BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES**.

NAME: CRISCITIELLO, MICHAEL FREDERICK

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

POSITION TITLE: Professor of Veterinary Pathobiology

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 North Carolina, Chapel Hill, NC	B.S.	05/1993	Biology
East Carolina University, Greenville, NC	M.S.	08/1997	Molecular Biology
University of Miami, Miami, FL	Ph.D.	05/2003	Microbiology and Immunology
University of Maryland, Baltimore, MD	Postdoctoral	06/2008	Immunology

A. Personal Statement

My Comparative Immunogenetics Laboratory studies immunology, molecular genetics and evolution. Most of our group's research focuses on the natural history and future application of the vertebrate adaptive immune system, with particular attention given to the genetics of lymphocyte antigen receptors. Particular expertise lies in the evolution of vertebrate immunoglobulin loci, T cell receptor loci and the major histocompatibility complex. Additionally, we are interested in the evolution of diversification mechanisms at work there (e.g., recombination activating genes (RAG), activation-induced cytidine deaminase (AID), and the high allelic polymorphism maintained by classical MHC genes). Most recently, we have been working on lymphocyte development in shark thymus that suggests plasticity across the B lymphocyte/T lymphocyte divide, immunoglobulin heavy and light chain isotype pairing in an amphibian system, immunogenetics in marine mammals of conservation importance, mucosal humoral immunity in diverse tetrapods and cattle antibodies with an unheralded domain extending for novel antigen binding possibilities.

My service is centered in graduate programs (Biomedical Sciences, Medical Sciences, Genetics, Biotechnology, Ecology and Evolutionary Biology, Toxicology and Reproductive Sciences), student committees, research infrastructure and high school science outreach. I serve as Associate Dean for Research and Graduate Studies in the College of Veterinary Medicine and Biomedical Sciences. My teaching is focused on immunology and genetics at the graduate and undergraduate levels.

B. Positions and Honors

Positions and Employment

2008-2013 Assistant Professor, Department of Veterinary Pathobiology, Texas A&M University
2008-Present Interdisciplinary Faculty of Genetics, Interdisciplinary Faculty of Reproductive Biology, Ecology and Evolutionary Biology Interdisciplinary Program, Texas A&M University
2010-Present Interdisciplinary Faculty of Toxicology, Professional Program in Biotechnology, Texas A&M University
2014-Present Joint Appointment, Department of Microbial Pathogenesis and Immunology, College of Medicine, Texas A&M Health Sciences Center, Texas A&M University
2014-Present Associate Professor with tenure, Department of Veterinary Pathobiology, Texas A&M University

2015-2017 Associate Department Head for Research and Graduate Studies, Department of Veterinary Pathobiology, Texas A&M University
2016-Present Track Leader: Infection and Immunity, Biomedical Sciences Graduate Program, Texas A&M University
2017-2021 Assistant Dean for Research and Graduate Studies, College of Veterinary Medicine & Biomedical Sciences, Texas A&M University
2019-Present Professor, Department of Veterinary Pathobiology, Texas A&M University
2021-Present Associate Dean for Research and Graduate Studies, College of Veterinary Medicine & Biomedical Sciences, Texas A&M University

Professional Memberships and Other Experiences

1996-Present International Society of Developmental and Comparative Immunologists (VP Americas)
2001-Present American Association of Immunologists (Vet Immuno Committee, Director HS Teachers)
2012-Present Society for Experimental Biology and Medicine (SEBM, Editorial Board 2011-2014)
2013-Present Society for Immunogenetics (IMGT, Editorial Board 2014-present)

Honors

2014 CVM Outstanding Scientific Achievement Award
2017 CVM Outstanding Graduate Student Mentor Award
2018-2021 TAMU Presidential Impact Fellow

C. Contribution to Science

1. We have discovered that all immunoglobulin light chains are related to four groups extant in sharks, and that their genomic organization schemes vary widely. Fig 7 from the EJI paper is routinely used in immunology texts to show the relationship of lambda and kappa to other vertebrate isotypes.
    a. Hsu, E. and **M.F. Criscitiello**. "Diverse immunoglobulin light chain organizations in fish retain potential to revise receptor specificities." *The Journal of Immunology*, 177(4):2452-62, 2006. PMC 16888007
    b. **Criscitiello, M.F.** and M.F. Flajnik. "Lambda and kappa are two of four primordial immunoglobulin light chain isotypes." *European Journal of Immunology*, 37(10):2683-94, 2007. PMC 17899545
    c. **Criscitiello, M.F.** "What the shark immune system can and cannot provide for the expanding design landscape of immunotherapy." *Expert Opinion on Drug Discovery* 9(7):725-739, 2014. PMC 24836096
    d. Ott, J.A., J. Harrison, M.F. Flajnik and **M.F. Criscitiello.** "Nurse shark T cell receptors employ somatic hypermutation preferentially to alter alpha/delta variable segments associated with alpha constant region." *European Journal of Immunology* in press 2020.

