

HUGH CROSS, PHD

I am a computational biologist with a background in ecology and evolutionary genetics. I work on projects across the tree of life, utilising many kinds of data and multiple approaches. With biodiversity studies as a centerpoint, I have naturally come to specialise in metagenomics research. To study any environment is to study a community of genes engaged in molecular dialogues—both within and between species, and this requires a community of researchers working together. I hope to find this team.

View this CV online with links at
hughcross.github.io/cv

EDUCATION

- | | | |
|------|--|--------------------|
| 2003 | ● Ph.D., Ecology and Evolutionary Biology
Columbia University | 📍 New York, NY |
| 1998 | ● M.Sc., Plant Breeding and Genetics
Colorado State University | 📍 Fort Collins, CO |
| 1993 | ● B.A., Anthropology
University of Colorado | 📍 Boulder, CO |

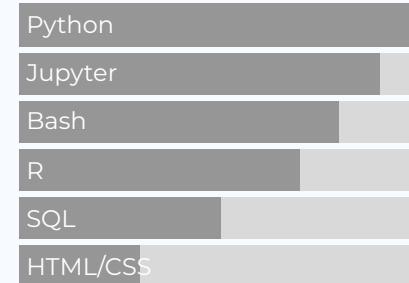
SUPPORT AND AWARDS

- | | |
|------|--|
| 2016 | ● Invertebrate Diversity in Common Ash Canopies with a Glimpse of Hidden Diversity Using Next Generation Sequencing
Norwegian Biodiversity Information Centre, 2.6 million Norwegian kroner (~\$US325,000)
· with K. Thunes |
| 2016 | ● Micro- and macroalgae interactions with bacteria and fungi to improve the viability of commercial algae production (MICMAC)
Norwegian Institute for Bioeconomy Research Development Pilot Grants, 1.5 million Norwegian kroner (~\$US187,500)
· With C. Bruckner, N. Nagy |
| 2012 | ● Soils to Satellites
Department of Innovation, Industry, Science and Research, Education Investment Fund (Australia), A\$184,568.29
· with A. Lowe (Chief Investigator), P. Doherty, C. Walker, G. Guerin |
| 2010 | ● Impact of grazing on lichens in Murray Basin
South Australia Native Vegetation Research Grant, A\$16,230 |

CONTACT

- ✉ hughcross@gmail.com
/github.com/hughcross
/hughcross.github.io/
📞 +64 (0) 21 980 027

PROGRAMMING SKILLS



FIELDWORK

Australia
Costa Rica
Mexico
USA: Colorado and Hawaii

FOREIGN LANGUAGE

Fluent in Spanish

Made with [pagedown](#) in R.

Source code:
github.com/hughcross/cv

Last updated on 2021-10-13.

- 2010 ● ***Environmental Genomics: Mining, climate change, water, crime and health***
ARC Linkage (Australia), A\$498,058.52
· with A. Cooper (Chief Investigator), Adelson D, Brook B, Facelli J, Stevens M, Paton J, Tuckweng K.
- 2009 ● ***21st Century Taxonomy - DNA barcoding of Grasses***
Taxonomy Research Initiative Network (Australia), A\$63,000
- 2009 ● ***Molecular genetics to improve the knowledge of plants in South Australia***
DEH Research Partnerships (Australia), A\$30,385.04
- 2002 ● ***Evolution and Domestication in the Genus Sechium***
Explorers Club Award, US\$1,200
- 2002 ● ***Genetic Diversity of Chayote***
Torrey Botanical Society Graduate Student Award Honorable Mention, US\$500
- 2002 ● ***Origins, Evolution, and Conservation of Crop Plants: A Molecular Approach***
Torrey Botanical Society Symposium Support Award, US\$2,500
· with co-organizers T.J. Motley and N. Zerega

