Xyrus X. Maurer-Alcalá

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GitHub: github.com/xxmalcala

Focus: I am an evolutionary biologist integrating computational and molecular approaches to analyze large-scale -omics data to explore questions related to the biodiversity and evolution of eukaryotes. I am particularly interested in deploying emergent computational (e.g., machine learning) and molecular approaches (e.g., reverse genetics) to understand the interplay between organismal life histories, genome/developmental biology and evolution over deep and shallow time scales using diverse microeukaryotes from locally sourced environments.

EDUCATION

2018 **Ph.D.**, Organismic and Evolutionary Biology, University of Massachusetts, Amherst

2011 **B.A.,** Ecology and Evolutionary Biology, University of Colorado, Boulder

APPOINTMENTS

2021 – Present **Postdoctoral Researcher**, American Museum of Natural History
Invertebrate Zoology; Institute for Comparative Genomics

2018 – 2021* **Postdoctoral Researcher**, Universität Bern
Institut für Zellbiologie
**Medical leave* Dec. 2019 - Dec. 2020

2012 – 2017 **Graduate Student**, University of Massachusetts
Organismic and Evolutionary Biology

2007 – 2010 **Undergraduate Research Fellow,** University of Colorado
Center for Limnology

RESEARCH

Grants and Fellowships

2021 **Simons Microbial Ecology and Evolution** $822,046
(Co-Investigator/Co-Author: **XXMA**; PI/Co-Author: E. Kim)
"Evolution of Genome Architecture and Gene Families in Microbial Eukaryotes"

2016 **NSF East Asia and Pacific Summer Institutes Fellow** $8,000
"Chromosome copy number variation, nuclear architecture, and paralog evolution in *Tokophrya lemnarum*"

Submitted

NSF - PurSUiT $1,881,127
(Co-PI/Co-Author: **XXMA**; PI/Co-Author: J. Burns)
"Accelerating discovery of major eukaryotic lineages with large-scale culture-based/independent approaches"

Prepped

NASA - Exobiology $686,918

(PI: **XXMA**)
"Assessing the Tempo of Gene Family Evolution across the Eukaryotic Tree of Life"

In Prep

Simons Early Career Investigator in Aquatic Microbial Ecology and Evolution
"Complex Developmental Processes and Genome Biology Influences Patterns of Local Adaptation in Microbial Eukaryotes"

Peer-Reviewed Publications (26 Total; 9: First-Author; 1 Senior Author; 7 with Undergrad Authors):
(***** undergraduate author, ♦ co-author/equal-contribution)

26. **Maurer-Alcalá X.X.**, E. Kim. ***Accepted.*** Machine Learning Approaches Improve Open Reading Frame and Contamination Inferences from Noisy Data. ***Genome Biology and Evolution.***

25. Sterner E.*, A. Cote-L'Heureux*, **X.X. Maurer-Alcalá**, L.A. Katz. ***Accepted***. Diverse genome structures among eukaryotes may have arisen in response to genetic conflict. ***Genome Biology and evolution.*** evae239

24. Cote-L'Heurex A.*, **X.X. Maurer-Alcalá**, E. Sterner*, L.A. Katz. ***Accepted.*** Extreme Codon Bias Underlies Emergent Genome Features in Foraminifera. ***mBio.***

23. Timmons C.M.*, K. Le*, E. Sterner*, H. Rappaport*, **X.X. Maurer-Alcalá**, L.A. Katz. 2024. Foraminifera as a model of eukaryotic genome dynamism. ***mBio.*** e03379-23.

22. **Maurer-Alcalá X.X.**, A. Cote-L'Heureux*, S.L. Kosakovsky Pond, L.A. Katz. 2024. Somatic genome architecture and molecular evolution are decoupled in "young" lineage-specific gene families in ciliates. ***PLoS One.*** 19(1):e0291688

21. Gyaltshen Y., A. Rozenberg, A. Paasch, J.A. Burns, S. Warring, R. Larson, **X.X. Maurer-Alcalá**, J. Dacks, E. Kim. 2023. An improved genome assembly for the green algal bacterivore *Cymbomonas tetramitiformis* and the genomes of its integrated viral elements. ***Genome Biology and Evolution*.** 15(11):evad194

20. Singh A.♦, **X.X. Maurer-Alcalá♦**, T. Solberg, S. Gisler, M. Ignarski, E.C. Swart, M. Nowacki. 2022. Chromatin remodeling is required for sRNA‐guided DNA elimination in Paramecium. ***EMBO Journal.*** 41(22):e111839

