# R. Blake Billmyre, PhD

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### **FACULTY POSITION**

Starting 2023 University of Georgia, Athens, GA

**Assistant Professor** 

Pharmaceutical and Biomedical Sciences, College of Pharmacy

Infectious Diseases, College of Veterinary Medicine

#### **EDUCATION**

2017 **Duke University**, Durham, NC

PhD, Genetics and Genomics

Certificate in Cell and Molecular Biology

"Genome evolution in the fungal pathogen Cryptococcus deuterogattii"

Advisor: Dr. Joseph Heitman

2009 **University of Maryland**, College Park, MD

Bachelor of Science, Cell Biology and Molecular Genetics

**Honors Citation** 

### RESEARCH EXPERIENCE

2017-2023 **Zanders Lab- Stowers Institute for Medical Research**, Kansas City, MO

Postdoctoral Associate

High-throughput genetics and genome evolution

2010-2017 **Heitman Lab- Duke University**, Durham, NC

Graduate Student

Genomics of the evolution of virulence in fungi

2009-2010 Mock Lab- National Cancer Institute, Bethesda, MD

Cancer Research Training Award Fellow

Role of mTOR in a murine model of plasmacytomagenesis

2008 **Baskakov Lab- University of Maryland**, Baltimore, MD

Summer Undergraduate Researcher

Photosynthetic bacterial fuel cells using Cyanobacterium

2006-2009 Cooke Lab- University of Maryland, College Park, MD

Undergraduate Research Assistant/Summer Undergraduate Research Fellow

Role of polar auxin transport in charophytes

2005-2009 **Gemstone Program- University of Maryland**, College Park, MD

Undergraduate Research Assistant

Aerotolerance of the electrogenic bacterium Geobacter ferrireducens

### **PUBLICATIONS**

- 1. **Billmyre RB\***, Eickbush MT\*, Craig CJ, Lange JL, Wood C, Helston RM, Zanders SE (2021). Genome-wide identification of sexual-reproduction genes in fission yeast via transposon-insertion sequencing. *bioRxiv*. https://doi.org/10.1101/2021.08.31.458362 \*Authors contributed equally **In press at** *PLOS Genetics*
- 2. **Billmyre RB** (2022). Drug Resistance and Evolvability in an Emerging Human Fungal Pathogen. *mBio*. e01876-22
- 3. De Carvalho M, Jia GS, Nidamangala Srinivasa A, **Billmyre RB**, Xu YH, Lange JJ, Sabbarini IM, Du LL, Zanders SE (2022). The wtf meiotic driver gene family has unexpectedly persisted for over 100 million years. *eLife*. 11:e81149
- 4. Lopez Hernandez JF, Helston RM, Lange JJ, **Billmyre RB**, Schaffner SH, Eickbush MT, McCroskey S, Zanders SE (2021). Diverse mating phenotypes impact the spread of wtf meiotic drivers in *S. pombe. eLife*. 10:e70812
- 5. **Billmyre RB\***, Clancey SA\*, Li L, Doering T, Heitman J (2020). 5-fluorocytosine resistance is associated with hypermutation and alterations in capsule biosynthesis in *Cryptococcus*. *Nature Communications*. 11(127). \*Authors contributed equally
- 6. Vellanki S, **Billmyre RB**, Lorenzen A, Campbell M, Turner B, Huh EY, Heitman J, Lee SC (2020). A novel resistance pathway for calcineurin inhibitors in the human-pathogenic Mucorales *Mucor circinelloides*. *mBio* 11(1), 10.1128/mBio.02949-19.
- 7. Pianalto KM, **Billmyre RB**, Telzrow CL, Alspaugh JA (2019). Roles for stress response and cell wall biosynthesis pathways in caspofungin tolerance in *Cryptococcus neoformans*. *Genetics* 213(1), 213-227.
- 8. Chang Z, **Billmyre RB**, Lee SC, Heitman J (2019). Broad antifungal resistance mediated by RNAi-dependent epimutation in the basal human fungal pathogen *Mucor circinelloides*. *PLOS Genetics* 15(2): e1007957.
- 9. Passer AR, Coelho MA, **Billmyre RB**, Nowrousian M, Mittelbach M, Yurkov AM, Averette AF, Cuomo CA, Sun S, Heitman J (2019). Genetic and genomic analyses reveal boundaries between species closely related to *Cryptococcus* pathogens, *mBio*, 10 (3), e00764-19.
- 10. Mueller KD, Zhang H, Serrano C, **Billmyre RB**, Huh EY, Wiemann P, Keller NP, Wang Y, Heitman J, Lee SC (2019). Gastrointestinal microbiota alteration induced by *Mucor circinelloides* in a murine model. *Journal of Microbiology*. 57, e1976-3794