► PROFESSIONAL & RESEARCH EXPERIENCE

- Present | 2017 ● **Bioinformatician**
Department of Anatomy, University of Otago
· Conducting bioinformatic analyses on several projects in the department, including genome and transcriptome assembly and annotation, gene expression, population and phylogenetic research
· Training staff and students in basic and advanced data analysis methods
- 2017 | 2013 ● **Scientist**
Department of Forest Health, Norwegian Institute for Bioeconomy Research (NIBIO)
· Primary responsibility was conducting bioinformatic analyses on several projects in the department of Forest Health at the institute, including genome and transcriptome assembly, gene expression, population and phylogenetic research of plants, animals, and fungus, and metagenomics

2013
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2008

● **Molecular Botanist**

State Herbarium of South Australia

- Conducted research in all areas of plant and fungal genomics, including genomic, transcriptomic, and bioinformatic applications for biodiversity and ecology
- Main coordinator for DNA Barcoding projects
- Trained and consulted with staff for next generation sequencing research

2013
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2008

● **Affiliate Research Fellow**

Australian Centre for Ancient DNA & Australian Centre for Evolutionary Biology and Biodiversity, University of Adelaide, SA, Australia

- Conducted research in ancient DNA of plants and fungi
- Led genetic components for major ecological research projects

2008
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2005

● **Research Associate/Laboratory Manager**

Pringle Lab, Dept of Organismic and Evolutionary Biology, Harvard University

- Responsible for setting up and maintaining the facility, training new users, establishing all protocols, and conducting research in molecular evolution, systematics, and population genetics
- Developed molecular markers for AFLP, ISSR, and DNA sequence data analyses of fungi and their plant hosts
- Developed methods for the molecular analysis of soil biota, including fungal-plant interactions, and DNA extraction from historical collections of fungus

2005
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2003

● **Laboratory Manager**

Leiden Ancient DNA Facility, National Herbarium of The Netherlands

- Responsible for establishing the facility, ordering equipment, establishing protocols for proper use
- Trained other researchers to use the facility
- Optimized protocols for extraction of DNA from museum materials

2005
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2003

● **Postdoctoral Researcher**

Leiden Herbarium, National Herbarium of The Netherlands

- Responsible for extraction, amplification, and sequencing of species of *Zehneria* and related genera to construct a molecular phylogeny of the genus
- Developed new molecular markers for Cucurbitaceae
- Conducted various projects in ancient DNA research in conjunction with researchers at the herbarium, the University of Leiden, and the Naturalis Natural History Museum

2003
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1999

● **PhD Fellow**

Cullman Laboratory for Molecular Systematics Studies, The New York Botanical Garden

- Conducted research in molecular genetics, including molecular sequencing, and molecular marker data (AFLP)
- Trained graduate students, postdoctoral students, and visiting scientists in molecular techniques and analyses

2002
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2001

● **DNA Database Manager and Technician**

Cullman Laboratory for Molecular Systematics Studies, The New York Botanical Garden

- Set up the DNA database for the collection at the Cullman Laboratory using Freezerworks software
- Transferred data from lab files and fieldbooks; labeled DNA and dried-silica collections

PUBLICATIONS

2021

● **First mitochondrial genome of the Caucasian squirrel *Sciurus anomalus* (Rodentia, Sciuridae)**

Mitochondrial DNA Part B 6: 883-885

- Boukhoud, L., Parker, L.D., McInerney, N.R., Saliba, C., Kahale, R., Cross, H.B., Matisoo-Smith, L., Maldonado, J.E., Bou Dagher Kharrat, M.

2021

● **First mitochondrial genome of the marbled polecat *Vormela peregusna* (Carnivora, Mustelidae)**

Mitochondrial DNA Part B 6: 1009-1011

- Boukhoud, L., Parker, L.D., McInerney, N.R., Saliba, C., Kahale, R., Cross, H.B., Matisoo-Smith, L., Maldonado, J.E., Bou Dagher Kharrat, M.

