
Thomas Harrop

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I work with large-scale genetic, genomic and transcriptomic datasets.
I use R and python to tidy, analyse and visualise data and communicate results.
I generate data using 2nd- and 3rd-generation sequencing.

About me

Technical skills

My main tools for programming and data analysis are Python and R. I'm also experienced with bash scripting. I visualise and communicate my results with ggplot2, Markdown, Pandoc, TeX and a bit of html & css. I use git, Snakemake, Singularity and Docker to keep my work reproducible. I've used job schedulers like SLURM, LSF and SGE for managing jobs in high-performance computing environments. I'm comfortable working with, installing and administrating *nix operating systems (Linux, macOS and FreeBSD).

I'm an experienced molecular biologist. I am skilled at the entire wet-lab workflow for producing short and long read sequencing libraries, from nucleic acid extraction to library preparation and running sequencing instruments. I have experience with classical genetic approaches with live organisms, including transformation, crosses, microdissection and bioassays.

Research

I'm interested in research related to agriculture and development, tools and techniques in bioinformatics and evolutionary and comparative biology.

Personal information

Languages English (native)
 German ([TELC Level](#) B2)
 French ([TELC Level](#) B1)

Nationalities Australian and British

Experience

Research & University positions

- 2021–Present Academic Specialist (B)**, Melbourne Bioinformatics, University of Melbourne, Australia.
In my current position, I provide training and support to researchers and projects using bioinformatics in Melbourne's biosciences precinct.
- 2020–2021 Research Fellow**, Biochemistry Department, University of Otago, Dunedin, New Zealand.
After promotion to Research Fellow, I began developing an independent genomics and bioinformatics research program.
- 2017–2020 Post-doctoral researcher**, Laboratory for Evolution and Development, Biochemistry Department, University of Otago, Dunedin, New Zealand.
In this postdoc position I worked on a project to develop and apply tools to integrate genomic selection to breeding programmes to improve honeybee performance.
- 2016–2017 Post-doctoral researcher**, Laboratory for Evolution and Development, Biochemistry Department, University of Otago, Dunedin, New Zealand.
I worked on a bioprotection project investigating the resistance of Argentine stem weevil to its biological control agent.
- 2014–2016 Post-doctoral researcher**, UMR DIADE, Institut de Recherche pour le Développement (IRD), Montpellier, France.
We used RNA sequencing to characterise molecular events that occur during development of inflorescence architecture in rice, which affects crop yield, and applied these results to study the effects of selection on gene expression during the parallel domestications of African and Asian rice.
- 2013–2014 Post-doctoral researcher**, Department of Plant Breeding and Genetics, Max Planck Institute for Plant Breeding Research, Cologne, Germany.
At the Max Planck Institute I worked on a bioinformatic and molecular biology project to compare the transcriptional response of different land plants to UV-B exposure, which acts as an environmental signal.

Professional positions

- 2004–2007** **Medical scientist**, Network Pathology, the Austin Hospital, Heidelberg, Australia.
- 2001–2004** **Laboratory assistant**, Network Pathology, the Austin Hospital, Heidelberg, Australia.

Education

- 2006–2012** **Doctor of Philosophy**, Department of Genetics, the University of Melbourne, Parkville, Australia.
Thesis: *The functions of cytochrome P450s in Drosophila.*
During my Ph.D. I used classical genetics and modern molecular biology, including transgenic manipulation of gene expression and comparative studies of gene function, to investigate the functions of cytochrome P450 genes in the *Drosophila* genus.
- 2002–2005** **Bachelor of Science with Honours (first class)**, the University of Melbourne, Parkville, Australia.
- Awards** **2006–2009**, Australian Postgraduate Award

Teaching

- 2021** **COMP90014, Algorithms for Bioinformatics**, Masters of Bioinformatics, The University of Melbourne. Subject coordinator and lecturer.
- BINF90002, Elements of Bioinformatics & COMP90016, Computational Genomics**. Guest lecturer.
- 2020** **GENE412**, Genetics Department, The University of Otago.
- 2017–2019** **GENE312** project supervisor, Genetics Department, The University of Otago.
- 2007–2011** **3rd Year Genetics**, Department of Genetics, The University of Melbourne, Parkville, Australia.
- 2006–2009** **High School Biology**, Department of Genetics, The University of Melbourne, Parkville, Australia.
- 2006–2008** **High School Biology**, Gene Technology Access Centre, The University High School, Parkville, Australia.
- 2005–2008** **1st Year Genetics**, The University of Melbourne, Parkville, Australia.

