

*I am currently a postdoctoral researcher at INRAE of Dijon (UMR1347 - BIOCOM team). My overarching research career goal is to use High-Throughput Sequencing and more specifically the meta-omics for understanding the structure, function and diversity of various microbiome within various ecological niches. My academic training in biology and computer science was supplemented by a doctorate in microbial ecology. My research interests cover the areas of Big Data, Software Development and Microbial Ecology.*

### Education & Academic achievements

- 2017 **PhD in Biologie de l'environnement, des populations, écologie**, UGSF - Université de Lille, France, with Highest Honours.
- 2013 **M. Sc. in bioinformatics**, Université de Bordeaux, France, with Highest Honours.
- 2011 **Three-year university degree in Biologie molecular, cellular et physiology**, Université de Bordeaux, France.
- 2009 **Two-year technical degree in biotechnologies**, Lycée St. Louis (Bordeaux, France), with honors.

### Research experiences

#### Post-graduates

- June 2018 – current **Studies in soil microbial ecology**,  
Advisors: D<sup>r</sup> **Lionel RANJARD** (Senior Scientist), D<sup>r</sup> **Sébastien TERRAT** (Lecturer), BIOCOM team – INRAE Dijon UMR1347, France.

#### Development in bioinformatics:

1. Setting up a database on micro-eukaryotes (**µgreen-db**),
2. Participation in the development of a post-clustering method (**ReClustOR**),
3. Participation in the development of a metabarcoding data analysis pipeline (**BIOCOM-PIPE**).

#### FungiMic-RMQS project: Biogeography and spatial ecology of soil fungi in France (2019 – 03/2020 / 09/2020 – current)

- Evaluate precisely the diversity of fungi in French soils in terms of diversity index and specific richness.
- Make an exhaustive inventory of the fungal populations (abundant and rare key player).
- Define biogeographical patterns and determinism of soil fungal diversity.
- Better understand the ecological attributes of fungal populations thanks to a better knowledge of their habitat.
- Better understand the regulation and changes in soil fungal diversity across various environmental disturbances (soil climate, land use, plant cover).
- Evaluate for the first time the area-species relationship and the diversification strategies
- Study the networks of biotic interactions, translate taxonomic diversity into functional diversity, estimate the services and functions provided by soils.
- Redaction of French Molecular Atlas of fungal soils.

#### Project: **APORTHE** : What is the impact of manure spreading practices of mixed “pig-cattle” systems in Massif Central grasslands on soil microbiology?

Advisor: D<sup>re</sup> **Sophie SADET-BOURGETEAU** (Lecturer),

- Study of microbial indicators to assess the impact of the spreading practices of mixed livestock manure.
- Generate soil microbiological quality diagnostic sheets.
- Multiple presentations of the results and a day of reports with the actors of the sector.

#### Project: **Study of the technosols microbiology (2018 - 2019)**

Advisor: D<sup>r</sup> **Pierre-Alain MARON** (Senior Scientist),

- Project manager within the framework of a study on microbial indicators in order to evaluate a new Technosol intended for urban renewal developed by **VICAT** company.

## PhD thesis

- Nov. 2013 – **Study of bacterial and fungal diversity during flax dew-retting by using metabarcoding**,  
Déc. 2017 *Advisors: D<sup>r</sup> Sébastien GREC and P<sup>r</sup> Simon HAWKINS*, UGSF – University of Lille, France.  
*jury members* : D<sup>re</sup> Fabienne GUILLON (Examiner, Senior Scientist at INRAE of Nantes), D<sup>r</sup> Lionel RANJARD (Examiner, Senior Scientist at INRAE of Dijon), D<sup>re</sup> Brigitte CHABBERT (Assessor, CR at INRAE of Reims), D<sup>r</sup> Kjell SERGEANT (Assessor, Senior Scientist in Luxembourg Institute of Science and Technology), D<sup>re</sup> Anne HARDUIN-LEPERS (Assessor, Chairperson, Senior Scientist CNRS at UGSF - University of Lille).
- 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

## M.Sc. internship

- Mars – Août 2013 **Development of metabarcoding pipelines for classify and clustering 16S rRNA gene sequences**,  
*Advisor: Jérôme Mariette*, INRAE – GenoToul, Toulouse – Fr.
- Development of pipelines (Roche 454 and Illumina MiSeq platform) with **Jflow** API based on **Makeflow** and **Weaver** and be integrated in NGS pipelines 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: D<sup>r</sup> Denis DUPUY (molecular biology) et D<sup>re</sup> Marie BEURTON-AIMAR (informatics)*, 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.
  - Development of iGEM Bordeaux team website **notre projet**
  - Participation of oral and poster communication in Amsterdam, 5th – 7th Oct. 2012, team won a bronze medal

