Club Macrophage
Grand Ouest
&co

Programme

4ième Journée du Club Macrophage & Co - Grand Ouest

Jeudi (après-midi) 26 - Vendredi (matinée) 27 Novembre 2026

Salle Senghor au lycée Descartes, Tours



ISP Fighting Pathogens · BD · 10x GENOMICS® · Olink® · InvivoGen Innovation within reach

BIENVENUE A LA 4ième JOURNEE DU CLUB MACROPHAGE DU GRAND OUEST

Cher(e)s Macrophage aficionados,



Jean Fouquet, peintre originaire de Tours, peignant un macrophage (ChatGPT).

Nous sommes ravis de vous acceuillir à Tours pour cette 4ième itération de notre journée du Club Macrophage pour un moment d'échange scientifique que nous espérons riche en nouvelles idées.

Après quatre ans et après être passés par nos quatre villes (Rennes, Nantes, Angers et enfin Tours), le moment est idéal pour dresser le bilan de notre Club Macrophage.

Nous avons donc créé un Framaform permettant de compiler vos idées, vos critiques ou vos louanges tout au long de ce congrès. N'hésitez pas, cela nous permettra de nous améliorer !

Scannez simplement ce QR-code :

Nous espérons que cette journée sera le point de départ d'une multitude de projets entre nos différentes équipes.

Nous vous souhaitons une mac-gnifique journée !

Le COPIL

Club Macrophage Grand Ouest &co

26 - 27 Novembre 2026 , Tours, France

Programme provisoire TOURS 2026

Jeudi 26 Novembre 2026 (après-midi)

13h00 Accueil des participants

13h20 Introduction. *Ronan Kapetanovic (Tours)*

13h30-14h00 **THE ALVEOLAR COMPARTMENT** (15 min + 5 min questions). *Chair : Valérie Lecureur (Rennes)*

- **Antoine, Guillon**, CEPR, Tours. Human Alveolar Macrophages Constitute a Previously Unrecognized Replication Niche for Influenza Virus
- **Ferdinand Roesch**, ISP, INRAE, Tours. Modulation of innate immune signaling pathways in ASFV-infected primary alveolar macrophages

14H00-14h15 **PRÉSENTATIONS FLASH** (3 min + 2 min questions). *Chair : Ronan Kapetanovic (Tours)*

- **Juliette Jamoneau**, RMeS, Nantes, Pro-resolving mediators and macrophages: toward an extracellular vesicle-based drug delivery strategy
- **Noémie Fournier**, CEPR, TOURS, Anti-Pseudomonas antibody induces innate immune memory hallmarks in alveolar macrophages
- **Soraya Sadiqi**, ISP, Tours, Linking Copper and Oxidative Stress: Investigating a new host antimicrobial strategy against *Salmonella*

14h15-15h15 Invité : **Johan Garaude,** *Mitochondrial Biology and Innate Immunity Team. ImmunoConcEpT, Bordeaux, France*

Microbial viability drives immunometabolic responses of macrophages

Chair : Aurélie Moreau (Nantes)

15h15-16h00 Pause-café et échanges

16h00-17h00 **SPONSORS & PLATEFORMS in TOURS** : (10 min + 5 min questions)

- Presentation BD
- Presentation IMI – Julien Pichon
- Presentation PIXANIM - Ana Paula Teixeira
- Présentation Infrastructure Spatial Omics and Technologies SpOT – Marie-Astrid Boutet

17h00-18h00 **EMERGING MECHANISMS IN MYELOID CELLS** (15 min + 5 min questions). *Chair : Yves Delneste* (Angers)

- **Maya Katby**, IRSET, Rennes, Deciphering macrophage heterogeneity with mass cytometry immunophenotyping in a mouse model of alveolar echinococcosis
- **Mael Seite**, CR2TI, Nantes, Autologous Tolerogenic Dendritic Cells induces Treg through lactate secretion
- **Etienne Boucard**, ISP, Tours, Metal meets microbe: exploring zinc-mediated immunity in chicken macrophages

18h00 - 20h00 Repas Buffet + Poster

Vendredi 27 Novembre 2026 (matinée)

09h00 Accueil des participants

09h30-10h30 **MACROPHAGES AND INFLAMMATION** (15 min +5 min questions). *Chair: Ronan Kapetanovic (Tours)*

