus (HCMV) is a -herpesvirus that establishes a lifelong latent infection. Latent infections are maintained in hematopoietic progenitor cells (HPCs). Large gaps in our mechanistic understanding of this switch between HCMV latency and reactivation exist. Our work has identified viral genes important to infection and latency in HPCs: UL138 is suppressive to virus replication and required for the establishment of latency, while UL135 is required for reactivation. Recent work suggests that UL136 functions to fine tune the switch between latency and reactivation. UL136 encodes five protein isoforms that accumulate at later times in infection relative to UL135 and UL138, and the isoforms have distinct roles in regulating latent and replicative states in HPCs. The full-length UL136-33kDa protein (p33) is required for reactivation from latency and is strikingly unstable relative to the other UL136 isoforms. Viral genome synthesis triggers increased accumulation of p33. We hypothesize that the rapid turnover of p33 may be important in establishing latency or that increased accumulation of p33 is required for reactivation. In support, stabilization of p33 results in a failure to establish latency and the virus replicates without reactivation stimulus. How p33 concentrations are regulated and how they impact infection is unknown. Here we demonstrate when p33 is stabilized other viral genes required for replication exhibit increased expression. In addition, stabilization of p33 overcomes defects in viral gene expression associated with disruption of UL135, a protein required for reactivation. Taken together, these results suggest a model whereby viral genome synthesis stimulates an increase in p33 concentration that promotes an increase in other viral genes required for reactivation and replication. Our work defines UL136 as a key determinant of the switch controlling latency and reactivation and supports our future mechanistic studies to understand how UL136 functions in reactivation.

Human Cytomegalovirus uses a Host Stress Response to Balance the Elongation of Saturated/Monounsaturated and Polyunsaturated Very Long Chain Fatty Acids

***Yuecheng Xi*,[1] Lena Lindenmayer[3], Ian Kline[1], Jens von Einem[3], and John G. Purdy[1,2]**

[1]Department of Immunobiology, [2]BIO5 Institute, University of Arizona, Tucson, Arizona, [3]Institute of Virology, Ulm University Medical Center, Ulm, Germany

Human cytomegalovirus (HCMV) asymptomatically infects most of the world's population. HCMV causes life-threatening illnesses in immunocompromised people, including transplant recipients and cancer patients. HCMV infection is also a leading cause of congenital disabilities. HCMV infection regulates host lipid metabolism by inducing fatty acid (FA) elongation and increasing the abundance of lipids with very long-chain FA tails (VLCFAs). While molecular-mediators of stress responses can reprogram metabolism, the role of stress in HCMV reprogramming of lipid metabolism is poorly understood. We engineered cells to knockout PKR-like ER kinase (PERK) in the ER stress pathway and measured lipid changes using lipidomics to determine if PERK is needed for lipid changes associated with HCMV infection. In HCMV-infected cells, PERK promotes the increase in the levels of phospholipids with saturated FA (SFA) and monounsaturated FA (MUFA) VLCFAs tails. Consistent with the SFA/MUFA lipidome changes, PERK enhances the protein levels of FA elongase 7 (ELOVL7), which elongates SFA and MUFA VLCFAs. Additionally, we found that increases in the elongation of polyunsaturated fatty acids (PUFAs) associated with HCMV infection was independent of PERK and that lipids with PUFA tails accumulated in HCMV-infected PERK knockout cells. Consistent with the PUFA lipidome changes, the protein levels of ELOVL5, which elongates PUFAs, are increased by HCMV infection through a PERK-independent mechanism. These observations show that PERK differentially regulates ELOVL7 and ELOVL5, creating a balance between the synthesis of lipids with SFA/MUFA tails and PUFA tails. Additionally, we found that PERK was necessary for virus replication and the infectivity of released viral progeny. Overall, our findings indicate that PERK—and more broadly, ER stress—may be necessary for membrane biogenesis needed to generate infectious HCMV virions.