2021

● **Genomic sequencing confirms absence of introgression despite past hybridisation between a common and critically endangered bird**

Global Ecology and Conservation 28: e01681

- Forsdick, N.J., Martini, D., Brown, L., Cross, H.B., Maloney, R.F., Steeves, T.E., Knapp, M.

2020

● **Genomic screening reveals that the endangered *Eucalyptus paludicola* (Myrtaceae) is a hybrid**

Diversity 12: 468

- van Dijk, K., Waycott, M., Quarmby, J., Bickerton, D., Thornhill, A.H., Cross, H.B., Biffin, E.

2020

● **Molecular underpinnings of long-term methyl jasmonate-induced resistance in Norway spruce**

Plant Cell & Environment 43: 1827-1843.

- Magerøy, M., Wilkinson, S., Tengs, T., Cross, H.B., Almvik, M., Petriacq, P., Vivian-Smith, A., Zhao, T., Fossdal, C.G., Krokene, P.

[Publications Overview](#):

Citations: 1400

h-index: 14

[Google Scholar profile](#)

- 2020
- **Stress, novel sex genes and epigenetic reprogramming orchestrate socially-controlled sex change**
Science Advances 7 eaaw7006
 - Todd, E.V., Ortega-Recalde, O., Liu, H., Lamm, M.S., Rutherford, K.M., **Cross, H.B.**, Black, M.A., Kardailsky, O., Marshall Graves, J.A., Hore, T.A., Godwin, J.R., Gemmell, N.J.
- 2019
- **One thousand plant transcriptomes and the phylogenomics of green plants**
Nature 574: 679-685.
 - Leebens-Mack, J. et al.
- 2018
- **The Sturt pea through 300 years of Australian botanical exploration**
Swainsona 30: 1-8.
 - Cross, H.B., Biffin, E., Waycott, M.
- 2017
- **Ash dieback in Norway - current situation**
In: *Dieback of European Ash (*Fraxinus spp.*) - Consequences and Guidelines for Sustainable Management* (Eds: Vasaitis, R. & Enderle, R.), pp. 166-175. COST.
 - Børja, I., Timmermann, V., Hietala, A.M., Tollefsrud, M.M., Nagy, N.E., Vivian-Smith, A., **Cross, H.B.**, Sønstebo, J.H., Myking, T., Solheim, H.
 - **Fungal diversity and seasonal succession in ash leaves infected by the invasive ascomycete *Hymenoscyphus fraxineus***
New Phytologist, 213(3): 1405-1417
 - Cross, H.B., Sønstebo, J.H., Nagy, N.E., Timmermann, V., Solheim, H., Børja, I., Kauserud, H., Carlsen, T., Rzepka, B., Wasak, K., Vivian-Smith, A., Hietala, A.M.
- 2016
- **Effective application of next generation sequencing (NGS) approaches in systematics and population genetics - case studies in *Eucalyptus* and *Acacia***
Australian Systematic Botany 29(3): 235-246
 - Cross, H.B., Biffin, E., van Dijk, K., Lowe, A., Waycott, M.
- 2015
- **Molecular phylogenetic analyses of Cucurbitaceae tribe Benincaseae urge for merging of *Pilogyne* with *Zehneria***
Phytotaxa, 236(2): 173-183
 - de Boer, H.J., Cross, H.B., de Wilde, J.J.O., Duyfjes, B.E.E., Gravendeel, B.
- 2015
- **Using phylogenetic diversity to identify ancient rain forest refugia and diversification zones in a biodiversity hotspot.**
Diversity and Distributions 21: 279-289
 - Costion, C., Edwards, W., Ford, A., Metcalfe, D., **Cross, H.B.**, Harrington, M., Richardson, J., Hilbert, D., Lowe, A., Crayn, D.