- **Maaike Suuring**, CEPR, Tours, GAG from Aspergillus fumigatus modulates human macrophage responses through TLR2-MMR signaling and inflammasome activation
- **Valérie Lecureur**, IRSET, Rennes, Efferocytosis in systemic sclerosis: from physiopathology to therapeutic approaches
- **Christophe Blanquart,** CRCI2NA, INSERM, Nantes, Heterogeneity of macrophages in pleural mesothelioma

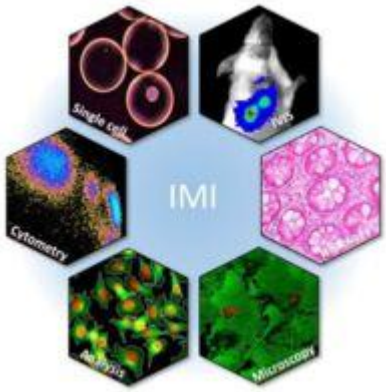
10h30-11h15 Pause-café et échanges

11h15 - 11h45 Table ronde *menée par Christophe Blanquart* :

- *Projet de demande de financement commune (qui fait quoi?)*
- *Quelles plateformes existent pour la communauté macrophage ?*
- *Quels outils mettre en place pour la communauté macrophage?*
- Après 4 ans, quelle suite pour ce Club Macrophage

12h00-12h30 Clôture de la journée, remise des prix (meilleur talk doctorant)

Plateforms



IMI - imagerie et infectiologie

IMI est un plateau technique d'imagerie spécialisée dans l'étude du processus infectieux. L'équipe possède une expertise scientifique pluridisciplinaire et est spécialisée dans le monitoring de pathogènes dans leur environnement, la caractérisation de la physiopathologie infectieuse et l'étude des interactions hôte-pathogène. Elle bénéficie du regroupement d'un ensemble d'approches méthodologiques complémentaires permettant une exploration multi-échelle allant de l'animal entier jusqu'à la cellule unique, pour l'étude du vivant en environnement confiné de niveau 2 (BSL2). Localisée sur le site de Nouzilly, l'équipe IMI est ouverte aux demandes extérieures sur un large panel de questions biologiques dns la limite de la capacité de ses équipements.

Equipements

L'équipe IMI met à disposition des utilisateurs des équipements de pointe pour l'étude d'échantillons vivants et fixés au sein de laboratoires confinés de niveau 2 :

> Imagerie *in vivo*

Imageur IVIS Spectrum

> Histologie Automate de déshydratation et d'inclusion en paraffine, Station d'inclusion en paraffine, Microtome manuel, Microtome automatique, Cryomicrotome, Automate à colorations histologiques

> Microscopie photonique

Microscope champ large Nikon Eclipse 80i (lumière blanche et fluorescence), Microscope confocal spectral Leica SP8

> Analyse d'images

Station d'analyse d'images, Logiciels dédiés à l'analyse d'images

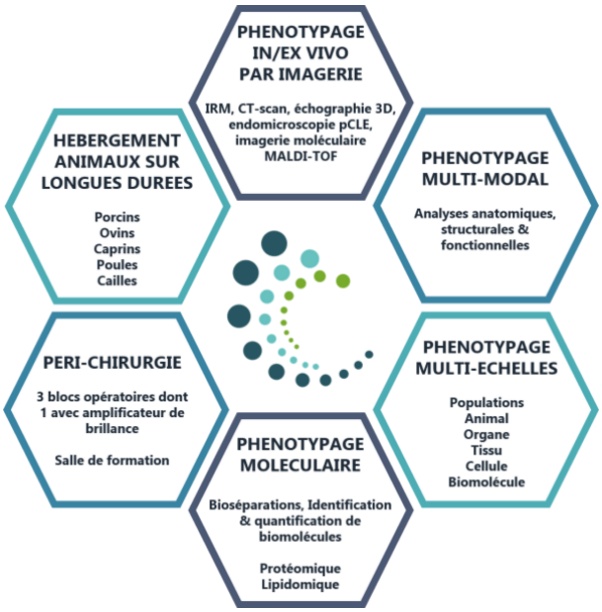
> Cytométrie en flux

Analyseur de recherche à 4 lasers LSR FortessaTM X-20 (Becton-Dickinson), Trieur de cellules à grande vitesse à 4 lasers avec module de clonage MoFlo Astrios EQ (BeckmanCoulter)

> Préparation d'échantillons pour des approches de Single cell/nuclei

Chromium Controller 10X Genomics

PIXANIM - Phénotypage par Imagerie in et ex vivo de l'Animal à la Molécule



Une plateforme expérimentale et analytique au service de la recherche agronomique et médicale, de la formation et de l'innovation.

