28ÈME ÉDITION DES JOURNÉES DE L'ÉCOLE DOCTORALE

Sciences de la Vie, Santé, Agronomie, Environnement

UCA UNIVERSITÉ Clermont Auvergne

UCA ÉCOLE DOCTORALE DES SCIENCES DE LA VIE, SANTÉ, AGRONOMIE, ENVIRONNEMENT

Blanche-Neige ET LA POMME MÉDIATIQUE

La Rotonde - Amphi A5
26 av. Léon Blum
63000 Clermont-Ferrand

22-23 mai 2025

Vendredi 23 mai
à 15h00

TABLE RONDE

La manipulation du grand public par les médias, la science et les réseaux.

Comment être moins naïf que Blanche-Neige?

Introduit par :

- **Catherine Bertrand Ferrandis**

Fondatrice OLYLO, spécialiste en communication des risques santé, Vétérinaire
Paris

Suivi d'une table ronde avec :

- **Déborah Adoh**

Journaliste & fondadrice d'Endémik

- **Julien Scanzi**

Gastroentérologue
CHU Estaing, CH Thiers

- **Nicolas Fradet**

Doctorant en Sciences de l'Education
Laboratoire ACTé, Clermont-Ferrand

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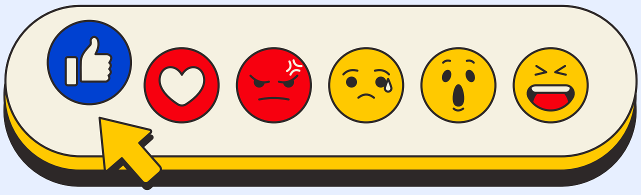
Volvic EAU MINÉRALE NATURELLE · les Crous · UCA EUROPEAN CENTRE FOR HEALTH AND HUMAN MOBILITY Université Clermont Auvergne · UCA INTERNATIONAL RESEARCH CENTRE ON SUSTAINABLE AGROECOSYSTEMS Université Clermont Auvergne · CRÉDIT AGRICOLE · OZYME Des femmes et des hommes au service de vos recherches · BIOPÔLE CLERMONT-LIMAGNE · HELIXIO BRINGS GENOMICS TO LIGHT

Livret de la 28e édition

DES JOURNÉES DE L’ÉCOLE DOCTORALE

Sciences de la Vie, Santé, Agronomie, Environnement



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OZYME
Des femmes et des hommes au service de vos recherches

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JED 2025
Sciences de la Vie, Santé, Agronomie, Environnement

L'équipe organisatrice
DES JEDS 2025

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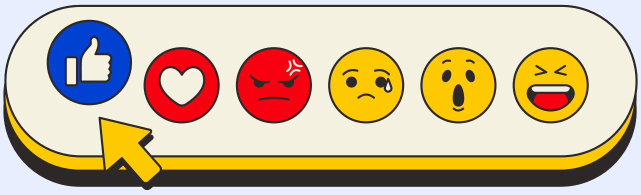

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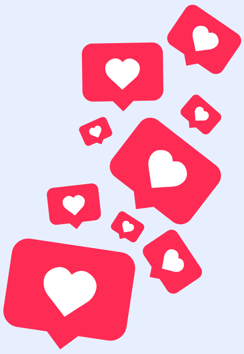

Nous tenons tout d'abord à remercier chaleureusement nos **sponsors et partenaires** pour leur soutien précieux dans l'organisation de cette nouvelle édition des Journées de l'Ecole Doctorale (JEDs) SVSAE : **Doct'Auvergne, Ozyme, Centre Jean Perrin, Biopôle Clermont-Limagne, Cystem, INRAE, Clermont Auvergne Métropôle, Fondation UCA, Crédit Agricole, CIR1, CIR3, CICS, Helixio, ED SVSAE, Volvic, Patapain, CROUS, Inserm, Miltenyi et Biose industrie**.

Nous souhaitons également adresser nos sincères remerciements à l'ensemble des **intervenant.es de l'Université Clermont Auvergne** pour leur aide et leur implication dans l'organisation de ces journées. Une pensée particulière à **Marie-Annick Martin, Karen Vergnol-Remont** et notre indispensable **Perrine Cluzel** toujours de bonne humeur et prête à nous épauler en toute circonstance.

Nous remercions sincèrement les **membres du jury** pour leur disponibilité et leur participation à l'évaluation des présentations des doctorant·es : **Devon Kavanaugh, Olivier Le Bacquer, Imen Difhallah, Christophe Tatout et Lore Metz**.

Un grand merci à l'ensemble des **intervenant·es** de la **table ronde** pour leur présence et la pertinence de leurs interventions, parfaitement en lien avec la thématique abordée : **Catherine Bertrand Ferrandis, Julien Scanzi, Déborah Adoh et Nicolas Fradet**.

Nous remercions vivement **l'ensemble des doctorant.es** qui présentent leurs travaux au cours de ces deux journées annuelles riches en échanges scientifiques.

Enfin, nous adressons toute notre gratitude à **Patrick Vernet** et **Mathilde Bonnet**, sans qui cette édition des JEDs n'aurait tout simplement pas été possible. Leur confiance, leur disponibilité, leurs conseils avisés et leur soutien indéfectible tout au long de la préparation ont été une véritable source de motivation et d'inspiration pour toute l'équipe.

JED 2025
Sciences de la Vie, Santé, Agronomie, Environnement

Programme de la 28e édition
DES JOURNÉES DE L'ÉCOLE DOCTORALE

Sciences de la Vie, Santé, Agronomie, Environnement

Jeudi
22 mai
2025

8h00-8h10 : Ouverture des Journées de l'ED SVSAE

Thème 1 : Environnement, Agronomie & Biologie Végétale - Environnement

Communications orales (8h10-9h30)

🇬🇧 **8h10 : FRIZOT Nathan** - Riding the Heatwave: When recovery and nutrition make the difference (p.20)

🇬🇧 **8h30 : GONZALEZ Alexandre** - Physiological mechanisms of drought-induced leaf cell death: the role of stress speed and intensity (p.21)

🇬🇧 **8h50 : MARTIN Elise** - Enzyme-Driven Valorisation of Lignin: Understanding the Lignolytic Mechanisms to Unlock its Potential in the Material Field (p.22)

🇬🇧 **9h10 : PAPIN Marie** - Trace metal elements and microplastics ingestion during biowaste recycling by black soldier fly larvae (p.23)

Flash Posters (9h30-9h50)

🇬🇧 **9h30 : BLACHE Nolwenn** - Scrub typhus in Nan province (Thailand): seventeen years of data to understand the impact of land cover change (p.24)

🇫🇷 **9h36 : ESCURA Marine** - Macroalgae in stream food webs: are we missing an important trophic link? (p.25)

🇫🇷 **9h42 : LALLOUE Pierre-Louis** - How does temperature influence microcystin-LR content in acclimated Microcystis aeruginosa PCC7806? (p.26)

Thème 2 : Santé publique - Maladies & Comorbidités

Communications orales (9h50-10h10)

🇫🇷 **9h50 : NJOUONKEP SIME Steve** - Prevalence and determinants of metabolic syndrome and pre-frailty comorbidity in older adults: Results from the Whitehall II study (p.27)

Flash Posters (10h10-10h15)

🇫🇷 **10h10 : COMBARET Nicolas** - Spontaneous coronary artery dissection: insights from the French registry (p.28)

les Crous **10h15-10h45 : PAUSE Café offerte par le CROUS** les Crous

Thème 3 : Biologie Santé - Génétique et biologie moléculaire

Communications orales (10h45-11h45)

🇬🇧 **10h45 : LAMBERT Louise** - Impact of pathological variants in the LRPPRC/SLIRP complex (p.29)

🇫🇷 **11h05 : SUTTER Jade** - Radiomodulating properties of hibernating bear serum on human cells (p.30)

🇬🇧 **11h25 : TESTE Camille** - Identication of Ten-Eleven Translocation's partners and function in drosophila (p.31)

Flash Posters (11h45-12h10)

🇬🇧 **11h45 : GHAMDI Zainab** - Acute Effects of Low Carbohydrate Meals on Energy Intake, Appetite, and Food Reward in Adolescents with Obesity (p.32)

🇫🇷 **11h51 : LUGOBONI Margot** - Transcriptional regulation mechanisms by m6A RNA modification in Drosophila melanogaster (p.33)

🇬🇧 **11h57 : RAUCROY Maxime** - Plant proteins and methionine restriction: a strategy for preventing obesity and type 2 diabetes (p.34)

🇬🇧 **12h03 : PRIKSHIT Prikshit** - Contribution of NMPs to the diversification of axial segments in chicken embryos (p.35)

CRÉDIT AGRICOLE

12h10-13h10 : REPAS financé par le Crédit Agricole

CRÉDIT AGRICOLE

Thème 1 : Environnement, Agronomie & Biologie Végétale - Agronomie

Communications orales (13h10-14h30)

🇬🇧 **13h10 : MICHELOTTI Tainara Cristina** - Endogenous bovine FFAR2/GPR43 ligands display distinct pharmacological properties (p.36)

🇫🇷 **13h30 : LIROT Helene** - Longitudinal analysis reveals transitions in pathogens profiles associated with mastitis in dairy cows (p.37)

🇬🇧 **13h50 : PRIEUR Vincent**- Does the molecular content of plasmatic small Extracellular Vesicles from crossbred heifers reflect variability in feed efficiency, meat quality, body composition and husbandry practices? (p.38)

Flash Posters (14h10-14h30)

🇬🇧 **14h10 : BECU Thomas** - Combining wheat and diverse prairies to promote positive ecological interactions and better regulation of C and N biogeochemical cycles in agroecosystems (p.39)

🇬🇧 **14h16 : BESSON Lisa** - Combining wheat and diverse perennial species: What is the impact on Z.tritici development and the wheat microbiome? (p.40)

🇬🇧 **14h22 : MORA Blandine** - Screening of 16 Mediterranean agro-industrial by-products rich in bioactive compounds to modulate in vitro ruminal fermentation (p.41)

Thème 3 : Biologie Santé - Reproduction

Communications orales (14h30-14h50)

🇬🇧 **14h30 : KARAM Germaine** - Functional characterization of a novel parental-effect histone protein during mammalian reproduction (p.42)

Flash Posters (14h50-15h20)

🇬🇧 **14h50 : CARCY Oriana** - What is the impact of ionizing radiation on the nuclear and epigenetic integrity of human sperm? (p.43)

🇫🇷 **14h56 : CHALEIL Florian** - Hyper-SUMOylation and ovarian insufficiency (p.44)

🇫🇷 **15h02 : KAHOUADJI Samy** - CX3CL1/Fractalkine as a biomarker for early pregnancy prediction of preterm premature rupture of membranes (p.45)

🇬🇧 **15h08 : POITRINAL Alice** - Assessment of the impact of breast cancer on human folliculogenesis (p.46)

🇬🇧 **15h14 : MOAZAMIAN Aron** - The dual nature of micronutrients on fertility: too much of a good thing? (p.47)

Thème 2 : Santé publique - Santé psycho-sociale

Flash Posters (15h20-15h30)

🇫🇷 **15h20 : DELAMARRE Louis** - Validation of visual analog scale of effort reward imbalance in workers (p.48)

🇬🇧 **15h26 : GRAMPAYRE Manon** - Improvement of women's and partners' experience in peri-and post-natal period (p.49)

:Patapain **15h30-16h00 : PAUSE Café offerte par Patapain** :Patapain

Thème 3 : Biologie Santé - Mobilité Santé

Communications orales (16h00-17h15)

🇬🇧 **16h00 : DE CLERCQ Fanny** - Development of a probiotics and plant extracts combination targeting Adherent-Invasive Escherichia coli strains associated with Crohn's disease (p.50)

🇬🇧 **16h20 : DELABRISE Coralie** - Human blood biomarkers of skeletal muscle atrophy (p.51)

🇫🇷 **16h40 : VIOLIN Maxime** - Effect of maturity status on lower-limb strength testing reliability in academy football players from an elite professional club (p.52)

Flash Posters (17h00-17h15)

🇬🇧 **17h00 : COUVERT Anaelle**- Acute Metabolic and Nutritional Responses to Isoenergetic HIIT Cycling vs. Running Sessions in Men with Overweight or Obesity (p.53)

🇫🇷 **17h06 : LANHERS Charlotte** - Analytical approaches of the questionnaires used in chronic low back pain – towards a use in personalized care (p.54)

Vendredi
23 mai
2025

Thème 1 : Environnement, Agronomie & Biologie Végétale - Biologie Végétale

Communications orales (8h00-8h20)

🇬🇧 **8h00 : PETIOT Valntine** - Dual role of Arabidopsis thaliana SRS2 helicase in meiotic recombination (p.56)

Flash Posters (8h20-9h00)

🇬🇧 **8h20 : FEIT Lea** - Study of GH1-domain proteins in chromatin organization and transcription regulation in Arabidopsis thaliana (p.57)

🇬🇧 **8h26 : FREY Caroline** - The robustness of Stb resistance genes (p.58)

🇬🇧 **8h32 : KHAN Kinza** - Postural control in Arabidopsis: a focus on actin network and auxin signalling in proprioception process (p.59)

🇬🇧 **8h38 : MAGLIARASCHI Ninon** - Unravelling the role of a regulatory hub of wheat susceptibility to Fusarium head blight in bread wheat (p.60)

🇬🇧 **8h44 : PALTRINIERI Stefania** - Nuclear and chromatin organization are reprogrammed during seed germination (p.61)

🇬🇧 **8h50 : SIRETA Gilles** - Automation of an RNA-seq analysis workflow to facilitate data processing and reproducibility (p.62)

Thème 2 : Santé publique - Technologies et outils en santé publique

Communications orales (9h00-9h20)

🇬🇧 **9h00 : FAKIH Aya** - Volatolomics to phenotype Listeria monocytogenes behavior: impact of growth and acid stress (p.63)

Flash Posters (9h20-9h50)

🇫🇷 **9h20 : PARAYRE Ines** - Environmental Health in Perinatal Care: Professional Perceptions and Territorial Dynamics – The ProSET Study (p.64)

🇫🇷 **9h26 : FANTELLI Reshad** - Aerosolization during cheeses wiping as a major factor of microbial transfer in ripening cellar (p.65)

🇫🇷 **9h32 : LECHAUVE Jean-Baptiste** - Evaluation of the impact of a smartphone application on adherence to an exercise program in people with chronic low back pain: a randomized controlled trial (p.66)

🇫🇷 **9h38 : RICHARD Amelie** - Prescription-free consultation, “the art of doing without” (p.67)

🇬🇧 **9h44 : SALANON Elfried** - Assessing the variability structure of analytical measurements using bivariate dispersion (p.68)

10h15-10h45 : PAUSE Café offerte par le CROUS

Thème 3 : Biologie Santé - Cancer

Communications orales (10h20-11h00)

🇬🇧 **10h20 : BAABDATY Elissa** - Study of the mechanisms of the initiation and evolution of early epithelial tumors. Implications for prostate carcinogenesis (p.69)

🇬🇧 **10h40 : DUBOIS Maxime** - LightSpot®-FL-1, an innovative tool for evaluating the Permeability-glycoprotein as a predictive biomarker of tumor resistance in acute leukemia models (p.70)

Flash Posters (11h00-11h30)

🇬🇧 **11h00 : BESOMBES Joevin** - The CML clone at diagnosis exhibits intra-clonal heterogeneity in telomere dynamics at the CD34+ hierarchical level (p.71)

🇬🇧 **11h06 : CHANCHOU Marion** - ^{99m}Tc-NTP 15-5, proteoglycan tracer: Phase I trial (CARSPECT) (p.72)

🇬🇧 **11h12 : CHAUSSIN Benjamin** - Development of a 3D in vitro model of triple-negative breast cancer for the evaluation of radiobiological effects (p.73)

🇫🇷 **11h18 : CROIZIER Carolyne** - Venetoclax resistance in real-life chronic lymphocytic leukemia cohort: RAVEN study (p.74)

🇬🇧 **11h24 : PINARD Celeste** - Identification of circulating protein candidates for prediction of response to neoadjuvant chemotherapy in triple negative breast cancer: preliminary results from the INSTIGO study (p.75)

Thème 3 : Biologie Santé - Microbiologie

Communications orales (11h30-12h50)

🇬🇧 **11h30 : BRON Auriane** - How plant extracts designed to prevent MASH impact in vitro human colon microbiota and hepatic steatosis (p.76)

🇬🇧 **11h50 : DAMBRINE Flavie** - Role of the bacterial deacetylase cobB in the virulence of adherent and invasive Escherichia coli (AIEC) bacteria associated with Crohn's disease (p.77)

🇬🇧 **12h10 : CARRIERE Eugenie** - Illuminating the live-cell dynamics of the early neutrophil-Encephalitozoon cuniculi interplay as a “Trojan horse” strategy (p.78)

🇬🇧 **12h30 : KAUR Manjyot** - Unravelling the aggregation mechanism in Lactobacillus crispatus and its role in probiotic functionality (p.79)

Flash Posters (12h50-13h10)

🇬🇧 **12h50 : CARTIER Alizee** - Assessment of corneal sensitivity in a mouse model of ocular rosacea induced by ultraviolet-B exposure (p.80)

🇬🇧 **12h56 : DESSEUX Coline** - Cytotoxic necrotizing factor-producing Escherichia coli enhance tumorigenesis in a pre-clinical mouse model of colorectal cancer with intestinal epithelial cell-specific autophagy deficiency (p.81)

🇫🇷 **13h02 : VERCRUYSSE Leslie** - The impact of the microsporidia Encephalitozoon intestinalis on colorectal carcinogenesis (p.82)

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13h10-14h30 : REPAS financé par Clermont Auvergne Métropole

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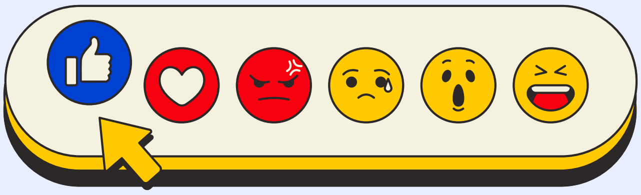

Remise des prix

14H30 - 15H00

Meilleure communication orale :
prix du jury (300€)
CICS Centre Imagerie Cellulaire Santé

Meilleure communication orale :
prix du public (300€)
ED SVSAE

Meilleur poster :
prix du jury (300€)
HELIXIO BRINGS GENOMICS TO LIGHT

Meilleur poster :
prix du public (300€)
FONDATION UNIVERSITÉ Clermont Auvergne

Meilleure communication orale :
Thème **“Biologie Santé”** (250€)
INTERNATIONAL RESEARCH CENTRE ON SUSTAINABLE AGROECOSYSTEMS
Université Clermont Auvergne

Meilleure communication orale :
Thème **“Environnement, Agronomie et Biologie Végétale”** (250€)
INTERNATIONAL RESEARCH CENTRE ON SUSTAINABLE AGROECOSYSTEMS
Université Clermont Auvergne

Meilleure communication orale :
Thème **“Santé Publique”** (250€)
CRÉDIT AGRICOLE

Meilleure communication orale :
Sous-thème **“Mobilité Santé”** (250€)
EUROPEAN CENTRE FOR HEALTH AND HUMAN MOBILITY
Université Clermont Auvergne

Meilleure communication orale :
Sous-thème **“Cancer”** (250€)
Centre Jean PERRIN
unicancer Clermont Auvergne Métropole

JED 2025
Sciences de la Vie, Santé, Agronomie, Environnement

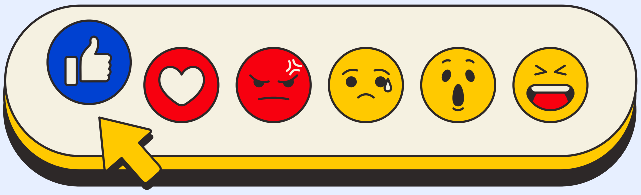

Table ronde grand public

15H00-17H00

Face à l'explosion des informations en santé, entre vérités, approximations et “fake news”, il devient de plus en plus difficile de s'y retrouver. L'**infodémie**, cette surabondance de contenus souvent contradictoires, nourrit la **défiance envers les scientifiques** et bouleverse notre rapport à la santé. Cette rencontre sera l'occasion d'explorer les racines de cette désinformation, d'en mesurer l'**impact émotionnel** et de réfléchir ensemble aux moyens d'y répondre : **mieux vérifier l'information, mieux comprendre les enjeux de santé, mais aussi, et surtout, repenser la manière de communiquer, avec plus d'humanité.**

Introduit par :

en vidéo.