- 11. Roth C, Sun S, **Billmyre RB**, Heitman J, Magwene P (2018). A high-resolution map of meiotic recombination in *Cryptococcus deneoformans* demonstrates decreased recombination in unisexual reproduction. *Genetics* 209(2), 567-578.
- 12. Yadav V, Sun S, **Billmyre RB**, Thimmappa BC, Bakkeren G, Cuomo C, Heitman J, Sanyal K (2018). RNAi-dependent centromere evolution in closely related fungal species. *PNAS*. 10.1073/pnas.1713725115
- 13. Persinoti GF, Martinez DA, Li W, Dogen A, **Billmyre RB**, Averette A, Goldberg JM, Shea T, Young S, Zeng Q, Oliver BG, Barton R, Metin B, Hilmioglu-Polat S, Ilkit M, Graser Y, Martinez-Rossi NM, White TC, Heitman J, Cuomo CA (2018). Whole genome analysis illustrates global clonal population structure of the ubiquitous dermatophyte pathogen *Trichophyton rubrum. Genetics*. 208 (4) 1657-1669.
- 14. **Billmyre RB**, Clancey SA, Heitman J (2017). Natural mismatch repair mutations mediate phenotypic diversity and drug resistance in *Cryptococcus deuterogattii*. *eLife*, 6, e28802.
- 15. **Billmyre RB**, Heitman J (2017). Genetic and epigenetic engines of diversity in pathogenic microbes. *PLoS Pathog* 13(9): e1006468.
- Hagen F, Lumbsch HT, Arsenijevic VA, Badali H, Bertout S, **Billmyre RB**, Bragulat MR, Cabañes FJ, Carbia M, Chakrabarti A, Chaturvedi S, Chaturvedi V, Chen M, Chowdhary A, Colom M-F, Cornely OA, Crous PW, Cuétara MS, Diaz MR, Espinel-Ingroff A, Fakhim H, Falk R, Fang W, Herkert PF, Rodríguez CF, Fraser JA, Gené J, Guarro J, Idnurm A, Illnait-Zaragozi M-T, Khan Z, Khayhan K, Kolecka A, Kurtzman CP, Lagrou K, Liao W, Linares C, Meis JF, Nielsen K, Nyazika TK, Pan W, Pekmezovic M, Polacheck I, Posteraro B, Telles FdQ, Romeo O, Sánchez M, Sampaio A, Sanguinetti M, Sriburee P, Sugita T, Taj-Aldeen SJ, Takashima M, Taylor JW, Theelen B, Verweij PE, Wahyuningsih R, Wang P, Boekhout T (2017). Importance of Resolving Fungal Nomenclature: The Case of Multiple Pathogenic Species in the *Cryptococcus* Genus. *mSphere*, 2(4), e00238–17.
- 17. Sun S, Yadav V, **Billmyre RB**, Cuomo CA, Nowrousian M, Wang L, Souciet J-L, Boekhout T, Porcel B, Wincker P, Granek JA, Sanyal K, Heitman J (2017). Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. *PLOS Biology* 15(8): e2002527.
- 18. Chow EWL, Clancey SA, **Billmyre RB**, Averette AF, Granek JA, Mieczkowski P, Cardenas ME, Heitman J (2017). Elucidation of the calcineurin-Crz1 stress response transcriptional network in the human fungal pathogen *Cryptococcus neoformans*. *PLOS Genetics* 13(4): e1006667.

