BIOGRAPHICAL SKETCH

NAME: Dewey Mitchel Magee

eRA COMMONS USER NAME (credential, e.g., agency login): mmagee1

POSITION TITLE: Research Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Texas Medical Branch, Galveston, TX	B.S.	1978	Medical Technology (ASCP) 123098
Texas A&M University, College Station, TX	Ph. D.	1985	Microbiology
The University of Pittsburgh, Pittsburgh, PA	Post-Doc	1987	Infectious Diseases

A. Personal Statement

D. Mitchell Magee joined the Virginia G Piper Center for Personalized Diagnostics as part of a team of scientists and engineers to assist with discovery of high throughput methods for analysis of protein-protein interaction and biomarker discovery. He attended the University of Texas Medical Branch and obtained a B.S. in Medical Technology. After several years' experience in clinical and research laboratories, he matriculated to Texas A&M University and obtained a Ph.D. in Microbiology. His post-doctoral fellowship was performed at the University of Pittsburgh. He has been working extensively in interdisciplinary teams for high-throughput sample handling and analysis efforts. He helped initiate one of laboratories as part of the CDC's National Tuberculosis Genotyping and Surveillance Network in which we performed RFLP typing of clinical isolates of *Mycobacterium tuberculosis*. Here we catalogued information on over 5,000 clinical tuberculosis isolates and established and validated DNA extraction and DNA fingerprinting analyses protocols. Additional experience with high throughput functional studies occurred in several projects of vaccine candidate discovery in models of coccidioidomycosis, smallpox, and glanders. These studies combined efforts of bioinformatics, molecular biologists and biologists to identify immunodominant proteins functionally through their protective effects against microbial challenge. He was also a key member of ASU's efforts as part of the Tularemia Vaccine Development contract where he coordinated and performed gene expression microarray analyses of bacterial RNA harvested from the tissues of infected animals. Most recently, as part of the Biological Advanced Research and Development Authority contract to identify genes responsive to ionizing radiation, he instituted high throughput sample preparation standard operating procedures for preparing cDNA from blood for RNA-Seq and qPCR analyses. These large scale studies of gene expression, peptide and protein microarrays, provide a firm foundation for high throughput studies with an emphasis on developing and refining sample preparation and analysis protocols.

B. Positions and Honors

1985-1987 Postdoctoral Fellow, Dept. of Medicine, University of Pittsburgh School of Medicine
1987-1988 Research Assistant Professor of Medicine, Dept. of Medicine, University of Pittsburgh School of Medicine,.
1988–1991 Assistant Professor of Medicine, Dept. of Medicine, University of Texas Health Science Center at San Antonio
1991-2000 Research Assistant Director, Department of Clinical Investigation, Texas Center for Infectious Disease

2000-2004 Research Assistant Professor, Department of Microbiology, University of Texas Health Science Center at San Antonio
2004-2005 Research Assistant Professor, Center for Biomedical Inventions, The University of Texas Southwestern Medical Center at Dallas
2005-2009 Research Assistant Professor, Center for Innovations in Medicine, Arizona State University
2008 Member, NIH Scientific Review Committee, ZAI1-DDS-M J1
2009 - Research Assistant Professor, Center for Personalized Diagnostics, Arizona State University
2012 - Member, Institutional Biosafety Committee, Arizona State University

C. Contributions to Science

1. Biology colony stimulating factors. My long standing interest in host response to infectious diseases ranges back to the very early part of my career. One infection model I was keenly interested in was that of *Listeria monocytogenes*, a model infection for tuberculosis, which causes a specific increase in mononuclear phagocytes during infection. I began studying the production of colony stimulating factors (CSF) during infection and mechanisms of CSF action on phagocyte function. We collaborated with one of the first groups to create a purified human CSF-1 and investigate its role in on macrophage function. We further investigated production of multiple CSFs and their effects on progenitor cells during vaccination. This cumulative expertise lead to an early clinical trial of recombinant human GM-CSF on phagocyte production and function.

a. Wing EJ, **Magee DM**, Pearson AC, Waheed A, Shadduck RK. Peritoneal macrophages exposed to purified macrophage colony-stimulating factor (M-CSF) suppress mitogen- and antigen-stimulated lymphocyte proliferation. J Immunol. 1986;137(9):2768-73. PMID: 3489777.
b. **Magee DM**, Wing EJ, Ampel NM, Waheed A, Shadduck RK. Macrophage colony-stimulating factor enhances the expression of Fc receptors on murine peritoneal macrophages. Immunology. 1987;62(3):373-8. PMID: 3499377; PMCID: PMC1454134.
c. **Magee DM**, Wing EJ. Secretion of colony-stimulating factors by T cell clones. Role in adoptive protection against *Listeria monocytogenes*. J Immunol. 1989;143(7):2336-41. PMID: 2674280.
d. Wing EJ, **Magee DM**, Whiteside TL, Kaplan SS, Shadduck RK. Recombinant human granulocyte/macrophage colony-stimulating factor enhances monocyte cytotoxicity and secretion of tumor necrosis factor alpha and interferon in cancer patients. Blood. 1989;73(3):643-6. PMID: 2465038.