2. Our work has led to the understanding that multiple immunogenetic mechanisms exist to diversify T cell receptor repertoires in sharks and other classes of vertebrates. These include allelic polymorphism at TCR constant domain genes, somatic hypermutation of TCR, and immunoglobulin variable gene use for TCR and doubly-rearranging TCR delta chains with two variable domains.
    a. **Criscitiello, M.F.**, M. Saltis, and M.F. Flajnik. "An evolutionarily mobile antigen receptor variable region gene: doubly rearranging NAR-TcR genes in sharks." *Proceedings of the National Academy of Sciences USA,* 103(13):5036-41, 2006. PMC 16549799
    b. **Criscitiello M.F.**, Ohta Y., Saltis M., McKinney E.C., and Flajnik M.F. "Evolutionarily conserved TCR binding sites, identification of T cells in primary lymphoid tissues, and surprising trans-rearrangements in nurse shark." *Journal of Immunology*, 184(12):6950-60, 2010. PMC 20488795
    c. Ott, J.O., C.D. Castro, T.C. Deiss, Y. Ohta, M.F. Flajnik and **M.F. Criscitiello**. "Somatic hypermutation for αβ primary T cell repertoire generation in shark." *eLife* 7:e28477, 2018. DOI: 10.7554/eLife.28477. PMID: 29664399
    d. **Criscitiello, M.F.** "Unusual T cell receptor in opossum." *Science* 371:1308-1309, 2021.

3. We have elucidated conserved features and areas of plasticity in the natural history of the vertebrate MHC and antigen processing.

    a. Wright K.L., B.J. Vilen, Y.I. Lindstrom, T.L. Moore, G. Li, **M.F. Criscitiello**, P. Cogswell, J.B. Clarke, and J.P. Ting. "CCAAT box binding protein NF-Y facilitates *in vivo* recruitment of upstream DNA binding transcription factors." *The European Molecular Biology Organization (EMBO) Journal* 13, 4042-4053, 1994. PMC 8076600

    b. Ohta Y., E.C. McKinney, **M.F. Criscitiello**, and M.F. Flajnik. "Proteasome, transporter associated with antigen processing, and class I genes in the nurse shark *Ginglymostoma cirratum*: evidence for a stable class I region and MHC haplotype lineages." *The Journal of Immunology*, 168, 771-781, 2002. PMC 11777971

    c. **Criscitiello M.F.**, Y. Ohta, M.D. Graham, J.O. Eubanks, P.L. Chen, and M.F. Flajnik. "Shark class II invariant chain reveals ancient conserved relationships with cathepsins and MHC class II." *Developmental and Comparative Immunology* 36:521-533, 2012. PMC 21996610

    d. **Criscitiello, M.F.,** M.B. Dickman J.E. Samuel and P. de Figueiredo. "Tripping on acid: trans-kingdom perspectives on biological acids in immunity and pathogenesis." *PLoS Pathogens* 9(7):e1003402, 2013. PMC 23874196

4. We have brought next-generation sequencing –omics to the white-leg shrimp (L. vannamei, the dominant crustacean in global aquaculture) and used this model as an innate model of immunity. We have extended next-generation sequence analysis to antigen receptor repertoire and population level MHC analyses for protected marine mammals including Amazonian manatee and California sea lion.

    a. **Criscitiello, M.F.** and P. de Figueiredo. "Fifty shades of immune defense." *PLoS Pathogens*, 9(2) e1003110, 2013. PMC 23408882

    b. Breaux, B., T.C. Deiss, P.L. Chen, M. P. Cruz-Schneider, L. Sena, M.E. Hunter, R. Bonde and **M.F. Criscitiello**. "The Florida manatee (*Trichechus manatus latirostris*) immunoglobulin hevy chain suggests the importance of clan III variable segments in repertoire diversity." *Developmental and Comparative Immunology* 72:57-68, 2017. PMID: 28131767

    c. López-Zavala, A.A., J.S. Carrasco-Miranda, K.D. Garcia-Orozco, R. Sugich-Miranda, J.M. Hernandez- Flores, **M.F. Criscitiello**, Luis G. Brieba, Rogerio R. Sotelo-Mundo and Enrique Rudiño-Piñera. "Crystal structure of shrimp arginine kinase in binary complex with arginine - a molecular view of the phosphagen precursor binding to the enzyme." *Journal of Bioenergetics and Biomembranes* 45(6):511-8, 2013. PMC 23746848

    d. Ghaffari, N., A. Sanchez-Flores, R. Doan, K.D. Garcia-Orozco, P.L. Chen, A. Ochoa-Leyva, A.A. Lopez-Zavala, J.S. Carrasco, C. Hong, L.G. Brieba, E. Rudiño-Piñra, P.D. Blood, J.E. Sawyer, C.D. Johnson, S.V. Dindot, R.R. Sotelo-Mundo and **M.F. Criscitiello.** "Novel transcriptome assembly and improved annotation of the whiteleg shrimp (*Litopenaeus vannamei*), a dominant crustacean in global seafood mariculture." *Scientific Reports* 4:7081, 2014. PMC 25420880