- 2014
- **Global change community ecology beyond species-sorting: a quantitative framework based on mediterranean-biome examples**
Global Ecology and Biogeography 23: 1062-1072
 - Guerin, G., Martín-Forés, I., Biffin, E., Baruch, Z., Breed, M., Christmas, M., Cross, H.B., Lowe, A.J.
- 2013
- **A spatially predictive baseline for monitoring multivariate species occurrences and phylogenetic shifts in mediterranean southern Australia**
Journal of Vegetation Science 25: 338-348
 - Guerin, G.R., Biffin, E., Jardine, D.I., Cross, H.B., Lowe, A.J.
- 2011
- **The application of DNA methods to timber tracking and origin verification**
IAWA Journal 32 (2): 251-262
 - Lowe, A.J. & Cross, H.B.
- 2011
- **Plant DNA barcodes can accurately estimate species richness in poorly known floras**
PloS ONE 6(11): e26841
 - Costion, C., Ford, A., Cross, H.B., Crayn, D., Harrington, M., Lowe, A.J.
- 2010
- **DNA barcoding of Invasive Species**
In *Fifty Years of Invasion Ecology: The Legacy of Charles Elton* (Ed. Richardson D.). Chapter 22. Wiley-Blackwell, Oxford
 - Cross H.B., Lowe A.J., Gurgel C.F.D.
- 2010
- **Distribution and abundance of the introduced ectomycorrhizal fungus, *Amanita phalloides*, in North America**
New Phytologist 185: 803-816
 - Wolfe B.E., Richard, F., Cross, H.B., and Pringle A.
- 2009
- **The ectomycorrhizal fungus *Amanita phalloides* was introduced and is expanding its range on the west coast of North America**
Molecular Ecology 18: 817-833
 - Pringle, A., Rachel I. Adams, R. I., Cross, H.B., Bruns, T.D.
- 2008
- **The ecological implications of a Yakutian mammoth's last meal**
Quaternary Research 69: 361-376
 - van Geel, B., Aptroot, A., Baittinger, C., Birks, H.H., Bull, I.D., Kompanje, E.J.O., Cross, H.B., Evershed, R.P., Gravendeel, B., Kuperus, P., Nierop, K.G.J., Mol, D., Pals, J.P., Tikhonov, A. N., van Reenen, G., and van Tienderen, P.H.
- 2008
- **The use of orchid pollinia or pollinaria for taxonomic identification**
Selbyana 29(1): 6-19
 - Singer, R. B., Gravendeel, B., Cross, H.B., Ramirez, S. R.

- 2008
- **Assessment of age and greenness of herbarium specimens as predictor for successful extraction and amplification of DNA**
Blumea 53: 407-428
• Erkens, R. H. J., Cross, H.B., Maas, J. W., Hoenselaar, K., and Chartrou, L. W.
- 2006
- **Origin and diversification of chayote**
In: *Darwin's Harvest: New Approaches to the Origins, Evolution, and Conservation of Crops* (Motley, Zerega, and Cross eds.). Columbia University Press
• Cross, H.B., Lira Saade, R., and Motley, T. J.
- 2006
- ***Darwin's Harvest: New Approaches to the Origins, Evolution, and Conservation of Crops***
Columbia University Press
• Motley, T. J., N. Zerega, and H.B. Cross, (editors)
- 2003
- **Regulating access to genetic resources: An analysis of selected case studies**
Biodiversity and Conservation 12(7), 1511-1524
• Dávalos, L.M., Sears, R., Raygorodetsky, G., Simmons, B., Cross, H.B., Grant, T., Barnes, T., Putzel, L. and Porzecanski, A.L.
- 2002
- **Phenotypic and genetic diversity of chayote germplasm**
Proceedings of the 2002 Cucurbitaceae Congress: 138-143
• Cross, H.B., and Motley, T. J.
- 2001
- **Natural History of Mesoamerica**
In: *Oxford Encyclopedia of Mesoamerican Cultures*, Carrasco et al. (editors). Oxford University Press, New York
• Cross, H.B.
- 2001
- **Rainforests of Mesoamerica**
In: *Oxford Encyclopedia of Mesoamerican Cultures*, Carrasco et al. (editors). Oxford University Press, New York
• Cross, H.B.
- 2000
- **Inheritance of resistance to Fusarium wilt in two common bean races**
Crop Science 40(4), 954-958
• Cross, H.B., Brick, M.A., Schwartz, H.F., Panella, L.W., Byrne, P.F.