- Zhu Y\*, Engström PG\*, Tellgren-Roth C, Baudo C, Kennell JC, Sun S, Billmyre RB, Schroeder M, Andersson A, Holm T, Sigurgeirsson B, Wu G, Sankaranarayanan SR, Siddharthan R, Sanyal K, Lundeberg J, Nystedt B, Boekhout T, Dawson TL, Heitman J, Scheynius A, Lehtiö J (2017). Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of *Malassezia sympodialis*. *Nucleic Acids Research*, 45(5), 2629–2643. \*Authors contributed equally
- 20. Rayner S, Bruhn S, Vallhov H, Andersson A, **Billmyre RB**, Scheynius A (2017). Identification of small RNAs in extracellular vesicles from the commensal yeast *Malassezia sympodialis*. *Scientific Reports*, 7, 39742.
- 21. Gladieux P, Byrnes EJ, Aguileta G, Fisher M, **Billmyre RB**, Heitman J, Giraud T (2017). Epidemiology and evolution of fungal pathogens in plants and animals. *Genetics and Evolution of Infectious Diseases*. 71-98.
- 22. Kingsbury JM, Shamaprasad N, **Billmyre RB**, Cardenas ME, Heitman J (2016). Cancer-associated mitochondrial isocitrate dehydrogenase mutations induce mitochondrial DNA instability in *Saccharomyces cerevisiae*. *Human Molecular Genetics*
- Feretzaki M\*, **Billmyre RB\***, Clancey SA, Wang X, Heitman J (2016). Gene network polymorphism illuminates loss and retention of novel RNAi silencing components in the *Cryptococcus* pathogenic species complex. *PLOS Genetics*, 12:e1005868. \*Authors contributed equally
- Wu G, Zhao H, Li C, Rajapakse MP, Wong WC, Xu J, Saunders CW, Reeder NL, Reilman RA, Scheynius A, Sun S, **Billmyre RB**, Li W, Averette A, Mieczkowski P, Heitman J, Theelen B, Schroder M, Sessions PFD, Butler G, Maurer-Stroh S, Boekhout T, Nagarajan N, Dawson TL (2015). Genus-wide comparative genomics of *Malassezia* delineates its phylogeny, physiology, and niche adaptation on human skin. *PLOS Genetics*, 11:e1005614.
- 25. Fu C, Sun S, **Billmyre RB**, Roach KC, Heitman J (2015). Unisexual versus bisexual mating in *Cryptococcus neoformans*: Consequences and biological impacts. *Fungal Genetics and Biology*, 78, 65-75.
- 26. Sun S, **Billmyre RB**, Mieczkowski P, Heitman J (2014). Unisexual reproduction drives meiotic recombination and phenotypic and karyotypic plasticity in *Cryptococcus neoformans*. *PLOS Genetics*, 10, e1004849
- 27. **Billmyre RB**, Croll D, Li W, Mieczkowski P, Carter D, Cuomo CA, Kronstad JW, Heitman J (2014). Highly recombinant VGII *Cryptococcus gattii* population develops clonal outbreak clusters through both sexual

macroevolution and asexual microevolution. mBio, 5, e01494-14.

