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.

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

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 Senior Scientist Cancer Research Center of Lyon,

e-mail: barbara.testoni@inserm.fr,

tel: +33 (0)4 72 68 19 65.

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

e-mail: helene.polveche@ens-lyon.fr,

tel: +33 (0)4 72 72 80 48.