La plateforme PIXANIM vous accompagne dans l'exploration fonctionnelle des différents systèmes biologiques d'un animal allant de l'animal entier (ou populations) jusqu'à la biomolécule en passant par toutes les échelles intermédiaires (organes, tissus, cellules pro- et eucaryotes, fluides).

PIXANIM vous propose des stratégies avec de multiples modalités d'imagerie in et ex/vivo qui peuvent être appliquées et combinées entre elles ou avec des outils d'analyses moléculaires en protéomique (peptides, protéines) et lipidomique (lipides), pour phénotyper finement ces systèmes biologiques et caractériser les mécanismes explicitant ces phénotypes. La plateforme dispose également de capacités d'hébergements (porcins, ovins, caprins pendant plusieurs semaines ou mois) et de suivis expérimentaux (prélèvements biologiques, bien-être) permettant la réalisation d'études longitudinales.

PIXANIM est une Infrastructure Scientifique Collective (ISC) de INRAE, labellisée par le GIS et certifiée ISO 9001. Placée sous la tutelle de INRAE, et la cotutelle de l'Université de Tours et du CHU de Tours, elle est rattachée au département PHASE (Physiologie Animale et Systèmes d'Elevage) sous la direction de l'UMR PRC(Physiologie de la Reproduction et des Comportements), sur le centre INRAE Val de Loire à Nouzilly.

Depuis 2021, PIXANIM est intégrée à l'Infrastructure de Recherche (IR) nationale LiPh4SAS (Livestock Phenotyping for Sustainable Agro ecoSystems) offrant des services de phénotypage pour les animaux d'élevage (bovins, petits ruminants, porcs et poissons).

Equipements

> Imagerie

- IRM 3 Teslas Magnetom Skyra® (Siemens)
- CT-scan Somatom® Definition AS 128 (Siemens)
- Endomicroscope confocal laser Cellvizio Dual Band® (Mauna Kea Technologies)
- Kratoscope - block face monté sur microtome ou cryostat (Keer Labs®)

> Spectrométrie

- Spectromètre de masse MALDI-TOF RapifleX TissueTyper & Biotyper (Bruker Daltonics)
- Spectromètre de masse à haute résolution - Tribrid Orbitrap ASCEND équipé de la mobilité ionique FAIMS Pro Duo - (Thermofisher)
- Système chromatographique NanoLC à basse et haute pression Evosep One (Proteigene)
- Système de chromatographie NanoLC Vanquish Neo UPLC (Thermofisher)
- Système chromatographique UPLC Ultimate 3000 (Thermofisher)

Sponsors

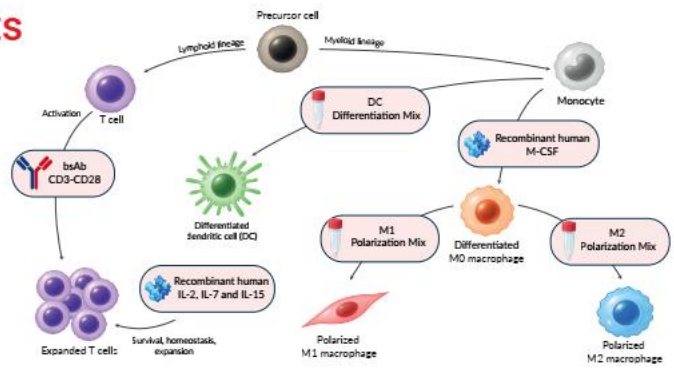
Nous remercions la générosité de nos sponsors
We would like to thank our generous sponsors