Catherine Bertrand-Ferrandis
Fondatrice OLYLO,
Spécialiste en communication des risques santé, Vétérinaire
Paris

OLYLO
bridging for health

Suivi d'un débat avec :

Julien Scanzi
Gastroentérologue
CHU Estaing, CH Thiers

CHU CLERMONT-FERRAND CENTRE HOSPITALIER UNIVERSITAIRE
Centre Hospitalier de THIERS

Déborah Adoh
Journaliste et fondatrice d'Endémik

Endémik Information

Nicolas Fradet
Doctorant en Sciences de l'éducation
Laboratoire ACTé

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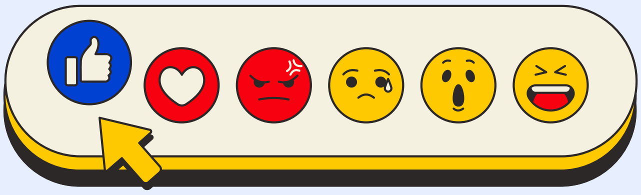

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Fondation Université Clermont Auvergne
La fondation favorise la visibilité de l'Université Clermont Auvergne (UCA) à l'échelle nationale, en soutenant les étudiants et les entreprises du secteur socio-économique.
Cette année, la Fondation UCA décerne le prix du public du meilleur poster.

Clermont Auvergne Métropole
La métropole clermontoise, capitale universitaire, culturelle et économique de l'Auvergne, accompagne financièrement notre évènement.

CAP 20-25 I-Site Clermont
Le Centre International de Recherche 1 et 3 (CIR1 et CIR3) a pour objectif d'explorer les facteurs d'intervention sur l'appareil locomoteur et proposer des stratégies d'optimisation de la santé humaine via la mobilité.

Le CIR3 sponsorise le prix pour la meilleure communication pour le sous-thème “Mobilité Santé”.

Le CIR1 sponsorise deux prix cette année : un pour la meilleure communication orale dans le thème “Biologie Santé” et un autre dans le thème “Environnement, Agronomie et Biologie Végétale”

Biopôle Clermont-Limagne
Le Biopôle Clermont-Limagne offre des services spécialisés pour accueillir et accompagner les entreprises opérant dans le domaine des sciences de la vie. Cette année encore, la technopole auvergnate nous fait le privilège de soutenir financièrement ces journées.

INRAe
L'INRAe est un institut de renommée mondiale dédié à la recherche scientifique de pointe dans les domaines de l'agriculture, de l'alimentation et de l'environnement, contribuant ainsi de manière significative au progrès et à la durabilité de ces secteurs clés.
L'institut a décidé de soutenir financièrement ces journées une année de plus.

Centre Jean Perrin
Le Centre Jean Perrin fait partie des 18 Centres de Lutte Contre le Cancer (CLCC) en France qui sont regroupés au sein d'UNICANCER, le seul réseau hospitalier français entièrement dévoué à la lutte contre le cancer.
Comme chaque année, le centre nous a accordé un généreux soutien financier et participe notamment au prix de la meilleur communication orale pour le sous-thème “Cancer”.

BIOSE

BIOSE est une entreprise pharmaceutique spécialisée dans le développement industriel et technologique, ainsi que dans la production clinique et commerciale de médicaments microbiotiques.
L’entreprise a participé au soutien des JEDs 2025 en fournissant des goodies.

CICS

Le Centre d’Imagerie Cellulaire & Santé est composé de plusieurs plateaux techniques équipés de technologies de pointe permettant l'aboutissement de projets de la communauté scientifique et industrielle.
Le CICS nous accompagne en récompensant financièrement le prix du jury de la meilleur communication orale.

CYSTEM

La plateforme CYSTEM (Cytometry, Sort & Transmission Electronic Microscopy) est rattachée au LMGE de l'UCA. C'est un partenaire privilégié dans la réalisation de nombreux projets scientifiques.
La plateforme participe cette année encore en soutenant financièrement l'organisation des JEDs 2025.

Volvic

Volvic est une entreprise emblématique qui propose une eau minérale naturelle d'une pureté exceptionnelle, issue de sources volcaniques préservées, offrant ainsi une expérience rafraîchissante et saine pour les consommateurs du monde entier.
Elle nous apporte un soutien matériel en fournissant des bouteilles d'eau pour tous les participants de l'évènement.

CROUS Clermont Auvergne

Le Crous Clermont Auvergne, acteur dans la vie quotidienne des étudiant.e.s pendant leurs études supérieures, a pour mission d'améliorer les conditions de vie et d'études à travers l'attribution de bourses, logements ou encore d'aides sociales.
La générosité de cet organisme s'étend aux JEDs 2025 à travers les financements de pause-café.

Helixio

Helixio est une société spécialisée dans les solutions en génomique, transcriptomique et bio-informatique, offrant des services avancés dans divers domaines, tels que la santé, la cosmétique, le vétérinaire, l’agroalimentaire et l’environnement. Grâce à son expertise en technologie à haut débit (NGS, séquençage nouvelle génération) et en analyses bioinformatiques, Helixio accompagne les chercheurs et laboratoires dans leurs projets scientifiques.
Pour les JEDs 2025, Helixio a financé le prix du jury pour le meilleur poster.

Doct’Auvergne

Créée en 2013, Doct'Auvergne est une association fondée par et pour les doctorant.es et jeunes chercheur.es d'Auvergne. À travers ses actions et évènements, l'association vise à créer et renforcer les liens sociaux entre doctorant.es et jeunes docteur.es, à promouvoir leurs recherches auprès de la société par la médiation scientifique, et à soutenir leur insertion professionnelle après-thèse.
Cette année, l’association s’est porté bénévole en animant un stand lors des JEDs 2025. Nota Bene : les premiers qui donneront le mot de passe “Doc’Team” aux membres qui tiennent le stand gagneront un petit cadeau...

Crédit Agricole Centre France

Fort de ses 2 400 collaborateurs et ses 230 agences, le Crédit Agricole Centre France est une banque responsable, au service de ses 900 000 clients. Présent dans l'Allier, le Cantal, la Corrèze, la Creuse et le Puy-de-Dôme, il s'engage au quotidien dans les initiatives en faveur du développement de son territoire, dont il est un acteur majeur. Il attache une grande importance à l'attractivité et la croissance économique de celui-ci. C'est pourquoi, il s'investit quotidiennement dans les initiatives et démarches innovantes. Le Crédit Agricole Centre France accompagne ses clients particuliers, professionnels, agriculteurs, entreprises, collectivités publiques… dans leurs projets ; il est également impliqué aux côtés de start-up grâce à son accélérateur, le Village by CACF.

Le Crédit Agricole Centre France a apporté une fois de plus un joli soutien financier pour l'organisation générale des JEDs ainsi que la remise d’un prix pour la meilleure communication orale du sous-thème “Santé publique”.

Ozyme

Spécialiste depuis 1984 dans la fourniture de produits pour la recherche, Ozyme sélectionne des réactifs et équipements issus des plus grands noms de la biologie cellulaire, moléculaire et de l’immunologie. Ce qui guide la 40aine de collaborateurs chez OZYME, c’est d’apporter des solutions innovantes (intégrant réactifs & équipements) pour répondre aux besoins et défis quotidiens des laboratoires de recherche en biologie. Son équipe accompagne les chercheurs sur le plan technique et commercial en mettant un point d'honneur à offrir un service réactif et adapté. L’engagement d’OZYME depuis 40 ans est d’être aux côtés des scientifiques pour faire avancer leur recherche.

Pour les JEDs 2025, Ozyme a apporté un soutien financier et sera présent sur un stand. N’hésitez pas à aller échanger avec eux !

Milteyi

Depuis plus de 30 ans, Miltenyi Biotec joue un rôle important dans la conception, le développement, la fabrication et l’intégration de produits qui favorisent l’avancement de la recherche biomédicale et permettent la thérapie cellulaire et génique. L’entreprise s’engage à faire progresser la compréhension scientifique et la médecine en proposant des solutions pour pour changer la façon de traiter certaines maladies communes.

Pour les JEDs 2025, Miltenyi Biotec a offert des goodies.

Patapain

Fondée en 1986 à Bourges par François Prély, Patàpain est une chaîne française de restauration rapide. L'enseigne propose une offre variée de pains, viennoiseries, sandwichs, salades et plats chauds, préparés sur place avec des produits frais. Présente principalement dans le centre et l'ouest de la France, elle compte plus de 50 établissements.

Lors des JEDs 2025, Patàpain a soutenu l'événement en fournissant des pauses-café, offrant ainsi aux participants des moments de convivialité bien mérités.

Inserm

Fondé en 1964, l’Inserm (Institut national de la santé et de la recherche médicale) est un établissement public à caractère scientifique et technologique, placé sous la tutelle des ministères de la Santé et de la Recherche. Entièrement dédié à la recherche biomédicale et à la santé humaine, il intervient du laboratoire jusqu’au chevet du patient, en lien avec les plus grandes institutions de recherche mondiales.

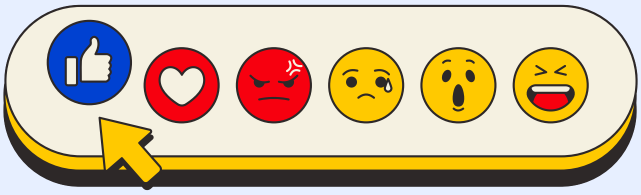
L’Inserm a soutenu les JEDs 2025 en fournissant des goodies.

ED SVSAE

L’Ecole Doctorale Sciences de la Vie, Santé, Agronomie, Environnement (ED SVSAE) de l’Université Clermont Auvergne regroupe des acteurs majeurs de la recherche en Auvergne, avec des partenaires comme le CNRS, l’INSERM, l’INRAe, le CHU, le Centre Jean Perrin et plusieurs écoles d’ingénieurs. Elle fédère plus de 550 chercheurs et enseignants-chercheurs et forme chaque année 50 à 60 nouveaux docteurs, dans des domaines aussi variés que la biologie, la santé, l’agronomie et l’environnement. L’ED SVSAE offre une formation de haute qualité, soutenue par plus de 20 laboratoires d’accueil bénéficiant d'un environnement technologique de pointe.

Grâce à son soutien à toutes les étapes de l’organisation, l’ED SVSAE participe à la bonne réalisation de ces journées permettant le rassemblement de la communauté scientifique clermontoise autour de ses jeunes chercheurs et chercheuses.

Pour les JEDs 2025, l'ED sponsorise le prix du public pour la meilleure communication orale.



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DES JEDS 2025

Olivier Le Bacquer
Chargé de recherche -
INRAe - UNH
Equipe : ASMS

Imen Dhifallah
Maître de conférence - MEDIS
Equipe : Thème GALINN

Lore Metz
Maître de conférence - AME2P
Equipe : Programme A

Christophe TATOUT
Professeur Universitaire - iGReD
Equipe : CODED

Devon Kavanaugh
ATER - M2iSH
Equipe : Axe 1

Jeudi
22 mai
2025

Résumés des communications orales et flash posters

DES JOURNÉES DE L'ÉCOLE DOCTORALE

Sciences de la Vie, Santé, Agronomie, Environnement

Family name: Frizot
First name: Nathan
Year of PhD: 3rd
Research team and Laboratory: LMGE - Equipe Interactions Réseaux Trophiques Aquatiques (IRTA)
PhD supervisors: Alexandre Bec and Apostolos-Manuel Koussoroplis
Email: nathan.frizot@uca.fr
Language of presentation: English

Riding the Heatwave: When recovery and nutrition make the difference

Nathan Frizot[1], Alexandre Bec[1], Apostolos-Manuel Koussoroplis[1]
[1]Université Clermont Auvergne, CNRS, LMGE, F-63000 Clermont–Ferrand, France.

Heatwaves are becoming more frequent and intense, threatening aquatic organisms' survival. Thermal tolerance—the ability to endure extreme temperatures—depends on heat-stress duration, intensity, prior exposure, and nutrition. During heat-stress, organisms accumulate damage until reaching a lethal threshold. However, temperature fluctuations during heatwaves allow recovery periods, during which organisms may repair damage and enhance tolerance (i.e. hardening). Despite extensive research on heat-stress, recovery periods remain understudied.

We studied heat injury repair in *Daphnia magna*, a planktonic crustacean feeding on microbial communities. We investigated how the biochemical composition (high vs. low sterols and PUFAs) of their resources upon modulates heat injury repair rate at various recovery temperatures (18°, 20°, 24°, 26°, 28°, 30°C). We find that repair rate is a unimodal function to recovery temperature. Yet, the nutritional quality had much stronger effects than temperature. Repair rate in *Daphnia* fed with sterols- and PUFAs-poor food was strongly reduced and *Daphnia* were unable to recover even after 12 hours at optimal recovery temperature.

Our findings highlight the importance nutritional context in predicting the long-term impacts of heatwaves on aquatic organisms.

Keywords: Thermal tolerance, recovery period, repair, food quality, heatwave

Family name: Gonzalez
First name: Alexandre
Year of PhD: 3rd
Research team and Laboratory: UMR 547 PIAF
PhD supervisor: Stéphane Herbette
Email: alexandre.gonzalez@doctorant.uca.fr
Language of presentation: English

Physiological mechanisms of drought-induced leaf cell death: the role of stress speed and intensity

Alexandre J. H. Gonzalez[1], José M. Torres-Ruiz[2], Julien Cartailler[1], Hervé Cochard[1], Christelle Blavignac[3], and Stéphane Herbette[1]
[1]Université Clermont Auvergne, INRAE, PIAF, 63000 Clermont-Ferrand, France
[2]Instituto de Recursos Naturales y Agrobiología (IRNAS), Consejo Superior de Investigaciones Científicas (CSIC), Seville, Spain
[3]Centre Imagerie Cellulaire Sante – UCA PARTNER, 63000 Clermont-Ferrand, France

Predictions from global climate models indicate a forthcoming escalation in the frequency and severity of drought events. These events have already demonstrated consequences on tree survival due to impacts on xylem function and key living tissues. Understanding how future climate conditions impact xylem integrity and, consequently, plant cell survival is a critical research challenge to improve. Despite numerous studies on the mechanisms for drought-induced tree mortality, those considering the impact of drought dynamics on these mechanisms are scarce. Thus, one of the main objectives of this research challenge is to understand the mechanisms behind tree mortality and the impact of drought dynamics on theses mechanisms.

To better characterize and understand the processes that occur during drought and lead to leaf cell death in trees, we applied three drought conditions with contrasting dynamics to *Laurus nobilis* plants in a greenhouse. We monitored various key physiological traits indicative of mild to severe stress conditions up to cell death.

Our results show how differences in drought speed and intensity have a substantial impact on tree's response encouraging a reconsideration of existing approaches to studying tree mortality under drought conditions.

Keywords: tree, leaf, drought, xylem, cell mortality

Family name: Martin
First name: Elise
Year of PhD: 3rd
Research team and Laboratory: Institut Pascal
PhD supervisor: Philippe Michaud
Email: elise.martin@uca.fr
Language of presentation: English

Enzyme-Driven Valorisation of Lignin: Understanding the Lignolytic Mechanisms to Unlock its Potential in the Material Field

Elise Martin[1], Pascal Dubessay[1], Eric Record[2], Fabrice Audonnet[1], and Philippe Michaud[1]

[1]Université Clermont Auvergne, Clermont Auvergne INP, CNRS, Institut Pascal, F-63000 Clermont-Ferrand, France; fabrice.audonnet@uca.fr (F.A.); pascal.dubessay@uca.fr (P.D.); elise.martin@uca.fr (E.M.) philippe.michaud@uca.fr (P.M)

[2]UMR1163, Biodiversité et Biotechnologie Fongiques, Aix-Marseille Université, INRAE, 13288 Marseille, France; eric.record@inrae.fr (E.R.)

Lignins are plant biopolymers composed of three monolignols: p-coumaryl, coniferyl and sinapyl alcohols. In biorefinery and paper industries, lignin is a by-product typically burned for energy production. However, it holds significant potential for higher-value applications, as a renewable biopolymer for applications in material field for example. This particular application requires chemical modifications of lignin so that it acquires specific functionalities. The resistance of lignins to most chemical treatments encourages investigations for their modification and bioconversion using enzymes such as fungal laccases, which oxidize and break down them while reducing oxygen to water.

A fungal laccase from *Pycnoporus cinnabarinus* (EC 1.10.3.2) was used to modify lignosulfonates, enhancing the mechanical properties of lignin-based composites reinforced with wood fibers. The enzymatic treatment significantly improved the flexural modulus and fracture strength, achieving values of 3.51 GPa and 17.5 MPa, respectively. But the accurate mechanism of laccase action on lignin remains unclear. To investigate this, an innovative electrochemical method was developed to monitor and better understand these interactions. This work highlights the benefits of enzymatic modification in lignin-based composites and provides new insights into the mechanism of laccase action in lignin modification.

Keywords: Lignin, enzymatic modification, laccases, valorisation, composites

Family name: Papin
First name: Marie
Year of PhD: 3rd
Research team and Laboratory: QuaPA (qualité des Produits Animaux), équipe MASS-INRAE-Theix
PhD supervisors: Erwan Engel, Christelle Planche and Patrick Borel
Email: marie.papin@inrae.fr
Language of presentation: English

Trace metal elements and microplastics ingestion during biowaste recycling by black soldier fly larvae

Marie Papin[1,2], Maxime Pattier[3], Solenn Reguer[4], Christophe Sandt[4], Camille Rivard[4], Patrick Borel[2], Mélanie Davranche[3], Erwan Engel[1], Christelle Planche[1]

[1]INRAE, UR 370 Animal Products Quality Unit, MASS Group, 63122 Saint-Genès-Champanelle, France
[2]Center for CardioVascular and Nutrition Research, C2VN, Aix Marseille Univ, INSERM, INRAE, Marseille, France
[3]Géosciences, CNRS Université Rennes 1, UMR 6118 35000 Rennes, France
[4]Synchrotron SOLEIL, L'Orme des Merisiers, 91190 Saint-Aubin, France

Insects such as Black Soldier Fly larvae (BSFL), *Hermetia Illucens*, are increasingly used in the feed industry for their nutritional and environmental benefits. BSFL can indeed efficiently convert biowaste into high-quality proteins. However, biowaste can contain several chemical hazards and their fate in BSFL remains largely unexplored. Preliminary results have shown that trace metal elements (TMEs) and microplastics are of the utmost importance for the evaluation of the chemical safety of BSFL. In this study, BSFL were reared on Gainesville diet spiked with polyethylene (PE) or with three different concentrations of cadmium and lead. The final concentrations of PE and both metals in BSFL were determined using respectively Py-GC/MS and ICP-MS and used to draw bioaccumulation models. The PE presence in the digestive tract of BSFL was confirmed using a Raman technique and lead was localized in BSFL using Synchrotron X-ray Diffraction. No effect of the different conditions was noticed concerning the main rearing parameters such as larval weight, survival or feed conversion ratio. These results give a better understanding of the bioaccumulation phenomenon of TMEs and microplastics in BSFL, with the final purpose of studying TMEs vectorization by microplastics.

Keywords: insect, chemical contaminants, lead, cadmium, polyethylene

Family name: BLACHE
First name: Nolwenn
Year of PhD: 3rd
Research team and Laboratory: Vetagro Sup, UMR EPIA et Territoires
PhD supervisors: Karine Chalvet-Monfray and Christophe Dépres
Email: nolwenn.blache@vetagro-sup.fr
Language of presentation: English

Scrub typhus in Nan province (Thailand): seventeen years of data to understand the impact of land cover change

Nolwenn Blache[1,2], Karine Chalvet-Monfray[2], Rawadee Kumlert[3], Soawapak Hinjoy[4], Serge Morand[5]

[1]Université Clermont Auvergne, UMR Territoires, VetAgro Sup, Lempdes, France
[2]Université de Lyon, UMR EPIA, INRAE, VetAgro Sup, Marcy l'Etoile, France
[3]Division of Vector-Borne Diseases, Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand
[4]Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand.
[5]IRL HealthDEEP CNRS – Kasetsart University – Mahidol University, Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand, Department of Social and Environmental Medicine, Mahidol University, Bangkok, Thailand

Scrub typhus, caused by *Orientia tsutsugamushi* and transmitted by chigger mites (*Leptotrombidium*), is a major health problem in northern Thailand, particularly in Nan province. This study investigated the impact of land cover changes on scrub typhus transmission in Nan Province between 2003 and 2019. Using the open land cover data of the European Spatial Agency Climate Change Initiative (ESA CCI), we quantified land cover composition and changes and integrated public health data on scrub typhus cases, as well as information on elevation, population, and slope. Generalized Additive Models were applied to assess the effects of land cover changes on annual scrub typhus cases.

Cases increased with shrubland and mosaic land, displayed an inverted U-shaped relationship with broadleaf forest, and decreased with needleleaf forest. Key land cover change factors included shrubland transitions, stable rainfed cropland, cropland to urban shifts. Reforestation (from shrubland to broadleaf forest) showed an inverted U-shaped relationship with cases, while loss of shrubland to grassland and loss of cropland to urban decreased the number of scrub typhus cases.

This study highlights the importance of land cover changes in understanding disease transmission and suggests that landscapes disturbance may create optimal conditions for *O. tsutsugamushi* transmission.

Keywords: Scrub typhus, vector-borne disease, land cover change, forest dynamic, Thailand

Family name: Escura
First name: Marine
Year of PhD: 3rd
Research team and Laboratory: LMGE, Equipe IRTA
PhD supervisors: Christian Desvilettes and Apostolos-Manuel Koussoroplis
Email: marine.escura@uca.fr
Language of presentation: French

Macroalgae in stream food webs: are we missing an important trophic link?

