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 have experience 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

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

Education

2006–2012 **Doctor of Philosophy**, Department of Genetics, the University of Melbourne, Victoria, 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, Victoria, Australia.

Research positions

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 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 now applying these results

to study the effects of selection on gene expression during the parallel domestications of African and Asian rice. Working on this project allowed my to expand my skills in bioinformatic analysis and statistics and my 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 Insitute 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 allowed me to expand my programming and bioinformatic skills.

Teaching experience

2007–2011 **3rd Year Genetics**, Department of Genetics, The University of Melbourne, Victoria, Australia.

2006–2009 **High School Biology**, Department of Genetics, The University of Melbourne, Victoria, Australia.

2006–2008 **High School Biology**, Gene Technology Access Centre, The University High School, Victoria, Australia.

2005–2008 **1st Year Genetics**, The University of Melbourne, Victoria, Australia.

Professional experience

2004–2007 **Medical scientist**, Network Pathology, the Austin Hospital, Victoria, Australia.

2001–2004 **Laboratory assistant**, Network Pathology, the Austin Hospital, Victoria, 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.[§], 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.

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.

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.

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.

[§] Equal contribution

Selected conference presentations

Thomas W. R. Harrop, 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.

Technical Experience

Should I write about other skills here or leave it in the blockquote?

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