5. Our work has detailed the evolution of the mucosal immunoglobulin isotypes IgZ/T and IgX/A, as well as the unheralded gut somatic hypermutation enabling cattle antibodies to diversify an additional antigen binding domain with ultralong third complementarity determining regions. These remarkable ultralong CDR3 "cattlebodies" have recently been shown to rapidly diversify in the immunized animal to produce remarkably broadly neutralizing antibodies against HIV gp120.

    a. Mashoof, S., A. Goodroe, C.C. Du, J.O. Eubanks, N. Jacobs, J.M. Steiner, I. Tizard, J.S. Suchodolski, and **M.F. Criscitiello**. "Ancient T-independence of mucosal IgX/A: gut microbiota unaffected by larval thymectomy in *Xenopus laevis*." *Mucosal Immunology* 6(2):358-68, 2013. PMC 22929561

    b. Wang, F., D.C. Ekiert, I. Ahmad, W. Yu, Y. Zhang, O. Bazirgan, A. Torkamani, T. Raudsepp, W. Mwangi, **M.F. Criscitiello**, I.A. Wilson, P.G. Schultz, V.V. Smider. "Reshaping antibody diversity." *Cell* 153:1379-1393, 2013. PMC 23746848

    c. Mashoof, S.M., C. Pohlenz, P.C. Chen, D. Gatlin, A. Buentello and **M.F. Criscitiello**. "Expressed IgH μ and τ transcripts share diversity segment in ranched *Thunnus orientalis*." *Developmental and Comparative Immunology* 43(1):76-86, 2014.PMC 24231183

    d. Sok, D., K.M. Le, M. Vadnais, K. Saye-Francisco, J.G. Jardine, J. Torres, Z.T. Berndsen, L. Kong, R. Stanfield, J. Ruiz, A. Ramos, C.H. Liang, P.L. Chen, **M.F. Criscitiello**, W. Mwangi, I.A. Wilson,

A.B. Ward, V.V. Smider and D.R. Burton. “Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows.” *Nature* 548(7665):108-111, 2017. PMID: 28726771

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/michael.criscitiello.1/bibliography/50888741/public/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

2021-67015-34534 Wu (PD) 07/01/2021-06/30/2024
USDA / NIFA
Impact of dietary glutamate on the development of gut mucosal immunity in hybrid striped bass
This project identifies immune response differences caused by glutamate supplementation in aquaculture feed.

R01AI141607 de Figueiredo (PI) 06/07/2019-05/31/2024
National Institutes of Health / NIAID
Development of a high-throughput microfluidics-enabled functional assay for rapidly identifying neutralizing antibodies
The goal is to provide a system that offers dramatic improvements in throughput and reduction in cost when compared to conventional nAb discovery strategies. In addition, the system can be configured for the rapid discovery of nAbs against a wide variety of viral pathogens.
Role: Co-PI

IOS-1656870 Criscitiello (PI) 07/01/2017-06/30/2022
National Science Foundation/ IOS-SDSR
Evolution of diversification mechanisms for lymphocyte antigen receptors
The goal of this project is to determine the role of AID mediated versus RAG mediated diversification mechanisms in the origins of vertebrate adaptive immune repertoires.
Role: PI

R21AR074635 Alge (PI) 03/10/2019-02/28/2022
National Institutes of Health / NIAMS (R21)
Impact of the anti-PEG response on the efficacy of PEG hydrogel-mediated bone regeneration
This project determines the effect of anti-PEG antibodies and other immune responses in bone healing.
Role: Co-PI

Completed Research Support

R21AI139738 de Figueiredo (PI) 01/24/2020-12/31/2021
National Institutes of Health / NIAID
Accelerating discovery of neutralizing paratopes with Functional Antibody Screening Technology
This proposal is to develop and utilize a microfluidic platform that can screening functionality of antibodies produced by B cells towards viral neutralization assays.
Role: Co-PI

DBI-2029949 de Figueiredo (PI) 05/01/2020-04/30/2021
National Science Foundation
RAPID: Large-scale functional analysis of Ab repertoires elicited by SARS-CoV-2
This project proposes to use high throughput methods to profile antibody repertoires against SARS-CoV-2
Role: Co-PI

R21AI140178 Taylor (PI) 09/01/2018-05/31/2020
National Institutes of Health / NIAID (R21)
Evaluation of novel INF-epsilon across human pregnancy

This project's goal is to determine the maternal demographic characteristics that influence IFN epsilon levels in the vagina across pregnancy and whether those levels are associated with maternal and infant health indicators.
Role: Co-PI