Marine Escura[1], Apostolos-Manuel Koussoroplis[1], Christian Desvilettes[1]

[1]Université Clermont Auvergne, CNRS, Laboratoire Microorganismes : Génome et Environnement, UMR 6023, 63000 Clermont-Ferrand, France

In headwater streams, the macroinvertebrate community plays a key role in the flow of matter and energy, mainly relying on allochthonous matter. Despite its relative scarcity, autochthonous matter has a high functional importance for the macroinvertebrates, as it constitutes a high-quality resource for primary consumers. Among the autochthonous matter sources for stream consumers, the trophic role of periphytic biofilms has been largely studied over the last decades while macroalgae (Rhodophyta, Ochrophyta) have been completely overlooked. Here, we investigate the trophic role of macroalgae compared to the most studied resources in headwater streams. We fed two ubiquitous macroinvertebrates species, *Gammarus pulex* (Crustacea) and *Halesus digitatus* (Trichoptera), with four different resource treatments, combining well-studied allochthonous and autochthonous resources, mixed or not with two previously unstudied macroalgae present in headwater streams. Our results show that macroalgae significantly impact primary consumers fitness, highlighting for the first time the trophic role of macroalgae as a high-quality resource for headwater stream macroinvertebrates.

Keywords: Headwater stream, Macroinvertebrates, Macroalgae, Food webs

Family name: Lalloué
First name: Pierre-Louis
Year of PhD: 3rd
Research team and Laboratory: LMGE, équipe Interactions dans les réseaux trophiques aquatiques (IRTA)
PhD supervisors: Delphine Latour and Clarisse Mallet
Email: pierre.louis.lalloue@gmail.com
Language of presentation: French

How does temperature influence microcystin-LR content in acclimated *Microcystis aeruginosa* PCC7806?

Pierre-Louis Lalloué[1], Fanny Perrière[1], Célia Kerbrat[1], Anne-Hélène Lejeune[1], Alexandre Bec[1], Apostolos-Manuel Koussoroplis[1], Clarisse Mallet[1], Delphine Latour[1]
[1]Laboratoire microorganismes : génome et environnement, CNRS, UCA, Aubière, France

In a warming world, cyanobacteria are expected to grow faster, increasing the frequency and severity of blooms. Among the threats they pose, cyanotoxins—particularly microcystins—are a major concern due to their toxicity and widespread occurrence. While numerous studies have explored the influence of temperature on microcystin production, findings remain inconsistent, with reports of both increases and decreases at higher temperatures. We hypothesize theses discrepancies might stem from methodological differences between studies. To clarify this, we investigated *Microcystis aeruginosa* PCC7806 cultures fully acclimated to temperatures ranging from 17°C to 35°C. Growth rates were estimated from cell density measurements, and intracellular microcystin-LR was quantified using HPLC, alongside optical microscope cell volume assessments. Our results highlight that temperature effects vary depending on how microcystins are expressed. When normalized per cell, microcystin content increases as temperature decreases, consistent with recent findings. However, when expressed per biovolume unit, the relationship is non-linear, with an optimum at 26°C. These findings contribute to resolving discrepancies in the literature and emphasize the importance of considering cell volume when assessing microcystin production under changing environmental conditions. Moreover, these results provide new insights into the effects of future temperature increases on cyanobacterial toxicity.

Keywords: Cyanobacteria, microcystin, temperature, thermal performance curves, cell volume

Family name: Njouonkep Sime
First name: Steve Kevin
Year of PhD: 3rd
Research team and Laboratory: Unité de Nutrition Humaine (UNH)
PhD supervisor: Blandine COMTE
Email: steve-kevin.njouonkep-sime@inrae.fr
Language of presentation: French

Prevalence and determinants of metabolic syndrome and pre-frailty comorbidity in older adults: Results from the Whitehall II study

Steve Kevin Njouonkep Sime[1], Estelle Pujos-Guillot[1], Blandine Comte[1], Léopold K. Fezeu[2]

[1]University Clermont Auvergne, INRAE, UNH, Platform of Metabolism Exploration, MetaboHUB Clermont, F63122 Saint-Genès Champanelle, France.
[2]Sorbonne Paris Cité Epidemiology and Statistics Research Center (CRESS), Nutritional Epidemiology Research Team (EREN), Inserm U1153, Inrae U1125, Cnam, University of Paris 13, Bobigny, France.

Background: Metabolic Syndrome (MetS) and frailty are independently associated with adverse health outcomes, with frailty being a stronger predictor of mortality. MetS has been implicated in frailty onset, making frailty prevention in older adults with MetS crucial. Pre-frailty represents an earlier, more reversible stage in the frailty continuum. Understanding the prevalence and determinants of MetS-pre-frailty co-occurrence is essential for targeted interventions.

Methods: This cross-sectional study analysed data from the 2015-2016 wave of the Whitehall II cohort, including 3,398 participants aged 62–82 years. MetS was defined using the harmonized criteria, while pre-frailty was assessed via the Fried phenotype. Multivariable multinomial logistic regressions identified determinants of MetS-pre-frailty co-occurrence.

Results: MetS-pre-frailty co-occurrence was observed in 23.2% of participants. Significant determinants included age (OR: 1.11, 95% CI: 1.08–1.13), male gender (OR: 1.55, 1.20–1.99), being single (OR: 1.76, 1.27–2.41), low fruit and vegetable intake (OR: 1.51, 1.16–1.95), high sedentary behaviour (OR: 1.86, 1.47–2.36), low SF-36 physical component score (OR: 2.80, 2.13–3.66), and self-reported depression (OR: 4.05, 2.16–7.39).

Conclusion: The high prevalence of MetS-pre-frailty co-occurrence highlights the need for early identification and prevention strategies. Its distinct set of determinants suggests it may represent a specific pathological state requiring further longitudinal research.

Keywords: Metabolic syndrome, pre-frailty, co-occurrence, geriatric syndrome, Healty ageing

Family name: Combaret
First name: Nicolas
Year of PhD: 3rd
Research team and Laboratory: UMR 6602 - UCA/CNRS
PhD supervisor: Pascal Motreff
Email: nicolas.combaret@doctorant.uca.fr
Language of presentation: French

Spontaneous coronary artery dissection: insights from the French registry

Nicolas Combaret[1,2], Pascal Motreff[1,2]

[1]Service de cardiologie du CHU Gabriel Montpied, Clermont-Ferrand

[2]Institut Pascal, UMR 6602 ; Thérapies guidées par l'Image (TGI) ; Cardio-Vascular Interventional Therapy and Imaging (CaVITI).

Context: Data on spontaneous coronary artery dissection are scarce, particularly in European countries.

Methods: Data from a national French registry of SCAD cases, were analysed prospectively and retrospectively. Clinical and angiographic data and management strategy were collected. Major adverse cardiovascular events (MACE) were analysed after one-year follow-up. Subjects were screened for fibromuscular dysplasia (FMD) and blood was collected for DNA extraction.

Results: 373 SCAD cases were confirmed by the core lab. Mean age was 51.5 years. Patients were mostly women (90.6%) and 54.7% of cases had less than two cardiovascular risk factors. At 1 year, 295 patients (79.1%) were treated conservatively and the MACE rate was 12.3%, and no case of mortality. Recurrence rate of SCAD was 3.3%. FMD was found at ≥1 arterial site in 45.0% of cases. We also confirmed the genetic association between the *PHACTR1* locus and SCAD (odds ratio=1.66, $P=7.08\times10^{-8}$).

Conclusion: Here we describe the largest European SCAD cohort where FMD was found in 45% of cases and the genetic association with *PHACTR1* was confirmed. This nationwide cohort is a valuable resource for future clinical and genetic investigation to understand SCAD aetiology.

Keywords: Spontaneous coronary artery dissection - fibromuscular dysplasia – acute coronary syndrome – genetic loci

Family name: Lambert
First name: Louise
Year of PhD: 3rd
Research team and Laboratory: LPCA - équipe santé - radiobiologie
PhD supervisors: Géraldine Farge and Maria Falkenberg
Email: louise.lambert@doctorant.uca.fr
Language of presentation: English

Impact of pathological variants in the LRPPRC/SLIRP complex

Louise Lambert[1], Urska Rovnik[2], Mãdãlina Sãcultanu[2], Adèle Porcan[1], Bertil Macao[2], Xuefeng Zhu[2], Siet Van Den Wildenberg[1,3], Amandine Moretton[1], Maria Falkenberg[2], Géraldine Farge[1]

[1]Université Clermont Auvergne, CNRS, Laboratoire de Physique de Clermont Auvergne, F-63000 Clermont-Ferrand, France

[2]Department of Medical Biochemistry and Cell Biology, University of Gothenburg, P.O. Box 440, SE-405 30 Gothenburg, Sweden

[3]Université Clermont Auvergne, CNRS, IRD, Université Jean Monnet Saint Etienne, LMV, F-63000 Clermont-Ferrand, France

Mitochondria are crucial cell organelles containing their own circular genome, the mitochondrial DNA, which encodes key subunits of the oxidative phosphorylation system. After transcription, it is important for mitochondrial messengers RNAs to be correctly processed in order to ensure their stability until translation. Several proteins are involved in mt-mRNAs processing, and we are particularly interested in the protein complex composed of the Leucin Rich Pentatricopeptide Repeat (LRPPRC) and the Stem-loop-interacting RNA-binding protein (SLIRP). Deletions or pathological variants of these two proteins cause serious disease; neurodevelopmental problems, cardiomyopathy, or congenital malformations. This complex is proposed to stabilize mt-RNAs, through its involvement in the mRNA polyadenylation process and the channeling of mt-RNAs to the mitoribosomes. However, the precise mechanism involved remains unclear and our goal is to understand these interactions at the single-molecule level.

First, we used Electrophoretic Mobility Shift Assays to study the interactions between the LRPPRC/SLIRP complex or its pathological variants with various mt-RNAs. In parallel, we investigate using Acoustic Force Spectroscopy and Total Internal Reflection Fluorescence microscopy, two single-molecule biophysics approaches, the effect of the complex on mRNA compaction. Finally, Cryogenic Electron Microscopy will give us insight into the molecular mechanisms of LRPPRC/SLIRP binding to mt-mRNAs.

Keywords: mitochondria, mtRNA, single-molecule, LRPPRC, SLIRP

Family name: Sutter
First name: Jade
Year of PhD: 3rd
Research team and Laboratory: LPCA
PhD supervisor: Patrick Vernet
Email: jade.sutter@doctorant.uca.fr
Language of presentation: French

Radiomodulating properties of hibernating bear serum on human cells

Jade Sutter[1], Alexandre Geffroy[2], Shabnam Huseynova[2], Mathilde Lefebvre[1], Guillaume Rivrais[1], Adèle Porcan[1], Isabelle Garreau-Balandier[1], Fabrice Bertile[2], Patrick Vernet[1]
[1] Université Clermont Auvergne, CNRS, LPCA, F-63000 Clermont–Ferrand, France
[2] Université de Strasbourg, CNRS, IPHC UMR7178, Strasbourg, France

Hibernation, a state of metabolic slowdown, might provide protection against cosmic radiations. We have previously shown that serum from hibernating brown bears significantly effects human muscle cells *in vitro*, notably through protein catabolism inhibition. Here, we hypothesized that hibernating bear serum may also modulate cellular responses to ionizing radiations. To test this, we used tumor (PC3) and healthy (HFF) human cell lines.

An initial large-scale approach showed that incubating human cells with bear serum led to profound proteome remodeling. The functional impact of these modifications was then assessed following exposure to X-rays. Surprisingly our results (cell survival, clonogenic capacity,..) revealed a radiosensitizing effect of hibernating bear serum. To better understand the metabolic mechanisms, we analyzed cell cycle changes, DNA damage signaling pathways, and mitochondrial alterations. We observed modifications in cell cycle phases distribution after incubation with bear serum combined with irradiation, as well as changes in mitochondrial homeostasis, which may partially explain the sensitivity towards irradiation.

In conclusion, studying the impact of bear serum on human cell lines allowed us to identify radiosensitizing mechanisms that could pave the way for advancements in radiotherapy. Focusing on specific serum compounds responsible for these effects should be the next steps.

Keywords: Biomimetism, Radiosensitization, Hibernation, Brown Bear

Family name: Teste
First name: Camille
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisors: Lucas Waltzer and Laurence Vandel
Email: camille.teste@uca.fr
Language of presentation: English

Identification of Ten-Eleven Translocation's partners and function in drosophila

Camille Teste[1], Yoan Renaud[1], Nadège Anglaret[1], Laurence Vandel[1] and Lucas Waltzer[1]
[1]Institut de Génétique Reproduction Développement, Université Clermont Auvergne

Ten-Eleven Translocation (TET) proteins are key regulator of transcription, and their dysfunction is highly associated to cancers. While they are mainly described through their role in 5 methyl-cytosine (5mC) demethylation, TET enzymes can act on other substrate, such as RNA, or independently of their enzymatic activity. The Drosophila model, which lacks 5mC on DNA, provides an interesting model to explore these alternative functions.

My thesis aims to characterize new function and mechanisms of TET, through the identification of its protein interaction network. Therefore, I developed an adapted TurboID tool combined with a GFP directed nanobody, that allows me to study the interactome of any GFP knocked-in protein. This tool allowed me to identify more than 100 different partners, both in the larval brain and wing disk of the drosophila, including known interactors. Yet, new partners involved in mRNA splicing were specifically detected in the brain. Study of RNAseq data from different TET mutants revealed over 150 differential alternative splicing events. These results suggest that TET may influence alternative splicing, through direct demethylation of mRNA, and/or by interacting with splicing factors. The next part of my work will consist in the description of those splicing events, as well as the description of TET role in mRNA splicing. Those mechanisms, still unknown, could be a new insight in the study of TET.

Keywords: Epigenetics, drosophila, interactions

Family name: Ghamdi
First name: Zainab
Year of PhD: 3rd
Research team and Laboratory: AME2P, CRNH
PhD supervisor: David Thivel
Email: zainab.GHAMDI@doctorant.uca.fr
Language of presentation: English

Acute Effects of Low Carbohydrate Meals on Energy Intake, Appetite, and Food Reward in Adolescents with Obesity

Ghamdi Zainab[1], Moore Halim[1], Siroux Julie[1], Beraud Duane[1], Shaea Alkahtani[5], Abdullah F. Alghannam[4], Pereira Bruno[5], Masurier Julie[7], Finlayson Graham[6], Julian Valérie[8], Isacco Laurie[1], Thivel David[1,2]

[1]Clermont Auvergne University, EA 3533, Laboratory of the Metabolic Adaptations to Exercise under Physiological and Pathological Conditions (AME2P), CRNH Auvergne, Clermont-Ferrand, France
[2]International Research Chair Health in Motion, Clermont Auvergne University Foundation, Clermont-Ferrand, France . [3]Unit of Biostatistics (DRCI), Clermont-Ferrand University Hospital, Clermont-Ferrand, France
[4]Lifestyle & Health Research Center, Health Sciences Research Center (HSRC), Princess Nourah bint, Abdulrahman University (PNU), Riyadh, Saudi Arabia (Abdullah F. Alghannam)
[5]College of Sport Sciences and Physical Activity, King Saud University, Saudi Arabia, PO Box: 1949 Riyadh 11441 Saudi Arabia (Shaea Alkahtani). [6]Appetite Control & Energy Balance Research Group, School of Psychology, Faculty of Medicine & Health, University of Leeds, Leeds, West Yorkshire, UK
[7]SSR Obesité Nutrition UGECAM, Clermont-Ferrand, France. [8]Clermont-Ferrand University Hospital, department of Sport Medicine, Respiratory and Functional evaluations. Clermont-Ferrand, France.

Lowering the carbohydrate-to-fat ratio proposed alternative caloric restriction that may improve satiety, thus avoiding dietary compensation. However, this strategy remained inconclusive in children. Whether consumption of meals varying in the proportions of carbohydrate and fat, but not protein, modulate energy intake, appetite sensations, food reward in adolescents with obesity. In randomized crossover trial, 15 adolescents with obesity in 3 conditions consumed isocaloric meals that were moderate, low, VLC with adjusted fat content and matched protein. Adolescents appetite sensations rated at regular intervals throughout test day. Food reward recorded pre, post lunch, prior to *ad libitum* dinner, energy and macronutrient intake quantified. No significant differences in energy, macronutrient intake during meal detected between conditions. Similarly, meals macronutrient content have no effect on liking energy dense or sweet foods. Sweet foods choice invariably increased (p =.048). Eating desire were marginally higher after VLC meal relative to others (p =.062). Whilst these trends appeared similar among other appetite sensations, none were significant.

Even severe Carbohydrate to fat ratio reduction does not significantly alter daily appetite sensations, reward responsivity, or dietary intake during meal test in adolescents with obesity.

Keywords: VLC, Appetite, Food Reward, Obesity, Adolescents

Family name: Lugoboni
First name: Margot
Year of PhD: 3rd
Research team and Laboratory: iGReD-Equipe Jagla
PhD supervisor: Guillaume Junion
Email: margot.lugoboni@uca.fr
Language of presentation: French

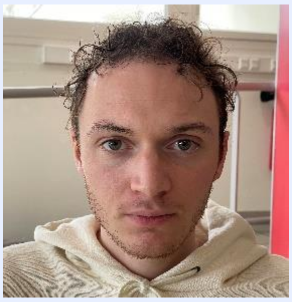
Transcriptional regulation mechanisms by m6A RNA modification in drosophila melanogaster

Margot Lugoboni, Paul Terzian, Yoan Renaud, Guillaume Junion

Gene expression regulation is a multi-layer process. The first regulated step is transcription, modulated by chromatin landscape allowing transcription factors recruitment and leading to transcription initiation. Nevertheless, more than 50 years ago, another regulated step of transcription was underly, RNAPII pausing. Downstream the TSS, RNAPII undergo a short stop in its transcription activity, called "pausing". The team showed that the release of RNAPII is partly dependant of m6A deposited on nascent RNA. The aim of my thesis is to unveil which molecular mechanisms allow the release of paused RNAPII through the m^6A epitranscriptomic mark. We hypothesized that another genomic structure, called R-loops, could be the pivot of such mechanism. We conducted whole genomic analysis, employing BisMapR-seq, to analyse R-loops landscape in drosophila and study effect of R-loops and m6A modulators. We also want to uncover the transcriptional effect of such structure by modulating their regulators and performing CUT&RUN-seq against RNAPII. We have now validated that most of R-loops are formed at promoters and present at active enhancers and are correlated with m6A modulators and m6A RNA at the promoters.

Keywords: transcription, m6A, R-loops, RNAPII pausing

Family name: Raucroy
First name: Maxime
Year of PhD: 3rd
Research team and Laboratory: UNH - Proteostasis
PhD supervisor: Julien Averous
Email: maxime.raucroy@uca.fr
Language of presentation: English



Plant proteins and methionine restriction: a strategy for preventing obesity and type 2 diabetes

Maxime Raucroy[1], Valérie Carraro[1], Laurent Parry[1], Isabelle Papet[1], Anne-Catherine Maurin[1], Céline Jousse[1], Alain Bruhat[1], Julien Averous[1]

[1]Unité de nutrition humaine UMR 1019 INRAE Université Clermont Auvergne, INRAE, Clermont-Ferrand, France

Methionine restriction (MR) is a promising dietary strategy for improving metabolic health and longevity. Essential amino acids (EAA), like methionine, cannot be synthesized or stored, and their restriction triggers adaptive responses that may prevent obesity and type 2 diabetes (T2D). MR's metabolic benefits involve complex signalling pathways, notably the eIF2α/ATF4 pathway, which regulates fibroblast growth factor 21 (FGF21), a key metabolic hormone. While short-term MR benefits have been observed in humans, synthetic MR diets are impractical for long-term use. This study explores plant proteins naturally low in methionine as a feasible alternative.

Adult mice were fed either a standard or plant protein-based diet with different methionine-unbalanced sources. The activation of the eIF2α/ATF4 pathway was assessed in various organs by measuring ATF4 target gene expression, including Fgf21, via qPCR. Plasma FGF21 levels were quantified using ELISA.

A plant protein-based diet significantly increased hepatic Fgf21 expression and plasma FGF21 levels, indicating activation of the eIF2α/ATF4 pathway. These findings support plant proteins as a viable MR strategy for metabolic health improvement.

Keywords: Methionine restriction, FGF21, eIF2α/ATF4 pathway, plant proteins, metabolic health

Family name: Prikshit
First name: Prikshit
Year of PhD: 3rd
Research team and Laboratory: iGRED, Guillot team
PhD supervisors: Krzysztof Jagla and Charlène Guillot
Email: prikshit@uca.fr
Language of presentation: English

Contribution of NMPs to the diversification of axial segments in chicken embryos

Prikshit[1], Jonas Cruzel[1], Felipe Maurelia Gaeta[1], Romane Bertrand[1] and Charlène Guillot[1]
[1]iGReD (Institut Génétique, Reproduction et Développement), Université Clermont Auvergne

The elongation of the vertebrate anterior-posterior axis relies on NMPs or axis stem cells, which are bipotent progenitors capable of differentiating into neural and mesodermal cells across various axial segments, from cervical to sacral regions (*Brown & Storey, 2000; Cambray & Wilson, 2007; Forlani et al., 2003; Gentsch et al., 2013; Tzouanacou et al., 2009; Guillot et al., 2021)*. Emerging evidence suggests that during this process, axis stem cells acquire axial positional information before differentiation (*Metzis et al., 2018*). Several key transcription factors (TFs) during this process are shown to act as pioneer factors, recruiting chromatin remodeling machinery essential for spatiotemporal information (*Verzi et al., 2013; Saxena et al., 2017; Neijts et al., 2017; Metzis et al., 2018; Amin et al., 2016*). However, the functional redundancy among these TFs, has made it challenging to dissect their individual roles (*Neijts et al., 2017)*. This has left unresolved gene regulatory networks during axial segment specification.