- 28. Springer DJ, **Billmyre RB**, Filler E, Voelz K, Pursall R, Mieczkowski P, Larsen R, Dietrich F, May R, Filler S, Heitman J (2014). *Cryptococcus gattii* VGIII isolates causing infections in HIV/AIDS patients in Southern California: Identification of the local environmental source as arboreal. *PLOS Pathogens*, 10, e1004285.
- 29. Lee SC, **Billmyre RB**, Li A, Carson S, Sykes SM, Huh EY, Mieczkowski P, Ko D, Cuomo CA, Heitman J (2014). Analysis of a foodborne fungal pathogen outbreak: virulence and genome of a *Mucor circinelloides isolate* from yogurt. *mBio*, 5, e01390-14.
- Janbon G, Ormerod KL, Paulet D, Byrnes EJ, Yadav V, Chatterjee G, Mullapudi N, Hon C, **Billmyre RB**, Brunel F, Bahn YS, Chen W, Chen Y, Chow EWL, Coppee JY, Floyd-Averette A, Gaillardin C, Gerik KJ, Goldberg J, Gonzalez-Hilarion S, Gujja S, Hamlin JL, Hsueh YP, Ianiri G, Jones S, Kodira CD, Kozubowski L, Lam W, Marra M, Mesner LD, Mieczkowski P, Moyrand F, Nielsen K, Proux C, Rossignol T, Schein JE, Sun S, Wollschlaeger C, Wood IA, Zeng Q, Neuveglise C, Newlon C, Perfect JR, Lodge JK, Idnurm A, Stajich JE, Kronstad JW, Sanyal K, Heitman J, Fraser JA, Cuomo CA, Dietrich FS (2014). Analysis of the genome and transcriptome of *Cryptococcus neoformans* var. *grubii* reveals complex RNA expression and microevolution leading to virulence attenuation. *PLOS Genetics*, 10, e1004261.
- 31. **Billmyre RB**, Calo S, Feretzaki M, Wang X, Heitman J (2013). RNAi function, diversity, and loss in the fungal kingdom. *Chromosome Research*, 21, 561-572.
- 32. Calo S, **Billmyre RB**, Heitman, J (2013). Generators of phenotypic diversity in the evolution of pathogenic microorganisms. *PLOS Pathogens*, 9, e1003181.
- 33. Springer DJ, Phadke S, **Billmyre RB**, & Heitman J (2012). *Cryptococcus gattii*, no longer an accidental pathogen? *Current Fungal Infection Reports*, 6, 245-256.
- 34. Zou Y, Pisciotta J, **Billmyre RB**, & Baskakov IV (2009). Photosynthetic microbial fuel cells with positive light response. *Biotechnology and Bioengineering*, 104, 939-946.

#### PRESENTATIONS AND POSTERS

2022 High throughput transposon mutagenesis and essential gene discovery in *Cryptococcus neoformans*Talk, Stowers Research Conference: Genetics and Genomics- Stuck on Repeat, Kansas City, MO

2022	High throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, Pennsylvania State University, State College, PA
2022	High throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, Virginia Tech, Blacksburg, VA
2022	High throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, Fungal Biology Group, University of Georgia, Athens GA
2022	High-throughput genetics and essential gene discovery in <i>Cryptococcus neoformans</i> Poster, 31 <sup>st</sup> Fungal Genetics Conference, Asilomar CA
2022	Genome-wide identification of sexual-reproduction genes in fission yeast via transposon-insertion sequencing Poster, 31st Fungal Genetics Conference, Asilomar CA
2022	High throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, University of Georgia, Athens GA
2022	High throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, University of Massachusetts Medical School, Worcester, MA
2022	Genome-wide identification of sexual-reproduction genes in fission yeast via transposon-insertion sequencing Talk, Sporulation Meeting, Virtual
2021	High-throughput genetics and essential gene discovery in <i>Cryptococcus neoformans</i> Poster, Molecular Mycology 25 <sup>th</sup> Reunion and Conference, Woods Hole, MA
2021	High-throughput genetics and essential gene discovery Talk, Mycology Working Group, Virtual
2021	Using transposons to identify sex and meiosis genes Talk, Young Investigators Science Retreat, Kansas City, MO
2021	Genome-wide identification of sexual-reproduction genes in fission yeast via transposon-insertion sequencing Talk, Mayosis series, Virtual

2021	Designing high throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, Translational Research Seminar, Kansas City, MO
2021	Transposon mutagenesis in two fungi: sex and silencing Talk, Duke University Mycology Unity, Durham, NC
2021	Using transposons to identify sex and meiosis genes Talk, Friday Science Club, Kansas City, MO
2020	Designing high throughput genetic approaches to understand drug resistance in a human fungal pathogen Talk, Friday Science Club, Kansas City, MO
2019	Using transposon-insertion sequencing to identify genes required for sexual reproduction across the <i>Schizosaccharomyces</i> genus Flash Talk and Poster, EMBO Comparative Genomics of Eukaryotic Microbes, Sant Feliu de Guixols, Spain
2019	Building a transposon-insertion sequencing approach for high-throughput genetics in eukaryotic microbes Poster, Young Investigator's Science Retreat, Kansas City, MO
2019	Promiscuous retrotransposition and intron evolution in the <i>Cryptococcus</i> genus Poster, 30 <sup>th</sup> Fungal Genetics Conference, Asilomar CA
2018	Using long reads to tell one WTF from another WTF Talk and Poster, Nanopore Community Meeting, San Francisco, CA
2018	Collateral mutations caused by promiscuous retrotransposons Poster, Young Investigator's Science Retreat, Kansas City, MO
2018	Collateral mutations caused by promiscuous retrotransposons Talk, Open Mic Talk series, Kansas City, MO
2017	Natural mismatch repair mutations mediate phenotypic diversity and drug resistance in <i>Cryptococcus deuterogattii</i> Talk, EMBO Comparative Genomics of Eukaryotic Microbes: Dissecting Sources of Evolutionary Diversity, Sant Feliu de Guixols, Spain
2017	Naturally occurring mismatch repair mutants mediate rapid phenotypic changes and drug resistance in the Pacific Northwest Cryptococcus gattii outbreak Poster, First Annual EPIC Symposium, Durham, NC

