

William Pearman

Curriculum vitae

Research summary

I am a broadly trained molecular and microbial ecologist with principal expertise in population genomics and microbial ecology. I specialise in developing eco-evolutionary simulations of microbial communities to develop hypotheses which I then test using observational data and experiments. My research background is a combination of population genomics and microbial ecology, with my current research interests working to align these two fields to understand the evolution of host-microbe relationships. My current work combines eco-evolutionary modelling of holobiont evolution, and experimental work with *Daphnia* to determine microbial contributions to host fitness and to understand host-microbial responses to environmental perturbations. In addition to these areas, I am also actively involved in the application and optimisation of new molecular biology protocols for non-model organisms.

Contact

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Awards and honours

2022	Best PhD Presentation - New Zealand Molecular Ecology Conference
2020	Best PhD Presentation - New Zealand Molecular Ecology Conference
2020	New Zealand Marine Sciences Society Student Research Award (\$1,500)
2020	University of Otago Doctoral Scholarship (\$27,500)
2019	Massey University Masters Scholarship (\$15,000)
2018	Presentation Bursary - Oxford Nanopore Technologies
2018	Massey Graduate Scholarship, Sciences - Massey University (\$5,000)
2018	Natural Sciences Masters Scholarship - Massey University (\$10,000)
2017	Best Student Presentation - New Zealand Molecular Ecology Conference
2015	Vice Chancellors Natural Science Excellence Scholarship, Massey University (\$15,000)

Education

2023	PhD Marine Science , University of Otago, Dunedin, New Zealand
2020	MNatSci (Distinction) Genetics , Massey University, Auckland, New Zealand
2018	BNatSci Genetics , Massey University, Auckland, New Zealand

Selected major grants

2025	Mana Tūāpapa Future Leader Fellowship (\$820,000 NZD) - Independent 4-year fellowship to explore <i>Daphnia</i> microbial ecology
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2025	Te Pūnaha Matatini Seed Fund (\$4,880 NZD)
2025	ISME Scholar Mobility Award (\$3,000 NZD)
2025	Emerging Researchers Network - Seed Fund (\$2,500 NZD)
2025	Genetics Society of Australasia - Workshop Support Fund (\$1,000 NZD)
2025	Center for Computational Evolution - Workshop Fund Award (\$3,500 NZD)
2025	Genomics Aotearoa - Workshop Fund Award (\$5,000 NZD)
2024	University of Auckland Research Fellow Society Seed Funding (\$5,000)

Selected teaching experience

- Contributed course material — BIOSCI 761, University of Auckland
- Workshop instructor — SLiM eco-evolutionary simulation workshop
- Workshop instructor (upcoming) — eDNA bioinformatics workshop
- Undergraduate teaching laboratory instructor / demonstrator
- Postgraduate student supervision (multiple students)

Selected talks

- 2024 Invited talk — Center for Computational Evolution's 2024 Research Showcase
- 2022 Conference presentation — New Zealand Molecular Ecology Conference (awarded Best PhD Presentation)
- 2020 Conference presentation — New Zealand Molecular Ecology Conference (awarded Best PhD Presentation)
- 2020 Invited participant — Ira Moana Investigator Workshop
- 2019 Invited participant — Ira Moana Project Early Career Workshop
- 2017 Conference presentation — New Zealand Molecular Ecology Conference (awarded Best Student Presentation)

Selected service

- 2025- Co-chair - University of Auckland
present Faculty of Science Research Fellow Society
- 2025- Member - University of Auckland
present Faculty of Science Research Committee
- 2024 EEB Representative - University of Auckland Faculty of Science Research Fellow Society

Professional development

- 2026 Visiting Scholar - KU Leuven
- 2020 Invited participant - Ira Moana Investigator Workshop
- 2019 Invited participant - Ira Moana Project Early Career Workshop