19. Wang C., T. Solberg, **X.X. Maurer-Alcalá**, E.C. Swart, F. Gao, M. Nowacki. 2022. A small RNA-guided PRC2 complex eliminates DNA as an extreme form of transposon silencing. ***Cell Reports***. 40(8):111263

18. Cote-L'Heurex A.*, **X.X. Maurer-Alcalá**, L.A. Katz. 2022. Old Genes in New Places: A Taxon-Rich Analysis of Interdomain Lateral Gene Transfer Events. ***PLoS Genetics***. 18(6): e1010239

17. Bechara S.T., L.E.S. Kabbani, **X.X. Maurer-Alcalá**, M. Nowacki. 2022. Identification of novel, functional long non-coding RNAs involved in programmed, large-scale genome rearrangements. ***RNA***. 28: 1110-1127

16. Sierra R., F. Mauffrey, J. Cruz, M. Holzmann, A.J. Gooday, **X.X. Maurer-Alcalá**, R. Thakur, M. Greco, A.K.M. Weiner, L.A. Katz, J. Pawlowski. 2022. Taxon-rich transcriptomics supports higher-level phylogeny and major evolutionary trends in Foraminifera. ***Molecular Phylogenetics and Evolution***. 107546.

15. Li Y., Y. Wang, S. Zhang, **X.X. Maurer-Alcalá**, Y. Yan. 2022. How ciliated protists survive adverse environments: some key points during encystment and excystment. ***Frontiers in Microbiology***. 13:785502.

14. Ma M.♦, Y. Li♦, Q. Yuan, T. Zhang, **X.X. Maurer-Alcalá**, Y. Wang, Y. Yan. 2022. Deciphering phylogenetic relationships in class Karyorelictea (Protista, Ciliophora) based on updated multi-gene information with establishment of a new order Wilbertomorphida n. ord. ***Molecular Phylogenetics and Evolution***. 169: 107406.

13. Smith S., **X.X. Maurer-Alcalá**, Y. Yan, L.A. Katz, L. Santoferrara, G. McManus. 2020. Combined genome and transcriptome analyses of the ciliate *Schmidingerella arcuata* (Spirotrichea) reveal patterns of DNA elimination, scrambling, and inversion. ***Genome Biology and Evolution***. 12(9):1616-1622.

12. Rzeszutek I., **X.X. Maurer-Alcalá**, M. Nowacki. 2020. Programmed Genome Rearrangements in Ciliates. ***Cellular and Molecular Life Sciences***. *77*(22), 4615-4629.

11. Ribeiro G.M., A. L. Porfírio-Sousa, **X.X. Maurer-Alcalá**, L.A. Katz, D.J.G. Lahr. 2020. *De novo* Sequencing, Assembly, and Annotation of the Transcriptome for the Free-Living Testate Amoeba *Arcella intermedia*. ***Journal of Eukaryotic Microbiology***. 67(3):383-392.

10. Yan Y.♦, **X.X. Maurer-Alcalá♦**, R. Knight, S.L. Kosakovsky Pond, L.A. Katz. 2019. Single cell transcriptomics reveal a correlation between genome architecture and gene family evolution in ciliates. ***mBio***. 10(6): e02524-19.

9. **Maurer-Alcalá X.X.,** M. Nowacki. 2019. Evolutionary origins and impacts of genome architecture in ciliates. ***Annals of the New York Academy of Sciences***. 1447(1): 110.

8. Céron-Romero M.A., **X.X. Maurer-Alcalá**, J.D. Grattepanche, Y. Yan, M.M Fonseca, L.A. Katz. 2019. PhyloToL: A taxon and gene rich phylogenomic pipeline for exploring genome evolution from diverse eukaryotes. ***Molecular Biology and Evolution***.36(8): 1831 -1842.

7. **Maurer-Alcalá X.X.♦,** Y. Yan♦, O.A. Pilling*, R. Knight, L.A. Katz. 2018. Twisted Tales: Insights into Genome Diversity of Ciliates Using Single-Cell Genomics. ***Genome Biology and Evolution***. 10(8): 1927-1939.

