



LES 1ER ET 2 JUIN



BÂTIMENT IMAG, UNIVERSITÉ GRENOBLE ALPES
150 PLACE DU TORRENT, 38400 SAINT-MARTIN-D'HÈRES

JOURNÉES DU PROTEOME ET PEPTIDOME VERTS 2026

- GRENOBLE -

ORGANISÉES AVEC LE SOUTIEN DE:



CBH Graduate School
Université Grenoble Alpes



PROGRAMME

Lundi 1er juin

13h30 - Accueil

14h - Présentation des journées (Stéphane Ravanel & Jonathan Przybyla-Toscano, LPCV - Grenoble)

Session 1 - Animateur: Stéphane Ravanel, LPCV - Grenoble

14h10 - Benoît Bernay, Proteogen - Université de Caen
Analyser un peptidome, compréhension et verrous technologiques

14h50 - Olivier Langella, GQE/PAPPSO - Gif-sur-Yvette
SpecpeptidOMS software to identify peptides without a priori in a peptidomics context

15h10 - Chloée Tymen, IBS - Grenoble
Mass spectrometry on intact biomolecules: a pivotal tool for studying plant proteoforms and macromolecular complexes

15h30 - Emmanuelle Bancel, GDEC - Clermont Ferrand
What can peptidomic analysis of bread digestates teach us?

15h50-16h20 - Pause

Session 2 - Animatrice : Lorraine Pennera, LPCV - Grenoble

16h20 - Pascal Albanese, LPCV - Grenoble
Décrypter les commutateurs moléculaires de la photosynthèse : une vision dynamique des interactions protéiques

17h00 - Fabien Chardon, IJPB - Versailles
Approche intégrative du protéome foliaire et du peptidome phloémien au cours de la sénescence foliaire

17h20 - Bruno Guillotin, IPS2 - Gif-sur-Yvette
Toward the discovery of the proteo-mobilome shaping plant development

17h40 - Nicolas Frei Dit Frey, LRSV - Toulouse
A fungal autocrine tripeptide stimulates arbuscular mycorrhizal symbiosis

18h00 - Océane Parthenay, BioForA - Orléans

Signatures protéomiques associées à l'infestation des glands de chênes sessiles par les charançons du genre *Curculio*

19h00-20h30 - Buffet sur site

Mardi 2 juin

Session 3 - Animateur : Claude Alban, LPCV - Grenoble

9h00 - Christine Carapito, IPH, Strasbourg

Single cell proteomics explorations on a range of different cell types

9h40 - Lorraine Pennera, LPCV - Grenoble

Identification of nickel-binding proteins in *Noccaea caerulescens*

10h00-10h30 - Pause

Session 4 - Animatrice : Mélisande Blein-Nicolas, GQE/PAPPSO - Gif-sur-Yvette

10h30 - Anne-Marie Labandera-Nadeau, BioFora - Orléans

Identification et validation des cibles de la tyrosine phosphatase RLPH2 d'*Arabidopsis thaliana*

11h10 - Nathalie Berger, IPSiM - Montpellier

Study of the stability of PDR9, a key actor in *Arabidopsis thaliana* Fe uptake

11h30 - Zhichao Liu, IAM - Vandoeuvre-lès-Nancy

Deciphering the relationships between protein persulfidation and oxidative stress in poplar exposed to elevated ozone

11h50 - Willy Bienvenut, GQE/PAPPSO - Gif-sur-Yvette

Bridging the analytical gap: Characterisation of grape must oligopeptides using an adapted proteomics approach

12h30 - Buffet sur site

14h00 - Conseils scientifiques du Protéome et Peptidome verts et discussion générale

Fin des journées du Protéome et Peptidome verts

Analyser un peptidome, compréhension et verrous technologiques

Benoît Bernay¹

¹ Plateforme Proteogen, US EMerode, Université de Caen Normandie

Corresponding author: benoit.bernay@unicaen.fr

Depuis deux décennies, les analyses protéomiques ont connu un essor considérable grâce aux avancées technologiques de la spectrométrie de masse haute résolution et à l'automatisation du traitement bioinformatique. Ces développements permettent désormais, en routine et à partir de quelques nanogrammes d'échantillons, d'obtenir des annotations fonctionnelles précises sur les grandes voies de signalisation impliquées dans divers contextes physiologiques.

Cependant, les peptidomes endogènes demeurent la « boîte noire » de la protéomique. La peptidomique se heurte encore à de multiples verrous analytiques : une instabilité enzymatique inhérente, une complexité dynamique extrême et des difficultés de standardisation lors de la préparation des échantillons. Au-delà de l'identification, le retraitement des données pour l'interprétation biologique constitue un défi majeur.

Toutefois, nous assistons à une rupture technologique portée par l'essor des nouvelles puissances de calcul et l'apport massif des outils de Deep Learning. L'intégration de modèles de langage protéiques (PLM) permet aujourd'hui de dépasser le simple stade de l'inventaire pour s'orienter vers la prédiction d'activité biologique. L'utilisation de logiciels de pointe basés sur des architectures de type *Transformers* (tels que UniDL4BioPep¹) ouvre la voie au criblage à haut débit de milliers de séquences natives. Cette approche permet d'identifier des peptides à potentiel antimicrobien, antioxydant ou régulateur, transformant ainsi la peptidomique en un moteur de découverte pour les biotechnologies.

Keywords: Peptidomique, Biochimie, Bioinformatique, Deep Learning

References:

1. **Du, Z. et al.**, UniDL4BioPep: a universal deep learning architecture for binary classification in peptide bioactivity. *Briefings in Bioinformatics* 24(3), 1–10 (2023).

SpecpeptidOMS software to identify peptides without a priori in a peptidomics context

Olivier Langella¹

¹GQE-Le Moulon, Université Paris-Saclay, INRAE, CNRS, AgroParisTech, Gif-sur-Yvette, France

Corresponding author: olivier.langella@universite-paris-saclay.fr

Peptidomics is an emerging field of the omics sciences, that refers to the identification of the pool of peptides present in a biological fluid or tissue. In practice, most studies in peptidomics use software and workflows derived from bottom-up proteomics. However, the peptidome has distinct specificities compared with the peptides commonly studied in proteomics: proteomics peptides are usually generated by tryptic digestion and therefore have predictable termini, whereas peptidome peptides often have non-predictable ends, can be very short, and are frequently highly modified.

We developed SpecPeptidOMS, a software that was specifically designed for peptidomics. It directly aligns peptide fragmentation spectra to whole and undigested protein sequences. Thus, SpecPeptidOMS can perform alignments starting and ending anywhere in the protein sequence. The underlying computational method, which is based on a dynamic programming approach, is highly optimized and the algorithm was recently re-implemented in C++ and made compatible with CBOR format to handle the massive volumetry of peptidomics data. This new export is promising for interfacing with rescoring and prediction tools such as DeepLC or MS2Rescore. SpecPeptidOMS is open-source, cross-platform, and freely available.