Students co-supervised

- Sarah Robinson** **Bachelor of Science with Honours**, Genetics, University of Otago, Dunedin, New Zealand.
- Marissa Le Lec** **Bachelor of Science with Honours**, Genetics, University of Otago, Dunedin, New Zealand.
- Swarit Jaisal** **Master of Science**, Life Science Informatics, Universität Bonn, Germany.
- Axel Verdier** **Master of Science**, Sciences et Technologies de l'Information et de la Communication pour la Santé, Université de Montpellier, France.

Service

Community group	Founder and convenor of the <i>Bioinformaticians' Shed</i> , for people using bioinformatics around the Parkville precinct, hosted by Melbourne Bioinformatics.
RNA-seq	From reads to differentially expressed genes workshop for Australian BioCommons, 23–24 February 2021.
Reproducible research	Reproducible research workflows with containers webinar for New Zealand eScience Infrastructure (NeSI), 23 July 2020.
Sequencing workshop	Invited instructor for the Long-read, long-reach sequencing workshop . November 2019, ANU, Canberra, Australia.
MapNet	Main organiser for the 2018 MapNet conference . November 2018, Dunedin, New Zealand.
Nanopore workshop	Main organiser for Genomics Aotearoa's long-read sequencing workshop . April 2018, Dunedin, New Zealand.
Carpentries	Assisting instructor for Carpentries workshops: Data Carpentry, 2019 ; RNA-seq-workshop, 2020 .

Publications

Peer-reviewed journals

Harrop, T.W.R.[§], Guhlin, J.[§], McLaughlin, G.M., Permina, E., Stockwell, P., Gilligan, J., Le Lec, M.F., Gruber, M.A.M., Quinn, O., Lovegrove, M., Duncan, E.J., Remnant E.J., Langford, K.L., Kronenberg, Z., Press, M.O., Eacker, S.M., Wilson-Rankin, E.E., Purcell, J., Lester, P.J., Dearden, P.K. (2020). High-quality assemblies for three invasive social wasps from the *Vespula* genus. *G3: Genes, Genomes, Genetics* 10 (10): 3479–3488. [doi:10.1534/g3.120.401579](https://doi.org/10.1534/g3.120.401579).

Harrop, T.W.R., Le Lec, M.F., Jauregui, R., Taylor, S.E., Inwood, S.N., van Stijn, T., Henry, H., Skelly, J., Ganesh, S., Ashby, R.L., Jacobs, J.M.E., Goldson, S.L., Dearden, P.K. (2020). Genetic Diversity in Invasive Populations of Argentine Stem Weevil Associated with Adaptation to Biocontrol. *Insects* 11 (7): 441. [doi:10.3390/insects11070441](https://doi.org/10.3390/insects11070441).

Harrop, T.W.R., Mantegazza, O., Luong, A.M., Béthune, K., Lorieux, M., Jouannic, S., and Adam, H. (2019). A set of AP2-like genes is associated with inflorescence branching and architecture in domesticated rice. *Journal of Experimental Botany* 70, 5617–5629. [doi:10.1093/jxb/erz340](https://doi.org/10.1093/jxb/erz340).

Harrop, T.W.R.[§], Denecke, S.[§], Yang, Y.T., Chan, J., Daborn, P.J., Perry, T., Batterham, P., (2018). Evidence for activation of nitenpyram by a mitochondrial cytochrome P450 in *Drosophila melanogaster*. *Pest Management Science* 74, 1616–1622. [doi:10.1002/ps.4852](https://doi.org/10.1002/ps.4852).

Harrop, T.W.R.[§], Ud Din, I.[§], Gregis, V., Osnato, M., Jouannic, S., Adam, H. and Kater, M. (2016). Gene expression profiling of reproductive meristem types in early rice inflorescences by laser microdissection. *The Plant Journal* 86, 75–88. [doi:10.1111/tpj.13147](https://doi.org/10.1111/tpj.13147).

