Xavier Grand
MS. in Bioinformatics

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WORK EXPERIENCE

3.2021 - Today **Research Engineer in Bioinformatics,** CRCL & ENS Lyon.
Bioinformatician, RNAseq, ChIP-seq, alternative splicing analysis, Human and HBV.
Supersivion: Barbara Testoni, Senior Scientist (CRCL) & Cyril Bourgeois, Research Scientist (ENS).

4.2020 - 08.2020 **Bioinformatics Internship,** Institut de Mathématiques de Toulouse.
Use of kernel methods to analyse heterogenous biological data.
Supersivion: Sébastien Déjean, Biostatistics Research Engineer (IMT) & Jérôme Mariette, Bioinformatics Reasearch Engineer (INRAe).

5.2016 - 11.2017 **Reasearch scientist,** Biogemma Toulouse.
Genetic and biological characterization of sunflower resistance against Orobanche cumana.
Supersivion: Marie Coque, Sunflower Project Lead & Oilseeds genetics and phenotyping coordinator.

9.2014 - 4.2015 **Biostatistician, research scientist,** Limagrain Europe.
Simulation of plant breeding strategies.
Supersivion: Nicolas Heslot, Head of Biostatistics.

5.2014 - 8.2014 **Bioanalyst, research scientist,** Limagrain Europe.
Barley genome browser development.
Supersivion: Anne-Marie Bochard, Barley molecular breeding Project Leader.

10.2012 - 3.2014 **Bioanalyst, research scientist,** Biogemma Auvergne.
Candidate gene discovery process for plant traits and breeding by analyzing complex datasets in the context of biological pathways and omics data.
Supersivion: Stéphane Lafarge, Gene Discovery Project Leader.

10.2008 - 12.2011 **Ph.D reasearch studies,** INRA Montpellier/Bayer Cropscience Gent
Biological, genetic and molecular analysis of partial resistance of rice to Magnaporthe oryzae.
Supersivion: Jean-Benoît Morel, Group Leader (INRA) & John Jacobs, Senior Scientist (Bayer).

LANGUAGES

French Native.
English Fluent.

Spanish	Basic knowledge of writing and speaking.

SKILLS AND QUALIFICATIONS

PLANT BIOLOGY

Molecular genetics	Forward genetics and cloning (molecular mapping, GWAS, QTLs).
Reverse genetics	Mutant analysis.
Omics	NGS, Expression analysis.
Laboratory	Molecular biology (PCR, qPCR, DNA/RNA library, NGS).
Plant Biology	Plant inoculation and phenotyping, Cellular biology.

COMPUTER PROGRAMMING

Programming languages	R, Python, (Java, C++).
Database Management	SQL, MySQL and NoSQL, Neo4J/CYPHER.
Data Mining	Scikit-learn, Numpy, Scipy, Pandas.
Development env.	UNIX, tmux, VSCode, Rstudio, PyCharm.
Container/pipeline	Nextflow, singularity, docker.
UI development	R-shiny, R-shiny Dashboard, tkinter, Django (in progress).

BIOINFORMATICS & STATISTICS

NGS data analysis	Minimap2, STAR, StringTie2, Salmon, FastQC, SamTools...
RNA-seq	Illumina, Nanopore (Direct-mRNA, genomic, cDNA).
Biology dedicated tools	Bioconductor, Biopython, NCBI and biological databases.
MultiOmics	mixOmics, mixKernel.

REPOSITORIES AND TOOLS

GitLab	https://gitbio.ens-lyon.fr/xgrand
GitHub	https://github.com/XavierGrand?tab=repositories
Shiny Dashboard	https://xavier-grand.shinyapps.io/K-PCA_Machine/

EDUCATION

2019 - 2020	**Master in Bioinformatics** University of Montpellier. *Bioinformatics, information systems, knowledge extraction.*
2008 - 2011	**Ph.D in Integrative Plant Biology** Montpellier Supagro.
2006 - 2008	**Master in Integrative Plant Biology** University of Montpellier.
2006 - 2008	**Bachelor in Biochemistry** University of Nîmes.

PUBLICATIONS AND COMMUNICATIONS

1. Calderón-González A., Pouilly N., Muños S., Grand X., Coque M., Velasco L., Pérez-Vich B. An SSR-SNP Linkage Map of the Parasitic Weed Orobanche cumana Wallr. Including a Gene for Plant Pigmentation. Frontiers in Plant Science 2019: 10, 797.

2. Grand, X., Gauthier, A., André, I., Loras, S., Legrand, L., Gouzy, J., Grezes-Besset, B., Coque, M., Muños, S. Genetic and biological approach to decipher O.cumana resistance in sunflower wild relatives. Presented at The 14th World Congress on Parasitic Plants, Asilomar, CA, USA (2017-06-24 to 2017-06-30). Book of abstracts (p. 23).

3. Kroj, T., Chanclud, E., Michel, C., Grand, X., Morel, J.-B. Integration of decoy domains derived from protein targets of pathogen effectors into plant immune receptors is widespread. New Phytol 2016.

4. Grand, X., Espinoza, R., Michel, C., Cros, S., Chalvon, V., Jacobs, J. et Morel, J.-B. Identification of positive and negative regulators of disease resistance to rice blast fungus using constitutive gene expression patterns. Plant Biotechnology Journal 2012, 10, 840–850.

5. Vergne, E., Grand, X., Ballini, E., Chalvon, V., Saindrenan, P., Tharreau, D., Nottéghem, J.-L., Morel, J.-B. Preformed expression of defense is a hallmark of partial resistance to rice blast fungal pathogen Magnaporthe oryzae. BMC Plant Biology 2010, 10, 206-206.

6. Grand, X., Tharreau, D., Nottéghem, J.-L., Brunner, S., Jacobs, J., Morel, J.-B. Forward and reverse genetic approaches in rice to unravel control of partial resistance to pathogens.6th International Rice Genetics Symposium,16-19 November 2009; Manila, Philippines.

7. Dogimont, C., Boissot, N., Chovelon, V., Tual, S., Grand, X., Rittener-Ruff, V., Giovinazzo, N., Bendahmane, A. Aphid and virus resistance triggered by the CC-NBS-LRR Vat melon gene. In: Genetic control of plant pathogenic viruses and their vectors: towards new resistance strategies. Book of abstracts (p. 34). Presented at International Conference, Cadiz, ESP (2008-11-23 - 2008-11-27).

INTERESTS

Clarinet/Saxo	XXS trio, Union musicale d'Ambérieu en Bugey.
Sport	Mtb: Transvolcanique 2014, bike travelling, Ski: Derby Mont-Dore 2014.
Miscellaneous	Animation Capacity Diploma, First Aid Certificate.
Travel	*6.2015 - 12.2015* Working Holiday in Australia.

REFEREES

Barbara Testoni
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Hélène Polvèche
Bioinformatics Research Engineer I-STEM/ENS Lyon,
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