As a result, SpecPeptidOMS can process around 12,000 spectra per hour on an off-the-shelf laptop, with alignment performed against the entire maize proteome. In this presentation we will demonstrate how this new algorithm behaves compared to classical ones on classical Zea Mays samples. We will then present early results on peptidomics datasets and discuss on the relevance of this new algorithm to identify peptides in a peptidomics context.

Mass spectrometry on intact biomolecules: a pivotal tool for studying plant proteoforms and macromolecular complexes

Chloée Tymen¹, Elisabetta Boeri Erba¹

¹ Univ. Grenoble Alpes, CNRS, CEA, IRIG, IBS, 38000 Grenoble, France

Corresponding author: chloee.tymen@ibs.fr

Intact protein mass spectrometry (MS) and Native MS are complementary approaches to peptide-level proteomic workflows, bringing invaluable structural insights.

Intact protein MS allows gas-phase investigation of an intact protein in its denatured state. This enables in-depth characterization and differentiation of proteoforms within a sample by comparing theoretical masses calculated from sequences with experimental signals. Shifts are then assigned to post-translational modifications (PTMs), backbone cleavages (ex: signal peptides), point mutations, disulphide bridges, isotopic labelling (¹⁵N, ¹³C, Deuterium), or any modification causing a mass shift. In plant systems, this allows for the correction of mis-annotated N-termini, as seen with the Rubisco large subunit (Rbcl)¹, and the resolution of multiple small subunit (SSu) isoforms². This approach is fully complementary to Bottom-up MS. While Intact MS can identify coexisting modification on the same protein, Bottom-up MS can provide information on protein sequences and on the residues where these modifications occur. Beyond looking at single proteins, Native MS has emerged as a pivotal tool in structural biology. It preserves intra- and inter-molecular non-covalent bonds, allowing the study of macromolecular complexes. Native MS's broad scope encompasses oligomerisation state of a complex, ligand competition, binding dynamics and can even study membrane macromolecular assemblies. It has been successfully applied to plant-specific challenges, such as confirming the dimeric assembly of plastid PAP9 superoxide dismutase³ and identifying key β -signal recognition residues in chloroplast Oep80⁴. While extensively described for PPIs, its high sensitivity and accuracy also allow the study of protein binding to small molecules like ATPs or cofactors. It can capture weak, transient, or heterogeneous interactions, complementing cryo-EM.

Ultimately, intact mass and native MS provide essential information about the nature of protein isoforms present in a sample and their interactions. It is an invaluable tool for validating in silico prediction models such as AlphaFold and confirming the stoichiometry of assemblies.

Keywords: Intact biomolecule, Native Mass spectrometry, Non covalent interactions, Macromolecular complexes, Proteoform

Acknowledgments / Funding:

This work used the mass spectrometry platform of the Grenoble Instruct-ERIC center (ISBG ; UAR 3518 CNRS-CEA-UGA-EMBL) within the Grenoble Partnership for Structural Biology (PSB), supported by FRISBI (ANR-10-INBS-0005-02) and GRAL, financed within the University Grenoble Alpes graduate school (Ecoles Universitaires de Recherche) CBH-EUR-GS (ANR-17-EURE-0003).

References:

1. Wang, Q., Sun, L. & Knut Lundquist, P. Large-scale top-down proteomics of the *Arabidopsis thaliana* leaf and chloroplast proteomes. *Proteomics* **23**, e2100377 (2023).
2. Reynolds, T., Zhang, Z., Živković, D., Kelly, S. & Bolla, J. R. Small subunit isoform diversity underlies structural heterogeneity in native plant Rubisco. *Proc. Natl. Acad. Sci.* **123**, e2519949123 (2026).
3. Favier, A. *et al.* The Plastid-Encoded RNA Polymerase-Associated Protein PAP9 Is a Superoxide Dismutase With Unusual Structural Features. *Front. Plant Sci.* **12**, 668897 (2021).
4. Durant, R. J., Jarvis, R. P. & Bolla, J. R. Biochemical characterisation supports a central role for Oep80 from *Arabidopsis thaliana* in chloroplastic β -barrel protein assembly. *Commun. Biol.* **8**, 1265 (2025).

What can peptidomic analysis of bread digestates teach us?

Emmanuelle Bancel¹, Mélanie Lavoignat^{1,2}, Angéla Juhász³, Utpal Bose⁴, Thierry Sayd⁵, Christophe Chambon⁵, Sébastien Déjean⁶, Catherine Ravel¹

¹ Université Clermont Auvergne, INRAE, UMR1095 GDEC, F-63000 Clermont-Ferrand, France

² AgroParisTech, 75005, Paris, France

³ Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science, Edith Cowan University, School of Science, 270 Joondalup Dr, Joondalup, WA 6027, Australia

⁴ Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science, Edith Cowan University, School of Science, 270 Joondalup Dr, Joondalup, WA 6027, Australia; CSIRO Agriculture and Food, 306 Carmody Rd, St Lucia, QLD 4067, Australia

⁵ INRAE, Plateforme d'Exploration du Métabolisme Composante Protéomique (PFEMcp), F-63122 Saint-Genès Champanelle, France

⁶ Institut de Mathématiques de Toulouse, UMR5219, Université de Toulouse, CNRS, UPS, F-31062 Toulouse Cedex 9, France

Corresponding author: emmanuelle.bancel@inrae.fr

Wheat grain storage proteins consist in gliadins and glutenins, which are rich in glutamine and proline. These storage proteins form the gluten, a network with remarkable cohesiveness and viscoelasticity properties. Therefore, they are key determinants of the wheat end-use quality.

Resistance of gluten to gastrointestinal digestion is involved in adverse reactions to wheat. Indeed, several peptides produced by the incomplete digestion can trigger, in predisposed individuals, an immune response responsible for celiac disease. It could also be involved in other adverse reactions including allergies and non-celiac gluten sensitivity or non-celiac wheat sensitivity. This resistance to digestion could be modulated by the wheat cultivars and the baking process.

In this context, our study aims at developing an approach to highlight the links between wheat cultivars and the digestibility of gluten proteins in bread and to identify peptides discriminating genotypes with a high or low bread protein digestibility¹.

To address this question, a set of cultivars illustrating the bread wheat (*Triticum aestivum*) diversity was selected for baking. A dynamic gastrointestinal system was used to digest the breads prepared with the flour from single cultivar. The peptide pools from gastrointestinal digestion were characterized by LC-MS/MS.

After a 2-hours digestion, 1,104 peptides originating from gastric (987) and jejunal (117) compartments were evidenced². Within the detected peptides, 557 gastric (56.4%) and 117 jejunal peptides assigned to a protein accession were reported as unique evidence for a protein². Results showed differential patterns of digestibility of these proteins according to the cultivars. The peptide list obtained was also screened for *in silico* toxicity/immunogenicity risk assessment, with the aid of bioinformatics tools for epitopes matching in order to tackle implications for celiac disease or wheat allergy.

Such quantitative and qualitative differences between cultivars could help in the choice of varieties with an improved digestibility.

Keywords: wheat, bread, *in vitro* digestion, proteolysis, peptidomics

Acknowledgments / Funding:

This work was supported by the French Funds to support Plant Breeding (FSOV) in the context of the project “GlutNsafe” (2016Y) and by the French Government through the Research National Agency (ANR) thanks to the project ANR17-CE21-0009 GlutN. Acknowledgements are expressed to the French Ministry of Agriculture which partly funded the research activities.