Harrop, T.W.R.[§], Pearce, S.L.[§], Daborn, P.J. and Batterham, P. (2014). Whole-genome expression analysis in the third instar larval midgut of *Drosophila melanogaster*. *G3 (Bethesda)* 4, 2197–2205. [doi:10.1534/g3.114.013870](https://doi.org/10.1534/g3.114.013870).

Harrop, T.W.R., Sztal, T., Lumb, C., Good, R.T., Daborn, P.J., Batterham, P. and Chung, H. (2014). Evolutionary changes in gene expression, coding sequence and copy-number at the *Cyp6g1* locus contribute to resistance to multiple insecticides in *Drosophila*. *Plos One* 9, e84879. [doi:10.1371/journal.pone.0084879](https://doi.org/10.1371/journal.pone.0084879).

[§] Equal contribution

Contributions to peer-reviewed publications

- McCulloch, G.A., Guhlin, J., Dutoit, L., **Harrop, T.W.R.**, Dearden P.K., and Waters, J.M. (2021). Genomic Signatures of Parallel Alpine Adaptation in Recently Evolved Flightless Insects. *Molecular Ecology* 30 (24): 6677–86. [doi:10.1111/mec.16204](https://doi.org/10.1111/mec.16204).
- Dussex, N. *et al.* (2021). Population Genomics of the Critically Endangered Kākāpō. *Cell Genomics* 1 (1): 100002. [doi:10.1016/j.xgen.2021.100002](https://doi.org/10.1016/j.xgen.2021.100002).
- McCulloch, G.A., Foster, B.J., Dutoit, L., **Harrop, T.W.R.**, Guhlin, J., Dearden, P.K., Waters, J.M. (2020). Genomics Reveals Widespread Ecological Speciation in Flightless Insects. *Systematic Biology* syaa094. [doi:10.1093/sysbio/syaa094](https://doi.org/10.1093/sysbio/syaa094).
- Lamichhane, R., Munro, F., **Harrop, T.W.R.**, de la Harpe, S.M., Dearden, P.K., Vernall, A.J., McCall, J.L., Ussher, J.E. (2020). Human liver-derived MAIT cells differ from blood MAIT cells in their metabolism and response to TCR-independent activation. *European Journal of Immunology* 51: 879–892. [doi:10.1002/eji.202048830](https://doi.org/10.1002/eji.202048830).
- Morgan, B.M., Brown, A.N., Deo, N., **Harrop, T.W.R.**, Taiaroa, G., Mace, P.D., Wilbanks, S.M., Merriman, T.R., Williams, M.J.A., McCormick, S.P.A. (2020). Nonsynonymous SNPs in *LPA* homologous to plasminogen deficiency mutants represent novel null apo(a) alleles. *Journal of Lipid Research* 61(3), 432–44. [doi:10.1194/jlr.M094540](https://doi.org/10.1194/jlr.M094540).
- Lamichhane, R., Schneider, M., de la Harpe, S.M., **Harrop, T.W.R.**, Hannaway, R.F., Dearden, P.K., Kirman, J.R., Tyndall, J.D.A., Vernall, A.J., and Ussher, J.E. (2019). TCR- or Cytokine-Activated CD8⁺ Mucosal-Associated Invariant T Cells Are Rapid Polyfunctional Effectors That Can Coordinate Immune Responses. *Cell Reports* 28, 3061–3076.e5. [doi:10.1016/j.celrep.2019.08.054](https://doi.org/10.1016/j.celrep.2019.08.054).
- Guerrero, F.D., Bendele, K.G., Ghaffarim N., Guhlin, J., Gedy, K.R., Lawrence, K.E., Dearden, **Harrop, T.W.R.**, Heath, A.C.G, Lun, Y., Metz, R.P, Teel, P., Perez de Leon, A., Biggs, P.J., Pomroy, W.E., Johnson, C.D., Blood, P.D., Bellgard, S.E., Tompkins, D.M. (2019). The Pacific Biosciences *de novo* assembled genome dataset from a parthenogenetic New Zealand wild population of the longhorned tick, *Haemaphysalis longicornis* Neumann, 1901. Data in Brief 27, 104602. [doi:10.1016/j.dib.2019.104602](https://doi.org/10.1016/j.dib.2019.104602).
- Ta, K. N., Adam. H., Staedler, Y.M., Schönenberger, J., **Harrop. T.W.R.**, Tregear, J., Do, N.V., Gantet, P., Ghesquière, A., and Jouannic, S. (2017). Differences in meristem size and expression of branching genes are associated with variation in panicle phenotype in wild and domesticated African rice. *EvoDevo* 8: 2. [doi:10.1186/s13227-017-0065-y](https://doi.org/10.1186/s13227-017-0065-y).
- Daborn, P.J., Lumb, C., **Harrop, T.W.R.**, Blasetti, A., Pasricha, S., Morin, S., Mitchell, S.N., Donnelly, M.J., Müller, P. and Batterham, P. (2012). Using *Drosophila melanogaster*

