Christophe DJEMIEL

Ph.D. in Environmental, population biology and ecology

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I am a bioinformatician with a primary focus on meta-omics approaches for understanding the structure, function and diversity of various microbiome within different ecological niches. My training in biology and computer sciences is complemented by Ph.D. in microbial ecology. My research interests span the areas of big data, software development and microbial ecology.

Education

2017 **Ph.D. in Environmental, population biology and ecology**, *UGSF - University of Lille, France*, with high honors.

2013 **M.Sc. in Computer science**, *University of Bordeaux, France*, with high honors.

2011 **B.Sc. in Biology**, *University of Bordeaux, France*.

2009 **2-year technical college degree in Biotechnology**, *St. Louis High School (Bordeaux - Fr)*, with high honors.

Professional experiences

Postdoctoral Associate

Jun. 2018 – Current **Study of microbial communities** ,
Supervisors: Dr Lionel RANJARD (Research Director), Dr Pierre-Alain MARON (Research Director), Dr Sébastien TERRAT (Assistant Professor), BIOCOM – INRA Dijon UMR1347, France.
- Various topics (details are coming)

Ph.D. student

Nov. 2013 – Dec. 2017 **Study of bacterial and fungal diversity during flax dew-retting by using metabarcoding**,
Directors: Dr Sébastien GREC and P^r Simon HAWKINS, UGSF – University of Lille, France.
- Preparation of samples from field experimental design to Illumina sequencing
- Re-design universal primer of V3 – V4 rRNA gene subregion for plant-associated bacteria studies
- Experimentation of various methods to remove rRNA or enrich to mRNA from plant-associated microbiome for metatranscriptomic studies
- Implementation of pipelines and statistical analysis for microbial diversity datasets
- Interpretation of microbial structures and CAZymes markers during the plant cell wall degradation

Master's internship

Mar. – Aug. 2013 **Development of metabarcoding pipelines for classify and clustering 16S rRNA gene sequences**,
Supervisor: Dr Jérôme MARIETTE – Software engineer, INRA – GenoToul, Toulouse – Fr.
- Development of pipelines (Roche 454 and Illumina MiSeq plateform) with Jflow API based on Makeflow and Weaver and be integrated in NGSpipelines and NG6 environment
- Implementation Perl script to convert taxonomy file from mothur to hierarchical Krona
- Implementaion of jQuery plugin for comparing lists with Venn Diagrams: jvenn

International Genetically Engineered Machine competition (iGEM)

2011 – 2013 **Pseudo-bacterial eye**, *Advisors: Dr Denis DUPUY (molecular biology) and D^{re} Marie BEURTON-AIMAR (computer science)*, Bordeaux (France).
- Involvement in setting up of the first team of Bordeaux and management for the second participation (2012)
- Responsible for modeling and simulation of complex existing regulatory mechanisms from eukaryotic organisms into prokaryotes
- Creation of a wiki website for your project
- Participation of oral and poster communication in Amsterdam, 5th – 7th Oct. 2012, team won a bronze medal

BTS internship

2007 – 2009
(4 months) **Functional analysis of cell cycle genes regulator and endocycle from tomato**, *Directors: Pr Michel HERNOULD (UMR 1332 Biologie du Fruit et Pathologie - INRA University of Bordeaux – Fr) and Dre Élodie MATHIEU-RIVET (Glyco-MEV, University of Rouen – Fr).*, Bordeaux (France).
- Constructing various expression vectors of cell cycle genes for a transitoire approach by biolistic method and for a stable approach by *Agrobacterium tumefaciens*
- Development of plasmid manager tool (VBA langage) called 'Plasmidator' on my free time

Teaching

2013 – 2017 Generally, I supervised a group of about 30 students for the practical work. I was in charge the elaboration of quick quiz at beginning of lessons, the evaluation of scientific experiments and the correction of drawings. For the 'Initiation of computer science' course for a Next Generation Sequencing workshop for 15 M.Sc. students, I developed a lesson (duration 6h) with practical work.

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Period	Institution	Level	Module	Type	Duration
2016 – 2017	University of Lille 1	M.Sc. in Biotechnology	Initiation of computer science	Teaching assistant	6h
2015 – 2016	University of Lille 1	1st year of Bachelor degree	Plant biology	Pratical work	16h
	University of Lille 1	M.Sc. in Biotechnology	Initiation of computer science	Teaching assistant	4h
	University of Lille 1	1st year of Bachelor degree	Cellular biology	Pratical work	45h
2014 – 2015	University of Lille 1	1st year of Bachelor degree	Plant biology	Pratical work	58h
	University of Lille 1	M.Sc. in Biotechnology	Initiation of computer science	Teaching assistant	6h
2013 – 2014	University of Lille 1	1st year of Bachelor degree	Plant biology	Pratical work	64h
Total				**Pratical work**	183h
				Teaching assistant	16h

Achievements

Articles in international peer-reviewed scientific journals

Citations: 148, H-index:1 based on Google Scholar (June 2018)

2017 **[2] Characterization of Bacterial and Fungal Community Dynamics by High-Throughput Sequencing (HTS) Metabarcoding during Flax Dew-Retting**, *C. Djemiel, S. Grec and S. Hawkins*, Frontiers in Microbiology | https://doi.org/10.3389/fmicb.2017.02052.