References:

1. Lavoignat, M. *et al.*, Differences in bread protein digestibility traced to wheat cultivar traits. *Journal of Cereal Science*, 107 (2022), 10.1016/j.jcs.2022.103533
2. Lavoignat, M. *et al.*, Peptidomics analysis of *in vitro* digested wheat breads: Effect of genotype and environment on protein digestibility and release of celiac disease and wheat allergy related epitopes. *Food Chem.* (2024). doi: 10.1016/j.foodchem.2024.139148.

Deciphering the molecular switches of photosynthesis: a dynamic view of protein interactions

Pascal Albanese ^{1,2}

¹ Light, Photosynthesis & Metabolism (LPM), Laboratoire Physiologie Cellulaire & Végétale (LPCV), France

² Exploring the Dynamics of Proteomes (EDyP), Laboratoire Biosciences et Bioingénierie pour la Santé (BGE), France

Corresponding author: pascal.albanese@cea.fr

Sunlight triggers rapid rearrangements in the protein networks that power photosynthesis. Within seconds, plants adjust how they capture and manage light energy by forming or breaking specific protein contacts. In this talk, I will introduce how chemical crosslinking coupled to mass spectrometry can be used to capture these transient interactions and probe the structural organization of photosynthetic complexes *in vivo*, while also discussing the main strengths and limitations of the approach. Using time-resolved structural proteomics combined with fluorescence measurements of photosynthetic performance, we map interaction changes during rapid light transitions. By comparing normal light responses with conditions that block proton-gradient formation, we can distinguish light-driven effects from those controlled by the cell's fast protective mechanisms. This approach reveals molecular switches that balance efficiency, protection, and repair in the photosynthetic machinery.

Approche intégrative du protéome foliaire et du peptidome phloémien au cours de la sénescence foliaire

Fabien Chardon¹, Benoit Bernay², Anne Marmagne¹, Céline Masclaux-Daubresse¹

¹ Université Paris-Saclay, INRAE, AgroParisTech, Institute Jean-Pierre Bourgin for Plant Sciences, 78000, Versailles, France. ² Université de Caen Normandie, Plateforme Proteogen, US EMerode 4206, Caen, France

La sénescence foliaire est une étape clé de la remobilisation de l'azote des feuilles vers les organes puits. Elle repose sur une dégradation importante des protéines foliaires, mais les relations entre protéolyse, production de peptides et accumulation dans le phloème restent encore peu connues. Dans ce contexte, nous cherchons à déterminer si les peptides présents dans la sève phloémienne reflètent simplement la dégradation locale des protéines ou s'ils résultent de mécanismes plus sélectifs.

Nous avons combiné des analyses protéomiques de feuilles et peptidomiques de sève phloémienne chez le colza (*Brassica napus*), en comparant un génotype sauvage et le mutant *oci*, affecté dans un inhibiteur de protéase. Les feuilles ont été analysées selon leur rang, des plus jeunes aux plus âgées. L'analyse du protéome met en évidence une forte structuration des échantillons selon le rang foliaire, correspondant à un gradient de sénescence. Le mutant *oci* présente un profil protéomique décalé vers un état plus sénéscent que le génotype sauvage.

En parallèle, l'analyse peptidomique révèle que les peptides présents dans le phloème proviennent majoritairement de protéines ribosomales, mais aussi de protéines associées à la protéolyse, au transport de l'eau ou à la photosynthèse. L'analyse conjointe met également en évidence des peptides présents dans la sève alors que les protéines correspondantes ne sont pas détectées dans les feuilles analysées. Ces résultats suggèrent que certains peptides pourraient être générés, stabilisés ou transportés de manière sélective, ouvrant de nouvelles perspectives sur leur rôle potentiel dans le dialogue source-puits.

Financement : ANR hAPPEN, « Autophagie, protéases et performances agronomiques » (ANR-19-CE14-0009).

Toward the discovery of the proteo-mobilome shaping plant development

Apoorva Gupta ^{1,2}, Emmanuelle Bayer², **Bruno Guillotin**¹

¹ Institute of Plant Sciences of Paris-Saclay, UMR9213 CNRS, France

² Laboratory of Membrane Biogenesis UMR5200 CNRS, University of Bordeaux, France

Corresponding author: bruno.guillotin@universite-paris-saclay.fr

Permission to reproduce the abstract in the abstract book and to publish it in the Open Archive Hal: **No**

A fungal autocrine tripeptide stimulates arbuscular mycorrhizal symbiosis

Nathan Pavot, Léa Pedinotti, Morgane Le Marquer, Eve Coutant, Marielle Aguilar, Hélène San Clemente, Jean Keller, Guillaume Bécard, Virginie Puech-Pagès and **Nicolas Frei Dit Frey***

Laboratoire de Recherche en Sciences Végétales, UMR5546 CNRS-UPS-INP (Toulouse, France)

Corresponding author: nicolas.frei-dit-frey@utoulouse.fr

Most land plants, including crops, establish a mutualist association with arbuscular mycorrhizal (AM) fungi. During this interaction, plants acquire water and minerals from the fungus, that explores the soil far beyond the plant root system. In return, fungi are rewarded with sugars and lipids from the host plants. These exchanges occur in specialized structures, the arbuscules, that develop in plant cells through dichotomous branching of fungal hyphae. To allow fungal colonization and proper establishment of the symbiosis interface, cell-cell communication play crucial roles. Using a bioinformatics approach in the fungal model species *Rhizophagus irregularis*, we identified a family of five proteins predicted to deliver multiple copies of a secreted tripeptide. Interestingly, these proteins display canonical features of Ascomycota sexual pheromone precursors, suggesting a role in cell-cell communication during fungal development and/or symbiosis. Indeed, our data collectively show that these fungal peptide genes are induced by plant exudates and are strongly expressed during symbiosis. Moreover, the predicted tripeptides can be detected using targeted mass spectrometry in germinated spores and in mycorrhized roots. Furthermore, exogenous application with the synthetic peptide increases hyphal fusions *in vitro* and promotes symbiotic interaction with the model plant *Medicago truncatula*, thus highlighting the existence of a new fungal-derived pheromone regulating positively vegetative cell fusions and AM symbiosis.