## Two-year technical degree in biotechnologies internships

- 2007 – 2009 **Functional analysis of cell cycle genes regulator and endocycle from tomato**, *Advisors: P<sup>r</sup> Michel HERNOULD (UMR 1332 Biologie du Fruit et Pathologie - INRAE of Bordeaux – Fr) and D<sup>re</sup> 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 experiences

- 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. During my postdoc, I taught for the three-year university (professional career) in or in the last year of engineering school (AgroSup Dijon)..

School term	Institution	Level	Number of students	Fields	Type	Time
2021	University of Burgundy	3 <sup>rd</sup> years university	10	NGS	Lecture	6h
		3 <sup>rd</sup> years university	10	Bioinformatics	Lab work	4h
2020	AgroSup Dijon	3 <sup>rd</sup> years of engineering school	15	research and experimentation	Seminar	2h
	University of Burgundy	3 <sup>rd</sup> years university	10	NGS	Lecture	6h
		3 <sup>rd</sup> years university	10	Bioinformatics	Lab work	4h
2016 – 2017	University of Lille	M. Sc. Biotechnology	15	Computer science initiation	Lecture/Seminar	6h
2015 – 2016	University of Lille	1 <sup>st</sup> year university	30	Plant Physiology	Lab work	16h
		M. Sc. Biotechnology	15	Computer science initiation	Lecture/Seminar	4h
		1 <sup>st</sup> year university	30	Cell biology	Lab work	45h
2014 – 2015	University of Lille	1 <sup>st</sup> year university	30	Plant Physiology	Lab work	58h
		M. Sc. Biotechnology	15	Computer science initiation	Lecture/Seminar	6h
2013 – 2014	University of Lille	1 <sup>st</sup> year university	30	Plant Physiology	Lab work	64h
<b>Total</b>					<b>Lab work</b>	191h
					<b>Lecture/Seminar</b>	30h

## Qualification for a position as an assistant professor in a French University

2021 **CNU64, CNU67.**

2021 **CNU65, CNU68.**

## Major works

**2020 C. Djemiel et al.**

*BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons*

**BMC Bioinformatics**, 21 (1), 1-21

<https://doi.org/10.1186/s12859-020-03829-3>

Research context: This development work was carried out in parallel with the various post-doctorates carried out within the BIOCOM team. The analysis of metabarcoding data allowed me to integrate various computer components allowing a better interpretation of microbial diversity (see also **ReClustOR**). Contribution: Participation in the pipeline development, in the bioinformatics analysis of case study data and artificial data, in the tests. I wrote the first draft manuscript.

**2020 C. Djemiel et al.**

*µgreen-db: a reference database for the 23S rRNA gene of eukaryotic plastids and cyanobacteria*

**Scientific reports**, 10 (1), 1-11

<https://doi.org/10.1038/s41598-020-62555-1>

Research context: This development work was carried out in parallel with the various post-doctorates carried out within the BIOCOM team. This database is part of the BIOCOM-PIPE pipeline and provides an alternative for the scientific community to study the photosynthetic microeukaryotes based on 23S rRNA marker.

Contribution: Participation in the database development (data formatting and taxonomy curation),

in the bioinformatics analysis of case study data. I wrote the first draft manuscript and develop the website.

**2017 C. Djemiel et al.**

*Characterization of bacterial and fungal community dynamics by high-throughput sequencing (HTS) metabarcoding during flax dew-retting*

**Frontiers in microbiology**, 8, 2052

<https://doi.org/10.3389/fmicb.2017.02052>

Research context: This research work was carried out during my phd thesis. Welcomed within the Plant fibers team of the UGSF (University of Lille), I set up a metabarcoding approach to study the microbial ecology of the degradation of plant fibers, at the time not available in my team.

Contribution: I proposed the experimental design and participated in the sampling on test plots. I carried out the preparation of all samples (storage, extraction / purifications of DNAs and generation of amplicons by PCR), bioinformatics and statistical analysis as well as their interpretations and writing of the first draft manuscript.