Cell-intrinsic and -extrinsic Age-related Changes Influence the Peripheral Maintenance of Naive T Cells

***Sandip Ashok Sonar, PhD*[1], *Jennifer Uhrlaub, MS*[1], *and Janko Nikolich-Zugich, MD, PhD*[1]**

[1]*Department of Immunobiology, University of Arizona, Tucson, AZ*

The reduced thymic output and altered peripheral maintenance of TN cells contribute to immune decline in the elderly, rendering them more vulnerable to infections, cancer and poor response to vaccination. However, the exact time where these defects occur remains unknown. Using inducible TCRdCre.ER.ZsGreen mouse model, that indelibly marks recent thymic emigrants (RTEs), we longitudinally analyzed the age-related decline of TN cells in SLO during homeostasis. Our data show the early onset (6 months) decline of RTEs in the skin-draining (axillary and inguinal) LNs, while brachial LNs and spleen exhibit delayed (18 months). These defects in the seeding and retention of RTEs are in part due to reduced expression of LN homing chemokine receptor, CCR7, and a transient increase in the surface expression of sphingosine 1-phosphate receptor (S1P1). Interestingly, a similar early decline (6 mo) of TN cells observed when we longitudinally monitored reporter+ T cells generated at 2 months of age for lifelong. Finally, we show that structural and organizational alterations of the LN stromal compartment contribute to defects in the maintenance of newly generated T cells in the SLO. Altogether, this suggests that different SLO undergo age-related changes differently, and warrants mechanistic studies to better understand defects in TN cell peripheral maintenance during aging.

GILT and MHC Class II in Melanoma: Impact on Immune Recognition

Karen Taraszka Hastings, MD, PhD[1]

[1]Department of Basic Medical Sciences, College of Medicine-Phoenix, University of Arizona, Phoenix, AZ

The MHC class I antigen presentation pathway in melanoma cells has a well-established role in immune-mediated destruction of tumors. However, the clinical significance of the MHC class II antigen presentation pathway in melanoma cells is less clear. In antigen presenting cells, gamma-interferon-inducible lysosomal thiol reductase (GILT) is critical for MHC class II-restricted presentation of multiple melanoma antigens. While not expressed in benign melanocytes of nevi, GILT and MHC class II expression is induced in malignant melanocytes in a portion of melanoma specimens. Analysis of The Cancer Genome Atlas (TCGA) cutaneous melanoma dataset showed that high GILT mRNA expression was associated with improved overall survival. Expression of IFN-γ, TNF-α, and IL-1β was positively associated with GILT expression in melanoma specimens. These cytokines were capable of inducing GILT expression in human melanoma cells in vitro. GILT protein expression in melanocytes was induced in halo nevi, which are nevi undergoing immune-mediated regression, and is consistent with the association of GILT expression with improved survival in melanoma. To explore potential mechanisms of GILT's association with patient outcome, we investigated pathways related to GILT function and expression. In contrast to healthy skin specimens, where the MHC class II pathway was nearly uniformly expressed and intact, there was substantial variation in the MHC class II pathway in the TCGA melanoma specimens. Both an active and intact MHC class II pathway were associated with improved overall survival in melanoma. These studies support a role for GILT and the MHC class II antigen presentation pathway in melanoma outcome.

Virus-host Interactions Impacting Human Cytomegalovirus Latency and Reactivation

Sebastian Zeltzer, PhD[2], Kristen Maness[2], Pierce Longmire[2], Jason Buehler, PhD[3], Scott Terhune[4], PhD and Felicia Goodrum, PhD[1,2]

[1]Department of Immunobiology, [2]Bio5 Institute, University of Arizona, Tucson, AZ, **,** *[3]Imanis Life Sciences, Rochester, MN, [4]Medical College of Wisconsin, Milwaukee, WI*