Keywords: plant-microbe interaction, peptide hormone, signaling, symbiosis

Signatures protéomiques associées à l'infestation des glands de chênes sessiles par les charançons du genre *Curculio*

Océane Parthenay¹, Marie-claude Venner², Stéphane Claverol³, Samuel Venner², Brigitte Musch³,
Caroline Teyssier ¹

¹ BioForA, UMR INRAE–ONF, 2163 Avenue de la pomme de Pin, CS 40001 Ardon, 45075 Orléans

² LBBE - UMR CNRS-Université Claude Bernard Lyon 1, 43 Bd du 11 nov 1918, 69622 Villeurbanne cedex

³ Bordeaux Proteome, Université de Bordeaux, 146 rue Léo Saignat, 33076 Bordeaux Cedex

⁴ ONF, 2 bis avenue du Général Leclerc, 94700 Maisons-Alfort

Corresponding author: oceane.parthenay@inrae.fr

Les glands constituent une ressource alimentaire essentielle pour les charançons du genre *Curculio*, surtout à leur stade larvaire. Les conséquences peuvent être importantes pour la régénération des chênes, alors que les changements globaux compromettent régulièrement la production des glands et l'établissement de leurs semis. Comme le déterminisme et les répercussions moléculaires de ces interactions graines-insectes restent encore peu caractérisées, il est essentiel de comprendre ces mécanismes en évaluant l'impact de l'infestation sur les processus biologiques des glands avec une attention particulière aux mécanismes de défense susceptibles de limiter ces attaques. Lors de ma thèse, j'ai caractérisé les profils physiologiques et biochimiques des glands à différents niveaux biologiques dans un cadre d'analyses intégratives combinant spectroscopie proche infrarouge, analyses biochimiques, métabolomiques et protéomiques.

Afin d'identifier les signatures protéomiques associées au niveau d'attaque des arbres hôtes et à l'infestation des glands, deux comparaisons ont été réalisées :

- (1) Glands sains provenant d'arbres faiblement ou fortement attaqués par *Curculio*
- (2) Glands sains versus glands infestés.

Au total, 4696 protéines ont été identifiées par LC-MS/MS. La comparaison des glands sains selon le niveau d'attaque des arbres a révélé des signatures protéomiques distinctes, suggérant un état physiologique modulé en fonction du contexte écologique de l'arbre, avec un protéome orienté vers la défense chez les glands des arbres faiblement attaqués. L'analyse différentielle met en évidence une réorganisation importante du protéome des glands infestés, impliquant notamment des protéines liées aux réponses au stress, aux mécanismes de défense, au métabolisme lipidique et à la biosynthèse de métabolites secondaires. Ces résultats montrent que la protéomique permet de mieux comprendre les processus biologiques impliqués dans la réponse des glands à l'infestation et au contexte écologique de l'arbre hôte.

Keywords: glands, *Curculio*, protéomique, réponse au stress, métabolisme lipidique

Acknowledgments / Funding:

Ce travail a été financé par une bourse de thèse de la **Région Centre-Val de Loire**.

Single cell proteomics explorations on a range of different cell types

Charline Keller, Pauline Perdu-Alloy, Farida Salimova, Sunu Lama, Francis Onyeka Offor, Jeewan Babu Rijal, **Christine Carapito**

*Laboratoire de Spectrométrie de Masse BioOrganique (LSMBO), IPHC UMR7178, CNRS, Université de Strasbourg
Site strasbourgeois de l'Infrastructure Nationale de Protéomique ProFI, UAR2048*

Corresponding author: ccarapito@unistra.fr

Single-cell proteomics (SCP) has emerged as a transformative mass spectrometry-based approach for investigating cellular heterogeneity at the functional protein level. By enabling the quantification of proteins in individual cells, SCP complements single-cell transcriptomics and provides direct insight into cellular phenotypes, signaling pathways, and post-transcriptional regulation. Despite rapid technological progress, major analytical challenges remain, due to the minute protein content of single cells, sample losses during preparation, missing data, and the need to balance proteome depth with highest possible analytical throughput.

Recent advances in ultra-sensitive LC-MS/MS instrumentation, microfluidic sample handling, and computational workflows have substantially improved proteome coverage and robustness, allowing the identification of thousands of proteins from single mammalian cells.

In this presentation, workflow optimizations will be presented as well as SCP results achieved on reference Hela cells, but also small plasmocytes (150pg), lymphocytes (80pg), and down to thermophilic prokaryotes (femtogram range protein amounts), in various biological contexts.

Identification of nickel-binding proteins in *Noccaea caerulescens*

Lorraine Pennera¹, Fabienne Devime¹, Sylvie Figuet¹, Yohann Couté², Sylvain Merlot³, Claude Alban¹, Stéphane Ravanel¹ and Jonathan Przybyla-Toscano¹

¹Univ. Grenoble Alpes, CEA, INRAE, CNRS, IRIG, LPCV, 38000 Grenoble, France

²Univ. Grenoble Alpes, CEA, INSERM, UA13 BGE, CNRS, CEA, Grenoble, France

³LRSV, UMR5546 CNRS/UPS/INPT, 31000 Toulouse, France

Corresponding author: lorraine.pennera@cea.fr

Nickel (Ni) is an essential micronutrient for plants. This element is required for the activity of urease, an enzyme involved in nitrogen metabolism (Myrach *et al.*, 2017), as well as for certain Ni-dependent glyoxalases participating in detoxification processes (Jain *et al.*, 2016). Trace amounts of Ni are sufficient to support plant growth and development, whereas moderate soil concentrations can become toxic to most plant species. Some plant species have evolved mechanisms enabling them to tolerate and accumulate high amounts of Ni in their leaf tissues when growing on Ni-rich soils (Brooks *et al.*, 1977). Among these mechanisms, we hypothesize that nickel-binding proteins (NiBPs) may function as metal chelators, thereby efficiently mitigating Ni toxicity. To identify novel plant NiBPs, we developed a metalloproteomic approach using the Ni-hyperaccumulator species *Noccaea caerulescens*. The soluble leaf proteome from plants exposed to high Ni concentrations was first fractionated through successive liquid chromatography steps, while the presence of Ni in protein fractions was monitored by inductively coupled plasma mass spectrometry (ICP-MS). Ni-enriched protein fractions were subsequently sequenced by tandem mass spectrometry (MS/MS). The application of stringent selection criteria—including MS/MS quality parameters, manual validation, association with metal homeostasis, and correlation with transcriptomic datasets—enabled the identification of promising candidates. Detailed biochemical characterization of one identified protein revealed original properties, providing new insights into the molecular strategies underlying metal tolerance.

Keywords: metalloproteomics, nickel-binding proteins, hyperaccumulator species, *Noccaea caerulescens*

References:

1. Myrach, T., Zhu, A., and Witte, C.-P. (2017). The assembly of the plant urease activation complex and the essential role of the urease accessory protein G (UreG) in delivery of nickel to urease. *J Biol Chem* 292, 14556–14565.
2. Jain, M., Batth, R., Kumari, S., & Mustafiz, A. (2016). Arabidopsis thaliana Contains Both Ni²⁺ and Zn²⁺ Dependent Glyoxalase I Enzymes and Ectopic Expression of the Latter Contributes More towards Abiotic Stress Tolerance in E. coli. *PLoS one*, 11(7)
3. Brooks RR, Lee J, Reeves RD, and Jaffre T. (1977) Detection of nickeliferous rocks by analysis of herbarium specimens of indicator plants. *J. Geochem Explor.* 7, 49-57

Identification et validation des cibles de la tyrosine phosphatase RLPH2 d'*Arabidopsis thaliana*

Anne-Marie Labandera Nadeau^{1,2}, Ryan Toth¹, Sierra Mitchell¹, Jayde J Johnson¹, Brooklyn Kurucz¹, Juliette Puyaubert^{3,4}, Emmanuel Baudouin^{3,4}, Kenneth K.S. Ng^{1,5}, R Glen Uhrig^{6,7}, Greg B Moorhead¹