## Languages

French Mother tongue  
English Intermediate level

## Informatic skills

Operating system	GNU/Linux, macOS	OOP	Python, Java
IDE, collaboration	Eclipse, SVN, github	Web	HTML5/CSS3, jQuery/Bootstrap, PHP
Database	MySQL, PostgreSQL	Programming language	Perl, Shell, LISP, Hoc
Office software	L <sup>A</sup> T <sub>E</sub> X 2 <sub>ε</sub> /Beamer, LibreOffice	Graphic editors	Adobe Illustrator, Adobe Photoshop, ImageJ

## Data analysis

Meta-transcriptomic	Bowtie2, SAMtools, SortMeRNA	Ecological tools	BIOCOM-PIPE, Mothur, PIPTIS, PICRUST2, FUNGuild, LEfSe, Oligotyping
Statistics	Biogeography, Multivariate analyzes, variance partition and multiple comparisons with R	Visualization tools	Highcharts, Krona, jvenn, Tulip/Cytoscape

## Biology skills

Methods	Set up an experimental plan (sampling, storage)	Molecular technics	Extraction/purification RNA/DNA, quantification by picogreen with a lightCycler, normalization by epMotion robot, PCR, cloning
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## Journal Review and Funding

My peer reviews Molecular Ecology Ressources (2021 (1)), Frontiers in Plant Science (2021 (2)), MDPI Agronomy (2021 (1)), MDPI Life (2020 (1)), Geoderma (2019 (1))

Review Editor Frontiers in Plant Science Marine and Freshwater Plants

## Referees

D<sup>r</sup> Lionel RANJARD

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# Lists of publications, communications, awards and distinctions

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 publons

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October 26, 2021

Nota bene: The [terms](#) in magenta are hypertext links. The [terms](#) in blue refer to an activity carried out during my master's degree, the [terms](#) in green for my phd thesis and the [terms](#) in orange for my postdoctoral fellowship.

## 1 Publications

### 1.1 Articles in international peer-reviewed scientific journals

2021

- [1] [post-doc](#) N. Chemidlin Prévost-Bouré, B. Karimi, S. Sadet-Bourgeteau, **C. Djemiel**, M. Brie, J. Dumont, M. Campedelli, V. Nowak, P. Guyot, C. Letourneur, V. Manneville, F. Gillet, Y. Bouton, "Microbial transfers from permanent grassland ecosystems to milk in dairy farms in the Comté cheese area", *Scientific reports*, (2021), [10.1038/s41598-021-97373-6](https://doi.org/10.1038/s41598-021-97373-6).

2020

- [2] [post-doc](#) **C. Djemiel**, S. Dequiedt, B. Karimi, A. Cottin, T. Girier, Y. El Djoudi, P. Wincker, M. Lelièvre, S. Mondy, N. Chemidlin Prévost-Bouré, PA. Maron, L. Ranjard and S. Terrat, "BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons", *BMC Bioinformatics*, (2020), [10.1186/s12859-020-03829-3](https://doi.org/10.1186/s12859-020-03829-3).
- [3] [thesis](#) **C. Djemiel**, E. Goulas, N. Badalato, B. Chabbert, S. Hawkins and S. Grec, "Targeted metagenomics of retting in flax: the beginning of the quest to harness the secret powers of the microbiota", *Frontiers in genetics*, (2020), [10.3389/fgene.2020.581664](https://doi.org/10.3389/fgene.2020.581664).
- [4] [post-doc](#) B. Karimi, J. Villerd, S. Dequiedt, S. Terrat, N. Chemidlin Prévost-Bouré, **C. Djemiel**, M. Lelièvre, J. Tripied, V. Nowak, N. PA. Saby, A. Bispo, C. Jolivet, D. Arrouays, P. Wincker, C. Cruaud and L. Ranjard, "Biogeography of soil microbial habitats across France", *Global Ecology and Biogeography*, (2020), [10.1111/geb.13118](https://doi.org/10.1111/geb.13118).
- [5] [post-doc](#) **C. Djemiel**, D. Plassard, S. Terrat, O. Crouzet, J. Sauze, S. Mondy, V. Nowak, L. Wingate, J. Ogée and PA. Maron, " $\mu$ green-db: a reference database for the 23S rRNA gene of eukaryotic plastids and cyanobacteria", *Scientific reports*, (2020), [10.1038/s41598-020-62555-1](https://doi.org/10.1038/s41598-020-62555-1).
- [6] [thesis](#) B. Chabbert, J. Padovani, **C. Djemiel**, J. Ossemond, A. Lemaître, A. Yoshinaga, S. Hawkins, S. Grec, J. Beaugrand and B. Kurek, "Multimodal assessment of flax dew retting and its functional impact on fibers and natural fiber composites", *Industrial Crops and Products*, (2020), [10.1016/j.indcrop.2020.112255](https://doi.org/10.1016/j.indcrop.2020.112255).

