

# Dr Pierre-Yves Dupont

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🌐 <http://pydupont.github.io/CV/>

## PERSONAL

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

## EDUCATION

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**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

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**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, transcriptomics and promoter 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

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**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

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*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

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### **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.