2017	Naturally occurring mismatch repair mutants mediate rapid phenotypic changes and drug resistance in the Pacific Northwest Cryptococcus gattii outbreak  Talk, Eukaryotic Pathogens Investigators Club (EPIC), Durham, NC
2017	Naturally occurring mismatch repair mutants mediate rapid phenotypic changes and drug resistance in the Pacific Northwest <i>Cryptococcus gattii</i> outbreak Talk and Poster, 29 <sup>th</sup> Fungal Genetics Conference, Asilomar, CA
2017	Addition by subtraction: RNAi loss and mycoviruses Talk, University Program in Genetics and Genomics Recruitment, Durham, NC
2017	Genome evolution in the fungal pathogen <i>Cryptococcus deuterogattii</i> Talk, Thesis Defense, Durham, NC
2016	Natural strains of <i>Cryptococcus</i> with defects in mismatch repair exhibit enhanced phenotypic diversity Poster, Molecular Genetics and Microbiology Retreat, Wrightsville Beach, NC
2016	Cryptococcus gattii in North America Talk, University Program in Genetics and Genomics Retreat, Haw River, NC
2016	Whole genome typing of <i>Cryptococcus gattii</i> in North America: Mitotic microevolution and sexual macroevolution contributed to the development of an outbreak Poster, Calcineurin as the Target for Antifungal Drug Development Symposium, Durham, NC
2015	Gene network polymorphism illuminates loss and retention of novel RNAi silencing components in the <i>Cryptococcus</i> pathogenic species complex Talk and Poster, Inaugural Center for Host Microbial Interactions Symposium, Durham, NC
2015	Gene network polymorphism illuminates loss and retention of novel RNAi silencing components in the <i>Cryptococcus</i> pathogenic species complex Talk and Poster, EMBO Exploring the genomic complexity and diversity of eukaryotes, Sant Feliu de Guixols, Spain
2015	Whole genome insights into the micro and macroevolution of the Pacific Northwest <i>Cryptococcus gattii</i> outbreak Talk, University Program in Genetics and Genomics Student Seminar, Durham, NC
2015	Gene network polymorphism illuminates loss and retention of novel RNAi silencing components in the <i>Cryptococcus</i> pathogenic species complex