Our research aims to clarify how a single pool of axis stem cells contributes to the development of distinct axial segments and to unravel the specific or combinatorial roles of key TFs in this process. Using electroporation and confocal imaging, we first identified three developmental stages where axis stem cells contribute to cervical, thoracic, and lumbar regions using the avian model system. Using HCR-FISH, qPCR, and immunostaining, we report for the first time the spatiotemporal heterogeneity of key TFs involved in axial patterning at the single-cell level. To learn more about these findings, please visit my poster.

Keywords: Transcription factors, NMPs, Axial segments, Chicken embryo

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Family name: Michelotti

First name: Tainara Cristina
Year of PhD: 3rd
Research team and Laboratory: INRAE - Biomarkers team
PhD supervisors: Muriel Bonnet and Guillaume Durand
Email: tainara.michelotti@inrae.fr
Language of presentation: English

Endogenous bovine FFAR2/GPR43 ligands display distinct pharmacological properties

Tainara Cristina Michelotti[1], Valérie Lamothe[2], Frederic Jean-Alphonse[3,4], Eric Reiter[3,4], Muriel Bonnet[1], Guillaume Durand[1,2]

[1]INRAE, Université Clermont Auvergne, VetAgro Sup, UMR Herbivores, 63122 Saint Genès Champanelle, France
[2]Feed and Food department, Bordeaux Sciences Agro, 33175 Gradignan, France
[3]INRAE, CNRS, Université de Tours, PRC, 37380 Nouzilly, France.
[4]Inria, Inria Saclay-Ile-de-France, 91120 Palaiseau, France.

Free fatty acids (**FFAs**) are ligands for specific G protein-coupled receptors (**GPCR**) called free fatty acid receptors (**FFARs**). Among these receptors, there is a particular interest in the physiological roles of FFAR2 and its potential use as therapeutic target for health disorders. Despite great progress in other species, pharmacological properties of the bovine FFAR2 (**bFFAR2**) are not fully understood. We aimed to evaluate how a selection of FFAs (C2:0 to C8:0, and branched FFAs) activate and regulate bFFAR2. We used HEK293A cells and BRET assays to measure $G\alpha_i/G\alpha_q$ coupling and signaling, β-arrestin 2 recruitment, and receptor internalization/trafficking. SRE and NFAT-RE dependent transcription was assessed by luciferase reporter assay. Results show that bFFAR2 couples to $G\alpha_i$ and $G\alpha_q$ and recruits β-arrestin 2 when stimulated with FFAs up to 8 carbons. FFAs with 4 to 7 carbons plus 3-methyl-butanoic acid showed the greatest potency to activate bFFAR2 upstream and downstream signaling, while C2:0, C3:0 and 2-methylpropanoic acid (2MP) were the least potent. 2MP had little pharmacological activity towards β-arrestin 2, and although induced receptor internalization, trafficking to the early endosome was not observed. Overall, the number of carbons and methyl position of FFAs differentially regulates the activation of bFFAR2.

Keywords: cell signaling, cell surface receptor, fatty acid, G protein coupled receptor, bovine FFAR2

Family name: Lirot
First name: Hélène
Year of PhD: 3rd
Research team and Laboratory: INRAE - EPIA
PhD supervisor: Xavier Bailly
Email: helene.lirot@doctorant.uca.fr
Language of presentation: French

Longitudinal analysis reveals transitions in pathogens profiles associated with mastitis in dairy cows

Hélène Lirot[1], Laurent Crespin[1], Patrick Gasqui[1], Xavier Bailly[1] and Anaïs Bompard[1]

[1]Unité Mixte de Recherche d'épidémiologie des maladies animales et zoonotiques (UMR EPIA), Institut national de recherche pour l'agriculture, l'alimentation et l'environnement (INRAE) - Institut national d'enseignement supérieur et de recherche en alimentation, santé animale, sciences agronomiques et de l'environnement (VetAgro Sup), France

Mastitis is a multifactorial infection of the udder caused by a multitude of pathogens, varying in severity and prevalence. It is one of the most common diseases on dairy farms. Limited information is available on the interactions between pathogens in mastitis infections. The aim of this study was to investigate the dynamics of pathogens and their associations in the udder microbiota, and to assess their impact on mastitis risk. We also investigated the potential sources of the pathogens studied within the farm. To this objective, a large longitudinal study was carried out. We examined the abundance of 15 mastitis-causing pathogens by qPCR in milk, faeces, and environmental samples collected twice weekly for five months from dairy farms in Auvergne. Analysis of pathogen distribution on the farms indicates preferential routes of transmission and potential sources of contaminations. Ward's cluster analysis of milk-quarter samples reveals distinct pathogen profiles, associated with distinct somatic cell counts in the cow, and indicate that *Corynebacterium bovis*, *Streptococcus uberis* and *non-aureus Staphylococci* structure the cow pathobiome. Analysis of these pathogen profiles suggests that certain bacterial pathogens considered minor may indirectly cause a higher immune response and longer infections by major pathogens.

Keywords: Mastitis, Pathobiome, Dynamics, Pathogens

Family name: Prieur
First name: Vincent
Year of PhD: 3rd
Research team and Laboratory: UMRH-Biomarqueurs
PhD supervisors: Isabelle Cassar-Malek et Muriel Bonnet
Email: vincent.prieur@inrae.fr
Language of presentation: English

Does the molecular content of plasmatic small Extracellular Vesicles from crossbred heifers reflect variability in feed efficiency, meat quality, body composition and husbandry practices?

Vincent PRIEUR[1], Isabelle Cassar-Malek[1] et Muriel Bonnet[1]
[1]INRAE/VAS – UMRH - TEAM BIOMARQUEURS

Summary: We investigated the proteome of plasma extracellular vesicles from heifers to identify potential biomarkers associated with key phenotypes (feed efficiency, meat qualities, body composition).

In cattle production, key phenotypes such as feed efficiency (**FE**), meat quality (**MQ**; tenderness, adiposity), and body composition (**BC**) are difficult to measure routinely. We investigated plasma-derived small Extracellular Vesicles (**EVs**) — nanoparticles of 30-150 nm — as a source of biomolecules associated with phenotypes. Indeed, **EVs** are involved in inter-organ crosstalk, growth, health, and homeostasis. **EVs** share size and density characteristics with other particles, such as lipoproteins, which outnumber **EVs**. This makes them very difficult to extract. We have developed a protocol to isolate **EVs** from 4 mL of plasma from 38 crossbred heifers (Brown Swiss dams × ANgus-n=12, LImousin-n=16, SImmental-n=10 sires) reared with (**PA**) or without (**NP**) pasture. Particle morphology, size, concentration, precense of **EV**-specifics markers, purity (average: 4.8×10^8 particles/µg protein) and gene ontology analysis confirmed **EVs** isolation. Proteomic analyses (LC-MS/MS, PRM) identified 417 proteins and quantified abundance for 272 of them. Statistical analyses of the proteome of **EVs** suggests differences between the '**PA** vs **NP**' and '**AN** vs **LI**-**SI**' groups, and potential biomarker proteins of phenotypes (e.g. **FE**: FGL1. **MQ**-**BC**: OIT3, PEPD, PARVB…), to be validated.

Keywords: Extracellular Vesicle, Cattle, Phenotypes, Proteomic, Biomarkers

Family name: Bécu
First name: Thomas
Year of PhD: 3rd
Research team and Laboratory: INRAE - UREP
PhD supervisors: Sébastien Fontaine, Audrey Niboyet, Amélie Cantarel
Email: thomas.becu@inrae.fr
Language of presentation: English

Combining wheat and diverse prairies to promote positive ecological interactions and better regulation of C and N biogeochemical cycles in agroecosystems

Thomas Bécu[1], Elodie Pascon[1], Sébastien Fontaine[1], Audrey Niboyet[2,3], Gael Alvarez[1], Sebastien Barot[2], Lisa Besson[1], Amélie Cantarel[4], Olivier Duchene[5], Xavier Le Roux[3], Nicolas Gross[1]

[1]INRAE, VetAgro Sup, Université Clermont Auvergne, UMR Ecosystème Prairial (UREP), Clermont-Ferrand 63000, France
[2]Sorbonne Université, Université Paris Cité, UPEC, CNRS, INRAE, IRD, Institut d'Ecologie et des Sciences de l'Environnement de Paris (IEES-Paris), Paris 75005, France
[3]AgroParisTech, Palaiseau 91120, France
[4]INRAE, CNRS, Université Lyon 1, Laboratoire d'Ecologie Microbienne (LEM), UMR 1418 INRAE, Villeurbanne 69622, France
[5]ISARA, Agroecology and Environment Research Unit, Lyon 69364, France

In perennial and diverse temperate prairies, plant functional diversity interacts with soil microbial communities, resulting in a tight coupling between soil carbon (C) and nitrogen (N) cycles and favours the resource use efficiency of the system. That emerging property could be used in highly diversified agroecosystems but require to understand plant-plant interactions in order to promote positive plant-plant interactions and reduce competition. The overall objective of this study is to explore the potential benefits of these interactions in a new agroecosystem called "Agroprairies" that combine wheat with perennial prairies in altering strips. We implemented an experimental design that encompasses four varieties of winter wheat (*Triticum aestivum*) that vary in their functional traits, with four functionally different perennial prairies that vary across acquisition strategies and leguminous proportion, in two fertilization contexts. The effect of prairies on wheat were studied through their functional trait's expressions in the field. First results show variable and significant impact of the functional structure of prairies traits on wheat response in terms of height and nutrition, depending on N management. This study should bring a first view on the potential benefits of combining an annual crop with diverse prairies in agroprairies, and open perspectives to diversify agroecosystems.

Keywords: Agroecology, Functional diversity, Crop diversification, Plant-plant interactions, Functional traits expression

Family name: Besson
First name: Lisa
Year of PhD: 3rd
Research team and Laboratory: INRAe - UREP
PhD supervisor: Sébastien Fontaine
Email: lisa.besson@inrae.fr
Language of presentation: English

Combining wheat and diverse perennial species: What is the impact on *Z.tritici* development and the wheat microbiome?

Lisa Besson[1], Sébastien Fontaine[1], Gaël Alvarez[1,2], Thomas Becu[1], Olivier Duchene[4], Audrey Niboyet[5,6], Nicolas Gross[1], Gaëlle Marliac[2,3]

[1]INRAE, Unité Mixte de Recherche Ecosystème Prairial, VetAgro Sup, Université Clermont Auvergne, 5 chemin de Beaulieu, 63000 Clermont-Ferrand, France. [2]VetAgro Sup, Universite Clermont Auvergne, 89 Av. de l'Europe, 63370 Lempdes, France. [3]INRAE, GDEC, Universite Clermont Auvergne, 5 chemin de Beaulieu, 63000 Clermont-Ferrand, France. [4]ISARA, Research Unit Agroecology and Environment, 23 Rue Jean Baldassini, 69007 Lyon, France. [5]Sorbonne Université, Université Paris Cité, UPEC, CNRS, INRAE, IRD, Institut d'Ecologie et des Sciences de l'Environnement de Paris, 75005, Paris, France· [6]AgroParisTech, 91120, Palaiseau, France

Increasing biodiversity in agroecosystems, is desirable for maintaining ecosystem functions, including disease regulation. In this context, a new cropping system called “Agroprairie” has been designed resulting from the association of alternating strips of wheat and diverse prairies (>10 plant species). The aim of this study is to explore the effect of this new cropping system on the regulation of *Zymoseptoria tritici* the causal agent of Septoria tritici blotch (STB), one of the most damaging leaf diseases of wheat. To achieve this, four wheat cultivars with contrasting susceptibilities to STB, grown in “agroprairies” associated with four types of prairies were investigated to explore the influence of intra- and interspecific diversity on the development of STB. In addition, a reduced number of plots with the most STB-susceptible cultivar was inoculated with *Z.tritici* to test the resistance of the associated wheat to inoculation. In parallel, to explore the role of microbiome in disease development, rhizosphere and roots DNA from associated wheat and prairies samples was extracted and sequenced using 16S rDNA. Four different STB incidence and severity notations were recorded between flowering and ripening stage. The results showed that agroprairies with the highest biomass and proportion of legumes reduce the incidence of STB compared to wheat monoculture. However, the protection afforded to wheat by prairie strips is lost when *Z.tritici* is inoculated, which means that this protection may mainly come from a barrier effect. In parallel, preliminary results show that agroprairies modify the composition of the bacterial rhizospheric and root microbiome of wheat, and increase the abundance of known PGPRs.

Keywords: Crop diversification, disease regulation, wheat, perennial species, microbiome

Family name: Mora
First name: Blandine
Year of PhD: 3rd
Research team and Laboratory: INRAE- UMRH équipe DINAMIC
PhD supervisor: Vincent Niderkorn
Email: blandinemora40@gmail.com
Language of presentation: English

Screening of 16 Mediterranean agro-industrial by-products rich in bioactive compounds to modulate *in vitro* ruminal fermentation

Blandine Mora[1], Serena Calabrò[2], Monica Isabella Cutrignelli[2], Elodie Barbier[5], Serkos Haroutounian[4], Angélique Torrent[1], Alessandro Vastolo[2], Hervé Hoste[5], Vincent Niderkorn[1]

[1]Université Clermont Auvergne, INRAE, VetAgro Sup, UMR 1213 Herbivores, 63122 Saint-Genès Champanelle, France
[2]Department of Veterinary Medicine and Animal Production, University of Napoli Federico II, Via Federico Delpino, 80137 Naples, Italy
[3]MG2MIX, La basse haye, F-35220 Châteaubourg, France
[4]Department of Animal Science, School of Animal Biosciences, Agricultural University of Athens, Greece
[5]INRAE, ENVT, UMR IHAP, Route des Capelles, 31076 Toulouse, France

Using by-products in nutrition offers a sustainable way to reduce pollutant emissions in small ruminant farming. The potential of 16 polyphenol-rich agro-industrial by-products from France, Italy and Greece was evaluated as dietary supplements to mitigate pollutants produced on *in vitro* rumen fermentation. The aim was to identify the most promising by-products for reducing pollutants emissions while maintaining productivity. All by-products were analysed and tested at a 10% inclusion rate in a standard diet. Measurements included gas production (CH_4, CO_2), fermentation end-products (VFAs, NH_3), and *in vitro* dry matter degradability (IVDMD). The French grape sample significantly reduced CH_4 emissions ($P < 0.001$), with a milder effect from Italian hazelnut and Greek pomegranate ($P < 0.05$). The same grape sample, along with two pomegranate samples, also lowered NH_3 levels ($P < 0.001$, $P < 0.01$, $P < 0.01$). Polyphenol profiles were closely linked to CH_4 and NH_3 reductions and antioxidant activity. No adverse effects on productivity were observed. The most promising by-product was the French grape sample.

Keywords: Ammonia, Agro-industrial by-products, Bioactive compounds, Enteric methane, *in vitro* ruminal fermentation

Family name: Karam
First name: Germaine
Year of PhD: 3rd
Research team and Laboratory: iGReD - Equipe evolutionary epigenomics and genetic conflicts
PhD supervisor: Antoine Molaro
Email: germaine.karam@doctorant.uca.fr
Language of presentation: English

Functional characterization of a novel parental-effect histone protein during mammalian reproduction

Germaine Karam, Marine Fraisse, Joris Mordier and Antoine Molaro
Genetics, Reproduction and Development Institute (iGReD), UCA, CNRS UMR 6293, INSERM U1103, Clermont-Ferrand, France.

Genetic information is transmitted from parents to offspring through chromatin. Chromatin encompasses the DNA sequences as well as packaging proteins known as histones. Unlike histones that are found in somatic cells, specific histones and histone variants are present in sperm and oocytes to support gamete production. The unique functions and role of one such variant, known as H2A.B, remain undiscovered. In mice, H2A.B is expressed during male and female meiosis, but its most significant effect is seen after fertilization, in offspring. Genetic ablation of H2A.B in parents produces embryos with reduced weights and survival. This implies that H2A.B influences chromatin of both sperm and oocyte in currently unknown ways. Through proteomic analysis of mature sperm and genomic profiling of mature oocyte chromatin, I showed that H2A.B alters the type and amount of histone proteins that are present in mature sperm and helps in organizing oocyte genome and chromatin landscape. Whether H2A.B's 'imprints' on parental gametes are transmitted to the zygote and whether they can explain its parental effect remains unanswered. Understanding how parental chromatin is set up and its influence on reproduction is fundamental to improve the knowledge around fertility disorders.

Keywords: Histone variant, Chromatin, Oocyte, Sperm, Fertility

Family name: Carcy
First name: Oriana
Year of PhD: 3rd
Research team and Laboratory: UMR 1240 IMoST
PhD supervisor: Florent Cachin
Email: oriana.carcy@hotmail.fr
Language of presentation: English

What is the impact of ionizing radiation on the nuclear and epigenetic integrity of human sperm?

O. Carcy[1], N. Sas[1,2], T. Billoux[1,2], E. Jouberton[1,2], M. Chanchou[1,2], S. Desset[3], C. Tatout[3], A. Tchirkov[4], M. Berger[5], C. Bourgne[5], B. Pereira[6], E. Miot-Noirault[1], F. Cachin[1,2], F. Brugnon[1,7], H. Pons-Rejraji[1,7]

[1]Clermont Auvergne University, INSERM U1240- Imagerie Moléculaire et Stratégies Théranostiques IMoST, Clermont-Ferrand, France.
[2]Jean Perrin Center, Nuclear Medecine Department, Clermont-Ferrand, France.
[3]Clermont Auvergne University, INSERM U1103- CNRS 6293- iGReD, Clermont-Ferrand, France.
[4]Clermont-Ferrand University Hospital, Medical Cytogenetics Department, Clermont-Ferrand, France.
[5]Clermont-Ferrand University Hospital, Biological Hematology Laboratory, Clermont-Ferrand, France.
[6]Clermont-Ferrand University Hospital, DRCI Clinical Research and Innovation Delegation, Clermont-Ferrand, France. [7]Clermont-Ferrand University Hospital, ART -CECOS unit, Clermont-Ferrand, France.

The increasing use of ionizing radiation (IR) in medical diagnostics and treatments raises concerns about its impact on male fertility, which remains poorly understood. Our study aimed to assess the effects of IR on human sperm functional parameters and nuclear quality. In this order, we exposed human spermatozoa in vitro to increasing absorbed doses (AD) of IR mimicking epididymis irradiation during diagnostic CT imaging (AD: 14- 70 mGy) and radioiodine therapy for thyroid cancer (AD: 140 mGy). Each sample served as its own control to address inter-individual variability.

We showed significant reductions in sperm vitality ($p<0.001$) and motility across all AD, along with chromatin decondensation at 70 and 140 mGy ($p<0.05$ and <0.01). Individual-dependent changes in nuclear morphometry were observed, but no DNA fragmentation or telomeric damage was detected. Exposure to 140 mGy did not affect oxidative stress levels or capacitation markers.

Our work provides valuable insights into how IR might affect human spermatozoa and male fertility. Ongoing research focuses on epigenomic alterations in sperm cells and seminal fluid. In vivo studies in patients and animal models are essential to fully understand the impacts of IR on the regulatory pathways of spermatogenesis and epididymal maturation.

Keywords: Ionizing radiation, Functional parameters, Human Sperm integrity, Nuclear alterations, 3D morphometry

Family name: Chaleil
First name: Florian
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisor: Anne-Marie Martinez
Email: florian.chaleil@uca.fr
Language of presentation: French

Hyper-SUMOylation and ovarian insufficiency

F. Chaleil[1], D. Dufour[2], I. Sahut-Barnola[1], A. Martinez[1], AM. Lefrançois-Martinez[1]
[1]GReD Institute, Clermont-Ferrand, France
[2] Institute of Basic Medical Sciences, Department of Molecular Medicine, Oslo, Norway

Context: SUMOylation is a reversible post-translational mechanism that expands the functional repertory of nuclear proteins to drive genetic programs for cell differentiation throughout life. Inappropriate SUMOylations have been associated with human ovarian diseases such as premature ovarian insufficiency (POI) and ovarian tumors. We have previously shown that chronic hypo-SUMOylation *in vivo* leads to loss of function and disruption of ovarian identity maintenance in mice.

Methods: To clarify the role of SUMOylation in ovarian physiology, we developed a novel mouse model (Senp2cKO) of chronic targeted hyper-SUMOylation in ovarian somatic cells.