Corresponding author: anne-marie.labandera-nadeau@inrae.fr

¹Department of Biological Sciences, University of Calgary, Calgary, AB, Canada

²INRAE, ONF, UMR BioForA, Orléans, France

³Sorbonne Université, CNRS, Inserm, Development, Adaptation and Ageing, Dev2A, Paris, France

⁴Sorbonne Université, CNRS, Inserm, Institut de Biologie Paris-Seine, IBPS, Paris, France

⁵Department of Chemistry and Biochemistry, University of Windsor, Windsor, Ontario, Canada

⁶Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada

⁷Department of Biochemistry, University of Alberta, Edmonton, Alberta, Canada

L'étude de la phosphorylation en tyrosine chez les plantes est largement négligée en raison de l'absence de tyrosine kinases classiques et de la sous-représentation des tyrosine phosphatases. Cependant, des études de phospho-protéomiques avancées ont révélé que l'abondance des résidus de phospho-tyrosine chez les plantes est comparable à celle observée chez l'humain. Ceci suggère fortement que la phosphorylation en tyrosine est également importante chez les plantes, pourtant nos connaissances sur les acteurs responsables de ces processus restent limitées. La phosphatase *Rhizobiale*-like phosphatase 2 (RLPH2) d'*Arabidopsis thaliana* est une nouvelle protéine phosphatase absente chez les mammifères qui, selon une analyse bioinformatique, se regroupe avec le groupe des phosphoprotéines phosphatases (PPP) spécifiques de la sérine/thréonine. Nous démontrons ici que RLPH2 se comporte étonnamment comme une tyrosine phosphatase. RLPH2 est inhibée par l'orthovanadate, un inhibiteur spécifique des phosphatases en tyrosine, et déphosphoryle les substrats de phospho-tyrosine ne présentant pratiquement aucune activité envers les résidus de phospho-sérine/thréonine. Afin de commencer à comprendre cette préférence inattendue, nous avons élucidé la structure cristalline de RLPH2 en présence et en l'absence de tungstate (phospho-mimétique) à 1,8 et 2,0 Å, respectivement. Cela a permis de comprendre en détail les mécanismes de son mode d'action. La structure de RLPH2, associée à une validation biochimique, a révélé les conditions que ses substrats doivent remplir, faisant les protéines kinases Mitogen-Activated Protein kinases (MAPKs) des candidats parfaits. Finalement, pour identifier les substrats endogènes de RLPH2, une étude de phospho-protéomique a été réalisée en comparant les peptides phosphorylés en tyrosine provenant de plantes sauvages et de deux lignées knock-out (*rlph2*). RLPH2 a été identifiée et validée comme étant une tyrosine phosphatase spécifique du groupe D des MAPKs.

Study of the stability of PDR9, a key actor in *Arabidopsis thaliana* Fe uptake

Nathalie Berger¹, Meijie Li¹, Kévin Robe¹, Alice Rossile¹, Esther Izquierdo-Allegre¹, Valérie Rofidal¹,
Christian Dubos¹

¹IPSiM, CNRS, INRAE, Institut Agro, University Montpellier, Montpellier, France

Corresponding author: nathalie.berger@inrae.fr

Although Fe is one of the most abundant elements on earth, the extremely low availability of free Fe in most soils makes Fe deficiency a common nutritional disorder in plants, affecting plant growth and crop productivity. Tremendous efforts have led to the identification and characterization of several molecular actors regulating Fe uptake and partitioning within the plant. In the model plant *Arabidopsis thaliana*, it is well established that Fe-mobilizing coumarins (FMCs) biosynthesis and secretion into the rhizosphere have a major role in facilitating Fe uptake, predominantly in calcareous / neutral to alkaline soils (i.e., soils with low Fe availability). The ABC transporter PDR9 (ABCG37) is essential for FMCs secretion from the cortex to the rhizosphere via the epidermis. PDR9 accumulates under low Fe availability conditions at the external side of cortical and epidermal cells of the root. Because of the key role of PDR9 in plant Fe nutrition, we decided to investigate the role of posttranslational modifications in regulating PDR9 accumulation and localization. PDR9 is composed of two major domains: a transmembrane domain and a nucleotide binding domain (NBD). Thanks to a phosphoproteomic approach, we first identified 3 amino acid stretches in the NBD domain of PDR9 that are specifically enriched for phosphorylation modifications under Fe deficiency condition. The corresponding phospho-dead mutants cannot complement the *pdr9-2* knock out mutant phenotype (i.e., hypersensitivity to Fe deficiency). Secondly, the localization of the phospho-dead mutants is still polarized in the cortical and epidermal cells but seems to be less stable. Moreover, a PDR9 co-immunoprecipitation experiment followed by LC-MS/MS analysis yielded a list of kinases potentially responsible for the observed phosphorylation. Finally, a mutant affected in one of the LRR-kinases from this list showed a significant Fe deficiency sensitivity phenotype, mimicking that one of the *pdr9* mutants. The potential role of this LRR-kinases in PDR9 phosphorylation will be discussed.

Deciphering the relationships between protein persulfidation and oxidative stress in poplar exposed to elevated ozone

Zhichao Liu¹, Noémie Simon¹, Christophe Marchand², Anthony Gandin³ and Jérémy Couturier^{1,4}

¹ Université de Lorraine, IAM, Nancy, France

² Sorbonne Université, CNRS, Laboratoire de Biologie Computationnelle et Quantitative, Paris, France

³ Université de Lorraine, SILVA, F-54000 Nancy, France

⁴ Institut Universitaire de France, Paris, France

Protein persulfidation, the oxidative modification of cysteine residues to persulfides, is suggested to represent the main way by which hydrogen sulfide (H₂S) exerts its biological functions (Filipovic et al., 2018). In plants, persulfidated proteins are involved in a wide range of important processes such as carbon metabolism, responses to abiotic and biotic stress, growth and development, protein translation, and autophagy (Aroca et al., 2017). However, the role of protein persulfidation in the response to oxidative stress in plants has not yet been studied. Ozone (O₃) is not only a major air pollutant and real threat to plant health and productivity, but also an excellent tool to induce oxidative stress (Noctor et al., 2016). We investigated the relationships between protein persulfidation and oxidative stress in poplar in the context of an acute O₃ stress. First, the level of persulfidated proteins was assessed in leaves of various poplar genotypes (exhibiting various sensitivity to O₃) treated or not with 250 ppb O₃ for three days. Then, the dynamic of the levels of persulfidated proteins was studied over the time of O₃ treatment and compared to the antioxidant capacity (i.e. quantifying oxidized and reduced forms of ascorbate and glutathione). Finally, we performed a proteomic analysis of the O₃-dependent persulfidome of poplar and identified several enzymes involved in the ascorbate-glutathione pathway and in lignin biosynthesis. Overall, our findings suggest that the O₃-induced oxidative stress promotes the persulfidation of specific proteins that could determine better plant tolerance to oxidative stress. Further analysis of the impact of persulfidation on protein function for some candidates will advance our understanding of ozone-dependent protein persulfidation in poplar.