Publications

19. Ryder, F.J., Pearman, W.S., Layton, C., Parvizi, E., Johnson, C., Bellgrove, A. & Fraser, C.I. (In Press). Contrasting patterns of population structure in two habitat-forming kelp species in southeastern Australia. *Journal of Phycology*. DOI
18. Kroos, G.C., Fernandes, K., Seddon, P., Ashcroft, T., Pearman, W.S. & Gemmell, N.J. (2026). Targeted Airborne eDNA of an Invasive Wallaby: Effects of Sampler Type, Distance, and Environmental Conditions. *Environmental DNA*, 8(1), e70240. DOI
17. Pillay, P., dos Remedios, N., Pearman, W.S., Santure, A.W. & Allen, M.S. (2025). Bones, barcodes, and biodiversity: Optimising bulk bone metabarcoding analysis for tropical subfossil collections from Polynesia. *Quaternary International*, 110099. DOI
16. Pearman, W.S., Rodrigo, A.G. & Santure, A.W. (2025). Within-host microbial selection and multiple microbial generations buffer the loss of host fitness under environmental change. *FEMS Microbiology Ecology*, fiaf089. DOI
15. Morales, S.E., Tobias-Hünefeldt, S.P., Armstrong, E., Pearman, W.S. & Bogdanov, K. (2025). Marine phytoplankton impose strong selective pressures on in vitro microbiome assembly, but drift is the dominant process. *ISME Communications*, 5(1), ycaf001. DOI
14. Pearman, W.S., Duffy, G.A., Smith, R.O., Currie, K.I., Gemmell, N.J., Morales, S.E. & Fraser, C.I. (2024). Host dispersal relaxes selective pressures in rafting microbiomes and triggers successional changes. *Nature Communications*, 15(1), 10759. DOI
13. Pearman, W.S., Arranz, V., Carvajal, J.I., Whibley, A., Liau, Y., Johnson, K., Gray, R., Treece, J.M., Gemmell, N.J., Liggins, L., Fraser, C.I., Jensen, E.L. & Green, N.J. (2024). A cry for kelp: Evidence for polyphenolic inhibition of Oxford Nanopore sequencing of brown algae. *Journal of Phycology*, 60(6), 1601-1610. DOI
12. Pearman, W.S., Duffy, G.A., Gemmell, N.J., Morales, S.E. & Fraser, C.I. (2024). Long-distance movement dynamics shape host microbiome richness and turnover. *FEMS Microbiology Ecology*, fiac089. DOI
11. Pearman, W.S., Adams, C.I.M., Monteiro, M., Quesada, A. & Fraser, C.I. (2024). Fine-scale phylogenetic diversity gradients support the Antarctic geothermal refugia hypothesis. *Antarctic*

10. Pearman, W.S., Morales, S.E., Vaux, F., Gemmell, N.J. & Fraser, C.I. (2024). Host population crashes disrupt the diversity of associated marine microbiomes. *Environmental Microbiology*, 26(3), e16611. DOI
9. Pearman, W.S., Duffy, G.A., Liu, X.P., Gemmell, N.J., Morales, S.E. & Fraser, C.I. (2024). Macroalgal microbiome biogeography is shaped by environmental drivers rather than geographical distance. *Annals of Botany*, 133(1), 169-182. DOI
8. Thompson, B., Atsawawaranunt, K., Nehmens, M.C., Pearman, W.S., Perkins, E.O., Pipek, P., Rollins, L.A., Tan, H.Z., Whibley, A., Santure, A.W. & Stuart, K.C. (2024). Population Genetics and Invasion History of the European Starling Across Aotearoa New Zealand. *Molecular Ecology*, e17579. DOI
7. Pearman, W.S., Urban, L. & Alexander, A. (2022). Commonly used Hardy-Weinberg equilibrium filtering schemes impact population structure inferences using RADseq data. *Molecular Ecology Resources*, 22(7), 2599-2613. DOI
6. Liu, X.P., Duffy, G.A., Pearman, W.S., Pertierra, L.R. & Fraser, C.I. (2022). Meta-analysis of Antarctic phylogeography reveals strong sampling bias and critical knowledge gaps. *Ecography*, 2022(12), e06312. DOI
5. Fraser, C.I., Dutoit, L., Morrison, A.K., Pardo, L.M., Smith, S.D.A., Pearman, W.S., Parvizi, E., Waters, J. & Macaya, E.C. (2022). Southern Hemisphere coasts are biologically connected by frequent, long-distance rafting events. *Current Biology*, 32(14), 3154-3160.e3. DOI
4. Pearman, W.S., Wells, S.J., Dale, J., Silander, O.K. & Freed, N.E. (2022). Long-read sequencing reveals atypical mitochondrial genome structure in a New Zealand marine isopod. *Royal Society Open Science*, 9(1), 211550. DOI
3. Pearman, W.S., Wells, S.J., Silander, O.K., Freed, N.E. & Dale, J. (2020). Concordant geographic and genetic structure revealed by genotyping-by-sequencing in a New Zealand marine isopod. *Ecology and Evolution*, 10(24), 13624-13639. DOI
2. Arranz, V., Pearman, W.S., Aguirre, J.D. & Liggins, L. (2020). MARES, a replicable pipeline and curated reference database for marine eukaryote metabarcoding. *Scientific Data*, 7(1), 209. DOI
1. Pearman, W.S., Freed, N.E. & Silander, O.K. (2020). Testing the advantages and disadvantages of short- and long-read eukaryotic metagenomics using simulated reads. *BMC Bioinformatics*, 21(1), 1-15. DOI