Results: Senp2cKO mice develop hypo fertility at 8 weeks of age and complete POI at 3 months, associated with ovulation failure, absence of corpus luteum and elevated LH plasma levels. Transcriptomic comparisons (RNA-Seq) of Senp2cKO and ERßcKO ovaries revealed that 67.2% of the transcripts deregulated by ERß inactivation were also deregulated in the Senp2cKO ovary. These signatures confirm a defect in terminal folliculogenesis, and indicate alterations in the control of proliferation, ovulatory lytic activities and key regulators of terminal pre-ovulatory follicle growth.

Conclusion: Our results demonstrate that a transient and controlled hypo-SUMOylation is required in somatic cells of antral follicles for the initiation of terminal follicle maturation and ovulation programs.

Keywords: ovarian insufficiency, terminal folliculogenesis, transcriptomic and chromatin analysis

Family name: Kahouadji
First name: Samy
Year of PhD: 3rd
Research team and Laboratory: iGreD - équipe 10
PhD supervisor: Damien Bouvier
Email: skahouadji@chu-clermontferrand.fr
Language of presentation: French

CX3CL1/Fractalkine as a biomarker for early pregnancy prediction of preterm premature rupture of membranes

Samy Kahouadji[1,2], Yves Giguère[3], Salomé Lambert[2], Jean-Claude Forest[3], Nathalie Bernard[3], Loïc Blanchon[2], Geoffroy Marceau[1,2], Julie Durif[1], Bruno Pereira[4], Denis Gallot[2,5], Vincent Sapin[1,2], Damien Bouvier[1,2]

[1]Biochemistry and Molecular Genetic Department, CHU Clermont-Ferrand, Clermont-Ferrand, France.
[2] Faculty of Medicine, CNRS 6293, INSERM 1103, GReD, Université Clermont Auvergne, Clermont-Ferrand, France
[3]Centre de Recherche du Centre Hospitalier Universitaire (CHU) de Québec-Université Laval, Québec City, Canada
[4]Biostatistics Unit (DRCI), CHU Clermont-Ferrand, Clermont-Ferrand, France.
[5]Department of Obstetrics and Gynecology, CHU Clermont-Ferrand, Clermont-Ferrand, France.

<u>Context</u>: This study evaluated serum CX3CL1/Fractalkine, a monocyte/macrophage chemoattractant expressed in cytotrophoblasts and decidual cells, as a predictive biomarker for preterm premature rupture of membranes (PPROM).

<u>Methods</u>: A case-control study of 438 pregnancies, including 82 PPROM cases and 64 preterm labor cases with intact membranes, was conducted. Blood samples were collected in the first trimester, second trimester, and at delivery. The predictive value of CX3CL1 and maternal risk factors was assessed using receiver operating characteristic (ROC) curve analysis. A second independent cohort was used for validation.

<u>Results</u>: First-trimester CX3CL1 levels were significantly higher in PPROM cases ($p=0.008$). CX3CL1 alone predicted PPROM with 90% sensitivity and ~40% specificity. The area under the ROC curve (AUC) for first-trimester CX3CL1 was 0.64 (95% CI: 0.57–0.71), compared to 0.61 (95% CI: 0.54–0.68) for maternal risk factors (BMI <18.5 kg/m^2, nulliparity, tobacco use, and low education). Combining CX3CL1 with risk factors improved the AUC to 0.72 (95% CI: 0.66–0.79, $p<0.001$). Findings were validated in an independent cohort.

<u>Conclusion</u>: CX3CL1 is a promising first-trimester biomarker for early PPROM prediction.

Keywords: CX3CL1, fractalkine, prediction, PPROM, pregnancy

Family name: Poitrinal
First name: Alice
Year of PhD: 3rd
Research team and Laboratory: IMoST
PhD supervisor: Florence Brugnon
Email: alice.poitrinal@gmail.com
Language of presentation: English

Assessment of the impact of breast cancer on human folliculogenesis

A. Poitrinal, S. Carlet-Dollet, B. Pereira, C. Rodrigues, A.S. Gremeau, D. Lütjohann, G. Marteil, F. Brugnon

Task group Fertilité et Cancer - Equipe Robust - IMoST UMR1240 INSERM/UCA / Service d'Assistance Médicale à la Procréation, Centre Hospitalier Universitaire de Clermont-Ferrand

Breast cancer (BC) is the most frequent cancer in reproductive-aged women, and may exert a deleterious impact on the ovarian functions. Indeed, cancer patients undergoing fertility preservation before treatments show a poorer response to ovarian stimulation than healthy women. Nevertheless, this impact remains controversial, and the underlying mechanisms are poorly understood. **This study investigates the impact of BC itself on ovarian functions.**

21 BC patients (9 triple negative (TN), 5 hormone-receptor positive (HR+) and 7 HER2 positive (HER2+)) and 30 oocytes donors (OD) undergoing oocyte cryopreservation were included since January 2019. Ovarian response to stimulation was assessed. The levels of enzymes and regulators of the cholesterol biosynthesis pathway in cumulus cells (CC) were quantified by RT-qPCR. Cholesterol and its intermediates concentrations were measured in follicular fluids (FF) by GC-FID and GC-MS/SIM.

BC patients had a poorer ovarian response compared to OD. RT-qPCR revealed altered enzyme expression in CC, with upregulation in TN patients and downregulation in HER2+ patients. Cholesterol and its intermediates were reduced in FF from HER2+ patients.

Our findings confirm that BC exerts a deleterious impact on ovarian functions, which could, at least in part, be explained by the alteration of cholesterol homeostasis in ovarian follicles.

Keywords: Oncofertility, Breast cancer, Fertility preservation, Folliculogenesis, Cholesterol biosynthesis

Family name: Moazamian
First name: Aron
Year of PhD: PhD
Research team and Laboratory: iGReD
PhD supervisor: Joël Drevet
Email: aron.moazamian@celloxess.com
Language of presentation: English

Unravelling the aggregation mechanism in *Lactobacillus crispatus* and its role in probiotic functionality

Aron Moazamian[1,2], Elisa Hug[1], Pauline Villeneuve[1], Stéphanie Bravard[1], Richard Geurtsen[2], Jorge Hallak[3], Fabrice Saez[1], Robert John Aitken[4], Parviz Gharagozloo[2] and Joël R. Drevet[1]

[1]University Clermont Auvergne, EVALSEM- iGReD- CRBC- Faculté de Médecine, Clermont Ferrand, France.
[2]CellOxess Biotechnology, Research & Development, Ewing, U.S.A.lanher
[3]University of Sao Paulo Medical School, Division of Urology, Sao Paulo, Brazil.
[4]University of Newcastle, Priority Research Centre for Reproductive Science, Newcastle, Australia.

Objective: Evaluate how typically “safe” doses of antioxidant micronutrients (Vitamin C, Zinc, Folate, Carnitine) affect semen parameters, systemic redox balance, sperm DNA integrity, and fertility in mice.
Methods: In a dose-escalation study, healthy male mice received single antioxidant treatments over one spermatogenic cycle. Redox status was assessed in blood, while sperm count, motility, viability, and acrosome integrity were measured. DNA oxidation (8-OHdG), fragmentation (TUNEL), and decondensation (Toluidine Blue) were evaluated. Fertility outcomes were examined using the highest carnitine dose in both healthy and oxidatively stressed mice.
Results: In healthy mice, high-dose supplementation with any micronutrient disrupted redox balance and compromised sperm DNA integrity. Notably, high-dose carnitine caused severe DNA fragmentation, confirmed by decreased pregnancy rates and fewer pups. Conversely, in oxidatively stressed mice, high-dose carnitine improved sperm DNA integrity.
Conclusion: Although preconception antioxidants can enhance semen quality, excessive doses may induce reductive stress, damaging essential sperm structures and impairing fertility. Personalized antioxidant dosing, guided by oxidative stress assessment, is crucial to minimize potential harm and optimize reproductive outcomes.

Keywords: Oxidative stress, Reductive stress, Antioxidant micronutrient supplementation, Sperm DNA integrity, Male infertility

Family name: Delamarre
First name: Louis
Year of PhD: 3rd
Research team and Laboratory: UCA, CNRS, LaPSCo, Team 3
PhD supervisor: Frédéric Dutheil
Email: louis.delamarre@doctorant.uca.fr
Language of presentation: French

Validation of visual analog scale of effort reward imbalance in workers

Louis Delamarre[1], Bruno Pereira[2], Thomas Cornet[3], Samuel Dewavrin[3], Julien S Baker[4], Marek Zak[5], Ukadike Chris Ugbolue[6], Martial Mermillod[7], Frédéric Dutheil[1]

[1]Université Clermont Auvergne, CNRS, LaPSCo, Physiological and Psychosocial Stress, Team 3, Clermont-Ferrand, France. [2]CHU Clermont Ferrand. [3]Wittyfit, Paris, France. [4]Centre for Health and Exercise Science Research, Department of Sport, Physical Education and Health, Hong Kong Baptist University, Kowloon Tong, Hong Kong. [5]The Institute of Health Sciences, Collegium Medicum, The Jan Kochanowski University of Kielce, ul. Zeromskiego 5, 25-369, Kielce, Poland. [6]Institute for Clinical Exercise & Health Science, School of Health and Life Sciences, University of the West of Scotland. [7]Univ. Grenoble Alpes, CNRS, LPNC, Grenoble, France

While the 23-item effort-reward imbalance (ERI) questionnaire of Siegrist is effective, its complexity and length limit its use. We aimed to validate a Visual Analog Scale for ERI (ERI-VAS) as a simpler alternative. Workers were asked to complete a questionnaire with both Siegrist questionnaire and ERI-VAS, with a retest one week later. Internal validity of the ERI-VAS was assessed as a quantitative and qualitative variable, with ERI defined by an ERI ratio (ERI-Siegrist) >1. Cut-off for ERI-VAS was determined using ROC curve analysis. Reproducibility was evaluated using test-retest. External validity compared associations between sociodemographic and work-related factors vs. ERI-Siegrist or ERI-VAS. Among the 176 respondents, 116 completed both the ERI questionnaire and ERI-VAS. Acceptability was correct as there was no significant difference in the proportion of participants that did not complete the Siegrist questionnaire vs. the ERI-VAS, and only 5 (2.8%) answered the Siegrist questionnaire but not the ERI-VAS. The ERI-VAS had no floor or ceiling effects. The ERI-VAS correlated significantly with the ERI ratio (Spearman's $\rho = 0.30$, $p < 0.01$). The optimal ERI-VAS cut-off was 56/100 (sensitivity 0.78, specificity 0.76, ROC AUC = 0.81). ERI-VAS showed high test-retest reliability (Spearman's $\rho = 0.82$; Cohen's kappa = 0.78). External validity analyses showed consistent associations between ERI-VAS and health outcomes, such as perceived health (Cramer's V: 0.3), fatigue (0.23), anxiety (0.34), burnout (0.31), stress at work (0.31), compared to the ERI-Siegrist. ERI-VAS is a quick, valid, and reliable alternative to the ERI questionnaire, maintaining correct diagnostic accuracy while minimizing respondent burden. Workers scoring below 56 on ERI-VAS may be classified as at risk for ERI.

Keywords: Effort-Reward Imbalance, Visual Analog Scale, Occupational Health, Psychosocial Risks

Family name: Grampayre
First name: Manon
Year of PhD: 3rd
Research team and Laboratory: Axe TGI-Decision Support in Perinatal Health, Institut Pascal, CNRS-UMR 6602, Université Clermont Auvergne
PhD supervisors: Françoise Vendittelli and Chloé Barasinski
Email: mgrampayre@chu-clermontferrand.fr
Language of presentation: English

Improvement of women's and partners' experience in peri and post-natal period

Manon Grampayre[1], Chloé Barasinski[1], Françoise Vendittelli[1,2,3]
[1]Université Clermont Auvergne, CNRS, CHU Clermont-Ferrand, Institut Pascal, F-63000 Clermont-Ferrand, France
[2]Réseau de Santé en Périnatalité d’Auvergne, F-63000 Clermont-Ferrand, France
[3]AUDIPOG (Association des Utilisateurs de Dossiers Informatisés en Pédiatrie, Obstétrique et Gynécologie), RTH Laennec Medical University

At a time when suicide is one of the leading causes of maternal mortality, it is important to take an interest in the mental health of mothers, but also of co-parents, because couples are facing a period of upheaval, and we know that this can have consequences on their mental health. Taking an interest in their experiences is a key point in improving the quality of our care and offer tailored support to parents.

The first part of the thesis will focus on the impact of interventions on women's experience with two axes: evaluation of the impact of type of pushing during delivery on the women's experience (randomized controlled trial already carried out) and evaluation of the effect of tecartherapy on post-operative scarring pain (randomized controlled trial NoCePain, in progress). The second part of my thesis will focus on the evaluation of partners' affectivity in the perinatal period (validation in French of a questionnaire and survey of partners, in progress).

By identifying each parent's vulnerabilities, this could help reduce the negative family, social and professional consequences, and also, through appropriate actions, improve the quality of the parent-child bond, which is vital to the child and family's health.

Keywords: experience, perinatal period, postnatal period, quality of life, medical pratices assessment

Family name: De Clercq
First name: Fanny
Year of PhD: 3rd
Research team and Laboratory: M2iSH
PhD supervisor: Nathalie Boisseau
Email: fanny.de_clercq@uca.fr
Language of presentation: English

Development of a probiotics and plant extracts combination targeting Adherent-Invasive *Escherichia coli* strains associated with Crohn's disease

Fanny De Clercq[1], Charlotte Leclaire[1], Jeremy Denizot[1,2], Sophie Holowacz[3], Nathalie Boisseau[4], Nicolas Barnich[1, 2], Adeline Sivignon[1, 2]

[1] Université Clermont Auvergne, Inserm, INRAe, M2iSH, F-63000 Clermont-Ferrand, France
[2] Université Clermont Auvergne, IUT Clermont Auvergne, Inserm, INRAE, M2iSH, F-63000 Clermont-Ferrand, France
[3] Groupe PiLeJe, Paris, France
[4] Université Clermont Auvergne, AME2P, F-63000 Clermont-Ferrand, France

In Crohn's disease (CD) patients, an abnormal colonization of the ileal mucosa by Adherent-Invasive *Escherichia coli* (AIEC) contributes to intestinal inflammation. Since no curative treatment exists, new therapies targeting AIEC and the intestinal microbiota are needed. This study aimed to evaluate the anti-virulence properties of 17 probiotic strains (Bifidobacteria and Lactobacilli) and three plant extracts (green tea, walnut, and liquorice) against AIEC.

The effects of the compounds were assessed *in vitro* by measuring IL-8 secretion and AIEC adhesion to Caco-2/TC7 cells. Six Lactobacillus strains and one Bifidobacterium strain significantly reduced IL-8 secretion and AIEC adhesion. Plant extracts did not prevent inflammation or adhesion but inhibited AIEC growth, which was also observed with four Lactobacillus strains tested. *In vivo*, probiotics and plant extracts were administered to AIEC-infected mice treated with dextran sulfate sodium (DSS). Both probiotics and green tea/walnut extracts reduced colitis severity and AIEC colonization. The combination of two Lactobacillus strains and walnut extract notably reduced colitis scores, protected the intestinal mucosa, and eliminated AIEC in half of the mice.

These promising results suggest that combining specific probiotics with plant extracts could limit AIEC colonization in CD patients, though further research is necessary to understand the underlying mechanisms.

Keywords: Adherent-Invasive *Escherichia coli*, Crohn's disease, probiotic, plant extract

Family name: Delabrise
First name: Coralie
Year of PhD: 3rd
Research team and Laboratory: UNH
PhD supervisor: Daniel Taillandier
Email: coralie.delabrise@inrae.fr
Language of presentation: English

Human blood biomarkers of skeletal muscle atrophy

Coralie Delabrise[1], Julien Aniort[1,2], Cécile Polge[1], Agnès Claustre[1], Lydie Combaret[1], Carole Philipponet[2], Charlotte Uro-coste[2], Anais Poyet[2], Thomas Walter[3], Benjamin Gibert[4], Anne-Elisabeth Heng[1,2], Daniel Taillandier[1]

[1]Université Clermont Auvergne, INRAE, UNH, Unité de Nutrition Humaine, CRNH Auvergne, ClermontFerrand, France.
[2]Nephrology, dialysis and transplantation department, Gabriel Montpied University Hospital, University Hospital of Clermont-Ferrand, Clermont-Ferrand, France.
[3]Medical oncology department, Hôpital Edouard Herriot, Hospices civils de Lyon (HCL)
[4]Centre de Recherche en Cancérologie de Lyon (CRCL), INSERM U1052-CNRS UMR5286, Université de Lyon, Centre Léon Bérard, Lyon, France.

Skeletal muscle atrophy (SMA) is a common side effect in patients suffering from chronic pathologies (cancers, kidney failure (CKD), etc.) or during physiological situations such as ageing. Although SMA increases morbidity and mortality, clinical diagnosis is difficult to perform and no reliable and easy diagnostic method exists so far.

We previously identified blood mRNA biomarkers whose expression identifies ongoing muscle degradation in atrophying CKD or lung cancer patients. We now aim at evaluating the predictive potential and the kinetic of these biomarkers in cohorts of patients suffering from CKD or abdominal cancer and the impact of treatments (dialysate composition or chemotherapy respectively). We also aim at determining if these blood biomarkers could play a role in the establishment of SMA in muscles.

We found a progressive decreased expression of the biomarkers in CKD patients within a 1-year follow up, in accordance with the progressive muscle loss of CKD patients. However, no effect of the dialysate was found. Although preliminary, it seems that decreased biomarker levels prevail in cancer patients before muscle atrophy can be detected in clinic. Finally, we found that the 3 main biomarkers are differentially regulated upon catabolic situations [Dexamethasone or TNFα] in human cultured myotubes.

Keywords: Skeletal Muscle Atrophy, Biomarkers, Blood, Chronic Kidney failure, Cancers

Family name: Violin
First name: Maxime
Year of PhD: 3rd
Research team and Laboratory: Laboratoire AME2P - Équipe C
PhD supervisors: Sebastien Ratel and Abd-Elbasset Abaïdia
Email: maxime.violin@toulousefc.com
Language of presentation: French

Effect of maturity status on lower-limb strength testing reliability in academy football players from an elite professional club

Maxime Violin[1,2], Abd-Elbasset Abaïdia[3], Benjamin Barthelemy[2], Guillaume Rave[2], Sébastien Ratel[1]

[1]UR UCA 3533 AME2P Laboratoire des Adaptations Métaboliques à l'Exercice en conditions Physiologiques et Pathologiques, Université Clermont-Auvergne, Clermont-Ferrand, France
[2]Toulouse Football Club, 31400 Toulouse, France
[3]UR UPJV 3300 APERE Adaptations Physiologiques à l'Exercice et Réadaptation à l'Effort, Université de Picardie Jules Verne, Amiens, France

This study examined the test-retest reliability of dominant lower-limb strength in football players from an elite professional club academy, and compared the results based on maturity status and movement type.

Seventy players were divided into 3 groups: 24 pre-pubertal, 18 pubertal, and 28 postpubertal. After at least two familiarization sessions, they performed five maximum strength tests targeting adductor, abductor, posterior or anterior chain muscles of the dominant lower limb on two occasions one week apart. Coefficient of variation (CV) and intraclass correlation coefficient (ICC) were calculated for each test.

Most tests demonstrated good reliability within each maturity level (CV<10% and ICC>0.90). However, postpubertal players exhibited lower CV and higher ICC values than their pre-pubertal and pubertal counterparts. The least reliable tests were the standing posterior chain and standing abductor tests in prepubertal players (CV=12.3% and 8.4%; ICC=0.89 and 0.86; respectively).

Lower-limb strength testing reliability was influenced by maturity status, with pre-pubertal players showing relatively high reliability but higher CV and lower ICC than their more mature counterparts, notably for polyarticular movements. Therefore, lower-limb strength testing reliability is not interchangeable between maturity categories, and caution should be exercised when interpreting strength results for talent identification and long-term player development purposes.

Keywords: youth, testing, isometric, dynamometer

Family name: Couvert
First name: Annaëlle
Year of PhD: 3rd
Research team and Laboratory: AME2P
PhD supervisor: Nathalie Boisseau
Email: annaelle.couvert@uca.fr
Language of presentation: English

Acute Metabolic and Nutritional Responses to Isoenergetic HIIT Cycling vs. Running Sessions in Men with Overweight or Obesity

Couvert[1], M. Rance[2], E. Dore[1], V. Martin[1], C. Morel[2], B. Pereira[3], A.H JR Lancha [4], N. Boisseau[1]

[1]AME2P Laboratory, Clermont Auvergne University, Clermont-Ferrand; [2]Center of Resources, Expertise and Performance in Sports of Vichy; [3]Biostatistics unit (DRCI), University Hospital Center of Clermont-Ferrand, Clermont Auvergne University; [4]Laboratory of Applied Nutrition and Metabolism, School of Physical Education and Sport, University of São Paulo

Background: High Intensity Interval Training (HIIT) modality (cycling vs. running) may influence metabolic and nutritional responses to exercise. The objective was to compare the acute effects of isoenergetic HIIT modalities (HIIT-RUN and HIIT-BIKE) on post-exercise VO_2, fat oxidation and 24-hour energy balance.