6. **Maurer-Alcalá X.X.,** R. Knight, L.A. Katz. 2018. Exploration of the Germline Genome of the Ciliate *Chilodonella uncinata* through Single-Cell Omics (Transcriptomics and Genomics). ***mBio***. 9(1): e01836–e01817

5. Wancura M.*, Y. Yan, L.A. Katz, **X.X. Maurer-Alcalá**. 2017. Genome amplification, life cycle and nuclear inclusion in the ciliate *Blepharisma americanum*. ***Journal of Eukaryotic Microbiology***. 65(1): 4-11.

4. **Maurer-Alcalá X.X.**, L.A. Katz. 2016. Nuclear architecture and patterns of molecular evolution are correlated in the ciliate *Chilodonella uncinata*. ***Genome Biology and Evolution***. 8(6): 1634-1642.

3. Tekle Y.I., O.R. Anderson, L.A. Katz, **X.X. Maurer-Alcalá,** M.A. Cerón-Romero, R. Molestina. 2016. Phylogenomics of 'Discosea': A new molecular phylogenetic perspective on Amoebozoa with flat body forms. ***Molecular Phylogenetics and Evolution***. 99: 144-154.

2. **Maurer-Alcalá X.X.**, L.A. Katz 2015. An epigenetic toolkit allows for diverse genome architectures in eukaryotes. ***Current Opinion in Genetics & Development***. 35: 93-99.

1. Bellec L., **X.X. Maurer-Alcalá**, L.A. Katz. 2014. Characterization of the Life Cycle and Heteromeric Nature of the Macronucleus of the Ciliate *Chilodonella uncinata* Using Fluorescence Microscopy. ***Journal of Eukaryotic Microbiology***. 61(3): 313-316.

Manuscripts Submitted/In Review (4 Total; **1:** First-Author; **1** Senior Author; **1** with Undergrad Authors)**:**
(* undergraduate author, ♦ co-author/equal-contribution)

Jiang A.*♦, T. Sehein♦, L.A. Katz, **X.X. Maurer-Alcalá**. ***In Review.*** Lineage-specific genes highlight potential species boundaries in populations of testate amoebae from New England bogs and fens. ***Protist***

Gutierrez M.R., G. Szabo, **X.X. Maurer-Alcalá**, Y. Vasquez, E. Kim, T. Woyke, R. Stepanauskas, J.A. Burns, F. Schulz. ***In Review***. Data mining and phylogenomics uncovers numerous novel deep-branching eukaryotic phylum-level lineages. ***Nature Microbiology***

Maurer-Alcalá X.X., S. Warring, Y. Gyaltshen, A.A. Heiss, J.A. Burns, A. Narancia, E. Kim. ***Submitted.*** Independent Approaches Infer Robust Unexpected Relationships Across the Eukaryotic Tree of Life. ***PNAS***

Ahsan R., **X.X. Maurer-Alcalá**, L. Katz. ***Submitted.*** Genome content in the non-model ciliate *Chilodonella uncinata*: insights into nuclear architecture, gene-sized chromosomes among the total DNA in their somatic macronuclei during their development. ***Genes & Development***

Manuscripts in Preparation (Available Upon Request)**:**
(* undergraduate author, ♦ co-author/equal-contribution)

Warring S.♦, X.X. Maurer-Alcalá♦, J. Burns, E. Kim. Inferring the evolution of photosynthesis in the eukaryotic supergroup Cryptista.

Maurer-Alcalá X.X., C.-H. Cho, Y. Gyaltshen, E. Kim. Analyses of nearly all sequenced families in Discoba link rapid genome evolution to genome architecture and major transitions in life histories.

Maurer-Alcalá X.X., R. Stepanauskas, F. Schulz, E. Kim, J. Burns. Environmental sampling driven discovery of multiple new eukaryotic supergroups.

Selected **Presentations**

2024 *Deploying machine learning to overcome challenges with contamination for phylogenomic studies*
PSA-ISOP-ISEP. WA, USA. (oral comm.)

Making sense from chaos through RNA-mediated nuclear crosstalk
Ohio State University. OH, USA. (invited oral comm.)

Breaking Down Biases in Biology: Insights From Microeukaryotes
University of Nebraska-Lincoln. NE, USA. (invited oral comm.)

Genome evolution across the eukaryotic tree of life: linking organismal biology to genome evolution
Hofstra University. NY, USA. (invited oral comm.)

2023 *Throwing out the textbook: how microeukaryotes challenge the "rules of life".*
Purdue University. IN, USA. (invited oral comm.)