References:

- Aroca A, Benito JM, Gotor C, Romero LC** (2017) Persulfidation proteome reveals the regulation of protein function by hydrogen sulfide in diverse biological processes in Arabidopsis. *Journal of Experimental Botany* **68**:4915-4927
- Filipovic MR, Zivanovic J, Alvarez B, Banerjee R** (2018) Chemical Biology of H₂S Signaling through Persulfidation. *Chemical Reviews* **118**:1253-1337
- Noctor G, Mhamdi A, Foyer CH** (2016) Oxidative stress and antioxidative systems: recipes for successful data collection and interpretation. *Plant Cell and Environment* **39**:1140-1160

Bridging the analytical gap: Characterisation of grape must oligopeptides using an adapted proteomics approach

Laurencia Fera ¹, Ainhoa Bacque ², Jonathan Rixhon ², Marlène Daventure ¹, Thierry Balliau ¹, Catherine Chabaliér ², Evelyne Aguera ³, Hugo Devillers ², Thierry Doco ², Jessica Noble ⁴, David Ferreira ⁴, Virginie Galeote ², Mélisande Blein-Nicolas ¹, **Willy Bienvenut** ¹

¹ PAPPSO, GQE, IDEEV (EMR 9005), Univ Paris Saclay, INRAE, CNRS, AgroParisTech, 12 route 128, Gif sur Yvette, France

² SPO, Univ Montpellier, INRAE, Institut Agro, France, montpellier

³ UE Pech Rouge, Chemin de la Rouquette, Gruissan, France

⁴ LALLEMAND SAS, 19 Rue des Briquetiers, 31702 Blagnac

Corresponding author: willy.bienvenut@cnrs.fr

Small peptides are abundant in food-related processes such as fermentation and by-product hydrolysate, and naturally occur in grape juice and must. Their characterisation is essential for understanding their contribution to product quality, fermentation processes, and the properties of the final wine product. While conventional proteomics typically targets peptides larger than 8–10 amino acids and metabolomics focuses on free amino acids or di-/tri-peptides, the characterisation of intermediate-sized oligopeptides (4–8 amino acids) remains technically challenging.

To address this analytical gap, we developed a proteomics-adapted workflow for the identification of oligopeptides in grape must. Samples were chemically derivatised to increase peptide molecular weight and modify physicochemical properties, including hydrophobicity, prior to mass spectrometry analysis. Because existing peptide identification tools often show limited performance for very small peptides, alternative identification strategies were implemented. Our adapted workflow combined pseudo *de novo* sequencing using PEAKS™ software with searches against a *Vitis vinifera* reference database. Using this approach, several thousand peptide sequences were identified across must samples from different grape varieties.

For validation, approximately 100 peptides were synthesised using stable isotope-labelled amino acids. These synthetic standards were analysed under the same conditions as grape must samples, and their fragmentation spectra and HPLC retention times were compared with those of the identified endogenous peptides. This strategy enabled evaluation of the reliability of peptide identification and provided a high level of confidence in the validated sequences retained for subsequent studies, including quantitative analyses in natural must.

Overall, this proteomics-adapted workflow enabled the large-scale identification of several thousand small peptides in grape must. Validation using stable isotope-labelled synthetic peptides confirmed the robustness of the approach. The validated peptide set now provides a basis for future investigations into the role of oligopeptides in fermentation processes and their impact on final wine quality.

Keywords: Peptidomics, Chemical derivatisation, Stable isotope labelling, Mass spectrometry, Grape must

Acknowledgments / Funding:

This work was funded by the ANR-24-CE21-2141 YEASTPEPS project. Proteomics analyses were performed

on the PAPPISO facility (<https://doi.org/10.15454/1.5572393176364355E12>) which is supported by Paris Saclay University (<https://www.universite-paris-saclay.fr/en>), INRAE (<http://www.inrae.fr>), CNRS (<http://www.cnrs.fr>), AgroParisTech (<https://www.agroparistech.fr/en>), the Ile-de-France regional council (<https://www.iledefrance.fr/education-recherche>), IBISA (<https://www.ibisa.net>), Saclay Plant Sciences-SPS (ANR-17-EUR-0007), and Plant2Pro® (#24 CARN 0024-01).

Deciphering the Role of NatA in Pea Physiology and Stress Response

Le Signor Christine¹, Bienvenut Willy², Lamotte Olivier¹, Gayral Mathieu¹, Aimé Delphine¹, Jeannin Nicolas¹, Sanchez Myriam¹, Nadia Rossin¹, Marlène Davanture², Melisande Blein-Nicolas², Markus Wirtz³ and **Gallardo-Guerrero Karine**¹

¹ Université Bourgogne Europe, Institut Agro Dijon, INRAE, Agroécologie, Dijon, France

² GQE-Le Moulon, Université Paris-Saclay, INRAE, CNRS, AgroParisTech, Gif-sur-Yvette, France

³ Centre for Organismal Studies (COS), Heidelberg University, Heidelberg, Germany

Corresponding author: christine.le-signor@inrae.fr

The modulation of protein activity via post- and co-translational modifications plays a fundamental role in regulating plant development and stress tolerance. N-terminal acetylation (NTA) of proteins is one of the most common protein modifications in eukaryotes, the primary function of which is to direct misfolded, denatured or obsolete proteins in a targeted manner towards the ubiquitin-dependent proteasome degradation pathway¹. Three Nat systems (NatA, NatB and NatC) are responsible for the majority of NTA modifications. The NatA system has recently been studied in the model plant *Arabidopsis thaliana*: it is essential for embryogenesis, and reduced NatA expression is sufficient to induce a water stress response typically mediated by ABA² (stomatal closure, induction of ABA-dependent gene expression, and altered root development). The aim of this work was to investigate the role of the NatA system in pea, using the Caméor genotype, for which TILLING mutants³ are available. Pea mutants for two genes encoding components of this system, NAA10 (structural protein) and HYPK (complex effector), were identified. The *naa10* stop-codon mutant was lethal, as observed in *A. thaliana*, whereas the *hypk* stop-codon mutant was viable but displayed increased levels of ubiquitinated proteins in leaves. When grown under water stress conditions, the *hypk* mutant did not show increased tolerance compared to the wild type. However, preliminary data suggest a greater tolerance of this mutant to the phytopathogenic fungus *Botrytis cinerea* compared to the wild type. Under non-stress conditions, *hypk* plants showed reduced growth and smaller seeds than the wild type. Seed protein content and composition were also significantly altered. Analysis of the *hypk* seed acetylome at PAPPISO revealed a marked decrease in the acetylation of several proteins, particularly NatA substrates, independently of developmental stage. A comparative analysis of acetylome data from seeds and leaves will help identify NatA targets in pea.

Keywords: *Pisum sativum*, N-terminal acetylation, seed, stress tolerance

Acknowledgments / Funding:

This study was funded by the Graduate school TRANSBIO and the Région Bourgogne-Franche Comté as part of the HOLOSTRESS project.

