

Xyrus X. Maurer-Alcalá

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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

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 lemnae*”

Prep'd **NASA - Exobiology** \$286,000
(PI: **XXMA**)
“Employing Phylogenomics to Assess the Evolution and Tempo of Eukaryotic Innovations”

In Prep **Simons Early Career Investigator in Aquatic Microbial Ecology and Evolution**
“Genome Architecture Influences Patterns of Local Adaptation in Microbial Eukaryotes”

Peer-Reviewed Publications (22 Total; 8 First-Author; 1 Senior Author):
(undergraduate author*, § co-author/equal-contribution)

22. Gyaltsen Y., A. Rozenberg, A. Paasch, J.A. Burns, S. Warring, R. Larson, **X.X. Maurer-Alcalá**, J. Dacks, E. Kim. *Accepted*. An improved genome assembly for the green algal bacterivore

Cymbomonas tetramitiformis and the genomes of its integrated viral elements. **Genome Biology and Evolution**.

21. **Maurer-Alcalá X.X.**, A. Cote-L'Heureux*, S.L. Kosakovsky Pond, L.A. Katz. *In Press*. Genome Architecture Drives Lineage-Specific Gene Family Expansion but not Molecular Evolution in Ciliates. **PLoS One**.
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'Heureux 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 in Review/Submitted (Available Upon Request):
(undergraduate author*, § co-author/equal-contribution)

Sterner E.* , A. Cote-L’Heureux*, **X.X. Maurer-Alcalá**, L.A. Katz. *In Revision*. Diverse genome structures among eukaryotes may have arisen in response to genetic conflict. *Nature Reviews Genetics*

Timmons C.M.* , K. Le*, E. Sterner*, H. Rappaport*, **X.X. Maurer-Alcalá**, L.A. Katz. *In Revision*. Nuclear architecture and life cycle of the early-diverging foraminiferan *Allogromia laticollaris* CSH. *mBio*

Riberio G., **X.X. Maurer-Alcalá**, L.A. Katz, D.L.G. Lahr. *In Review*. Phylogenomics reveals potential low-oxygen adaptations in free-living testate amoebae. *Molecular Phylogenetics and Evolution*

Cote-L’Heureux A.* , **X.X. Maurer-Alcalá**, E. Sterner*, L.A. Katz. *In Review*. Extreme Codon Bias Underlies Emergent Genome Features in Foraminifera. *PLoS Genetics*

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

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

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

Maurer-Alcalá X.X., E. Kim. Finding a Home for Malawimonads: Placing Orphan Lineages on the Eukaryotic Tree of Life Using Complementary Approaches.

C.-H. Cho[§], **X.X. Maurer-Alcalá[§]**, E. Kim. Failure to Reproduce: Sister Relationship Between Picozoa and Archaeplastida is Artifactual.

Jiang A.^{*§}, T. Sehein[§], L.A. Katz, **X.X. Maurer-Alcalá**. Lineage-specific genes highlight potential species boundaries in populations of testate amoebae from New England bogs and fens.

Selected Presentations

(Presenting Author; * Undergraduate Presenter)

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

- 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 - 2023 **Science Research Mentoring Program**, *American Museum of Natural History*
 “*Microbial Matryoshka Dolls: Hunting for Microbes in Microbes*”
 “*Machine Learning for Inferring Microbial Evolution*”

- 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*