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# Thomas Harrop

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I am a genomics scientist working with large-scale bioinformatic and genetic datasets.

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## About me

### Technical skills

I'm an experienced bioinformatician, geneticist and 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 generate data using 2<sup>nd</sup>- and 3<sup>rd</sup>-generation sequencing. I have experience with classical genetic approaches with live organisms, including transformation, crosses, microdissection and bioassays.

My main tools for programming and data analysis are Python and R. I use workflow managers, version control, containerisation and high-performance computing for bioinformatics. I'm also experienced with bash scripting and \*nix system administration.

I'm comfortable communicating complex bioinformatics and genetic results to stakeholders and students. I visualise and share my results with ggplot2, Markdown, Pandoc, TeX and a bit of html & css. I teach complex bioinformatics algorithms to postgraduate students in classroom and one-on-one settings.

### Research

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

## Experience

### Research & University positions

**2021–Present Academic Specialist (B)**, Melbourne Bioinformatics,  
University of Melbourne, Australia.

**Bioinformatician**, Galaxy Australia.

In my current position, I provide training and support to

researchers and projects using bioinformatics in Melbourne's biosciences precinct. I am also part of the team that develops and runs Galaxy Australia.

**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

## Personal information

**Languages**   English (native)  
German (TELC Level B2)  
French (TELC Level B1)

**Nationalities**   Australian and British

## Teaching

**2021-present**   **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**   **3<sup>rd</sup> 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 **1<sup>st</sup> Year Genetics**, The University of Melbourne, Parkville, Australia.

## Students (co-)supervised

- Current** Three students, **Masters of Science (Bioinformatics)** University of Melbourne.
- 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 [\*Bioinformaticians' Shed\*](#), 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

See my [Google scholar](#) profile for the latest list.

### Journal articles

**Harrop, T.W.R.<sup>§</sup>**, Guhlin, J.<sup>§</sup>, 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](#).

**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](#).

**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](#).

**Harrop, T.W.R.<sup>§</sup>**, Denecke, S.<sup>§</sup>, 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](#).

**Harrop, T.W.R.<sup>§</sup>**, Ud Din, I.<sup>§</sup>, 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](#).

**Harrop, T.W.R.<sup>§</sup>**, Pearce, S.L.<sup>§</sup>, 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](#).

**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](#).

<sup>§</sup> Equal contribution

## Contributions to articles

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<sup>+</sup> 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 7<sup>th</sup> 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 10<sup>th</sup> 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 14<sup>th</sup> 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 6<sup>th</sup> 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 50<sup>th</sup> Annual Drosophila Research Conference, Chicago, USA, 2009.

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