TEACHING EXPERIENCE

Present
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2019

- **Instructor, Workshop in Environmental DNA**
University of Otago 📍 Dunedin & Auckland, NZ
 - Designed from bottom up course to teach methods & concepts for eDNA metabarcoding
- **Instructor, Software/Data Carpentry**
University of Otago 📍 Dunedin, NZ
 - Teaching basic and advanced bioinformatic skills using live coding in a team-teaching environment
- **Instructor, Advanced Bioinformatic Workshops**
University of Otago 📍 Dunedin, NZ
 - Teaching applied bioinformatic skills in specific fields, including population genetics and gene expression (RNAseq)
- 2019 ● **Instructor, Undergraduate honours course (ANAT458)**
University of Otago 📍 Dunedin, NZ
 - Gave lectures on data analysis for team-taught course to prepare honours students for their research component.
- 2004 ● **Lecture: Applications of Ancient DNA for archaeology**
Leiden University 📍 Leiden, The Netherlands
 - Invited lecture
- 2001 ● **Public Tour: Botanicals for Flavors and Scent**
The New York Botanical Garden 📍 New York, NY
 - Gave a tour of the Enid A. Haupt Conservatory, focusing on plants in the collection that are used as flavors and scents
- 2001 ● **Lecture: The evolution of stem and wood structure**
The Cooper Union School of Art 📍 New York, NY
 - General Botany for undergraduates
- 2000 | 1999 ● **Graduate Teaching Assistant**
Columbia University 📍 New York, NY
 - Taught recitation for introductory biology course
 - Helped professor design and grade exams
- 1998 ● **Instructor, Genetics course**
Colorado State University 📍 Fort Collins, CO
 - Taught midlevel genetics course required for all science majors
 - Covered basic and advanced genetics topics, including transmission, population, and molecular genetics

Certified Software Carpentry Instructor

[link to environmental DNA workshop](#)

I also run a [biweekly bioinformatics help session](#)

1998	<ul style="list-style-type: none"> Teaching Assistant, Genetics Colorado State University 	📍 Fort Collins, CO
1993	<ul style="list-style-type: none"> Teaching Assistant, Physical Anthropology University of Colorado 	📍 Boulder, CO
1992 1991	<ul style="list-style-type: none"> Teacher, English as a Second Language University of Guadalajara 	📍 Guadalajara, Mexico
	<ul style="list-style-type: none"> • Taught English as a second language from beginning to advanced levels to students of all ages 	

🎙 SELECTED ABSTRACTS AND PRESENTATIONS

- 2021
- Environmental DNA from pāua (*Haliotis spp.*) in New Zealand reflects common, but not rare, haplotypic variation in a field setting***
Presented at the Society for Molecular Biology and Evolution annual meeting (Virtual Meeting)
 - Adams, C.I.M., Hepburn, C., Cross, H.B., Taylor, H.R., Gemmell, N.J., Bunce, M., Jeunen, G-J., Knapp, M.
- 2019
- Origin and evolution of Tuberculosis in New Zealand***
Presented at Queenstown Molecular Biology Meeting, Queenstown, NZ
 - Knapp, M., McDonald, S.K., Buckley, H., Kardailsky, O., Aung, H.L., Cross, H.B., Jeunen, G-J., Matisoo-Smith, E., Walter, R., Cook, G.M.
- 2016
- Unraveling phenology: epigenetic memory adjusts bud set and bud burst in Picea***
Presented at NorPlantBio, Trondheim, Norway
 - Viejo, M., Carneros, E., Cross, H.B., Lee, Y.K., Yakovlev, I., Fossdal, C.G., Olsen, J.E.
- 2015
- Priming of plant immunity: molecular mechanisms of defense priming in Norway spruce***
Presented at 5th International Workshop on the Genetics of Tree-Parasite Interactions, Orleans, France
 - Krokene, P., Fossdal, C.G., Vivian-Smith, A., Cross, H.B., Zhao, T.
- 2015
- Effect of primed conifer defences on a tree-killing bark beetle-fungus complex***
Presented at IUFRO Tree Biotechnology Conference, Florence, Italy
 - Fossdal, C.G., Cross, H.B., Vivian-Smith, A., Krokene, P.