Methods: Twelve fasted men (44.4±14.5 years; BMI: 28.3±1.9 $kg{\cdot}m^{-2}$) completed both HIIT sessions. VO_2 and VCO_2 were measured before, during and for 2 hours post-exercise, while substrate oxidation was calculated before and after exercise. Appetite was assessed throughout each session using a visual analogue scale (VAS) and energy intake (EI) was recorded via a 24-hour dietary questionnaire.

Results: Both exercise modalities resulted in similar energy expenditure, but HIIE-BIKE elicited a significantly higher mean RER ($p < 0.01$). No significant effect of exercise modality or time × modality interaction was observed for VO_2 or energy expenditure (EE) during the 2-hour post-exercise period. Fat oxidation was significantly higher during recovery compared to pre-exercise levels ($p < 0.001$) but did not differ between modalities. Appetite and 24-hour energy intake remained unaffected by exercise modality.

Conclusion: Both acute isoenergetic HIIT sessions resulted in similar VO_2 and EE during the 2-hour recovery period, with both modalities promoting fat oxidation to a comparable extent.

Keywords: Exercise, Modality, Energy Expenditure, Fat Oxidation

Family name: Lanhers
First name: Charlotte
Year of PhD: 3rd
Research team and Laboratory: Neurodol
PhD supervisor: Christian Dualé
Email: clanhers@chu-clermontferrand.fr
Language of presentation: French

Analytical approaches of the questionnaires used in chronic low back pain – towards a use in personalized care

Charlotte Lanhers[1], Emmanuel Coudeyre[2], Bruno Pereira[3], Christian Dualé[1]
[1]UMR (Inserm/UCA) 1107 Neuro-Dol
[2]INRAE
[3]Direction Recherche Clinique, CHU Clermont-Ferrand

Background: Specific assessment questionnaires are essential for understanding chronic non-specific low back pain (CNLB), but their psychometric validation and their position in the biopsychosocial model are insufficiently known.

Methods:

- Literature review of the validation of function questionnaires in CNL using Rasch analysis (item response theory)
- French-language validation in the LCNS of two questionnaires (adherence to exercises and feeling of propensity to return to work)
- Study of the biopsychosocial model in LCNS patients at work or in specialist care
- Analysis of data from two cohorts of French patients.

Results: We validated the French-language version of the EARS and RTWSE questionnaires (publication completed or in progress). More generally, our observations encourage us to be more demanding in terms of the psychometric validity of the tools we use, and enable us to envisage their use in clinical practice in a more rational manner. It also seems important to study men and women separately, given their different biopsychosocial interactions (publication in progress).

Discussion: Thanks in particular to our cohort data, we now hope to be able to propose simpler and more relevant models for characterising LCNS patients at the start of their treatment programme, with a view to personalising them.

Keywords: Chronic low back pain, Rasch analysis, psychometry, outcomes, biopsychosocial model

Vendredi
23 mai
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Résumés des communications orales et flash posters

DES JOURNÉES DE L'ÉCOLE DOCTORALE

Sciences de la Vie, Santé, Agronomie, Environnement

JED 2025
Sciences de la Vie, Santé, Agronomie, Environnement

Family name: Petiot
First name: Valentine
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisor: Olivier Da Ines
Email: valentine.petiot@uca.fr
Language of presentation: English

Dual role of *Arabidopsis thaliana* SRS2 helicase in meiotic recombination

Valentine Petiot[1], Floriane Chéron[1, 2], Charles I. White[1], Olivier Da Ines[1]

[1]Institut Génétique, Reproduction et Développement (iGReD), UMR 6293 CNRS, U1103 INSERM, Clermont-Ferrand, France

[2]Adresse actuelle: INRAe, UMR 1095 INRAE - Université Clermont Auvergne, Genetics, Diversity & Ecophysiology of Cereals (GDEC), Clermont-Ferrand, France

Helicases are enzymes that use the energy derived from ATP hydrolysis to translocate along and unwind nucleic acids. Accordingly, helicases are instrumental in maintaining genomic integrity and ensuring genetic diversity. Srs2 is a multi-functional DNA helicase that dismantles Rad51 nucleofilaments and regulates DNA strand invasion to prevent excessive or inappropriate homologous recombination in yeast. Consistently, the deletion of Srs2 has significant consequences for the maintenance of genome integrity in mitotic cells. In contrast, its role in meiotic recombination remains less clear.

We present here substantial evidence that SRS2 plays an important role in meiotic recombination in the model plant *Arabidopsis thaliana*.

Arabidopsis *srs2* mutants exhibit moderate defects in DNA damage-induced RAD51 focus formation, but SRS2 is dispensable for DNA repair and RAD51-dependent recombination in somatic cells. Meiotic progression and fertility appear unaffected in *srs2* plants but strikingly, the absence of SRS2 leads to increased genetic interference accompanied by increased numbers of Class I COs and a reduction in MUS81-dependent Class II COs. SRS2 thus has both anti- and pro-CO roles during meiosis in *Arabidopsis thaliana* - acting as an anti-CO factor by influencing the stability and/or the dissociation of early recombination intermediates, while playing a pro-CO role by promoting MUS81- mediated resolution of meiotic recombination intermediates.

Keywords: *Arabidopsis thaliana*, meiosis, homologous recombination, cross-over

Family name: Feit
First name: Léa
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisor: Simon Amiard
Email: Lea.FEIT@doctorant.uca.fr
Language of presentation: English

Study of GH1-domain proteins in chromatin organization and transcription regulation in *Arabidopsis thaliana*

Léa Feit[1], Emmanuel Vanrobays[1], Clara Bourbousse[2,3], Fredy Barneche[2,3], Christophe Tatout[1], Aline. V. Probst[1], Simon Amiard[1]

[1]iGReD, CNRS, Inserm, Université Clermont Auvergne, 63000 Clermont-Ferrand, France

[2]Institut de biologie de l'Ecole normale supérieure (IBENS), Ecole normale supérieure, CNRS, INSERM, Université PSL, Paris, France

[3]Sorbonne Université, IBPS, CNRS UMR 7622, Laboratoire de Biologie du Développement (LBD), 75005, Paris, France

The linker histone H1, critical for chromatin compaction, interacts with DNA at the nucleosome dyad through its GH1 domain (Globular domain of histone H1). Notably, the Arabidopsis genome encodes additional protein families containing a GH1 domain: the GH1-HMGA family and the TRB family. Recent studies indicate that these proteins are involved in chromatin epigenetic organization and transcriptional regulation. The diverse functions of these GH1-containing proteins highlight their significance in orchestrating gene expression and chromatin dynamics in Arabidopsis.

Recent research suggests a dynamic interplay and/or competition among these proteins for DNA accessibility. The objective of our study is to investigate the interaction/competition among GH1 domain-containing proteins, with a focus on the GH1-HMGA protein family.

Although the genome binding patterns of Arabidopsis H1 proteins have been elucidated, such information is currently unavailable for GH1-HMGA1. To fill this gap, we have generated a custom antibody targeting GH1-HMGA1. Following validation through Western Blot (WB) and Chromatin Immunoprecipitation (ChIP) assays, we intend to use this antibody to map the genomic localization of GH1-HMGA1 under wild-type conditions and in plants lacking H1. This comprehensive analysis will enable us to determine whether H1 exhibit an attracting or repelling effect on GH1-HMGA1 at specific genomic loci.

Keywords: GH1 domain, *Arabidopsis Thaliana*, GH1-HMGAs, chromatin organization

Family name: Frey
First name: Caroline
Year of PhD: 3rd
Research team and Laboratory: GDEC
PhD supervisor: Thierry Langin
Email: caroline.frey@inrae.fr
Language of presentation: English

The robustness of Stb resistance genes

Caroline Frey[1], Florence Cambon[1], Marc-Henri Lebrun[2], Thierry Langin[1], Cyrille Saintenac[1]
[1]Université Clermont Auvergne INRAe GDEC, [2]Université Paris-Saclay CNRS I2BC

Genetic resistance is one of the most agroecologically relevant strategies to protect wheat from Septoria tritici blotch (STB), caused by the fungus *Zymoseptoria tritici*. To date, 23 *Stb* wheat resistance genes have been identified, some of which following a gene-for-gene model. In field conditions, efficiency of these resistance highly depends on factors such as the environment and the fungal pressure. To assess the robustness of resistance, we studied the impact of high fungal inoculum on *Stb16q* resistance by phenotyping near-isogenic lines with 11 isolates of *Z. tritici* using increased spore concentrations. Under these conditions, *Stb16q* efficacy decreased, with up to 50% leaf covered by pycnidia, as compared to no pycnidia at low concentrations. At high inoculum levels, 75% of stomata, considered a barrier to *Z. tritici*, experienced penetration attempts, while only 20% closed, potentially explaining efficacy loss. One of the five identified *AvrStb16q* alleles identified among the 11 isolates was associated with a greater loss of *Stb16q* efficacy suggesting a role of *AvrStb16q* alleles recognition in this loss. Unlike *Stb16q*, *Stb6* remains fully effective using high inoculum concentration. These findings demonstrate that, resistance confer by major *Stb* genes is more quantitative than qualitative with gene-dependent efficacy influenced by environmental factors.

Keywords: Phytopathology, Wheat, Resistance, *Zymoseptoria tritici*, Robustness

Family name: Khan
First name: Kinza
Year of PhD: 3rd
Research team and Laboratory: PIAF-UMR-biology
PhD supervisor: Nathalie Leblanc-Fournier
Email: kinza.khan@uca.fr
Language of presentation: English

Postural control in Arabidopsis: a focus on actin network and auxin signalling in proprioception process

Kinza Khan[1], Jérôme Franchel[1], Félix Hartman[1], Nicole Brunel[1], Mélanie Decourteix-Volle1, Valerie Legue[1], Jason Reed[2], Bruno Moulia[1], Nathalie Leblanc-Fournier[1]

[1]University of Clermont Auvergne, Department of Biology, Biomechanics, Clermont France.
[2]University of North Carolina at Chapel Hill, Department of Biology, Chapel Hill, France.

The ability of plant organs to sense their local curvature and driving the progressive establishment of organ straightening is known as proprioception. This is a key mechanism in achieving correct shape and regulating the growth dynamics in combination with gravisensing and light perception. In this study, we aim to explore molecular players driving proprioception in *Arabidopsis*. Previous experiment using myosin-XI mutants suggested a role of actin in this process. The proprioceptive insensitivity in this mutant could be either due to the disruption of their cargo function or due to the modification of tension in actin cables. To explore the role of actin filaments we analyzed actin network with confocal microscopy. In wild type, during the gravitropic-upward-curving-phase, these long actin bundles deviate from their straight-alignment and become wavy. During the de-curving-phase, these actin bundles regain their straight configuration. Then we produced RNAi-villin plants where actin configuration was specifically altered in fibre cells in stem. Using computational phenotypic tool, these lines appeared to be insensitive to proprioception confirming the importance of actin filament in controlling plant posture. We are exploring the actin configuration in both mutants and how it could modify the growth pattern and auxin action during plant movements.

Keywords: Proprioception, actin network, confocal microscopy, plant shape

Family name: Magliaraschi
First name: Ninon
Year of PhD: 3rd
Research team and Laboratory: GDEC - IPM
PhD supervisors: Ludovic Bonhomme and Thierry Langin
Email: ninon.magliaraschi@doctorant.uca.fr
Language of presentation: English

Unravelling the role of a regulatory hub of wheat susceptibility to Fusarium head blight in bread wheat

Ninon Magliaraschi[1], Florian Rocher[2], Anne Partier[1], Géraldine Philippe[1], Thierry Langin[1], Ludovic Bonhomme[1]

[1]GDEC
[2]Växtskyddsbiologi

Fusarium Head Blight (FHB), caused by *Fusarium graminearum*, is a disease affecting wheat heads. The infection process leverages unconventional mechanisms that exploit host susceptibility factors, diverging from classical determinants of host resistance. Our previous studies have revealed a conserved regulatory network across multiple wheat cultivars, linking fungal effector expression with core host-response modules and highlighting genes that act either upstream or downstream of the wheat response. In this study, two key genes were selected for functional validation using the Virus-Induced Gene Silencing (VIGS) method in spikes. The first belongs to the WRKY transcription factor family and is thought to be targeted by nuclear effectors of *F. graminearum*. It acts as a master regulator involved in responses to various stresses due to its broad impact on downstream gene regulation. The second belongs to the STP family and functions downstream of the WRKY gene. It plays a role in sugar transport and is involved in biotic stress responses. Silencing both genes prior to fungal infection resulted in a significant one-third reduction in FHB symptom severity, suggesting that both genes contribute to wheat susceptibility to FHB. These findings support their key roles in disease development and provide promising targets for breeding programs.

Keywords: wheat, FHB, WRKY, STP, VIGS

Family name: Paltrinieri
First name: Stefania
Year of PhD: 3rd
Research team and Laboratory: iGReD – Coded, équipe Probst-Tatout
PhD supervisor: Aline Probst
Email: stefania.paltrinieri@uca.fr
Language of presentation: English

Nuclear and chromatin organization are reprogrammed during seed germination

Stefania Paltrinieri[1], Samuel Le Goff[1], Paolo Lucas Rodrigues Silva[2], Lauriane Simon[1], Manon Verdier[1], Sylviane Cotterell[1], Vicente Rubio[2] and Aline V. Probst[1]

[1]CODED laboratory, CNRS, Inserm, GReD, Clermont-Ferrand, France

[2]Vicente Rubio Lab, Plant Molecular Genetics Dept., Centro Nacional de Biotecnología (CNB-CSIC), Madrid, Spain.

The plant embryo surrounded by endosperm and enclosed by the seed coat can survive long periods in a desiccated state. The severe water deficit is thought to inhibit most biological processes, including transcription and translation, and, in *Arabidopsis* dry seed embryos, the genetic material is organized in small nuclei with highly condensed chromatin. Successful germination and seedling establishment require major changes in gene expression as well as chromatin and nuclear organization.

Using the Brassicaceae species *B. napus* as a model system, and combining proteomics, molecular and imaging approaches, we are investigating the chromatin composition in rapeseeds and study how this organization is reprogrammed during seed germination and seedling establishment.

We find that chromatin in rapeseed dry seeds is characterized by particular histone variants and modifications, and that seed imbibition triggers the eviction of histone variants and the progressive enrichment in histone marks associated with transcriptional activation.

Keywords: Plant embryo, germination, histone, chromatin

Family name: Sireta
First name: Gilles
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisors: Aline Probst and Christophe Tatout
Email: gilles.sireta@uca.fr
Language of presentation: English

Automation of an RNA-seq analysis workflow to facilitate data processing and reproducibility

Gilles Sireta[1], Gwendal Cueff[2], Vincent Darbot[3], Marie Lefebvre[2], Simon Amiard[1], Aline V. Probst[1] and Christophe Tatout[1]

1 iGReD, Université Clermont Auvergne, CNRS, INSERM, BP 38, Clermont-Ferrand, 63001, France.

2 INRAE, Unité de Nutrition Humaine, Université Clermont Auvergne, UMR 1019, F-63000 Clermont-Ferrand, France

3 GenPhySE, Université de Toulouse, INRAE, ENVT, 31326 Castanet Tolosan, France

The analysis of next generation sequencing data allows an in depth understanding of biological processes, yet the complexity inherent in the multitude of available tools, each with their own parameters, negatively affects standardization and reproducibility of bioinformatic analyses. My aim is to conduct a meta-analysis of several RNA-seq datasets of *Arabidopsis thaliana* plants having undergone prolonged heat stress, a treatment useful to understand the role of transcriptional regulation in the plant’s response to heat stress. As such, I decided to systematize and automate the process of analyzing these datasets by creating a scalable solution for comprehensive transcriptomic profiling. This workflow is called CRESCENT (Comprehensive RNA-Seq Expression, Splicing, and Coding/non-coding Element Network Tool) and uses the workflow management tool Snakemake to process RNA-seq datasets from raw data all the way to differential analysis and functional enrichment analysis, both for expression and splicing. This workflow allows the user to set parameters relevant to their specific dataset in a software-agnostic way, choose among a selection of tools, then either launch parts of the pipeline or the entire process at once, at their discretion. This workflow has allowed me to easily handle multiple, sometimes large datasets very quickly and ensure reproducibility of my results.

Keywords: bioinformatics, meta-analysis, workflow, reproducibility, automation

Family name: Fakih
First name: Aya
Year of PhD: 3rd
Research team and Laboratory: INRAE, Unité QuaPA (Qualité des Produits Animaux)
PhD supervisor: Erwan Engel
Email: ayafakih9999@gmail.com
Language of presentation: English

Volatolomics to phenotype *Listeria monocytogenes* behavior: impact of growth and acid stress

[1]Aya Fakih, [1]Jérémy Ratel, [2]Dimitra Tsoureki, [1]Frédéric Mercier, [1]Nathalie Kondjoyan, [3]Nelly Caccia, [2]Cristian Botta, [2]Kalliopi Rantsiou, [1]Erwan Engel

[1]French National Research Institute for Agriculture, Food and Environment (INRAE), UR QuaPA, MASS Group, Saint-Genès-Champanelle, France.
[2]Department of Agricultural, Forest and Food Sciences, University of Turin, Turin, Italy.
[3]INRAE, Université Clermont Auvergne, UMR454 MEDiS, 63000 Clermont-Ferrand, France.

Volatolomics - branch of metabolomics focused on volatile organic compounds (VOCs) - provides a wealth of information for phenotyping key foodborne pathogens like *Listeria monocytogenes* (*L. monocytogenes*) in their culture medium.

Prior to investigate the bacterial volatolome, it is essential to determine the most informative sampling mode as there is no knowledge available in the literature on this topic. Taking *L. monocytogenes* as a model pathogen, volatolomics was performed by headspace solid phase microextraction - gas chromatography - Q Exactive - Orbitrap™ mass spectrometry, on three types of samples: Whole culture – which contains global information diluted by the growth medium and avoids any handling of bacterial samples; pellet – which contains bacterial cells; and supernatant – which contains what the bacteria can release into the growth medium. Results show that whole culture and pellet led to reveal the maximum number of candidate volatile markers of *L. monocytogenes*.

Furthermore, the study examined how the volatolome reflects variations during different growth phases of the pathogen and in response to stress factors, such as acidification of the culture medium. A large number of candidate markers were identified, including those that seem promising in the perspective of future development of diagnostic tools.

Keywords: Microbial volatolomics, foodborne pathogen, GC-HRMS, acid stress, untargeted screening

Family name: Parayre
First name: Inès
Year of PhD: 3rd
Research team and Laboratory: DeciSiPH
PhD supervisor: Marie-Pierre Sauvant-Rochat
Email: iparayre@hotmail.fr
Language of presentation: French

Environmental Health in Perinatal Care: Professional Perceptions and Territorial Dynamics – The ProSET Study

Inès Parayre[1], Marie-Pierre Sauvant-Rochat[1]
[1]Université Clermont Auvergne, Clermont Auvergne INP, CNRS, Institut Pascal, F-63000 Clermont-Ferrand, France

Introduction: The First 1000 Days Program in France highlights the importance of early environmental exposures—particularly to endocrine disruptors—on long-term health, in line with the Developmental Origins of Health and Disease (DOHaD) concept. This period of vulnerability requires coordinated action among perinatal professionals to promote healthier environments and raise families' awareness of environmental risks.
The ProSET study (Promotion of Environmental Health at the Territorial Level) explores how perinatal health professionals and policymakers in a rural area perceive and incorporate environmental health into their practices.

Method: A qualitative study was conducted in a rural area of Auvergne-Rhône-Alpes with 44 healthcare professionals, pharmacists, and local policymakers. Interviews were recorded and thematically analysed using NVivo15 until data saturation.

Results: Participants expressed interest in environmental health, but their knowledge—particularly about the DOHaD concept and the First 1000 Days—was often partial and informally acquired. While endocrine disruptors such as bisphenol A were commonly cited, knowledge regarding their exposure routes and sources remained limited. Engagement was driven by personal and ethical motivations. Barriers included lack of time, training, and territorial coordination.

Conclusion: Integrating environmental health represents a key opportunity to improve perinatal health, contingent on interprofessional collaboration, harmonised knowledge, and effective territorial governance.

Keywords: Environmental health – Health promotion – Public health – Perinatal care – Professional perceptions – Territorial dynamics

Family name: Fantelli
First name: Reshad
Year of PhD: 3rd
Research team and Laboratory: INRS - UMRF
PhD supervisors: Céline Delbès (UMRF) and Patricia Battais (INRS)
Email: reshad.fantelli@inrae.fr
Language of presentation: French

Aerosolization during cheeses wiping as a major factor of microbial transfer in ripening cellar

Reshad Fantelli[1,2], Sullivan Lechêne[3], Mathilde Lacalmontie[2], Sébastien Theil[2], Elisa Michel[2], Christophe Chassard[2], Philippe Duquenne[1], Patricia Battais[1], Céline Delbès[2]

[1]Laboratoire d'Analyses Spatiales et Temporelles des Expositions Chimiques, INRS, 54519 Vandœuvre-lès-Nancy Cedex, France. [2]Université Clermont Auvergne, INRAE, VetAgro Sup, UMR545 Fromage, 20 Côte de Reyne, 15000 Aurillac, France. [3]Laboratoire Aéraulique, Ventilation, Thermique et Qualité d'air, INRS, 54519 Vandœuvre-lès-Nancy Cedex, France

Various biological agents (bacteria, molds, yeasts…) contribute by their metabolic activity to cheese's ripening. In ripening cellar, cheese cares, like wiping, may disperse bioaerosols. Chronic inhalation of potential allergenic particles may cause the development of respiratory diseases. However, microorganisms' emissions and fluxes in ripening cellars remained poorly documented.