2. Role of T cells and B cells in protective immunity. Protective immunity against infectious disease has been one of the core missions of my scientific career. From the very beginning I have worked to understand the core components to protective immunity to primary infection and how vaccination modifies the underlying protective components. Early studies utilized T cell cloning to investigate discrete components of protection in the *Listeria* model. My interests broadened to other infection models including *Chlamydia*, *Histoplasma*, *Mycobacteria* and *Coccidioides*. A majority of my effort was in studying *Coccidioides* primary and vaccine-induced host responses. One of the key findings in this series of studies was the importance of B cells in vaccine-induced immunity. While the importance of T cells in immunity to *Coccidioides* is not to be understated, the importance of humoral immunity to Coccidioidomycosis was under appreciated until we published on this in 2005.

a. **Magee DM**, Wing EJ. Cloned L3T4+ T lymphocytes protect mice against *Listeria monocytogenes* by secreting IFN-gamma. J Immunol. 1988;141(9):3203-7. PMID: 2459247.
b. **Magee DM**, Cox RA. Roles of gamma interferon and interleukin-4 in genetically determined resistance to *Coccidioides immitis*. Infect Immun. 1995;63(9):3514-9. PMID: 7642285; PMCID: PMC173486.
c. Sampson SL, Mansfield KG, Carville A, **Magee DM**, Quitugua T, Howerth EW, Bloom BR, Hondalus MK. Extended safety and efficacy studies of a live attenuated double leucine and pantothenate auxotroph of *Mycobacterium tuberculosis* as a vaccine candidate. Vaccine. 2011;29(29-30):4839-47. PMID: 21549795; PMCID: PMC3146342.
d. **Magee DM**, Friedberg RL, Woitaske MD, Johnston SA, Cox RA. Role of B cells in vaccine-induced immunity against coccidioidomycosis. Infect Immun. 2005;73(10):7011-3. PMID: 16177382; PMCID: PMC1230979.

3. Technology Development. Providing tools, datasets, and technologies to the scientific community has been a long-term goal as part of my scientific career. Early on we utilized standard technologies to provide monoclonal antibodies to important antigens of Coccidioides. We were part of the National Tuberculosis Genotyping and Surveillance Network performing RFLP typing of tuberculosis clinical isolates in collaboration with the Centers for Disease control. More recently, I have been developing microarrays for performing serological screening to characterize immunoreactivity to proteins or epitopes. Most recently, we are developing a high-content protein microarrays for increasing throughput of samples across very large protein sets. These types of tools provide enhanced capabilities to perform high-throughput screening of serological reactivity to native proteins on a genome scale.

a. Cox RA, Dolan MJ**, Magee DM**, Galgiani JN. Production of a murine monoclonal antibody that recognizes an epitope specific to Coccidioides immitis antigen 2. Infect Immun. 1993;61(5):1895-9. PMID: 7682998; PMCID: PMC280781.
b. Quitugua TN, Seaworth BJ, Weis SE, Taylor JP, Gillette JS, Rosas, II, Jost Jr KC, Jr., **Magee DM**, Cox RA. Transmission of drug-resistant tuberculosis in Texas and Mexico. J Clin Microbiol. 2002;40(8):2716-24. PMID: 12149319; PMCID: PMC120686.
c. Legutki JB, **Magee DM**, Stafford P, Johnston SA. A general method for characterization of humoral immunity induced by a vaccine or infection. Vaccine. 2010;28(28):4529-37. PMID: 20450869.
d. Bian X, Wiktor P, Kahn P, Brunner A, Khela A, Karthikeyan K, Barker K, Yu X, **Magee M**, Wasserfall CH, Gibson D, Rooney ME, Qiu J, LaBaer J. Antiviral antibody profiling by high-density protein arrays. Proteomics. 2015. PMID: 25758251.