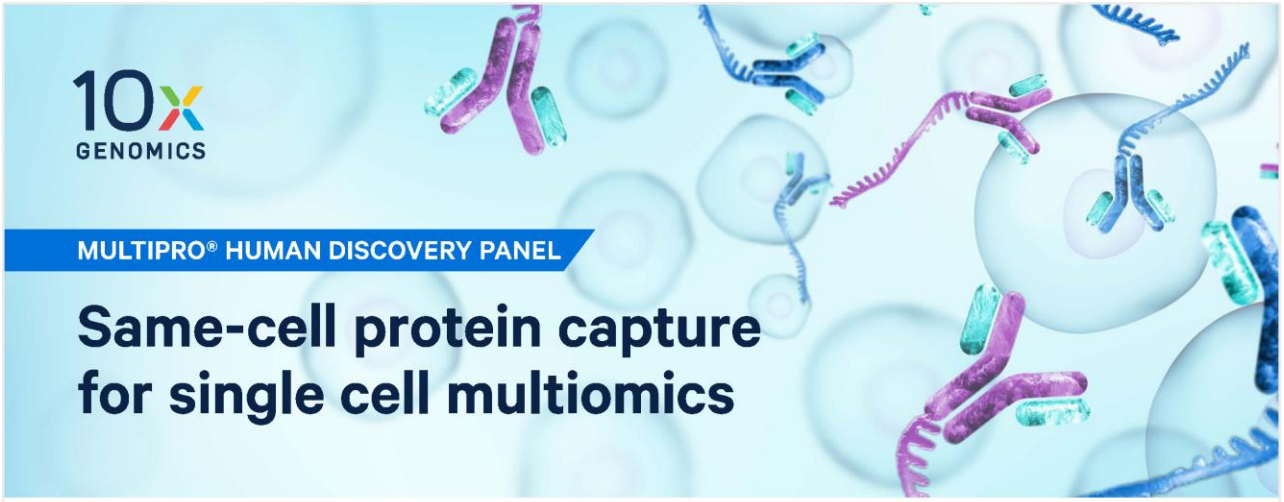
Functionally tested reagents for reproducible:

- Macrophage polarization
- Dendritic cell differentiation
- T-cell activation & expansion



InvivoGen
www.invivogen.com

More information contact: tech.eu@invivogen.com



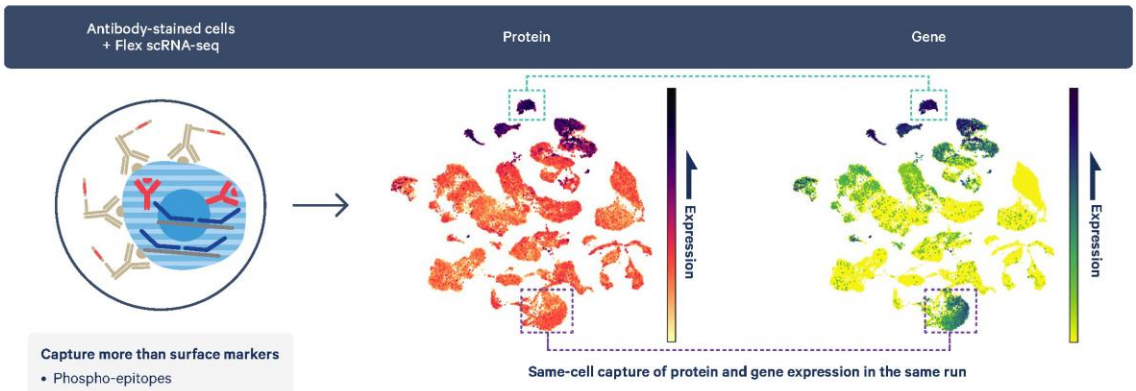
300+ proteins.
One workflow.
Full resolution.

Signaling activity. Post-translational modifications. Functional cell state. Biological details that can only be captured by measuring protein alongside RNA. And your Flex workflow is already set up to do exactly that.

The **MultiPro Human Discovery Panel** adds 347-antibody capture to your Flex run and integrates easily into your existing single cell workflow. No separate assay. No need to combine multiple datasets. Just a new layer of insight from the cells you're already profiling.

Highlights:

- Capture cell surface, cytoplasmic, and intranuclear proteins from the same cells
- Directly measure protein and RNA without combining datasets
- Identify phosphorylation state and active signaling pathways
- Count on reproducible results with pre-titrated, single-use panels



Capture more than surface markers

- Phospho-epitopes
- Transcription factors
- Cytokines
- And more...