To evaluate microorganisms transfer during cheese wiping, we focused on microbial community from long-ripened cheeses (CH_LR) and its dispersion in air (AR) and on short-ripened cheeses (CH_SR). Thirty-six Saint-Nectaire PDO cheeses (SR, LR), were stored and further wiped or not wiped, in 3 experimental cellars (INRAE, Aurillac). Samples were taken over 4 weeks in four environments: air, cellar walls, wiping cloth and cheese rinds. Levels of culturable bacteria and fungi were assessed (n=92) and microbial communities were analyzed by metabarcoding (16S RNA and ITS genes) (n=101).

Results showed airborne mold levels rising to 7 log UFC/m^3 during cheese wiping. Microbial profiles analyses revealed dominant genera, including Mucor, Penicillium, and Glutamicibacter on CH_LR rinds. Some of them were shared between cheese rinds, cloths and air. Wiping also contributed to dispersion of less abundant genera on cheeses rinds such as Chrysosporium since its relative abundance in air was greater in the cellar where CH_LR were wiped.

Keywords: ripening, experimental cellars, cheese, wiping activity, dispersion

Family name: Lechauve
First name: Jean-Baptiste
Year of PhD: 3rd
Research team and Laboratory: Institut Pascal
PhD supervisor: Emmanuel Coudeyre
Email: jblechauve@gmail.com
Language of presentation: French

Evaluation of the impact of a smartphone application on adherence to an exercise program in people with chronic low back pain: a randomized controlled trial

JB. Lechauve[1], L. Dobija[1], B. Pereira[2], M. Grolier[1], M. Pelletier[1], C. Lanhers[1], E. Coudeyre[1]
[1]Service de Médecine Physique et de Réadaptation, CHU Clermont-Ferrand
[2]Direction de la Recherche Clinique et de l'Innovation, unités de biostatistiques, CHU Clermont-Ferrand

The positive effects of multidisciplinary rehabilitation programs tend to fade over time due to low long-term patient adherence. We aimed to evaluate the impact of a smartphone application on adherence to an exercise program at 6 months for individuals with chronic low back pain (CLBP).
110 participants with CLBP were randomly assigned into two groups: 54 in the intervention group (IG), who received education on using the app in addition to usual care (multidisciplinary rehabilitation and self-management education), and 56 in the control group (CG) (only usual care). The Exercise Adherence Rating Scale (EARS) was the primary outcome. Secondary outcomes included pain, disability, barriers to physical activity, physical capacity, and qualitative adherence. Statistical analyses were performed using an intention-to-treat approach with a linear mixed model to compare the primary endpoint at 6 months.
71 participants were evaluated at 6 months. No significant differences were observed between the groups regarding adherence, pain, or disability. However, significant differences were found between the groups at 6 months for physical capacity and qualitative adherence in favor of the IG. Furthermore, the IG showed significant improvements in all outcomes compared to baseline, while the CG did not.
The smartphone application had no impact on exercise adherence at 6 months in individuals with CLBP. However, it may serve as a useful self-management tool, given the positive effects observed on pain, function, physical capacity, and exercise execution in the IG.

Keywords: Chronic low back pain, smartphone application, adherence, exercise

Family name: Richard
First name: Amélie
Year of PhD: 2nd
Research team and Laboratory: ACCePPT
PhD supervisors: Hélène Vaillant-Roussel and Catherine Laporte
Email: amelie.richard@uca.fr
Language of presentation: French

Prescription-free consultation, “the art of doing without”

Amélie Richard, Hélène Vaillant-Rousse, Catherine Laporte
ACCePTT AutomédiCation aCcompagnement Pluriprofessionnel Patient
Institut Pascal : Centre National de Recherche scientifique (CNRS) Université Clermont Auvergne, Clermont Auvergne INP, CHU Clermont-Ferrand.

This thesis is part of an approach aimed at studying and improving the relevance of care and the fight against over-medicalisation. In particular, reducing the excessive use of antibiotics is a priority in the face of the growing emergence of antibiotic resistance.

Consultations without a medical prescription were 24% (95% CI [20.11-27.41]). One limiting factors was ‘consultations for acute reasons’ (OR = 0.33). A poster shows a tool used in: the capillary CRP in Europe. The use of CRP in primary care in France was studied; 91 CRP measurements were taken. When the CRP concentration was < 20 mg/L, doctors prescribed fewer antibiotics (odds ratio: 12.0, 95% confidence interval: 1.91 to 75.8, p=0.008). The 45 patients in centre 1 had recovered after three months. The ACROPOLE protocol aims to evaluate the contribution of capillary CRP in a trial with a control group.

Consultations with drug prescriptions are infrequent in France, 24%, consultations for acute reasons increase the prescription of drugs (OR=0.33). Capillary CRP could help limit the prescription of antibiotics. In France, when the CRP concentration is < 20 mg/L, doctors prescribe fewer antibiotics. Antibiotic prescriptions appear to be decreasing in France with the use of capillary CRP. The protocol for a larger study on capillary CRP ACROPOLE is being submitted.

Keywords: Prescription-free consultation, Deprescribing, Capillary CRP, Primary care, antibiotics

Family name: Salanon
First name: Elfried
Year of PhD: 3rd
Research team and Laboratory: PFEM, UMR 1019 UNH INRAE
PhD supervisor: Estelle Pujos-Guillot
Email: elfried.salanon@gmail.com
Language of presentation: English

Assessing the variability structure of analytical measurements using bivariate dispersion

Elfried Salanon[1], Blandine Comte[1], Delphine Centeno[1], Stéphanie Durand[1], Estelle Pujos-Guillot[1], Julien Boccard[2]

[1]Université Clermont Auvergne, INRAE, UNH, Plateforme d'Exploration du Métabolisme, MetaboHUB Clermont, Clermont-Ferrand, France

[2]School of Pharmaceutical Sciences, University of Geneva, Geneva, Switzerland

Assessing repeatability and reproducibility in analytical chemistry often relies on dispersion indicators computed from repeated Quality Control (QC) measurements. However, classical indicators like standard deviation may fail to capture complex variability patterns. This study proposes a visualization method to better describe intra- and inter-batch dispersion structures.

A Euclidean space is defined using the "measurement order" (X-axis) and "intensity" (Y-axis). The convex hull (CH) of repeated QC measurements represents the smallest convex set containing all data points, allowing the visualization of dispersion patterns. This approach was evaluated on simulated data with different bias types (additive, multiplicative) and real metabolomics data from NIST SRM1950 analyzed over a year.

The method effectively described batch-wise drift and revealed distinct dispersion structures depending on bias type. It enabled the detection of non-constant bias and anomalies within the acquisition sequence. The approach also identified common behaviors among analytes.

This visualization method provides a comprehensive assessment of variability within and between batches. Combined with dispersion indicators, it facilitates identifying acquisition issues and supports selecting appropriate correction strategies.

Keywords: Reproducibility, Precision, LC/MS, Dispersion, Drift

Family name: Baabdaty
First name: Elissa
Year of PhD: 3rd
Research team and Laboratory: iGReD
PhD supervisor: Cyrille De Joussineau
Email: elissa.baabdaty@uca.fr
Language of presentation: English

Study of the mechanisms of the initiation and evolution of early epithelial tumors. Implications for prostate carcinogenesis

Elissa Baabdaty, Marine Vialat, Marielle Limoges, Amalia Trousson, Françoise Degoul, Jean-Marc A. Lobaccaro, Silvère Baron, Laurent Morel & Cyrille de Joussineau

The Notch signaling pathway is evolutionarily conserved and plays a crucial physiological role in cell fate determination, tissue homeostasis, but also a pathological role in carcinogenesis. However, its implication in prostate tumorigenesis remains ambiguous, with contradictory observations regarding its promoting or inhibitory effect on tumor growth and evolution, without a comprehensive understanding of the underlying mechanisms.

Our team has previously developed a model of prostate tumorigenesis in vivo, using a structural and functional equivalent of a prostatic acinus, the accessory gland of Drosophila melanogaster. This model is based on clonal expression of the oncogene EGFRλ which allows precise quantification of tumor formation following basal extrusion phenomenon, and the degree of tumor cell progression based on their localization, number and expression of markers of aggressiveness.

In this context, we have deciphered the influence of the different components of the Notch pathway on tumor initiation, progression and resistance. Remarkably, our results reveal the existence of two opposing signaling within the Notch pathway. On the one hand, canonical Notch-dependent signaling displays an anti-tumoral action. On the other hand, depending of Notch ligand Delta, a predominant and separated signaling occurs, which itself strongly promotes tumorigenesis.

These findings rationalize previous contradictory observations and suggest targeted therapeutic avenues to achieve specific anti-tumor effects.

Keywords: Tumor formation, signaling pathway, initiation, prostate

Family name: Dubois
First name: Maxime
Year of PhD: 3rd
Research team and Laboratory: IMoST
PhD supervisor: Mahchid Bamdad
Email: maxime.dubois@uca.fr
Language of presentation: English

LightSpot®-FL-1, an innovative tool for evaluating the Permeability-glycoprotein as a predictive biomarker of tumor resistance in acute leukemia models

Maxime Dubois[1], Antoine Goisnard[1]#, Céline Bourgne[2]#, Elodie Gay[1], Marie Depresle[1], Manon Roux[1], Allison Voisin[2], Marc Berger[2], Frédérique Penault-Llorca[3], Emmanuelle Mounetou[1]#, Pierre Daumar[1]#, Mahchid Bamdad[1]

[1]UMR INSERM/UCA U1240, Imagerie Moléculaire et Stratégies Théranostiques, Institut Universitaire de Technologie, Université Clermont Auvergne, 63000 Clermont-Ferrand, France. [2]Equipe d'accueil 7453 CHELTER, CHU Clermont-Ferrand, Hôpital Estaing, Université Clermont Auvergne, 63003 Clermont-Ferrand, France. [3]Centre de Lutte contre le Cancer Jean Perrin, Université Clermont Auvergne, UMR INSERM-UCA, U1240, Imagerie Moléculaire et Stratégies Théranostiques, 63000 Clermont-Ferrand, France. # equal contributions

MultiDrug Resistance (MDR) proteins contribute to chemotherapy resistance in various cancers. Among them, the P-glycoprotein (P-gp) has been the most investigated. These works aim to evaluate the efficacy of the new fluorescent tracer LightSpot®-FL-1 for quantifying P-gp in CCRF-CEM and KG-1a acute leukemia cell lines, as well as in blood samples from healthy donors and leukemic patients. First, flow cytometry analysis revealed the high specificity of LightSpot®-FL-1 in measuring P-gp expression in both cell lines and clinical samples. Then, in CCRF-CEM and KG-1a cells exposed to increasing concentrations of Daunorubicin (DNR) a significant drop in P-gp expression levels was detected as early as 3h following exposure to high doses. Moreover, this drop preceded a dose-dependent decline in cell viability detected after 24h of treatment. These findings suggest that P-gp downregulation could serve as a potential biomarker of treatment efficacy. Additionally, LightSpot®-FL-1 analysis of six acute myeloid leukemia patient blood samples allowed the identification of 14 distinct blast subpopulations, revealing substantial inter- and intra-individual heterogeneity in P-gp expression. Thus, these findings underscore the potential of LightSpot®-FL-1 as a valuable tool for re-evaluating the clinical relevance of P-gp in tumor resistance diagnosis.

Keywords: Multi-Drug Resistance, P-gp, LightSpot®-FL-1 fluorescent probe, Daunorubicin, Acute Leukemia

Family name: Besombes
First name: Joévin
Year of PhD: 3rd
Research team and Laboratory: EA 7453 CHELTER (UCA)
PhD supervisors: Marc Berger and Andrei Tchirkov
Email: joevin.besombes@gmail.com
Language of presentation: English

The CML clone at diagnosis exhibits intra-clonal heterogeneity in telomere dynamics at the CD34+ hierarchical level

Joévin Besombes[1,2], Thomas Tassin[1,2], Benjamin Lebecque[1,2], Candice Internicola[1], Estéban Louis[2], Farida Godeau[3], Éric Hermet[4], Marc G Berger[1,2], Andreï Tchirkov[1,3], Céline Bourgne[1,2].

[1]EA7453 CHELTER, UCA.
[2]Service d'hématologie biologique, CHU Clermont-Ferrand.
[3]Service de cytogénétique médicale, CHU de Clermont-Ferrand.
[4]Service d'hématologie clinique, CHU de Clermont-Ferrand.

Background: Tyrosine kinase inhibitors (TKIs) have significantly improved chronic myeloid leukemia (CML) outcomes, but individual responses vary, and few patients can discontinue treatment. Telomere shortening in CML correlates with lower deep molecular response rates and tumor burden in CD34+CD38− cells. This study investigates intra-clonal telomere dynamics at the CD34+ level.

Methods: Relative average telomere length (aTL) was measured by qPCR in total leukocytes (n=97) and CD34+ cells (n=32) from CML patients at diagnosis and compared to controls (n=92, n=22 respectively). Telomerase gene (hTERT) expression was quantified by digital PCR in 45 total leukocytes samples.

Results: CML leukocytes and CD34+ cells had shorter telomeres than controls. Two CML subgroups were identified: one with significantly shortened CD34+ telomeres ($p=0.002$) and another with CD34+ telomeres comparable to total leukocytes. The subgroup with equivalent telomere length between CD34+ and total leukocytes exhibited a higher rate of major molecular response at M12. hTERT expression was reduced in CML but overexpressed in high Sokal score patients ($p=0.0046$).

Discussion: Telomere shortening in CML, especially in CD34+ cells, and altered hTERT/RAP1 expression may influence prognosis. Further studies will evaluate their predictive value for therapy response and relapse risk after TKI discontinuation.

Keywords: chronic myeloid leukemia, telomere dynamics, tyrosine kinase inhibitors

Family name: Chanchou
First name: Marion
Year of PhD: 3rd
Research team and Laboratory: Inserm UMR1240 IMoST
PhD supervisor: Florent Cachin
Email: marion.chanchou@clermont.unicancer.fr
Language of presentation: English

^{99m}Tc-NTP 15-5, proteoglycan tracer: Phase I trial (CARSPECT)

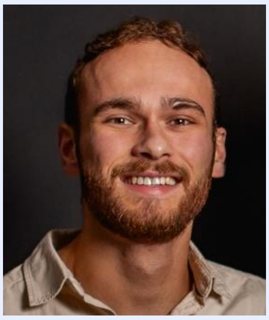
Marion Chanchou[1,2], Emilie Thivat[1,3,4], Sylvain Mathieu[5], Sophie Levesque[1,2,6], Nicolas Sas[1,7], Philippe Auzeloux[1], Tommy Billoux[1,7], Ioana Molnar[1,3,4], Elodie Jouberton[1,2], Jacques Rouanet[1,8], Giovanna Fois[9], Lydia Maigne[9], Frédérique Penault-Llorca[1,10], Elisabeth Miot-Noirault[1], Xavier Durando[1,3,4,11], Florent Cachin[1,2,3]

[1]INSERM U1240 IMoST, Université Clermont Auvergne, 63000 Clermont-Ferrand, France.[2]Service de Médecine Nucléaire, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.[3]Centre d'Investigation Clinique UMR501, F-63000 Clermont-Ferrand, France.[4]Département de Recherche Clinique, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.[5]Service de Rhumatologie, Université Clermont-Auvergne, CHU Gabriel Montpied, 63000 Clermont-Ferrand, France.[6]Unité de radiopharmacie, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.[7]Service de Physique Médicale, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.[8]Service de Dermatologie et d'Oncologie Cutanée, CHU Clermont-Ferrand, F-63000, France.[9]Laboratoire de Physique de Clermont, UMR6533, CNRS/IN2P3, Université Clermont Auvergne, France.[10]Département de biopathologie, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.[11]Département d'oncologie médicale, Centre Jean PERRIN, F-63000 Clermont-Ferrand, France.

^{99m}Tc-NTP 15-5 showed affinity for cartilage proteoglycans on preclinical studies but has not been tested in humans. This phase I trial aims to define the optimal of ^{99m}Tc-NTP 15-5 injected activity to obtain the best visual contrast of cartilage, without toxicity. Patients with unilateral knee osteoarthritis or breast cancer treated with hormonal therapy were eligible. Three activities were studied, from 5 to 15 MBq/kg. Visual tracer uptake of 31 joints was rated on scintigraphies, from 30 min to 6 h p.i, followed by 3D quantification on SPECT-CT. Pharmacokinetics, biodistribution and dosimetry were studied on urine, blood and scintigraphies. Tolerance was scored according to NCICTC 4.0 scale. Five patients were injected with ^{99m}Tc-NTP 15-5, without major toxicity. With a 15 MBq/Kg activity, the median rate of joint uptake higher than diaphysis was 80.6% (80.60 – 85.45) at 2 h p.i. and increased with time. Cartilage S/N ratio with muscular background was superior to 3 from 2h30 p.i. Uptake evolution discriminated cartilage from background and from ligaments and tendons for all examination times ($p < 0.001$). Pharmacokinetic, biodistribution and dosimetry were similar to preclinical studies. ^{99m}Tc-NTP 15-5 is a new tracer for cartilage human functional imaging.

Keywords: ^{99m}Tc-NTP 15-5, Cartilage, Scintigraphy, Pharmacology

Family name: Chaussin
First name: Benjamin
Year of PhD: 3rd
Research team and Laboratory: UMR 1240 Inserm / UCA IMoST
PhD supervisor: Florent Cachin
Email: benjamin.chaussin@doctorant.uca.fr
Language of presentation: English



Development of a 3D *in vitro* model of triple-negative breast cancer for the evaluation of radiobiological effects

Benjamin Chaussin[1], Marjorie Maillet[1], Alban Revy[2], Sophie Levesque[2] Emmanuel Chautard[3], Erwan Boutault[3], Christopher Montemagno[4], Jérôme Durivault[4], Sébastien Schmitt[1], Elisabeth Miot-Noirault[1], Florent Cachin[2], Elodie Jouberton[2]

[1]UMR1240 INSERM, Université Clermont Auvergne, 58, rue Montalembert, BP 184, 63005 Clermont-Ferrand, France
[2]Médecine Nucléaire, Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand
[3]Anathomopathologie, Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand
[4]Biomedical Department, Centre Scientifique de Monaco, 98000 Monaco, Monaco.

Molecular Radiotherapy (MRT) using ^{177}Lu-PSMA is a new promising therapeutic strategy particularly in Triple-Negative Breast Cancer (TNBC), the most aggressive subtype of breast cancer, characterized by high invasiveness and a poor prognosis. The emergence of this strategy requires the development of *in vitro* models representing tumour architecture and cellular interactions to study radiobiological effects. The mild overexpression of PSMA in TNBC suggests evaluating MRT alone or in combination with PARP inhibitors (Olaparib) in this pathology. The objective of this study is to propose a 3D *in vitro* culture model for TNBC to examine the radiobiological effects of 177Lu-PSMA. Two TNBC cell lines (MDA-MB-231 and MDA-MB-436) were cultured and transfected to express PSMA. Morphological characterization and cell count were performed. Doubling Time was evaluated for these two models: 89,3 ± 8,8 hours for MDA-MB-231 and 103,3 ± 3,5 hours for MDA-MB-436. An initial uptake study with 177Lu-PSMA-I&T demonstrated the stability of the radiopharmaceutical in the culture medium for 5 days, an uptake by TNBC spheroids (PSMA+) up to 5 days post-treatment. Dose-escalation of 177Lu-PSMA and Olaparib are ongoing to determine the dose for the combination of treatments. In short term, the efficacy of the therapeutic combination will be evaluated on 3D *in vitro* models. Ultimately, this approach could be transferred to *in vivo* models for further analysis and toxicities evaluation.