2019

- [7] **post-doc** S. Terrat, **C. Djemiel**, C. Journay, B. Karimi, S. Dequiedt, W. Horrigue, PA. Maron, N. Chemidlin Prévost-Bouré and L. Ranjard, "ReClustOR: a re-clustering tool using an open-reference method that improves operational taxonomic unit definition", *Methods in Ecology and Evolution*, (2019), [10.1111/2041-210X.13316](https://doi.org/10.1111/2041-210X.13316).

## 2018

- [8] **post-doc** U. Cenci, S. J. Sibbald, B. A. Curtis, R. Kamikawa, L. Eme, D. Moog, B. Henrissat, E. Maréchal, M. Chabi, **C. Djemiel**, A. J. Roger, E. Kim and J. M. Archibald, "Nuclear genome sequence of the plastid-lacking cryptomonad *Goniomonas avonlea* provides insights into the evolution of secondary plastids", *BMC biology*, (2018), [10.1186/s12915-018-0593-5](https://doi.org/10.1186/s12915-018-0593-5).

## 2017

- [9] **thesis** **C. Djemiel**, S. Grec and S. Hawkins, "Characterization of bacterial and fungal community dynamics by high-throughput sequencing (HTS) metabarcoding during flax dew-retting", *Frontiers in microbiology*, (2017), [10.3389/fmicb.2017.02052](https://doi.org/10.3389/fmicb.2017.02052).

## 2014

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

## 1.2 Popular Scientific Papers

### 2021

- [1] **post-doc** **C. Djemiel**, S. Dequiedt, A. Belsic, V. Nowak, F. Von Kerssenbrock, C. Husson, B. Dounies, S. Mugnier and S. Sadet-Bourgeteau, "Quel est l'impact des pratiques d'épandage des effluents d'élevage mixte « Porcin-Bovin » en zone herbagère du Massif Central sur la microbiologie des sols ?", *JRP 2021*, (2021).

### 2020

- [2] **post-doc** S. Dequiedt, B. Karimi, N. Chemidlin Prévost-Bouré, S. Terrat, W. Horrigue, **C. Djemiel**, M. Lelièvre, V. Nowak, P. Wincker, C. Jolivet, N. PA. Saby, D. Arrouays, A. Bispo, I. Feix, T. Eglin, P. Lemanceau, PA. Maron and L. Ranjard, "Le RMQS au service de l'écologie microbienne des sols français", *Etude et Gestion des Sols*, (2020), [link](#).

### 2019

- [3] **post-doc** **C. Djemiel** and S. Terrat, "Nouvelles techniques de méta-omiques pour le diagnostic de la qualité microbiologique des sols", *Editions T.I.*, (2019), [link](#).

### 2018

- [4] **post-doc** S. Terrat, B. Karimi, S. Dequiedt, N. Chemidlin Prévost-Bouré, W. Horrigue, **C. Djemiel** and L. Ranjard, "La caractérisation des communautés microbiennes du sol à l'échelle de la France pour évaluer l'effet de l'usage des sols", *Innovations Agronomiques*, (2018), [10.15454/IO3VXY](https://doi.org/10.15454/IO3VXY).

## 1.3 Articles submitted or under review

- [1] **post-doc** **C. Djemiel**, PA. Maron, S. Dequiedt, S. Terrat, A. Cottin and L. Ranjard, "Inferring microbiota functions from taxonomic genes: a review", *GigaScience*, (2021).
- [2] **post-doc** Sophie Sadet-Bourgeteau and **C. Djemiel**, "Impact des amendements organiques sur les communautés microbiennes des sols agricoles", *na*, (2020).

## 1.4 Articles being finalized

- [1] **post-doc** C. Djemiel, S. Dequiedt, W. Horrigue, A. Bailly, M. Lelièvre, J. Tripied, N. Saby, A. Bispo, A. Pierart, P. Winker, C. Cruaud, S. Terrat and L. Ranjard, "Biogeographical patterns and determinism of soil fungal alpha-diversity in France", *Fungal diversity*, (2021).
- [2] **post-doc** C. Djemiel, S. Dequiedt, J. Tripied, L. Ranjard and S. Terrat, "Biogeographical patterns and determinism of soil fungal:bacteria ratio in France", *Fungal diversity*, (2021).
- [3] **thesis** C. Djemiel, B. Kurek, B. Chabbert, S. Hawkins, I. Mangin, A. Day, "Microbial hemp retting : Current Status, Challenges and Future Perspectives.", *Bioresource Technology*, (2021).

