

Thomas Harrop

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.

Personal information

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

Education

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

Experience

2014–Present	<p>Post-doctoral researcher, 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.

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

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

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.[§], 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* (accepted manuscript). [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).

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).

[§] 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.

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 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 have a range of interests including building and riding bicycles, social football and basketball, cooking, programming and technology.

Awards

2006–2009, Australian Postgraduate Award

twharrop@gmail.com · [GitHub](#) · [stackoverflow](#)

Castelnau-le-Lez, Hérault, FRANCE