Keywords: Triple Negative Breast Cancer, Molecular Radiotherapy, spheroids, PSMA

Family name: Croizier
First name: Carolyne
Year of PhD: 3rd
Research team and Laboratory: CHELTER
PhD supervisor: Romain Guièze
Email: carolyne.croizier@gmail.com
Language of presentation: French

Venetoclax resistance in real-life chronic lymphocytic leukemia cohort: RAVEN study

Carolyne Croizier[1], Manon Garcia[1], Olivier Tournilhac[1], Bruno Pereira[2], Marie-Sarah Dilhuydy[3], Pierre Feugier[4], Vincent Levy[5], Anne-Sophie Michallet[6], Anne Quinquenel[7], Damien Roos-Weil[8], Loïc Ysebaert[9], Sylvain Carras[10], Pierre Morel[11], Morgane Nudel[12], Stéphanie Poulain[13], Annie Brion[14], Nataliya Dmytruk[15], Thérèse Aurran-Schleinitz[16], Emmanuelle Tchernonog[17], Gregory Lazarian[18], Lauren Véronèse[19], Romain Guièze[1]

[1]Service de thérapie Cellulaire et d'hématologie clinique, CHU Estaing, EA 7453 CHELTER, UCA, Clermont-Ferrand, [2]Département médico-économique et bio-statistique, DRCI CHU Clermont-Ferrand. [3]Service hématologie clinique, CHU Bordeaux. [4]Service hématologie clinique, CHU Nancy. [5]Service hématologie clinique, Bobigny, Paris. [6]Service hématologie clinique, Centre Leon Berard, Lyon. [7]Service hématologie clinique, CHU Reims.[8]Service hématologie clinique, La Pitié, Paris. [9]Service hématologie clinique, Oncopole, Toulouse. [10]Service hématologie clinique, CHU Grenoble. [11]Service hématologie clinique, CHU Amiens. [12]Service hématologie clinique, CHU Lille. [13]Laboratoire hématologie biologique, CHU Lille. [14]Service hématologie clinique, CHU Besançon. [15]Service hématologie clinique, CHU Limoges. [16]Service hématologie clinique, Institut Paoli Calmette, Marseille. [17]Service hématologie clinique, CHU Montpellier. [18]Laboratoire hématologie biologique, Bobigny, Paris. [19]Laboratoire cytogénétique médicale, CHU Estaing, CHU Estaing, EA 7453 CHELTER, UCA, Clermont-Ferrand.

Venetoclax, the first oral BCL2 inhibitor, is approved in both front-line and relapsed lines in chronic lymphocytic leukemia (CLL) and considerably improves its clinical outcomes. However, cases of resistance still exists and the characterization of resistance mechanisms is necessary to allow a personalized approach in term of patientcare. Mutations in the targeted-gene *BCL2* are first described as resistance mechanism (Blombery P. et al., *Cancer Discovery*, 2019). Another mechanism is the hyperexpression of MCL1, a protein of BCL2 familly, sometimes associated at amplification of the 1q21 region (Guièze R. et al., *Cancer Cell*, 2019). Both of these mechanisms are described into small separately cohorts. RAVEN is a multicentric, retrospective, translationnal study (NCT05246345) promoted by the CHU Clermont-Ferrand. Between March 2022 and Mars 2025, 74 CLL patients resistant to venetoclax were enrolled. *BCL2* mutations in NGS-sequencing were found in 27.45% (n=14/51) of the cases and 1q21 amplification in FISH was found in 36,53% (n=19/52) of the cases. Our study is the largest real-life CLL patient cohort with a venetoclax resistance.

Keywords: chronic lymphocytic leukemia, venetoclax, resistance, BCL2 inhibitor

Family name: Pinard
First name: Celeste
Year of PhD: 3rd
Research team and Laboratory: IMoST
PhD supervisors: Xavier Durando and Catherine Abrial
Email: celeste.PINARD@clermont.unicancer.fr
Language of presentation: English

Identification of circulating protein candidates for prediction of response to neoadjuvant chemotherapy in triple negative breast cancer: preliminary results from the INSTIGO study

Celeste Pinard[1-3], Angeline Ginzac[1-3] Ioana Molnar[1-3], Hugo Veyssiere[2], Yannick Bidet[4], Vincent Sapin[5], Julie Durif[5], Catherine Abrial[1-3], Frederique Penault-Llorca[1,8] Xavier Durando[1-3,6], Nina Radosevic-Robin[1,7,8]

[1]University Clermont Auvergne, INSERM U1240 "Molecular Imaging and Theragnostic Strategies (IMOST)", Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand, France. [2]Clinical Research Unit, Clinical Research & Innovation Department, Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand, France [3] Clinical Investigation Center, UMR501, F-63001, Clermont-Ferrand, France. [4]Oncogenetics Department, Molecular Oncology Laboratory, Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand, France. [5]Biochemistry and Molecular Genetics Department, CHU Gabriel Montpied, 58 rue Montalembert, 63003 Clermont-Ferrand. [6]Oncology Department, Centre Jean PERRIN, 58 rue Montalembert, 63011 Clermont-Ferrand, France. [7]Platform for Advanced and /or Novel Tissue Analyses (TANYA), Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand, France. [8]Department of Pathology, Centre Jean Perrin, 58 rue Montalembert, 63011 Clermont-Ferrand, France.

Triple-negative breast cancer (TNBC) is an aggressive subtype with high recurrence rates, where response to neoadjuvant chemotherapy (NACT) is a key prognostic factor. Liquid biopsy (LB) is emerging in TNBC management, with circulating proteins being promising biomarkers due to their role in cancer progression. The INSTIGO study aims to identify blood proteins predictive of pathological complete response (pCR) to NACT and analyze their dynamics during treatment. INSTIGO is a single-center, interventional prospective trial conducted by Centre Jean Perrin. Blood samples were collected at diagnosis and post-NACT surgery in 30 non-metastatic TNBC patients. NACT followed the standard carboplatin-paclitaxel and EC protocol. A panel of 21 proteins was quantified using multiplex immunoassays. Among 24 evaluable patients, 13 achieved pCR, while 11 did not. Higher baseline levels of CCL5, IL8, TIE2, and CXCL5 were observed in non-pCR patients. CXCL5 decreased after NACT in non-pCR patients ($p=0.04$). CD40, PD-L1, and CX3CL1 increased in pCR patients ($p=0.008$, $p=0.02$, $p=0.008$, respectively). ANGPT2 increased in both groups but was significantly higher in pCR patients ($p=0.04$). Our preliminary findings highlight the potential of circulating proteins as predictive biomarkers of TNBC response to NACT. These results must be validated once study has been completed for the entire cohort of 90 patients.

Keywords: triple negative breast cancer, circulating protein, predictive biomarker, pathological complete response, neoadjuvant chemotherapy

Family name: Bron
First name: Auriane
Year of PhD: 3rd
Research team and Laboratory: UMR MEDIS (France) / CMET (Belgique)
PhD supervisors: Stéphanie Blanquet-Diot and Tom Van de Wiele
Email: auriane.bron@doctorant.uca.fr
Language of presentation: English

How plant extracts designed to prevent MASH impact *in vitro* human colon microbiota and hepatic steatosis

Auriane Bron[1,2,3], Florian Le Joubioux[4], Sylvain Denis[1,3], Tom Van de Wiele[2,3], Claude Durif[1,3], Vivien Chavanelle[5], Pascal Sirvent[5], Yolanda F. Otero[5], Stéphanie Blanquet-Diot[1,3]

[1]Université Clermont Auvergne, INRAE, UMR 454 MEDIS, Microbiologie Environnement Digestif et Santé (MEDIS), CRNH Auvergne, Clermont-Ferrand, France. [2]Ghent University, Faculty of Bioscience Engineering, Center for Microbial Ecology and Technology (CMET), Ghent, Belgium. [3]International associated laboratory Host Microbes Interactions in the Human Gut (HOMIGUT). [4]Valbiotis R&D Périgny Center, Périgny, France. [5]Valbiotis R&D Riom Center, Riom, France.

The role of human gut microbiota in the development of metabolic dysfunction-associated steatohepatitis (MASH) remains unclear. Plant extracts appear as a promising multitargeted strategy to alleviate disease symptoms. This study investigated the effects of repeated exposure of Totum-448, a combination of polyphenol-rich plant extracts designed to prevent MASH, on human gut microbiota and hepatic steatosis using the Mucosal-ARtificial-COLon (M-ARCOL) combined with hepatocytes in culture. M-ARCOL bioreactors were inoculated with healthy human fresh stools (n=4) and daily treated with 1g/L of Totum-448 for two weeks. Gut microbiota composition, metabolic activities, and Totum-448 metabolites were daily monitored. Palmitic acid treated-hepatocytes were exposed to M-ARCOL supernatants with or without Totum-448, and 24h later, expression of key genes involved in liver inflammation was assessed. Proportions of *Veillonellaceae*, *Ruminococcaceae*, *Prevotellaceae* were higher with Totum-448 in both lumen and mucus compartments, while that of *Bacteroidaceae* was lower. For all donors, the main compounds of Totum-448 were quickly and highly metabolized leading to the production of several polyphenol metabolites. Reduction in inflammation and *de novo* lipogenesis in steatotic hepatocytes was observed in half of the donors. Our results suggest a key role of gut microbiota in plant extracts metabolization, likely shaping their effects in humans.

Keywords: Gut microbiota, *in vitro* gut model, MASH, hepatocyte steatosis, plant extracts

Family name: Dambrine
First name: Flavie
Year of PhD: 3rd
Research team and Laboratory: M2iSH
PhD supervisor: Jérémy DENIZOT
Email: flavie.dambrine@uca.fr
Language of presentation: English

Role of the bacterial deacetylase cobB in the virulence of adherent and invasive *Escherichia coli* (AIEC) bacteria associated with Crohn's disease

Flavie Dambrine, Florian Coudray, Perrine Bouvard, Nicolas Barnich, Jérémy Denizot
Microbes, intestin, inflammation et Susceptibilité de l'Hôte (« M2iSH »), INSERM U1071 USC-INRAE 1382, Université Clermont Auvergne (UCA), Clermont-Ferrand, France

Context: Adherent and invasive *E. coli* (AIEC) abnormally colonize the intestinal mucosa of Crohn's disease (CD) patients on a chronic basis, and their presence is associated with severe post-operative recurrences. The aim of this project is to identify and characterize a bacterial effector modulating host epigenetic markers, as well as the inflammatory response in favor of chronic colonization of the intestine by AIEC.

Methods/Results: A bacterial protein, cobB, was identified by bioinformatics analysis. Overexpression of cobB in intestinal cells shows nuclear localization, as well as the ability of cobB to efficiently deacetylate and delactylate host cell histones, indicating a potential role of cobB in regulating host gene expression during infection. Furthermore, deletion of the cobB gene in the reference AIEC strain (LF82) results in hyperacetylation of histones in infected intestinal cells. In addition, overexpression of cobB in the bacteria leads to improved entry into intestinal epithelial cells and enhanced intramacrophage replication.

Discussion/Conclusion: Our results show that the cobB protein appears to act as a nucleomodulin capable of modifying host epigenetic marks, where its activity could be central in the virulence of AIEC bacteria and in the chronicity of infection in CD patients.

Keywords: Crohn's disease, adherent-invasive *Escherichia coli*, inflammation, epigenetics, cobB

Family name: Carriere
First name: Eugénie
Year of PhD: 3rd
Research team and Laboratory: LMGE - IHP team
PhD supervisor: Pascale Gueirard
Email: eugenie.carriere@uca.fr
Language of presentation: English

Illuminating the live-cell dynamics of the early neutrophil- *Encephalitozoon cuniculi* interplay as a "Trojan horse" strategy

Eugénie Carriere, Juliette Gilbert, Julien Verlaguet, Marjolaine Vareille-Delarbre, Frédéric Delbac and Pascale Gueirard

Université Clermont Auvergne, CNRS UMR 6023, Laboratoire Microorganismes : Génome et Environnement, F-63000 Clermont-Ferrand, France

Encephalitozoon cuniculi is an obligate intracellular parasite of birds and mammals, including humans. It belongs to the phylum *Microsporidia* and causes severe infections in immunocompromised individuals. The innate immune system serves as the first line of defense against infection but only partially eliminates the parasite. Microsporidia are known to modulate the effector functions of phagocytes, such as macrophages (MOs), to evade destruction after phagocytosis. However, the role of neutrophils (PMNs) during microsporidiosis remains poorly understood.

Using live and static cell imaging, we explored the dynamics of interactions between murine PMNs and *E. cuniculi* in *in vitro* and *in vivo* models. Fluorescent PMNs purified from LysM-EGFP transgenic mice were exposed to fluorescent spores of *E. cuniculi*, and their behaviors were monitored over 48 hours using videomicroscopy, high-resolution confocal imaging, fluorescence in situ hybridization, and transmission electron microscopy.

Infected PMNs exhibited structural and functional modifications, including pseudopodia emission, altered motility, and neutrophil extracellular traps formation. A small proportion of viable parasites initiated intracellular development, with meront stages detected at 24 and 48 hours post-infection. Finally, infected PMNs harboring intact spores were phagocytosed by MOs, highlighting their role in the "Trojan horse" mechanism that facilitates *E. cuniculi* dissemination within host tissues.

Keywords: Microsporidia, Polymorphonuclear leukocyte, innate immunity, live-cell imaging, murine model

Family name: Kaur
First name: Manjyot
Year of PhD: 3rd
Research team and Laboratory: LMGE
PhD supervisors: Christiane Forestier and Sylvie Miquel
Email: manjyot.kaur@uca.fr
Language of presentation: English

Unravelling the aggregation mechanism in *Lactobacillus crispatus* and its role in probiotic functionality

Manjyot Kaur[1], Caroline Dausset[2], Audrey Durand[2], Adrien Nivoliez[2], Christiane Forestier[1], Sylvie Miquel[1]
[1]Université Clermont Auvergne, CNRS, LMGE, F-63000 Clermont–Ferrand, France.
[2]Biose Industrie, Aurillac, 24 avenue Georges Pompidou, 15000, Aurillac, France.

Bacterial cells are predominantly studied in their planktonic form, yet in natural environments, they often exist within structured communities such as biofilms, exhibiting distinct physiological properties. Another, less characterized mode of bacterial life involves floating aggregates—dense clusters of viable cells embedded in extracellular DNA. This aggregation phenotype has been documented in several pathogens (*Pseudomonas aeruginosa*, *Campylobacter jejuni*, *Streptococcus pyogenes*, and *Staphylococcus aureus*), demonstrating biofilm-like properties, including reduced growth rates and enhanced resistance to phagocytosis and antibiotics. While auto-aggregation is also widespread among probiotic bacteria, its mechanisms and potential benefits remain poorly understood.This study aims to elucidate the aggregation mechanisms in *Lactobacillus crispatus* and their impact on probiotic functionality. Using an evolutionary enrichment approach, we generated two spontaneous mutants from an aggregative, biofilm-deficient *L. crispatus* strain: one incapable of aggregation and another that readily forms biofilms. Comparative phenotypic analysis revealed an inverse relationship between auto-aggregation and biofilm formation. Surface properties' analysis highlighted significant differences in hydrophobicity and surface charge among the wild-type and mutant strains.Whole-genome sequencing identified mutations primarily in genes encoding surface proteins and capsular polysaccharides associated with secretion pathways. Our preliminary findings suggest that *L. crispatus* can adopt two distinct lifestyles, each potentially conferring specific adaptive advantages. These insights contribute to a deeper understanding of *Lactobacilli* aggregation and may inform strategies to enhance probiotic efficacy.

Keywords: *Lactobacilli*, aggregation, biofilm, probiotic, surface properties

Family name: Cartier
First name: Alizée
Year of PhD: 3rd
Research team and Laboratory: NeuroDol
PhD supervisor: David Cia
Email: alizee.cartier@doctorant.uca.fr
Language of presentation: English

Assessment of corneal sensitivity in a mouse model of ocular rosacea induced by ultraviolet-B exposure

Alizée Cartier[1], Maxime Hitier[1], Christine Cercy[1], Frédéric A. Carvalho[1], David Cia[1]

[1]UMR 1107 NeuroDOL INSERM/Université Clermont Auvergne, France

Ocular rosacea is a chronic inflammatory disease affecting the ocular surface. Its causes telangiectasias, blepharitis, conjunctivitis and keratitis. It often provokes redness and painful sensations such as burning, stinging and itching. This pathology is multifactorial and can be triggered by various factors such as sunlight exposure. We aimed to develop a model by exposing mouse eyes to ultraviolet-B (UVB) radiation. Eyes were exposed to UVB at 3,94mW/cm² for 3 minutes per day for one, three or five days. To assess the validity of the model, we evaluated ocular surface sensitivity using eye-wiping and ocular Von Frey tests. Additionally, corneal inflammation was measured by ELISA using lipocalin-2, MPO and IL-8 markers. We found that one-day exposure did not alter corneal sensitivity. After three days' exposure, an increase in corneal sensitivity was detected only with the eye-wiping test. After five-days' exposure, corneal sensibility increased with the eye-wiping test but decreased with the Von Frey test. In addition, UVB exposure for five days resulted in a significant increase in corneal inflammatory markers, indicating increased ocular inflammation compared to control mice. These results demonstrate that repeated exposure for five days is necessary to increase sensitivity and inflammation of the ocular surface.

Keywords: ocular rosacea, UVB, corneal sensitivity, inflammation

Family name: Desseux
First name: Coline
Year of PhD: 3rd
Research team and Laboratory: M2ISH
PhD supervisor: Hang Nguyen
Email: coline.desseux@uca.fr
Language of presentation: English

Cytotoxic necrotizing factor-producing *Escherichia coli* enhance tumorigenesis in a pre-clinical mouse model of colorectal cancer with intestinal epithelial cell-specific autophagy deficiency

Coline Desseux[1], Alison Da Silva[1], Julien Delmas[1], Anaëlle Tassini[1], Pierre Sauvanet[1], Nicolas Barnich[1], Guillaume Dalmasso[1], Hang Nguyen[1]

[1]M2iSH, UMR 1071 Inserm, Université Clermont Auvergne, INRAE USC 1382, CNRH, 63001 Clermont-Ferrand, France.

In patients with colorectal cancer (CRC), intestinal dysbiosis has been observed, with abnormal colonization of the colonic mucosa by pathogenic *Escherichia coli* strains producing a cyclomodulin named cytotoxic necrotizing factor (CNF). Cyclomodulins are bacterial toxins capable of altering the cell cycle of the infected cell. One of the mechanisms involved in host defence against pathogens and in carcinogenesis is autophagy. The study aimed to investigate the role of autophagy in colorectal carcinogenesis in the context of CyPEC infection.

Mice predisposed to CRC development with autophagy deficiency specifically in intestinal epithelial cells were infected with clinical CyPEC strain (21F8) or a mutant strain that does not produce CNF (21F8Δcnf).

Results showed that infection with either strain did not affect tumor development in control mice with functional autophagy. However, in autophagy-deficient mice, infection with the CyPEC 21F8 strain led to an increase in both the size and number of colonic tumors, and it seems to be CNF-dependent. This was associated with increased cell proliferation, and decreased apoptosis in colonic epithelial cells.

Our results suggest that autophagy deficiency, combined with colonization by CyPEC strains, could be a risk factor for CRC development.

Keywords: *Escherichia coli*, CNF, colorectal cancer, autophagy

Family name: Vercruysse
First name: Leslie
Year of PhD: 3rd
Research team and Laboratory: M2iSH
PhD supervisor: Philippe Poirier
Email: leslie.vercruysse@uca.fr
Language of presentation: French

The impact of the microsporidia *Encephalitozoon intestinalis* on colorectal carcinogenesis

Leslie Vercruysse[1], Virginie Bonnin[1], Aurore Dubuffet[2], Mathilde Bonnet[1], Céline Nourrisson[1,3,4], Philippe Poirier[1,3,4]

[1]Microbes, Intestin, Inflammation et Susceptibilité de l'hôte. INSERM U1071 USC-INRAE 1382. Université Clermont Auvergne, Clermont-Ferrand, France.

[2]Université Clermont Auvergne, CNRS, Laboratoire Microorganismes : Génomes et Environnement, F-63000 Clermont-Ferrand, France.

[3]Service de Parasitologie-Mycologie, 3IHP, CHU Clermont-Ferrand, Clermont-Ferrand, France.

[4]National Reference Center for Cryptosporidiosis, Microsporidia and Other Digestive Protozoa, Clermont-Ferrand, France.

Introduction: Colorectal cancer (CRC) is influenced by genetic, environmental, and microbial factors. Among them, *Encephalitozoon intestinalis*, an intestinal microsporidium, which is known to disrupts the cell cycle and inhibits apoptosis, suggesting a potential procarcinogenic role. Recent studies indicate a higher seroprevalence of *Encephalitozoon* in CRC patients.

Aim of this subject is to precise impact of infection on epithelial cells.

Materials and Methods: Vero E6 and HT-29 cells were infected for 24h and 48h to evaluate apoptosis, cell cycle, and proliferation using flow cytometry (TUNEL assay, cell cycle analysis), immunofluorescence (p53, Ki67), RT-qPCR and Western Blot (PCNA, Cyclins E/A/D, Rb, p21). A culture insert system assessed the effect of the secretome from infected cells on non-infected cells.

Results and Discussion: *E. intestinalis* induced cell cycle arrest in S/G2 phases, increased cyclins E (24h) and A (48h), and decreased PCNA (48h). It reduced *p53* and *bax* gene expression and p21 protein expression, inhibiting apoptosis. Secreted factors from infected cells also induced S and G2 arrest in non-infected cells.

Conclusion: These findings suggest that *E. intestinalis* promotes a pro-tumor environment by disrupting cell cycle regulation, reducing proliferation, and inhibiting apoptosis, potentially contributing to CRC development.

Keywords: Colorectal cancer, infection, microsporidia, cell cycle, apoptosis

Evaluation des communications orales

Nom	Avis	Note
Nathan Frizot		
Alexandre Gonzalez		
Elise Martin		
Marie Papin		
Steve Kevin Njouonkep-Sime		
Louise Lambert		
Jade Sutter		
Camille Teste		
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Coline Desseux		
Leslie Vercruysse