

# Thomas Harrop

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I am a post-doctoral researcher with a background in bioinformatics, genetics and molecular biology and interests in data science and research relating to agriculture.

I have advanced programming skills in R, Python and shell scripting. I am experienced working in molecular, plant, animal and medical laboratories and installing, maintaining and using computers running Unix, Linux and MacOS.

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## Personal information

**Nationalities** Australian and British

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

## 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.

## Experience

- 2014–Present** **Post-doctoral researcher**, UMR DIADE, Institut de Recherche pour le Développement (IRD), Montpellier, France.  
In my current project I am working on the development of inflorescence architecture in rice, which is related to grain yield potential. We used a laser microdissection and RNA sequencing approach to characterise molecular events that occur during the transitions between meristem types in the developing inflorescence. We are now applying these results to study the effects of selection on gene expression during the parallel domestications of African and Asian rice. Whilst working on this project I have expanded my skills in bioinformatic analysis and statistics and gained a knowledge of plant biology and agronomy.
- 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 project to compare the

transcriptional response of several different land plants to UV-B exposure, which acts as an environmental signal. This position provided hands-on experience with plant biology and a foundation to apply my programming and bioinformatic skills.

### Professional positions

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

### 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

- 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

- 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

### Selected scientific presentations

**Harrop, T.W.R.** Gene expression during *O. sativa* panicle development. Invited seminar, 19 November 2015, LMI RICE, Hanoi, Vietnam.

**Harrop, T.W.R.**, Gregis, V., Ud Din, I., Kater, M., Jouannic, S. and Adam, H. *Molecular mechanisms underlying the phenotypic convergence of inflorescence architecture in domesticated rice species*. Society for Molecular Biology and Evolution annual meeting, 2015, Vienna, Austria

**Harrop, T.W.R.**, Ud Din, I., Gregis, V., Osnato, M., Jouannic, S., Adam, H. and Kater, M. *Transcriptomic analysis of early developmental stages of the rice panicle*. Workshop in Molecular Mechanisms Controlling Flowering, 2015, Aiguablava, Spain.

**Harrop, T.W.R.**, Batterham, P. and Daborn, P.J. *RNA interference of the Cytochrome P450 redox partners Cpr and dare uncovers novel P450 functions in Drosophila melanogaster*. The 50th Annual Drosophila Research Conference, 2009, Chicago, USA.

### Other information

**Research** My interests include plant and insect research related to agronomy, tools and techniques in bioinformatics and evolutionary and comparative biology.

**Technical** Aside from daily use of R, Python and bash scripts, I also use Markdown regularly and have experience with Perl, LaTeX, html and css. I use git and GitHub for version control and strive to follow the principles of reproducible research when coding. I have used several different workload managers for cluster computing including SGE and LSF, and I maintain an installation of SLURM on my personal workstation.

I have experience in molecular biology techniques such as quantitative real-time PCR, cloning, nucleic acid extraction and cDNA library preparation, as well as classical genetic approaches with live organisms, such as transformation, crosses, microdissection and bioassays.

**About me** Outside work I enjoy building and riding bicycles, social football and basketball, cooking, programming and technology.

**Awards** 2006–2009, Australian Postgraduate Award

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