2014 **[1] jvenn: an interactive Venn diagram viewer**, *P. Bardou, J. Mariette, F. Escudié, C. Djemiel and C. Klopp.*, BMC Bioinformatics | https://doi.org/10.1186/1471-2105-15-293.

Awards

2017 **Best poster price RFP**, *Seminar Reseau Francais des Parois*, Orléans (Fr).

2012 **Bronze medal Europe Jamboree Championship**, *iGEM*, Amsterdam (Nl).

Invited Talks

2018 **[6] Etude de la dynamique des communautés microbiennes au cours du rouissage du lin par metabarcoding**, *FARE Seminar*, INRA Reims (Fr), 45 minutes.

2018 **[5] Les méta-omiques au service des écosystèmes microbiens**, *Conférence sur l'appui des techniques "omiques"*, ULCO Boulogne-sur-Mer (Fr), 45 minutes.

International conference with proceedings

2016 **[4] Phenotyping microbial diversity during flax dew-retting by using targeted-metagenomics**, *Cost meeting*, University of Copenhagen (Dk), 15 minutes.

National conference with proceedings

2016 **[3] Microbial diversity of retting - From cultured to uncultured genome sequences**, *Multihemp workshop*, University of Lille 1 (Fr), 15 minutes.

2015 **[2] Dynamics of bacterial and fungal communities during the dew-retting of flax**, *Transatlantic Flax Research meeting*, University of Lille 1 (Fr), 20 minutes.

Seminar and oral communications without proceedings

2014 **[1] Study of cell wall degrading during the dew-retting of flax by targeted-metagenomics**, *UGSF seminar*, University of Lille 1 (Fr), 45 minutes in french.

Posters

2017 **[10] Microbial diversity and plant cell wall-degrading enzyme dynamics during dew-retting of flax – one of the oldest applications of biotechnology to textile**, *JOBIM,*, Lille (Fr).

[9] Structural variability in the caulosphere and rhizosphere microbiome during flax dew-retting, *Réseau Français des Parois*, Orélans (Fr), Best poster price.

2016 **[8] Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics and metatranscriptomics**, *ISME*, Montréal (Ca).

[7] Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics, *JOBIM*, Lyon (Fr).

[6] Microbial diversity and cell wall-degrading enzymes prediction during flax dew-retting, *Exploring Lignocellulosic Biomass*, Reims (Fr).

[5] Characterization of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics, metatranscriptomics and biochemistry, *Cell Wall Meeting*, Chania (Gr).

[4] Meta-omics for a better understanding of the early stages of flax fiber extraction during retting, *Polytech seminar*, Lille (Fr).

2014 **[3] Study of cell wall degrading during the dew-retting of flax by targeted-metagenomics**, *Réseau Français des Parois*, Amiens (Fr).

[2] "Like looking for a needle in a flax stack", *Bioinformatics for Environmental Genomics workshop*, Lyon (Fr).

2013 **[1] Integrated next generation sequencing storage and processing environment**, *JOBIM – Open days in Biology, Computer Science and Mathematics*, Toulouse (Fr).

Languages

| English | Good |
| French | Native |

Computer skills

Operating system	GNU/Linux, macOS	OOP	Python, Java
IDE, collaboration	Eclipse, SVN, github	Web	HTML5/CSS3, jQuey/Bootstrap, PHP
Database	MySQL, PostgreSQL	Programming languages	Perl, Shell, LISP, Hoc
Office software	LATEX 2$_\varepsilon$/Beamer, LibreOffice	Graphic Editors	Adobe Illustrator, Adobe Photoshop, ImageJ

Data analysis

| Meta-transcriptomic | Bowtie 2, SAMtools, SortMeRNA | Diversity tools | Mothur, PIPTIS, Picrust, FUNGuild, LEfSe, Oligotyping |
| Statistics | Multivariate and Multiple comparison analysis with R | Visualization tools | Highcharts, Krona, jvenn, Tulip/Cytoscape |

Biology

Methodology	Set up experimental design (sampling, storage)	Molecular technics	RNA/DNA extraction/purification, quantification by picogreen using lightCycler instrument, normalization by epMotion system, PCR, cloning

References

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