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# 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 2<sup>nd</sup>- and 3<sup>rd</sup>-generation sequencing.

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## 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 workflow managers (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 positions

- 2017–Present** **Post-doctoral researcher**, Laboratory for Evolution and Development, Biochemistry Department, University of Otago, Dunedin, New Zealand.  
I am currently working 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.  
In this project, 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.  
I used machine learning, data mining, statistical analyses and other bioinformatic techniques to study the development of inflorescence architecture in rice, which affects crop yield. We used laser microdissection and RNA sequencing to characterise molecular events that occur in the developing inflorescence, 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

- 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

- 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.

## Publications

### Peer-reviewed journals

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).
- 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).
- Guerrero, F.D., Bendele, K.G., Ghaffari, N., Guhlin, J., Gedye, K.R., Lawrence, K.E., Dearden, P.K., **Harrop, T.W.R.**, Heath, A.C.G., Lun, Y., et al. (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).
- Harrop, T.W.**<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](https://doi.org/10.1002/ps.4852).
- 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).
- 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](https://doi.org/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](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).

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).

<sup>§</sup> Equal contribution

### 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

*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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