- 2015 ● ***Community profiling of ash leaf mycoflora at a stand heavily affected by ash dieback***
Presented at seminar Advances in Fungal Genomics, Ås, Norway
· Cross, H.B., Hietala, A.
- 2014 ● ***Transcriptomic analysis of the spruce bark beetle***
Presented at the annual meeting of the Society for Bioinformatics in Northern Europe, Oslo, Norway
· Cross, H.B., Fossdal, C. G., Vivian-Smith, A., Krokene, P.
- 2013 ● ***Exploring plant genomic biodiversity in South Australia***
Presented at the CBA Biodiversity Genomics Conference, Canberra, Australia
· Cross, H.B., Biffin, E., van Dijk, K. Waycott, M.
- 2011 ● ***Tales from the cryptogams, fungal DNA from museum collections***
Plenary speaker at the Fourth International Barcode of Life Conference, Adelaide, Australia
· Cross, H.B., Pringle, A.
- 2011 ● ***Strangers in a strange land: camel impact on Australian native flora***
Presented at the Fourth International Barcode of Life Conference, Adelaide, Australia
· Cross, H.B., Armstrong, K., Bauman, U., Thomson, V. Jardine, D. Cooper, A.
- 2011 ● ***Utilizing Grass DNA barcodes to Explore Australian Ecosystems***
Presented at the International Botanical Congress, Melbourne, Australia
· Cross, H.B., Murphy, D., Brown, A., Gardner, S., Syme, A., Jardine, D., Cantrill, D., Lowe, A.J.
- 2011 ● ***Paleoecology from the ground up: ancient DNA of fungi***
Presented at the International Botanical Congress, Melbourne, Australia
· Cross, H.B., Cooper, A.
- 2007 ● ***Ancient DNA of a Mammoth's Last Meal***
Invited Seminar Speaker, Department of Geology, Johns Hopkins University, Baltimore, MD
· Cross, H.B.
- 2005 ● ***Obtaining plant DNA from museum material***
Presented at the International Botanical Congress, Vienna, Austria
· Cross, H.B., Gravendeel, B.

SYMPOSIA AND WORKSHOPS ORGANISED

- 2019 • ***Environmental DNA Workshop***
 University of Otago, Dunedin, NZ
- 2011 • ***Plant Ancient Biomolecules: Human History and Changing Climates***
 Symposium at the International Botanical Congress, Melbourne, Australia
- 2005 • ***Current Research in Ancient Plant DNA***
 Symposium at the International Botanical Congress, Vienna, Austria
 · co-organized with Terry Brown
- 2004 • ***Ancient DNA***
 Naturalis Museum  Leiden, The Netherlands
- 2002 • ***Origins, Evolution, and Conservation of Crop Plants: A Molecular Approach***
 The New York Botanical Garden  Bronx, NY
 · Co-organized with Timothy J. Motley and Nyree Zerega
 · Sponsored symposium at the Society for Economic Botany annual meeting
- ***Application of Next Generation DNA Sequencing in Environmental Monitoring and Assessment: Current Status and Future Directions***
 Adelaide University  Adelaide