	Talk, Genomics of Microbial Systems work in progress meeting, Durham, NC
2015	Gene network polymorphism illuminates loss and retention of novel RNAi silencing components in the <i>Cryptococcus</i> pathogenic species complex Talk, Molecular Genetics and Microbiology Retreat, Wrightsville Beach, NC
2015	Whole genome sequencing of the <i>Mucor circinelloides</i> species complex: identification of yogurt contaminants associated with GI illness in consumers  Talk, University Program in Genetics and Genomics Retreat, Lake Lure, NC
2015	Whole genome sequencing of the <i>Mucor circinelloides</i> species complex: identification of yogurt contaminants associated with GI illness in consumers  Talk, 19 <sup>th</sup> International Society for Human and Animal Mycology Congress, Melbourne, Australia
2015	Whole genome typing of <i>Cryptococcus gattii</i> in North America: Mitotic microevolution and sexual macroevolution contributed to the development of an outbreak  Talk and poster, 19 <sup>th</sup> International Society for Human and Animal Mycology Congress, Melbourne, Australia
2015	Whole genome insights into the micro and macroevolution of the Pacific Northwest <i>Cryptococcus gattii</i> outbreak Talk, Small Eukaryotes Meeting, Durham, NC
2015	Evolution of an outbreak: Hypermutators and the <i>Cryptococcus gattii</i> outbreak Talk and Poster, 28 <sup>th</sup> Fungal Genetics Conference, Asilomar, CA
2015	A hypermutator lineage preceded the Pacific Northwest outbreak of <i>Cryptococcus gattii</i> Poster, Antifungal Drug Development Symposium, Durham, NC
2015	Origins of an outbreak: Hypermutators in the Pacific Northwest outbreak of <i>Cryptococcus gattii</i> Talk, Molecular Genetics and Microbiology Departmental Seminar, Durham, NC
2014	A hypermutator lineage preceded the Pacific Northwest outbreak of <i>Cryptococcus gattii</i> Poster, Molecular Genetics and Microbiology Retreat, Wrightsville Beach, NC
2014	Anatomy of an outbreak: Recombining clonal clusters comprise the VGII Cryptococcus gattii population

	Talk and Poster, 9th International Conference on <i>Cryptococccus</i> and Cryptococcosis, Amsterdam, The Netherlands
2013	Development of an outbreak: Whole genome analysis of population Structure in <i>C. gattii</i> Talk, Genomics of Microbial Systems work in progress meeting, Durham, NC
2013	RNAi loss in <i>Cryptococcus gattii</i> : Don't know what you've got till it's gone Talk, Cell and Molecular Biology Student Seminar, Durham, NC
2013	Loss of the RNAi pathway in VGII <i>Cryptococcus gattii</i> sheds light on the intact system in <i>Cryptococcus neoformans</i> Poster, Molecular Genetics and Microbiology Retreat, Wrightsville Beach, NC
2013	RNAi loss in <i>Cryptococcus gattii</i> : Don't know what you've got till it's gone Talk, Genomics of Microbial Systems work in progress meeting, Durham, NC
2013	RNAi loss in <i>Cryptococcus gattii</i> : Don't know what you've got till it's gone Talk, University Program in Genetics and Genomics Retreat, Lake Lure, NC
2013	Loss of the RNAi pathway in VGII <i>Cryptococcus gattii</i> sheds light on the intact system in <i>Cryptococcus neoformans</i> Poster, 27th Fungal Genetics Conference, Asilomar, CA
2012	Addition by Subtraction: RNAi loss in <i>Cryptococcus gattii</i> Poster, Duke Epigenetics and Epigenomics Colloquium, Durham, NC
2012	RNAi loss in <i>Cryptococcus gattii</i> : addition by subtraction? Talk, Molecular Genetics and Microbiology Retreat, Durham, NC
2012	Addition by Subtraction: RNAi loss in <i>Cryptococcus gattii</i> Poster, Duke Symposium in Celebration of Mycology and Mycologists, Durham, NC
2012	Addition by Subtraction: RNAi loss in <i>Cryptococcus gattii</i> Talk, Young One's Student Seminar, Durham, NC
2011	Addition by Subtraction: RNAi loss in <i>Cryptococcus gattii</i> Talk, University Program in Genetics and Genomics Student Seminar, Durham, NC
2008	Examining the Roots of Plant Evolution: Polar Auxin Transport in Charophytes  Poster, American Society of Plant Biology International Meeting, Merida, Mexico

### TEACHING EXPERIENCE

2019	Guest Lecture- Genetics Module
2017	Stowers Institute Graduate School, Kansas City, MO
2018	Guest Lecture- Genetics Module
	Stowers Institute Graduate School, Kansas City, MO
2015	Guest Lecture- Frontiers in Medicine
	Duke University, Durham, NC
	Gave a guest lecture on fungal pathogens for a non-major biology class
2015	Teaching Assistant- Whole Genome Analysis Workshop
	Duke University, Durham, NC
	Helped run a one-day genome analysis workshop focusing on RNAseq analysis
2013	Teaching Assistant – Ethics Retreat
2013	Duke University Marine Lab, Beaufort, NC
	Dake Chivelen's Marine Dao, Beautoff, IVC