4. High Throughput screens for immunoreactivity. Utilization of the aforementioned tools has allowed for high throughput screens of open-reading frames as either potential vaccine candidates or immunological targets. Most of this work has dealt with genetic vaccination utilizing large scale cDNA libraries of open-reading frames from various microorganisms. In models of Coccidioides, Vaccinia, and Burkholderia, new potential vaccine candidates were discovered utilizing a functional screen to determine which clones provided protection against a lethal challenge of target organism. Most recently, in a model of tuberculosis vaccine, we were able to identify protein targets of humoral immunity from mice immunized with membrane vesicles of *Mycobacterium tuberculosis.* The utilization of high-content technology to screen genome-wide protein content provides a rapid way to identify immunodominance in an unbiased fashion.

a. Ivey FD, **Magee DM**, Woitaske MD, Johnston SA, Cox RA. Identification of a protective antigen of Coccidioides immitis by expression library immunization. Vaccine. 2003;21(27-30):4359-67. PMID: 14505918.
b. Borovkov A, **Magee DM**, Loskutov A, Cano JA, Selinsky C, Zsemlye J, Lyons CR, Sykes K. New classes of orthopoxvirus vaccine candidates by functionally screening a synthetic library for protective antigens. Virology. 2009;395(1):97-113. PMID: 19800089; PMCID: PMC2784938
c. Whitlock GC, Robida MD, Judy BM, Qazi O, Brown KA, Deeraksa A, Taylor K, Massey S, Loskutov A, Borovkov A, Brown K, Cano JA, **Magee DM**, Torres AG, Estes DM, Sykes KF. Protective antigens against glanders identified by expression library immunization. Front Microbiol. 2011;2:1-14. PMCID: PMCPMC3221416
d. Prados-Rosales R, Carreno LJ, Batista-Gonzalez A, Baena A, Venkataswamy MM, Xu J, Yu X, Wallstrom G, **Magee DM**, LaBaer J, Achkar JM, Jacobs WR, Jr., Chan J, Porcelli SA, Casadevall A. Mycobacterial membrane vesicles administered systemically in mice induce a protective immune response to surface compartments of *Mycobacterium tuberculosis*. mBio. 2014;5(5):e01921-14. PMID: 25271291.

Complete List of Published Work in MyBibliography:

http://www.ncbi.nlm.nih.gov/sites/myncbi/d. mitchell.magee.1/bibliography/48102612/public/?sort=date&direction=ascending

D. Research Support

Ongoing Research Support

HHS0100201000008C LaBaer (PI) 12/17/2009-07/29/2016

Integrated Biosymetry System (IBiS) for High Throughput Medical Care After Radiologic and Nuclear Events
Biomedical Advanced Research and Development Authority (BARDA)

The proposed IBiS system exploits novel radiation-related molecular signatures to measure a person's radiation exposure. The IBiS system offers a High Throughput platform suitable for processing at least 2000 victim's samples per day for centralized analysis, but it is also suitable for future integration of its functional components into a portable instrument.
Role: Co-PI

FP00001458 Magee (PI) 08/01/14-12/21/16
Design and Creation of a Registry for Housing Standard Procurement Operating Procedures for Tissue Collection
GBSI
We propose to create a common, shared registry that stores all SOPs used in sample collection.
Role: PI

ASUF 30006685 Magee (PI) 7/20/2015-07/19/16
Does Mycobacterium tuberculosis use cellular modifications to survive in human macrophages
Kleberg Foundation
Since treatment options for XDR-TB are limited and the TB drug pipeline is insufficient to address global treatment needs (4), new therapeutic intervention strategies are needed. Our efforts could help identify a novel area for Mtb intervention.
Role: PI

Completed Research Support

1R01AI096213-01 Magee (PI) 08/15/11-07/31/14
Antibody Biomarkers for Early Detection of Tuberculosis
National Institutes of Health

We will finalize the construction of a nucleic acid programmable protein array (NAPPA) for the *M. tuberculosis genome*. We will screen tuberculosis patient sera, from both HIV+ and HIV-, patients for unique serological responses in the HIV+ patient subpopulation
Role: PI

1U54DK093449-01 Chaput (PI) 09/25/11-07/31/14
Developing a Pipeline for the Production of Bivalent Synthetic Antibodies to the Human Proteome
National Institutes of Health

We are developing a high throughput pipeline to create synthetic binding ligands for 90 human kinases. This program will establish the protocol for creating nucleic-acid/peptide heteroconjugates that have high affinity and specificity to a cognate protein.
Role: Co-Investigator

5R01DK047936-15 Mandarino (PI) 02/12-06/13 (current start and end dates 02/01/12-01/31/2017)
Molecular Regulation of Muscle Glucose Metabolism in Man
National Institutes of Health

We are characterizing the binding affinity of phosphorylation events on PI3 Kinase to better understand regulation of the insulin receptor substrate-1 during insulin resistance.
Role: Co-Investigator

10056577 Claffey (PI) 07/10-06/13
Discovery Platform for Cancer Antigens
NIH Subcontract through the University of Connecticut
We will utilize a targeted human nucleic acid programmable protein array (NAPPA), to assess recombinant single chain variable (SCFV) regions proteins cloned from B cells of patients with breast cancer to determine potential autoantigen reactivity to potential biomarker proteins for breast cancer.
Role: Co-Investigator