Dr Pierre-Yves Dupont

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PERSONAL

Date of Birth	24/4/1984
Nationality	French
Residency	Permanent New Zealand resident
Languages	French (mother tongue), English (advanced)

EDUCATION

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

2008: **Masters in Computational Biology**, Bordeaux University, *Top of Class*

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

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

POSITIONS

Postdoctoral researcher in computational biology at Massey University, Palmerston North, New Zealand

Time to fight back: harnessing molecular determinants of virulence and adaptation in kauri dieback pathogens. 2016 – current

Postdoctoral researcher in computational biology at Massey University, Palmerston North, New Zealand

Lateral gene transfer in fungi: Identifying the cross-species toolbox for metabolic innovation. 2012 – 2016

PhD studentship at INRA, Clermont Ferrand, France

Thesis on developing bioinformatics tools to combine information from metabolomics, transcritomics and promotor studies to characterise metabolic pathways involved in liver cancers. 2008 – 2011

Masters Internship at European Institute of Biology and Chemistry, Bordeaux, France, 2008

Bachelor Internship at Bordeaux University, Bordeaux, France, 2007

SKILLS

Bioinformatics: Phylogeny: Neighbor Joining, Maximum Likelihood, super trees, consensus trees; multiple sequence alignment; protein structure analysis and visualisation; next generation sequencing; population genetics.

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

PUBLICATIONS

Analysis of simple sequence repeat (SSR) structure and sequence within Epichloë endophyte genomes reveals impacts on gene structure and insights into ancestral hybridization events - Clayton W, Eaton CJ, **Dupont PY**, Gillanders T, Cameron N, Saikia S, Scott B; PLoS ONE, *in press*

Evolution of polyketide synthesis in a Dothideomycete forest pathogen - Ozturk IK, Chettri P, **Dupont PY**, Barnes I, McDougal RL, Moore GG, Sim A Bradshaw RE; Fungal Genetics and Biology, 2017

Host tissue environment directs activities of an Epichloë Endophyte, while it induces systemic hormone and defense responses in its native perennial ryegrass host - Schmid J, Day R, Zhang N, **Dupont PY**, Cox MP, Schardl CL, Minards N, Truglio M, Moore N, Harris DH, Zhou Y; Molecular Plant-Microbe Interactions, 2017

Genomic data quality impacts automatic detection of lateral gene transfer in fungi - **Dupont PY**, Cox MP; Genes | Genomes | Genetics, 2017

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, 2015

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; 2015

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

Genomes of plant-associated clavicipitaceae - Schardl CL, Young CA, Moore N, Krom N, **Dupont PY**, Pan J, Farman ML; Advances in Botanical Research, 2014

Computational identification of transcriptionally co-regulated genes, validation with the four ANT isoform genes - **Dupont PY**, Guttin A, Issartel JP, Stepien G; BMC Genomics, 2012

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, 2011

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, 2010

SOFTWARE AND DATABASES

Genomic annotation of *Epichloë 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

Geneprom

Geneprom is a Ruby on Rails web application developed during my PhD. It allowed me to study regulatory elements present in gene promoters.

MPSA

Metabolic Pathway Software Analyzer. It is a Java plugin for the software VANTED. It allows the integration of data from different biological analysis methods to have a better understanding of metabolic pathways and their regulation.