## 2 Communications

### 2.1 Invited Talks

11. **Biogeographical patterns and determinism of soil fungal alpha-diversity in France**  
C. Djemiel, S. Terrat, S. Dequiedt, PA. Maron and L. Ranjard  
**PEPI IBIS** 🇫🇷 Toulouse (France) 📅 November 16 - 18, 2021 ⌚ 20min 📄 [Proceedings](#)
10. **Study of the dynamics of microbial communities during retting of flax by metabarcoding**  
C. Djemiel  
**FARE Seminar** 🇫🇷 INRA Reims (France) 📅 February 09, 2018 ⌚ 45min
9. **Meta-omics at the service of the study of microbial ecosystems**  
C. Djemiel  
**Conférence sur l'appui des techniques "omiques"** 🇫🇷 ULCO Boulogne-sur-Mer (France) 📅 February 08, 2018 ⌚ 45min



### 2.2 International conferences with proceedings

8. **Phenotyping microbial diversity during flax dew-retting by using targeted-metagenomics**  
C. Djemiel, S. Grec and S. Hawkins  
**2<sup>nd</sup> general COST meeting (European Cooperation in Science and Technology)** 🇩🇰 Copenhagen (Denmark) 📅 April 18 - 20, 2016 ⌚ 20min 📄 [Proceedings](#)
7. **Tracking dynamics of fax retting by evolution in stem architecture, call wall structure, and biological activities**  
B. Chabbert, C. Djemiel, A. Portelette, J. Ossemond, S. Grec, S. Hawkins, Bernard Kurek  
**LIGNO BIOTECH IV** 🇪🇸 Madrid (Spain) 📅 June 19 - 22, 2016 ⌚ 20min

### 2.3 National conferences with proceedings

6. **Biogeographical patterns and determinism of soil fungal alpha-diversity in France**  
C. Djemiel, S. Terrat, S. Dequiedt, PA. Maron and L. Ranjard  
**EAGS** 🇫🇷 Tours (France) 📅 October 27 - 29, 2021 ⌚ 20min 📄 [Proceedings](#)
5. **What is the impact of the spreading practices of mixed "pig-cattle" livestock manure in mountain areas on soil microbiology?**  
C. Djemiel, S. Dequiedt, A. Belsic, V. Nowak, F. Von Kerssenbrock, C. Husson, B. Dounies, S. Mugnier and S. Sadet-Bourgeteau  
**53<sup>rd</sup> Swine Days' Research** 🇫🇷 Paris (France) 📅 February 02 - 03, 2021



4. **Exploring microbial functions from taxonomic information: a state of the art of tools and methods**  
C. Djemiel, B. Karimi, S. Terrat, S. Dequiedt, PA. Maron and L. Ranjard  
GDRGE ■ ■ La Rochelle (France)  October 08 - 10, 2019  20min  [Proceedings](#)
  3. **Microbial diversity of retting - From cultured to uncultured genome sequences**  
C. Djemiel, S. Grec and S. Hawkins  
Multi hemp workshop ■ ■ Lille (France)  January 18, 2016  15min  [Proceedings](#)
  2. **Dynamics of bacterial and fungal communities during the dew-retting of flax: Metagenomics approaches**  
C. Djemiel, S. Grec, and S. Hawkins  
Transatlantic Flax Research meeting ■ ■ Lille (France)  June 9, 2015  20min  [Proceedings](#)
- ## 2.4 Seminar and oral communications without proceedings
1. **Study of cell wall degradation during flax retting: Approaches by functional metagenomics and taxonomic diversity**  
C. Djemiel, S. Grec and S. Hawkins  
UGSF Seminar ■ ■ Lille (France)  March 14, 2014  45min
- ## 2.5 Posters
15. **How do the breeders of mixed “pig-cattle” farms in the Massif Central manage their pig effluents?**  
F. Von Kerssenbrock, C. Husson, S. Dequiedt, C. Djemiel, B. Dounies, S. Sadet-Bourgeteau, S. Mugnier  
53<sup>rd</sup> Swine Days’ Research ■ ■ Paris (France)  February 02 - 03, 2021
  14. **Valorization of effluents in mixed cattle-pig farms in the Massif Central**  
F. Von Kerssenbrock, C. Husson, A. Beslic, S. Dequiedt, C. Djemiel, B. Dounies, V. Nowak, S. Bourgeteau-Sadet and S. Mugnier  
25<sup>th</sup> 3R International Congress ■ ■ Paris (France)  December 02 - 03, 2020
  13. **ReClustOR, a Re-Clustering method using an Open-Reference method that improves OTU definition for metabarcoding approaches**  
C. Djemiel, C. Journay, B. Karimi, W. Horrigue, S. Dequiedt, PA. Maron, N. Chemidlin Prévost-Bouré, L. Ranjard and S. Terrat  
20<sup>th</sup> JOBIM ■ ■ Nantes (France)  July 02 - 05, 2019
  12. **Deciphering controlled cell wall degradation during flax dew retting: exploring potential enzymatic activities by metatranscriptomics**  
N. Badalato, C. Djemiel, J. Ossemond, B. Chabbert, S. Hawkins and S. Grec  
Exploring Lignocellulosic Biomass ■ ■ Reims (France)  June 26 - 29, 2018
  11. **Microbial diversity and plant cell wall-degrading enzyme dynamics during dew-retting of flax – one of the oldest applications of biotechnology to textile**  
C. Djemiel, S. Grec and S. Hawkins  
18<sup>th</sup> JOBIM ■ ■ Lille (France)  July 03 - 06, 2017  [Proceedings](#)
  10. **Structural variability in the caulosphere and rhizosphere microbiome during flax dew-retting**

