

# Christopher CM Baker

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## Education

- 2008 – 2015 **PhD, Organismic and Evolutionary Biology**  
Harvard University (Cambridge MA, USA)  
Dissertation: Complexity in mutualisms: indirect interactions with multiple parties  
Advisor: Naomi E Pierce
- 1998 – 2001 **Bachelor of Economics (Honours Class I) and Bachelor of Science**  
Australian National University (Canberra ACT, Australia)  
Thesis: Endogenous ATM sharing with bilateral agreements  
Advisor: Rohan Pitchford

## Employment and professional training

- 2021 – present Soil Microbiologist (contractor), Centuria Corporation (2021-22) and CSMI (2022-)  
Soil Microbiology Group, US Army ERDC Cold Regions Research and Engineering Laboratory
- 2020 – 2021 Bioinformatics Analyst, nextSource  
Gehrke Lab, Massachusetts Institute of Technology
- 2017 – 2019 Postdoctoral Research Fellow, Harvard University  
Pierce Lab, Department of Organismic and Evolutionary Biology & Harvard Global Institute
- 2015 – 2017 Postdoctoral Research Associate, Princeton University  
Pringle and Tarnita Labs, Department of Ecology and Evolutionary Biology
- 2002 – 2008 Payments Policy and System Stability Departments  
Reserve Bank of Australia

## Peer-reviewed publications

- Thurston AK *et al.* (2025). Changes in permafrost bacterial community composition after thaw across multiple Alaskan locations. **Ecosphere** (doi:10.1002/ecs2.70260)
- Wang Z *et al.* (2024). Automated detection of an insect-induced keystone vegetation phenotype using airborne LiDAR. **Methods in Ecology and Evolution** (doi:10.1111/2041-210X.14298)
- Doherty SJ *et al.* (2023). Rhizosphere microbial community structure differs between constant subzero and freeze-thaw temperature regimes in a subarctic soil. **FEMS Microbiology Ecology** (doi:10.1093/femsec/fiad147)
- Espeland M *et al.* (2023). Rapid radiation of ant parasitic butterflies during the Miocene aridification of Africa. **Ecology and Evolution** (doi:10.1002/ece3.10046)
- Baker CCM *et al.* (2023). Seasonal variation in near-surface seasonally thawed active layer and permafrost soil microbial communities. **Environmental Research Letters** (doi:10.1088/1748-9326/acc542)
- Titcomb GC *et al.* (2022). Large-herbivore nemabiomes: patterns of parasite diversity and sharing. **Proceedings of the Royal Society B** (doi:10.1098/rspb.2021.2702)

- Ji Y\*, CCM Baker\* *et al.* (2022). Measuring Protected-Area Effectiveness using Vertebrate Distributions from Leech iDNA. **Nature Communications** (doi:10.1038/s41467-022028778-8) \* equal contributions
- Castillo Vardaro JA\*, JA Bonachela\* *et al.* (2021). Resource availability and heterogeneity shape the self-organization of regular spatial patterning. **Ecology Letters** (doi:10.1111/ele.13822) \* equal contributions
- Baker CCM *et al. et al.* (2020). Spatial patterning of soil microbial communities created by fungus-farming termites. **Molecular Ecology** (doi:10.1111/mec.15585)
- Whitaker MRL *et al.* (2019). Combining stable isotope analysis with DNA metabarcoding improves inferences of trophic ecology. **PLoS ONE** (doi:10.1371/journal.pone.0219070)
- Rosario K *et al.* (2018). Virus discovery in all three major lineages of terrestrial arthropods highlights the diversity of single-stranded DNA viruses associated with invertebrates. **PeerJ** (doi:10.7717/peerj.5761)
- Kerr M *et al.* (2018). Discovery of four novel circular single-stranded DNA viruses in fungus-farming termites. **Genome Announcements** (doi:10.1128/genomeA.00318-18)
- Baker CCM *et al.* (2017). Distinctive fungal communities in an obligate African ant plant mutualism. **Proceedings of the Royal Society B** (doi:10.1098/rspb.2016.2501)
- Baker CCM *et al.* (2016). Dissecting host-associated communities with DNA barcodes. **Philosophical Transactions of the Royal Society B** (doi:10.1098/rstb.2015.0328)
- Bittleston LS *et al.* (2016). Metabarcoding as a tool for investigating arthropod diversity in *Nepenthes* pitcher plants. **Austral Ecology** (doi:10.1111/aec.12271)
- Baker CCM *et al.* (2012). Kin selection and the evolution of social information use in animal conflict. **PLoS ONE** (doi:10.1371/journal.pone.0031664)
- Mushegian AA *et al.* (2011). Bacterial diversity across individual lichens. **Applied and Environmental Microbiology** (doi:10.1128/AEM.02850-10)

## Other publications

- Gonzalez LM *et al.* (2024). Ecological modeling of microbial community composition under variable temperatures. **US Army ERDC/CRREL Technical Report TR-24-2** (doi:10.21079/11681/48184)

## Software

- Baker CCM** (2016). `entrez_qiime`: a utility for generating QIIME input files from the NCBI databases. [https://github.com/bakerccm/entrez\\_qiime](https://github.com/bakerccm/entrez_qiime), release v2.0, 7 October 2016 (doi:10.5281/zenodo.159607)

## Teaching

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|-------------------------|--|
| Spring 2018, Fall 2018  | Instructor, <i>Of Mice and Microbes: How Microbes Drive Animal Behavior</i><br>Mind Brain Behavior Interfaculty Initiative, Harvard University |
| Spring 2010–11, 2013–15 | Teaching Fellow, <i>Animal Behavior</i><br>Department of Organismic and Evolutionary Biology, Harvard University                               |
| Fall 2014               | Teaching Fellow, <i>Biology of Fungi</i><br>Department of Organismic and Evolutionary Biology, Harvard University                              |
| Spring 2001             | Tutor, <i>Quantitative Methods for Business and Economics I</i><br>Department of Statistics and Econometrics, Australian National University   |