10xgen.com/SCProtein


Waters™
Biosciences
Formerly BD Biosciences
Redefining What's Possible in Flow Cytometry
BD FACSDiscover™ Family
One spectral platform. Continuous innovation. Consistent results.
Introducing the BD FACSDiscover™ A7.
FACSTruQ™ Technology
BD FACSDiscover™ A8
BD FACSDiscover™ A7
BD FACSDiscover™ S8
and
BD Horizon™ Real Dyes
They're just better dyes.
BD flow cytometers are Class 1 Laser Products. For Research Use Only. Not for use in diagnostic or therapeutic procedures. Waters, BD FACSDiscover, FACSTruQ, BD CellView, BD Horizon, and BD SpectralFX are trademarks of Waters Technologies Corporation. © 2026 BD. All rights reserved. BD and the BD Logo are trademarks of Becton, Dickinson and Company.

Olink

Olink® Target 48: Set your sights on cytokines

Olink® Target 48 Cytokine is the ultimate solution for studies of inflammation and the immune response. Our thorough assay selection allows for simultaneous quantification of 45 low abundance protein biomarkers, relevant across a variety of diseases. Perfect for understanding biological mechanisms in disease research and drug development.

Learn more



Cytokine-focused
45 inflammatory biomarkers involved in major disease areas.

pg/mL
Read-out in both absolute and relative quantification.

Validation data
Available for the panel.

1 µL
Volume input, 40 samples per kit.

Olink® Signature Q100

qPCR

Streamline your protein analysis workflow with Olink® Signature Q100 benchtop instrument.

Learn more



www.olink.com

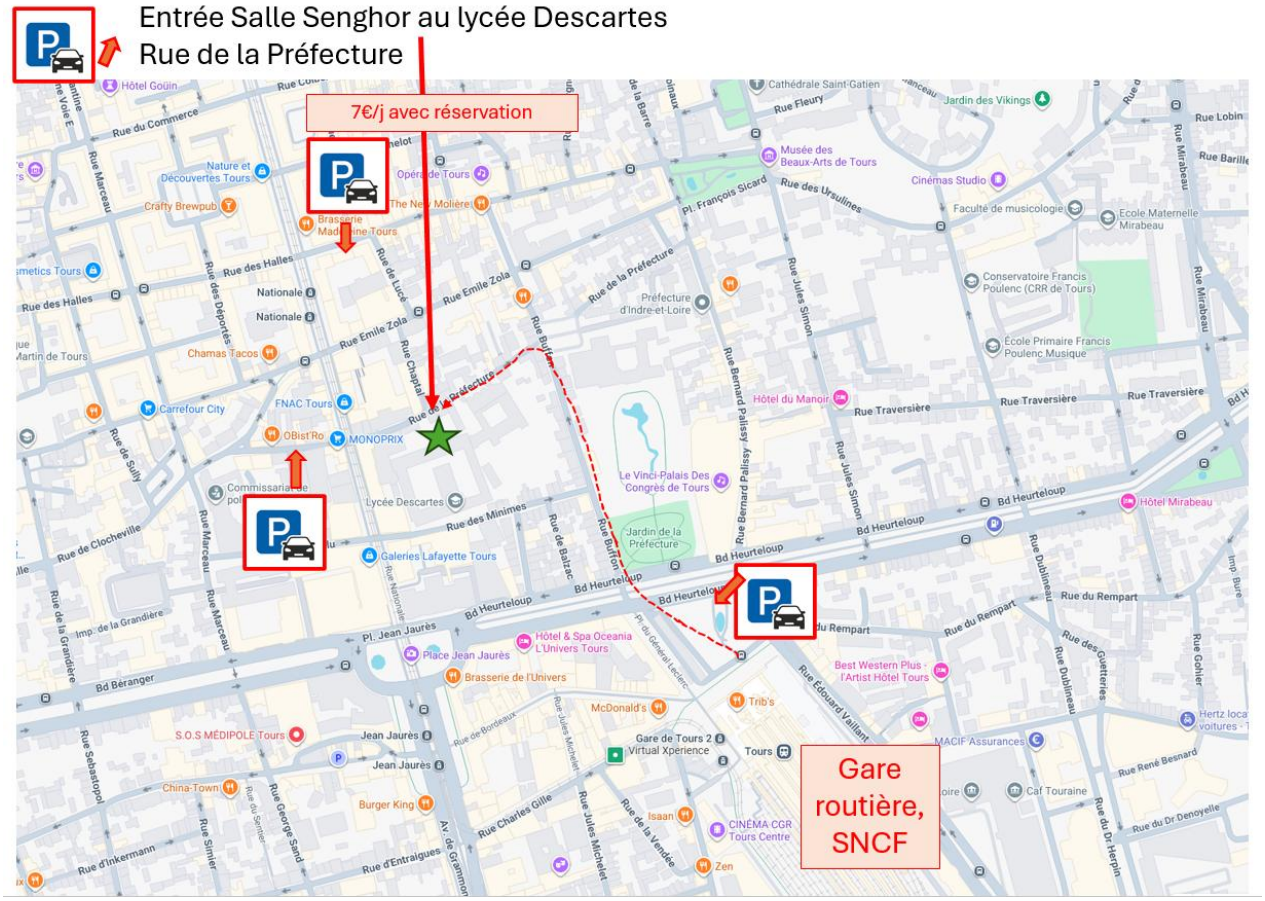
© 2023 Olink Proteomics AB.
Olink products and services are For Research Use Only and not for Use in Diagnostic Procedures.
This document is not intended to convey any warranties or representations of any kind.
1370, v1.1, 2023-04-25