C. Djemiel, S. Grec and S. Hawkins

11<sup>th</sup> RFP 🇫🇷 🇫🇷 Orléans (France) 📅 June 27 - 29, 2017 📄 Proceedings

9. **Microbial diversity and cell wall-degrading enzymes prediction during flax dew-retting**

Djemiel C, Grec S, Portelette A, J. Ossemond, Chabbert B and Hawkins S

Natural fibers and polymers conference 🇫🇷 🇫🇷 Troyes (France) 📅 September 15, 2016

8. **Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics and metatranscriptomics**

C. Djemiel, S. Grec and S. Hawkins

16<sup>th</sup> ISME 🇨🇦 🇨🇦 Montreal (Canada) 📅 August 21 - 26, 2016

7. **Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics**

C. Djemiel, S. Grec and S. Hawkins

17<sup>th</sup> JOBIM 🇫🇷 🇫🇷 Lyon (France) 📅 June 28 - 30, 2016 📄 Proceedings

6. **Microbial diversity and cell wall-degrading enzymes prediction during flax dew-retting**

C. Djemiel, S. Grec, A. Portelette, J. Ossemond, B. Chabbert and S. Hawkins

Exploring Lignocellulosic Biomass 🇫🇷 🇫🇷 Reims (France) 📅 June 23 - 24, 2016

5. **Characterization of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics, metatranscriptomics and biochemistry**

C. Djemiel, S. Grec and S. Hawkins

XIV Cell Wall Meeting 🇬🇷 🇬🇷 Chania (Greece) 📅 August 12 - 17, 2016

4. **Meta-omics for a better understanding of the early stages of flax fiber extraction during retting**

C. Djemiel, A. Portelette, B. Chabbert, B. Kurek, S. Grec and S. Hawkins

Polytech Seminar: Bio-based materials, biocomposites 🇫🇷 🇫🇷 Lille (France) 📅 March 24, 2016

3. **Study of cell wall degradation during flax retting**

C. Djemiel, S. Grec, and S. Hawkins

10<sup>th</sup> RFP 🇫🇷 🇫🇷 Amiens (France) 📅 July 07 - 09, 2014

2. **“Like looking for a needle in a flax stack”**

C. Djemiel, S. Grec, and S. Hawkins

Bioinformatics for Environmental Genomics 🇫🇷 🇫🇷 Lyon (France) 📅 May 27 - 28, 2014

1. **Integrated next generation sequencing storage and processing environment**

J. Mariette, F. Escudie, A. Leleu, C. Djemiel, P. Bardou, C. Kushly, G. Salin, C. Hoede, C. Noirot et C. Klopp

14<sup>th</sup> JOBIM 🇫🇷 🇫🇷 Toulouse (France) 📅 July 01- 04, 2013

### 3 Fellowships, Grants and Awards

- 2017 Best RFP poster award, [Results](#), Colloque Réseau Français des Parois, 🇫🇷 🇫🇷 Orléans (France)
- 2012 Bronze medal in the competition of the European gathering iGEM 2012., [Results](#), International Genetically Engineered Machine competition, 🇳🇱 🇳🇱 Amsterdam (Netherlands)