References:

1. Linster E, Wirtz M. N-terminal acetylation: an essential protein modification emerges as an important regulator of stress responses. *J Exp Bot.* 2018 Aug 31;69(19):4555-4568. doi: 10.1093/jxb/ery241.
2. Linster E, Stephan I, Bienvenut WV, Maple-Grødem J, Myklebust LM, Huber M, Reichelt M, Sticht C, Møller SG, Meinel T, Arnesen T, Giglione C, Hell R, Wirtz M. Downregulation of N-terminal acetylation triggers ABA-mediated drought responses in *Arabidopsis*. *Nat Commun.* 2015 Jul 17;6:7640. doi: 10.1038/ncomms8640.
3. Dalmais M, Schmidt J, Le Signor C, Moussy F, Burstin J, Savoie V, Aubert G, Brunaud V, de Oliveira Y, Guichard C, Thompson R, Bendahmane A. UTILLdb, a *Pisum sativum* in silico forward and reverse genetics tool. *Genome Biol.* 2008;9(2):R43. doi: 10.1186/gb-2008-9-2-r43.

Deciphering the relationships between protein persulfidation and oxidative stress in poplar exposed to elevated ozone

Zhichao Liu¹, Noémie Simon¹, Christophe Marchand², Anthony Gandin³ and Jérémy Couturier^{1,4}

¹ Université de Lorraine, IAM, Nancy, France

² Sorbonne Université, CNRS, Laboratoire de Biologie Computationnelle et Quantitative, Paris, France

³ Université de Lorraine, SILVA, F-54000 Nancy, France

⁴ Institut Universitaire de France, Paris, France

Protein persulfidation, the oxidative modification of cysteine residues to persulfides, is suggested to represent the main way by which hydrogen sulfide (H₂S) exerts its biological functions (Filipovic et al., 2018). In plants, persulfidated proteins are involved in a wide range of important processes such as carbon metabolism, responses to abiotic and biotic stress, growth and development, protein translation, and autophagy (Aroca et al., 2017). However, the role of protein persulfidation in the response to oxidative stress in plants has not yet been studied. Ozone (O₃) is not only a major air pollutant and real threat to plant health and productivity, but also an excellent tool to induce oxidative stress (Noctor et al., 2016). We investigated the relationships between protein persulfidation and oxidative stress in poplar in the context of an acute O₃ stress. First, the level of persulfidated proteins was assessed in leaves of various poplar genotypes (exhibiting various sensitivity to O₃) treated or not with 250 ppb O₃ for three days. Then, the dynamic of the levels of persulfidated proteins was studied over the time of O₃ treatment and compared to the antioxidant capacity (i.e. quantifying oxidized and reduced forms of ascorbate and glutathione). Finally, we performed a proteomic analysis of the O₃-dependent persulfidome of poplar and identified several enzymes involved in the ascorbate-glutathione pathway and in lignin biosynthesis. Overall, our findings suggest that the O₃-induced oxidative stress promotes the persulfidation of specific proteins that could determine better plant tolerance to oxidative stress. Further analysis of the impact of persulfidation on protein function for some candidates will advance our understanding of ozone-dependent protein persulfidation in poplar.

References:

- Aroca A, Benito JM, Gotor C, Romero LC** (2017) Persulfidation proteome reveals the regulation of protein function by hydrogen sulfide in diverse biological processes in Arabidopsis. *Journal of Experimental Botany* **68**:4915-4927
- Filipovic MR, Zivanovic J, Alvarez B, Banerjee R** (2018) Chemical Biology of H₂S Signaling through Persulfidation. *Chemical Reviews* **118**:1253-1337
- Noctor G, Mhamdi A, Foyer CH** (2016) Oxidative stress and antioxidative systems: recipes for successful data collection and interpretation. *Plant Cell and Environment* **39**:1140-1160

PsbS interacts with LHCII trimers and PSII core during NPQ induction in Spinach acclimated to different light intensities

Oriane Bethoux¹, Nicolas Francés^{1,2}, Giovanni Finazzi¹, Myriam Ferro², Pascal Albanese^{1,2}

¹ Light, Photosynthesis & Metabolism (LPM), Laboratoire Physiologie Cellulaire & Végétale (LPCV), France

² Exploring the Dynamics of Proteomes (EDyP), Laboratoire Biosciences et Bioingénierie pour la Santé (BGE), France

Non-photochemical quenching (NPQ) is an essential mechanism to dissipate excess energy as heat to avoid photodamage in land plants. Its major and fastest component energy-dependent quenching (qE) depends on the xanthophyll cycle and the thylakoid membrane protein PsbS. The molecular mechanism by which PsbS acts as a quencher remains largely unknown despite numerous studies. PsbS structure is known in a dimeric form, but the oligomerization state of the active/inactive form of this protein remains controversial. It has been demonstrated that PsbS mainly interacts with the Photosystem II and its antenna (LHCII), however these studies were not performed under active NPQ induction states.

In this work, we used a method of extraction allowing the use of functional thylakoids to perform chemical crosslinking during NPQ induction, followed by mass spectrometry analysis to decipher PsbS interactors. This method allows us to build a precise interactome under active physiological conditions. We observed that PsbS interacts with the PSII core protein PSBH, LHCII trimers (Lhcb1.1-1.3) and CP26, but not with CP29 nor CP24. The interactors were similar in both high and low light acclimated plants, however this seems to have an impact on the preferential interaction sites of PsbS. Further, we can attest that PsbS dimers are present during NPQ induction, suggesting a part of PsbS pool remains in a dimer state during this process. Whether this is because only a fraction of PsbS pool is active during NPQ induction resulting in partial monomerization or because it indeed functions as a dimer remains to be determined.

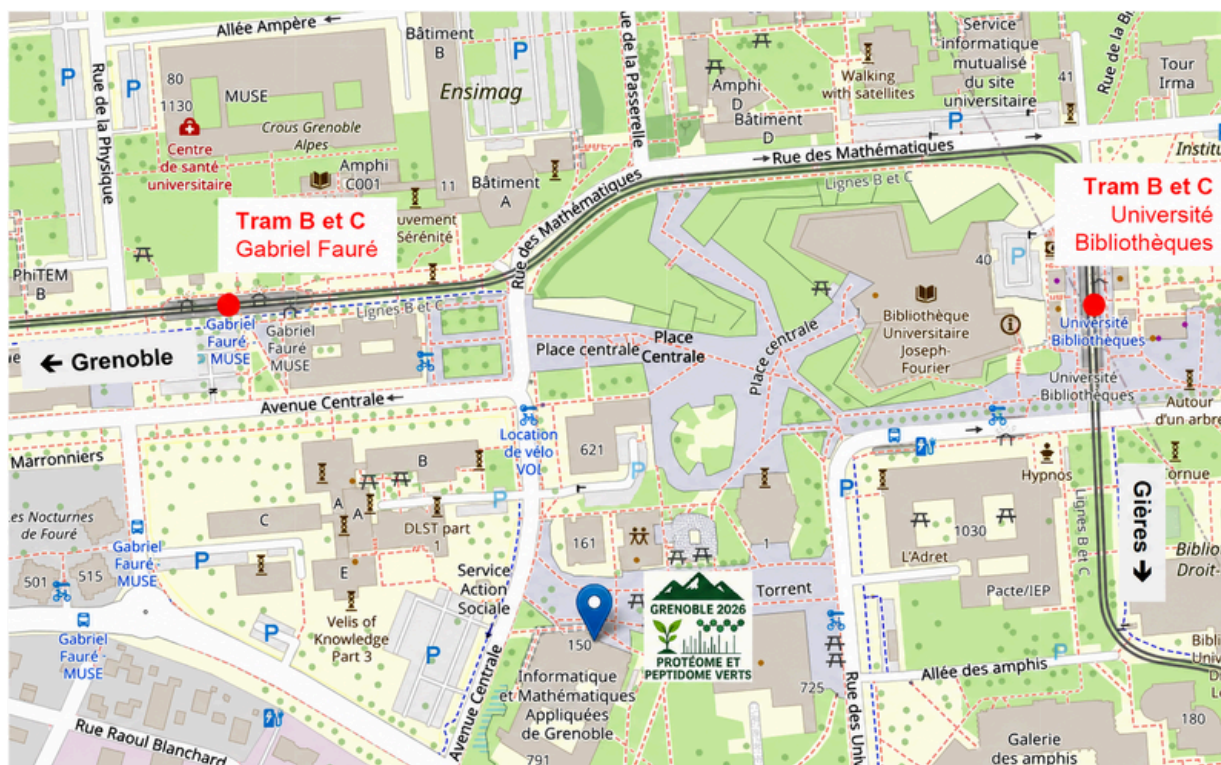
Keywords: Thylakoids; PsbS; Non-photochemical quenching; XL-MS

