

# Thomas Harrop

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I am a post-doctoral researcher with a background in bioinformatics, genetics and molecular biology and an interest in basic and applied 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

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| Date of birth | 25 December 1982  |
| Nationalities | Australian and British  |
| Languages     | English (native), German (TELC Level B2) and French (TELC Level B1) |

## Education

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| 2006–2012 | <p><b>Doctor of Philosophy</b>, Department of Genetics, the University of Melbourne, Parkville, Australia.</p> <p>Thesis: <a href="#"><i>The functions of cytochrome P450s in Drosophila.</i></a></p> <p>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 <i>Drosophila</i> genus.</p> |
| 2002–2005 | <p><b>Bachelor of Science with Honours (first class)</b>, the University of Melbourne, Parkville, Australia.</p>  |

## Research positions

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| 2014–Present | <p><b>Post-doctoral researcher</b>, UMR DIADE, Institut de Recherche pour le Développement (IRD), Montpellier, France.</p> <p>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 precise laser microdissection and RNA sequencing approach to characterise molecular events that occur during the transitions between meristem types in the developing inflorescence. We are</p> |
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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.

During my stay at the Max Planck Institute I worked on a short project to compare the transcriptional response of several different land plants to UV-B exposure, which acts as a developmental signal. This position provided my first hands-on experience with plant biology and a foundation to apply my programming and bioinformatic skills.

## Professional experience

**2004–2007**

**Medical scientist**, Network Pathology, the Austin Hospital, Heidelberg, Australia.

**2001–2004**

**Laboratory assistant**, Network Pathology, the Austin Hospital, Heidelberg, Australia.

## Teaching experience

**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

**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* (accepted manuscript). [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 conference presentations

**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.

## Awards

2006–2009                      Australian Postgraduate Award

## Other information

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

**Technical experience**     Aside from daily use of R, Python and bash scripts, I also use Markdown regularly and have basic 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 maintain an installation of SLURM on my personal workstation.

I have extensive 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 complex crossing experiments, microdissection and bioassays.

**About me**                 Outside work I have a wide range of interests including building and riding bicycles, social football and basketball, programming and technology.

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