

Chris Baker, PhD

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Education

- 2008 – 2015** **PhD, Organismic and Evolutionary Biology**
Harvard University (Cambridge MA, USA)
- 1998 – 2001** **Bachelor of Economics (Honours Class I) / Bachelor of Science**
Australian National University (Canberra ACT, Australia)

Employment and professional training

- 2021 – present** Bioinformatician/Microbiologist, Centuria (2021-22) and CSMI (2022-25) contractor
Soil Microbiology Group, US Army Cold Regions Research and Engineering Laboratory
- 2020 – 2021** Bioinformatician, nextSource consultant
Gehrke Lab, Massachusetts Institute of Technology
- 2017 – 2019** Postdoctoral Research Fellow, Harvard University
Pierce Lab, Department of Organismic and Evolutionary Biology
- 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

- Baker CCM *et al.* (submitted). Temperature and matric potential drive site-dependent shifts in microbial community structure and assembly in cold regions surface soils.
- Faber Q *et al.* (2026). Antimicrobial resistance varies with warming in active layer soil and permafrost. **Scientific Reports** 16:17281 (doi:10.1038/s41598-026-46295-2)
- Gaimaro L *et al.* (2026). Laboratory warming and wetting drives microbial respiration, enzyme activity, and community composition in a boreal forest soil. **FEMS Microbiology Ecology** (doi:10.1093/femsec/fiag003)
- Thurston AK *et al.* (2025). Genome sequences of a *Paenibacillus* sp. and two *Sporosarcina* spp. isolated from New Hampshire soil. **Microbiology Resource Announcements** (doi:10.1128/mra.00790-25)
- van Galen LG *et al.* (2025). A global database of soil microbial phospholipid fatty acids and enzyme activities. **Scientific Data** (doi:10.1038/s41597-025-05759-2)
- 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/s41467-022-28778-8) * 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.* (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)

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

Teaching

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