to validate metabolism-based insecticide resistance from insect pests. *Insect Biochemistry and Molecular Biology* 42, 918–924. [doi:10.1016/j.ibmb.2012.09.003](https://doi.org/10.1016/j.ibmb.2012.09.003).

Book chapters

Cridge, A., Harrop, T.W.R., Lovegrove, M., Remnant, E. & Dearden, P. (2017). *Nutrition and Epigenetic Change in Insects: Evidence and Implications*, in *Advances in Insect Physiology* (ed. Verlinden, H.) 53, 31–54 (Academic Press). [doi:10.1016/bs.aiip.2017.06.001](https://doi.org/10.1016/bs.aiip.2017.06.001)

Selected scientific presentations

Genetic diversity and biocontrol in Argentine stem weevils. Genomics Aotearoa seminar series, New Zealand, 2021.

The genomes of three invasive social wasps. **Oral presentation** at the Annual Conference of the Genetics Society of Australasia (GSA), Melbourne, Australia, 2019.

Symposium chair: Genomics & bioinformatics.

*Comparative genomics of sexual and asexual parasitoid wasps from the *Microctonus* genus*. **Poster presentation** at the 7th meeting of the European Society for Evolutionary Developmental Biology, Galway, Ireland, 2018.

Genomics of a weevil pest and its parasitoid biocontrol agent. **Poster presentation** at the Annual Conference of the Genetics Society of Australasia (GSA) with the New Zealand Society for Biochemistry and Molecular Biology (NZSBMB), Dunedin, New Zealand, 2017.

De novo sequencing of Argentine stem weevil and its parasitoid wasp biocontrol agent. **Poster presentation** at the 10th Annual Arthropod Genomics Symposium, Notre Dame University, South Bend, U.S.A., 2017.

*Sequencing and community annotation of the *Vespula vulgaris* genome*. **Oral presentation** at the Entomological Society of NZ Conference, Wellington, New Zealand, 2017.

Genes controlling transition of reproductive meristem identity during inflorescence development. **Oral presentation** at the 14th International Symposium on Rice Functional Genomics, Montpellier, France, 2016.

Mechanisms underlying the parallel evolution of inflorescence phenotype during independent domestication of African and Asian rice. **Contributed oral presentation** at the 6th meeting of the European Society for Evolutionary Developmental Biology, Uppsala, Sweden, 2016. **Joint symposium chair:** Branching across the tree of life.

*Gene expression during *O. sativa* panicle development*. **Invited seminar** at the Agricultural Genetics Institute, Hanoi, Vietnam, 2015.

Molecular mechanisms underlying the phenotypic convergence of inflorescence architecture in domesticated rice species. **Poster presentation** at the Society for Molecular Biology and Evolution annual meeting, Vienna, Austria, 2015.

*Transcriptomic analysis of early developmental stages of the rice panicle. **Poster presentation***
at the Workshop in Molecular Mechanisms Controlling Flowering, Aiguablava,
Spain, 2015

*RNA interference of the Cytochrome P450 redox partners Cpr and dare uncovers novel
P450 functions in Drosophila melanogaster. **Poster presentation*** at the 50th Annual
Drosophila Research Conference, Chicago, USA, 2009.

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