Human Cytomegalovirus (HCMV) is a beta herpesvirus that persists in majority of the population through the establishment of viral latency. HCMV latency occurs in hematopoietic cells through complex virus-host interactions that remain incompletely defined, as do the stress and differentiation pathways that trigger reactivation. Decisions to enter or exit latency have to be carefully negotiated in a noisy background of cellular inputs. Our research focuses on defining modulators of the decisions to enter and exit latency. We have defined a locus of genes spanning UL133-UL138 that are dispensable for virus replication in fibroblasts, but either impede or stimulate virus replication in hematopoietic cells. We have identified UL138 as a viral determinant of latency. When UL138 is disrupted, infected hematopoietic cells support a replicative rather than a latent infection, suggesting a suppressive role for UL138 in establishing latency. We have focused on interaction between UL138 and host factors in an effort to understand the mechanism by which UL138 contributes to latency. We have defined an interaction between UL138, ubiquitin specific peptidase-1 (USP1) and its scaffold protein, WDR48. WDR48 activates the deubiquitinase activity of USP1, which functions to downregulate the DNA damage response, while sustaining a pIRF3/pSTAT1 innate immune response. We have shown that UL138 activates USP1 activity, impacting the ubiquitination of DNA damage response and replication factors, PCNA and FANCD2, and the activity of pIRF3 and pSTAT1. The importance of the UL138-USP1 interaction is that loss of USP1 results in a loss of latency, marked by viral replication in hematopoietic cells in the absence of a stimulus for reactivation. This phenotype depends on the presence of UL138. Further, the DNA damage pathways and repair mechanisms factor importantly into HCMV genome synthesis and replication. This work advances our understanding of viruses sense and respond to cellular cues to modify infection programs. Ongoing studies are aims at understanding how DNA damage and innate immune pathways function in regulating latency and reactivation. The studies may provide insight as to how DNA damage and innate pathways are integrated.

Metabolic Reprogramming of the Brain as a New Treatment Approach for Post-Stroke Rehabilitation

***Sanna Loppi, PhD*[1], *Jennifer Frye*[1], *Jacob Zbesko, PhD*[1], *Helena Morrison, PhD RN*[2], *Marco Tavera-Garcia*[1], *Frankie Garcia*[1], *Natalie Scholpa, PhD*[3], *Rick Schnellmann, PhD*[3], *and Kristian Doyle, PhD*[1]**

[1]Department of Immunobiology, [2]College of Nursing, [3]College of Pharmacy, University of Arizona, Tucson, AZ

Ischemic stroke reduces the flow of oxygen and nutrients to the brain and can cause long-lasting disturbances in brain energy metabolism. There are no pharmacological treatments available to help people recover from stroke, and approximately one third of patients experience cognitive decline in the first year after the ischemic attack. Stroke research is in desperate need of novel approaches to help understand the mechanisms that govern the balance between cell death and cell survival in the weeks and months following stroke, and thus discover methods for enhancing recovery. To that end, we are exploring the approach that inducing mitochondrial biogenesis (MB) may be able to mitigate stroke induced deficits in brain energy metabolism. Specifically, the goals of this study are to I.) use global precision liquid chromatography mass spectrometry (LC-MS) metabolomics to determine how stroke alters metabolic homeostasis in the brain over time, and II.) test if the beta-2 adrenergic receptor agonist formoterol can induce MB, restore mitochondrial function and improve recovery after experimental stroke. We have previously shown that the beta-2 adrenergic receptor agonist formoterol is a potent inducer of MB and improves recovery from spinal cord injury. Our preliminary data indicate that stroke alters fatty acid and glucose metabolism in the brain, and that these changes persist for at least 7 weeks after stroke. Our preliminary data also show that formoterol treatment starting 24 hours following stroke is able to induce MB, reverse these effects, and bring the metabolic profile towards that of a healthy brain two weeks after ischemia. However, formoterol treatment also increased microglial activation and cytokine secretion, and worsened behavioral outcome. Therefore, we are currently modifying our treatment paradigm to determine if we can optimize the therapeutic effects of formoterol on brain energetics, while mitigating its negative effects on brain inflammation.

Research!America

Mary Woolley

The Research!America alliance advocates for science, discovery, and innovation to achieve better health for all. Together, with our member organizations that represent a vast array of medical, health and scientific fields, our goals are:

- Achieve funding for medical and health research from the public and private sectors at a level warranted by scientific opportunity and supported by public opinion.
- Better inform the public of the benefits of medical and health research and the institutions that perform research.
- Motivate the public to actively support medical and health research and the complementary sciences that make advances possible.
- Promote and empower a more active public and political life by individual members of the research community on behalf of medical and health research, public health, and science overall.

