

# 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 lemnarum*”
- 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 (21 Total; 8 First-Author; 1 Senior Author):**  
(undergraduate author\*, § co-author/equal-contribution)

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.<sup>§</sup>, **X.X. Maurer-Alcalá**<sup>§</sup>, 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. <sup>§</sup>, Y. Li<sup>§</sup>, 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.<sup>§</sup>, **X.X. Maurer-Alcalá**<sup>§</sup>, 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.**<sup>§</sup>, Y. Yan<sup>§</sup>, 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)

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

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<sup>§</sup>, **X.X. Maurer-Alcalá<sup>§</sup>**, E. Kim. Failure to Reproduce: Sister Relationship Between Picozoa and Archaeplastida is Artifactual.

Jiang A.\*<sup>§</sup>, T. Sehein<sup>§</sup>, 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*

## PROFESSIONAL REFERENCES

#### **Dr. Laura A. Katz** (Ph.D Advisor)

E-mail: lkatz@smith.edu  
Department of Biological Sciences  
Smith College, Northampton, MA

#### **Dr. Eunsoo Kim**

E-mail: ekim1@amnh.org; eunsookim@ewha.ac.kr  
Division of Invertebrate Zoology and Sackler 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