Dr Pierre-Yves Dupont

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🖶 http://pydupont.github.io/CV/

PERSONAL

Date of Birth	24/4/1984
Nationality	French
Languages	French (mother tongue), English (advanced)

EDUCATION

2011: **PhD in Computational Biology**, INRA, Clermont Ferrand

2008: **Masters in Computational Biology**, Bordeaux University, *Class Major*

2007: **Bachelor in Computer Sciences**, Bordeaux University

2005: **Bachelor in Biology, Geology and Earth Sciences**, Bordeaux University, Diploma to become High School biology and geology teacher

POSITIONS

Postdoctoral researcher in computational biology at Massey University, Palmerston North, New Zealand; 2012 – current
Lateral gene transfer in fungi: Identifying the cross-species toolbox for metabolic innovation.

PhD studentship at INRA, Clermont Ferrand, France; 2008 – 2011
Thesis on developing bioinformatics tools to combine information from metabolomics, transcriptomics and promotor studies to characterize metabolic pathways involved in liver cancers.This was in collaboration with the Polytechnic school (Palaiseau, France) and a IT startup company, Solusciences (Clermont-Ferrand, France) to develop software for biological pathway modelling and biochemical dynamics analysis.

Masters Internship at European Institute of Biology and Chemistry, Bordeaux, France; 2008
Evaluation of a docking software (Autodock v.4) and development of an automatic procedure to compute docking of multiple ligands on kinase receptors using a computation cluster.

Bachelor Internship at Bordeaux University, Bordeaux, France; 2007
Development of software for visualization and detection of internal movements in biomolecules.

SKILLS

Phylogeny: Neighbor Joining, Maximum Likelyhood (PHYLIP, PhyML, RAxML), super

trees, consensus trees. Multiple sequence alignments with mafft, clustal, kalign, muscle, etc.

Statistics: Good understanding of basic statistics, Markov chains and Monte Carlo statistics

Computer Sciences: Daily use of Windows and Linux (Fedora, Ubuntu, Mint) and command line interface. Good commad of languages Ruby (and Ruby on Rails), Python and Java, and web technologies (HTML 5, CSS3, JQuery). Common practice of C++, R (BioConductor) and Perl (BioPerl, EnsEMBL libraries). Good understanding of Agent-Based Models (Repast symphony) and Petri Nets

Protein structure analysis and visualisation: AutoDock, GOLD, VMD

PUBLICATIONS

Fungal endophyte infection of ryegrass reprogrammes host metabolism and alters development
Dupont PY, Eaton CJ, Wargent JJ, Fechtner S, Solomon P, Schmid J, Day RC, Scott B, Cox MP; New Phytologist; *In press*

A core gene set describes the molecular basis of mutualism and antagonism in Epichloë spp.
Eaton CJ, **Dupont PY**, Solomon P, Clayton W, Scott B, Cox MP; Molecular Plant-Microbe Interactions, 28(3), 218âĂŞ231; PubMed PMID: 25496592

HyLiTE: accurate and flexible analysis of gene expression in allopolyploid species
Duchemin W, **Dupont PY**, Campbell MA, Ganley A and Cox MP; BMC Bioinformatics, 2015; 16:8; PubMed PMID: 25592117

Chapter 10 - Genomes of plant-associated clavicipitaceae
Schardl CL, Young CA, Moore N, Krom N, **Dupont PY**, Pan J, Farman ML; Advances in Botanical Research, 70, 291-327, 2014; DOI: 10.1016/B978-0-12-397940-7.00010-0

Computational identification of transcriptionally co-regulated genes, validation with the four ANT isoform genes
Dupont PY, Guttin A, Issartel JP, Stepien G; BMC Genomics, 13:482, 9/2012; PubMed PMID: 22978616

Computational analysis of the transcriptional regulation of the adenine nucleotide translocator isoform 4 gene and its role in spermatozoid glycolytic metabolism
Dupont PY, Stepien G; Gene, 487(1):38-45, 11/2011; PubMed PMID: 21827840

Description and assessment of a model for GSK-3beta database virtual screening
Ventimila N, **Dupont PY**, Laguerre M, Dessolin J; J Enzyme Inhib Med Chem, 25(2):152-7, 4/2010; PubMed PMID: 20170337

CONFERENCE

Endophyte infection of ryegrass alters metabolism, development and response to stress - Pierre-Yves Dupont; Queenstown Molecular Biology Conference, 8/2014; Presented in both Plant and Main meetings

Fungal endophyte infection of ryegrass reprograms host metabolism and alters development - Pierre-Yves Dupont; Fungal Genetics Conference, 3/2015; Poster

SOFTWARE AND DATABASES

Genomic annotation of *Epichloe festucae* E2368 gene models

Publically available at: *http://epichloe.massey.ac.nz*. This database contains functional annotations predicted by sequence homology for all *E. festucae* E2368 gene models. It includes links to major international bioinformatics databases including Pfam, Gene Ontology (GO), KEGG, Interproscan and GenBank.

Genomic annotation of perennial ryegrass (*Lolium perenne*) gene models

Publically available at: *http://ryegrass.massey.ac.nz*. This database contains functional annotations predicted by sequence homology for over 50,000 predicted perennial ryegrass coding sequences. It includes links to the major international bioinformatics databases listed above.

Hybrid Lineage Transcriptome Explorer (HyLiTE)

Publically available at: *http://sourceforge.net/projects/hylite*. HyLiTE is a software allowing the analysis of high-throughput transcriptome data from allopolyploid species