### **MENTORING**

## **Mentored technicians**

2020-2022 Caroline Craig2018- current Michael Eickbush2013-2017 Shelly Clancey

## **Mentored visiting Masters Students**

2019 Maya Houmel

2018 Shona Gray-Switzman

### **Mentored Rotation Students**

2016	Kayla Sylvester
2015	Woonyung Hur
2015	Shelby Priest
2014	Jon Kastan
2014	Andrew Passer

## **Mentored Undergraduate Researchers**

2009-2010	Erin Ong
2010	Lindsey Draper

### **SERVICE**

2019	Session Chair – Sex, mating and meiosis - EMBO Comparative Genomics of Eukaryotic Microbes Sant Feliu de Guixols, Spain
2015-2017	Cofounder/organizer – Eukaryotic Pathogens Investigator Club (EPIC) Duke University, Durham, NC

2017	Organizer and chair – First Annual EPIC Symposium Duke University, Durham, NC
2014-2016	<b>Distinguished Lecture Series Committee</b> Duke University, Durham, NC
2014	Molecular Genetics and Microbiology Retreat Committee Duke University, Durham, NC
2010-2012	Cell and Molecular Biology Recruitment Committee Duke University, Durham, NC
OUTREACH	I
2019	DNA Day Visiting Scientist Northgate Middle School, Kansas City, MO Visited a local middle school for DNA day to talk to local students about biology, DNA, and careers in science
2019-2021	Project Lead the Way Biomed Contest Judge Kansas City, MO Served as a judge for portfolios submitted for a Project Lead the Way high school biomedical research competition
2010 & 2011	<b>Teaching Assistant- Microbial Stress Responses</b> North Carolina School of Science and Mathematics, Durham, NC Helped develop course material for a miniterm (~2 weeks) course for gifted high school students and taught a unit on bioinformatics
AWARDS	
2021	Best Postdoc Talk, Young Investigators Science Retreat
2019	Finalist, Life Sciences Research Fellowship
2017	Speaker Award – EMBO Comparative Genomics of Eukaryotic Microbes: Dissecting Sources of Evolutionary Diversity
2016	Speaker Award – UPGG Student Retreat
2015	Poster Award – EMBO Exploring the Genomic Complexity and Diversity of Eukaryotes
2015	Mitchell Meritorious Research Travel Award
2015	EMBO Travel Award

2015	DeLill Nasser Award for Professional Development in Genetics, GSA	
2015	Young ISHAM Travel Award	
2014	Mitchell Meritorious Research Travel Award	
2013	Asilomar Fungal Genetics Meeting Travel Grant	
2009-2010	Cancer Research Training Award Fellowship	
2009	Best Thesis Presentation- Gemstone Program	
2007-2009	Howard Hughes Medical Institute Undergraduate Research Fellowship	
2007	American Society of Plant Biologists Summer Undergraduate Research Fellowship	
2005-2009	Maryland Regents' Scholar	
2005-2009	National Merit Scholar	
2005-2009	Banneker/Key Scholar	
2005-2009	Maryland Distinguished Scholar	
SPECIAL COURSES/CERTIFICATIONS		
2021	Mental Health First Aid Bert Nash Community Mental Health Center	
2013	Molecular Mycology: Current Approaches to Fungal Pathogenesis Marine Biological Lab, Woods Hole, MA	
SOCIETY MEMBERSHIP		
2012-current	Member, Genetics Society of America	
2022-current	Member, American Society for Cell Biology	
2015-2017	Member, International Society for Human and Animal Mycology	

# **REVIEWING**

Guest editor:

PLOS Genetics

Guest grant reviewer: National Science Foundation

Reviewer:

**PLOS Genetics** 

PLOS Pathogens

*mBio* 

Microbiology Spectrum

*mSphere* 

Microbial Genomics

Genetics

*G3* 

Genome Biology and Evolution

Molecular Biology and Evolution

New Phytologist

BMC Evolutionary Biology

International Journal of Molecular Sciences

*Microorganisms* 

**Pathogens** 

Journal of Fungi

Microbiology and Molecular Biology Reviews

#### **REFERENCES**

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