Role of GILT and MHC Class II in Melanoma Cells on Regulating the Anti-tumor Immune Response

***Anne M. Macy, BS*[1], *Anngela C. Adams, MS*[1], *Karla F. Castro-Ochoa, PhD*[1], *Paul Kang, MS*[2], *MPH, Alexandra Charos, MD, PhD*[3], *Marcus Bosenberg, MD, PhD*[3], *and Karen Taraszka Hastings, MD, PhD*[14]**

[1]College of Medicine – Phoenix, [2]College of Public Health, University of Arizona – Phoenix, Phoenix, AZ, [3]Department of Dermatology, Yale University, New Haven, CT, [4]Arizona Cancer Center, University of Arizona, Tucson, AZ

The MHC class I antigen presentation pathway in melanoma cells has a well-established role in immune-mediated destruction of melanoma. However, the role of the MHC class II pathway in melanoma cells is not fully understood. Gamma-interferon-inducible lysosomal thiol reductase (GILT) is critical for MHC class II-restricted presentation of multiple melanoma antigens by antigen presenting cells. While GILT and MHC class II expression is typically limited to antigen presenting cells, GILT and MHC class II can be expressed constitutively or induced by IFN-γ in melanoma cells. In human melanoma specimens, high GILT expression and an active and intact MHC class II pathway are associated with improved survival. The goal of this project is to investigate a causal role for GILT and MHC class II in melanoma cells, using immunogenic Yale University Mouse Melanoma (YUMM) lines YUMM2.1, YUMMER1.7, and YUMMERG. These cell lines contain driver mutations present in human disease and respond to immune checkpoint blockade with anti-PD-1. These lines constitutively expressed GILT, and MHC class II expression was IFN-γ-inducible in a subset of cells under serum-free conditions. YUMM2.1 was selected as the primary model to assess the role of the MHC class II pathway in in vivo immune-mediated tumor destruction, because YUMM2.1 cells reliably formed tumors in mice and had high IFN-γ-inducible MHC class II expression in vitro and high MHC class II expression in vivo. We have genetically engineered YUMM2.1 cells without GILT and without MHC class II, verified the deletion, and selected clones with similar in vitro proliferation as the wild-type YUMM2.1 cells. We are in the process of determining the in vivo tumor growth and phenotype of the tumor-infiltrating T cells in MHC class II-/- and GILT-/- YUMM2.1 tumors compared to wild-type tumors.

Poster Titles

Poster Session 1

Poster	Author	Abstract Title
1	Kiah Sleiman	Tracking Th17-derived Tfh Cells in Germinal Centers
2	Yanmei Hu	Targeting Host and Viral Protease to Combat COVID-19
3	Anngela C. Adams	Solar Simulated Light Induces Cutaneous Squamous Cell Carcinoma in Inbred Mice: A Clinically Relevant Model to Investigate T Cell Responses
4	Kristen Maness	HCMV Latency Protein pUL138 Modulates STAT1 Signaling
5	Advait Jeevanandam	Role of Human Papillomavirus L2 C-terminus Cationic Region in Endosomal Membrane Destabilization and vDNA Trafficking
6	Kathryn McGovern	Amyloid Beta Protects Elderly Mice from Succumbing to Infection with Toxoplasma gondii.
7	Belen Molina	Human Cytomegalovirus Infection in Endothelial Cells Induces the Secretory Autophagy Pathway for Egress.

Poster Session 2

Poster	Author	Abstract Title
8	Natalie Iannuzo	Loss of Club Cell Secretory Protein Impacts Epithelial Response to Pathogen Challenge
9	Pierce Longmire	HCMV Hijacks Host DNA Damage Response for Latency
10	Luwanika Mlera	Human Cytomegalovirus Reorganizes Endothelial Cell Exosomes by Changing Protein Composition
11	Maria Love	Genetic Characterization of HIV-1 env and vpr genes from HIV-Infected Older Patients with Controlled Viremia on ART
12	Stephanie Lambert Tribble	Regulation of DCLK1 by the PRR, AIM2, During a Type 2 Innate Immune Response
13	Shio Kobayashi	A Biomimetic 5-Module Chimeric Antigen Receptor (5MCAR) Designed to Target Pathogenic T Cells
14	Josh Kochanowsky	Developing Platforms to Identify Host and Parasite Factors that Drive Toxoplasma gondii Strain-specific Differences in Encystment
15	Ian Kline	Human Cytomegalovirus Infection Promotes de novo Phosphatidylcholine Lipid Synthesis
16	Dakota Reinartz	Role of AIM2 in Head and Neck Squamous Cell Carcinoma Carcinogenesis
17	Mark Lee	Evolution has Imposed a Functional Requirement for CD4-Lck Association

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