Nom	Prénom	Email	Laboratoire/entreprise/plateforme
Aimé	Delphine	delphine.aimé@inrae.fr	Agroécologie
Alban	Claude	claud.alban@cea.fr	LPCV
Albanese	Pascal	pascal.albanese@cea.fr	LPCV/EDyP
Bancel	Emmanuelle	emmanuelle.bancel@inrae.fr	GDEC
Beille	Séverine	severine.beille2@cea.fr	LPCV
Bernay	Benoît	benoit.bernay@unicaen.fr	Proteogen
Berger	Nathalie	nathalie.berger@inrae.fr	IPSiM/MSPP
Bethoux	Oriane	Oriane.BETHOUX@cea.fr	LPCV
Bienvenut	Willy	willy.bienvenut@inrae.fr	GQE/PAPPSO
Blein Nicolas	Melisande	melisande.blein-nicolas@inrae.fr	GQE/PAPPSO
Bonnet-Blanes	Estelle	ebonnet@gattefosse.com	Gattefossé
Cadoux	Cécile	cecile.cadoux@ibs.fr	IBS
Camagna	Alba	Alba.CAMAGNA@cea.fr	LPCV
Carapito	Christine	ccarapito@unistra.fr	IPHC
Chardon	Fabien	fabien.chardon@inrae.fr	IJPB
Chaulaïc-Metais	Aurélien	Aurélien.CHAULAIC--METAIS@cea.fr	LPCV
Chauvet	Aurélié	Aurélié.CHAUVET@cea.fr	LPCV
Corellou	Florence	florence.corellou@cea.fr	LPCV
Couté	Yohann	yohann.coute@cea.fr	EDyP
Curien	Gilles	gilles.curien@cea.fr	LPCV
Demolombe-Liozu	Vincent	vincent.demolombe-liozu@inrae.fr	IPSiM/MSPP
Devime	Fabienne	fabienne.devime@cea.fr	LPCV
Dubos	Christian	christian.dubos@inrae.fr	IPSiM/MSPP
Durufle	Harold	Harold.Durufle@inrae.fr	BioForA
Ferro	Myriam	myriam.ferro@cea.fr	EDyP
Fortier	Emma	emma.fortier@roullier.com	Agro International Innovation
Frei-dit-Frey	Nicolas	nicolas.frei-dit-frey@utoulouse.fr	LRSV
Gallardo	Karine	karine.gallardo-guerrero@inrae.fr	Agroécologie
Galeone	Adrien	adrien.galeone2@cea.fr	LPCV
Gasser	Mélanie	melanie.gasser@cnsr.fr	IPSiM
Guillotin	Bruno	bruno.guillotin@universite-paris-saclay.fr	IPS2
Jacquot	Jean-Pierre	jacquot45@univ-lorraine.fr	IAM
Jamet	Elisabeth	elisabeth.jamet@utoulouse.fr	LRSV
Knibiehly	Jules	Jules.KNIBIEHLY@cea.fr	LPCV
Labandera-Nadeau	Anne-Marie	anne-marie.labandera-nadeau@inrae.fr	BioForA
Langella	Olivier	olivier.langella@universite-paris-saclay.fr	GQE/PAPPSO
Leriche	Pierre	pierre.leriche@inrae.fr	GQE/PAPPSO
Liu	Zhichao	zhichao.liu@univ-lorraine.fr	IAM
Marmagne	Anne	anne.marmagne@inrae.fr	IJPB
Merlino	Marielle	marielle.merlino@inrae.fr	GDEC
Pageau	Raphaël	raphael.pageau@inrae.fr	GQE/PAPPSO
Parthenay	Océane	oceane.parthenay@inrae.fr	BioForA
Pennera	Lorraine	lorraine.pennera@cea.fr	LPCV
Pichereaux	Carole	carole.pichereaux@ipbs.fr	ProteoToul
Przybyla-Toscano	Jonathan	jonathan.przybyla-toscano@cea.fr	LPCV
Quillerou Moreau	Manon	Manon.QUILLEROU MOREAU@cea.fr	LPCV
Ravanel	Stéphane	stephane.ravanel@cea.fr	LPCV
Rofidal	Valérie	valerie.rofidal@inrae.fr	IPSiM/MSPP
Seassau	Aurélié	aurelie.seassau@inrae.fr	PlantBIOS
Tauzin	Marc	marc.tauzin@inrae.fr	IPSiM/MSPP
Tymen	Chloée	chloe.tymen@ibs.fr	IBS
Vettor	Alexandre	alexandre.vettor@inrae.fr	IPSiM
Vieyetz	Maria	mvieyetz@gattefosse.com	Gattefossé

Lieu des conférences et accès en tram

Adresse: Bâtiment IMAG

150 place du Torrent - 38401 Saint Martin d'Hères



Accès depuis Grenoble en tram, arrêts Gabriel Fauré ou Université Bibliothèques

Ligne B: direction Gières Plaine des Sports

Ligne C: direction Université Condillac

Zone à privilégier pour la recherche d'un hôtel



Quelques suggestions d'hôtels:

- **Maison Barbillion:** 10 Rue Louis Barbillion, 38000 Grenoble
<https://www.maisonbarbillion.com>
- **1924:** 2 Rue Gabriel Péri, 38000 Grenoble
<https://www.1924hotel.com>
- **Hôtel d'Angleterre:** 5 Pl. Victor Hugo, 38000 Grenoble
<https://www.hotel-angleterre-grenoble.com/fr/>
- **RockyPop:** 7 Rue de Strasbourg, 38000 Grenoble
<https://www.rockypop.com/grenoble/>