Finding a home for orphans: evaluating the phylogenetic placement and genome evolution of malawimonads. NeLLi. Berkeley National Labs. CA, USA (oral comm.)

2022 *Exploring the Evolution of Lineage-Specific Gene Families in Microeukaryotes*. Biology of Genomes. Cold Spring Harbor Labs. NY, USA. (poster)

2019 *Small RNA-mediated nucleosome depletion is required for elimination of transposon-derived DNA*. NCCR RNA & Disease – Vienna RNA Biology Network. Fuchslee, Austria. (oral comm.)

2019 *Studying gene family evolution and genome diversity of ciliates using single-cell 'omics of uncultivable species*. Ecological and Evolutionary Genomics. NH, USA. (poster)

2018 *Applying single-cell -omics towards a greater understanding of ciliate germline genomes*. Ciliate Molecular Biology. Washington, D.C., USA. (oral comm.)

2017 *Single-cell –omics and Exploring the Evolutionary Impact of Germline-Soma Distinctions*. Society for Molecular Biology and Evolution. Houston. TX, USA. (poster)

2015 *Nuclear architecture of the ciliate, Chilodonella uncinata, correlates to patterns of molecular evolution.* Ciliate Molecular Biology. 2015, Camerino, Italy. (oral comm.)

TEACHING ACTIVITIES

2018 – 2020 **Teaching Assistant:** Applied Biostatistics I (104207; Universität Bern)

2014 – 2016 **Teaching Assistant**, Introductory Biology (BIO 153; University of Massachusetts)

2013 **Teaching Assistant**, Genomes and Genetic Analysis (BIO 230; Smith College)

SERVICE AND OUTREACH

Mentorship and Outreach

Undergraduate Researchers Supervised

2021 - 2023 Angela Jiang, Smith College (Honors Thesis)
2021 - 2023 Caitlin Timmons, UMass (Honors Thesis)
2018 - 2023 Auden Côte-L'Heureux, Northampton High-School/University of Massachusetts
2016 - 2017 Angela Lool, Smith College
2016 - 2017 Jacqueline Banuelos, Smith College
2016 - 2017 Monica Wilson, Smith College (Honors Thesis)
2015 - 2017 Anna Rogers, Smith College (Honors Thesis)
2014 - 2017 Olivia Pilling, Smith College (Honors Thesis)
2015 - 2016 Cynthia Masai, Smith College (Honors Thesis)
2015 - 2016 Megan Wancura, Smith College

Graduate Researchers Supervised

2018 - 2021 Sebastian Bechara (Ph.D.), Universität Bern
2018 - 2021 Iris Hug (Ph.D.), Universität Bern
2018 - 2021 Therese Solberg (Ph.D.), Universität Bern

2021 - 2024 **Science Research Mentoring Program,** *American Museum of Natural History*
"*Microbial Matryoshka Dolls: Hunting for Microbes in Microbes*"
"*Machine Learning for Inferring Microbial Evolution"*
"Central Park's Tree of Life"

2016 - 2017 Graduate Student Organizer, Pioneer Valley "Bio-Blitz"

Service

2020 **Invited Session Chair,** Genome Rearrangements, *Ciliate Molecular Biology*

2015 - 2016 **Organizer**, "Classic Papers in Biology" Seminar *University of Massachusetts, Amherst*

***Ad Hoc Reviewer*:** *BMC Evolutionary Biology*, *Genome Biology, Genome Biology and Evolution*, *Journal of Eukaryotic Microbiology*, *mBio, Microorganisms, Molecular Biology and Evolution*, *Nucleic Acids Research*, *PLoS Biology*, *Protist, Evolution*

PROFESSIONAL REFERENCES

Dr. Laura A. Katz (Ph.D Advisor)
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Smith College, Northampton, MA

Dr. Eunsoo Kim
E-mail: ekim1@amnh.org; eunsookim@ewha.ac.kr
Division of Invertebrate Zoology and Institute for Comparative Genomics
American Museum of Natural History, New York, NY
Current Address: Ewha Womans University, Seoul, South Korea

Dr. Sergei Kosakovsky Pond
E-mail: spond@temple.edu
Institute of Genomic and Evolutionary Medicine
Temple University, Philadelphia, PA

Dr. John A. Burns
E-mail: jburns@bigelow.org
Bigelow Laboratory for Ocean Sciences
East Boothbay, Maine 04544