Comment nous rejoindre ? *(How to get there ?)*

Salle Senghor du Lycée Descartes.
L'entrée se fait par le 1bis rue de la Préfecture – 37000 TOURS (à l'arrière du lycée)

Nous vous conseillons vivement le trajet en train.
Les TGV s'arrêtent souvent à Saint-Pierre des Corps. Une navette train relie St-Pierre des Corps à Tours centre.

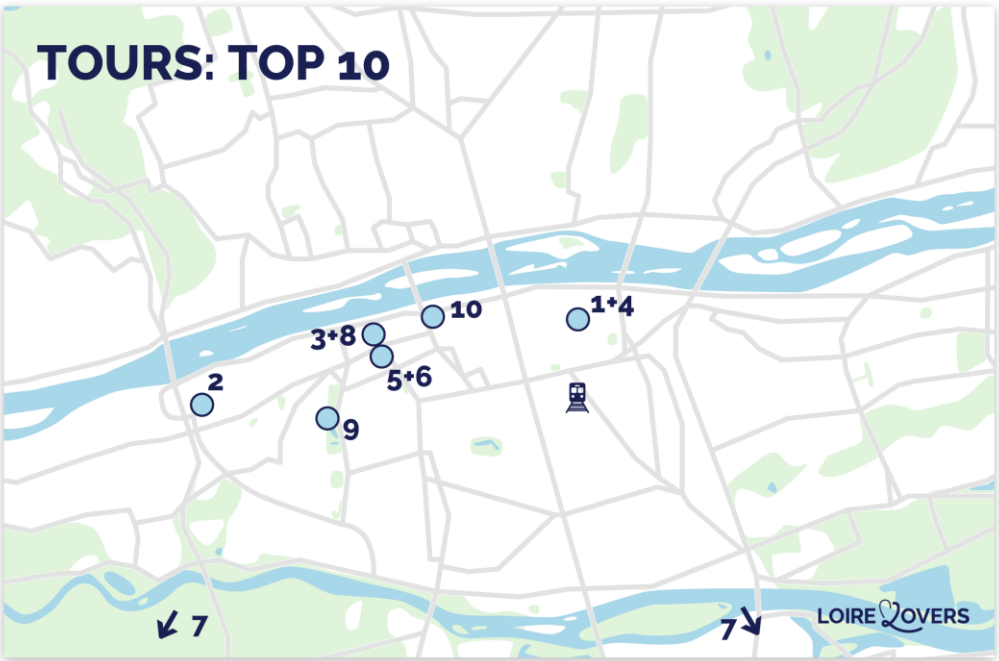
Les places de parking voitures sont extrêmement limitées dans la rue. Vous pouvez réserver des places de parking à la journée dans les parkings aux alentours (autour de 7 euros par jour)



Que faire en attendant votre train ou sur le WE ?



6 - Place Plumereau est l'endroit parfait pour aller prendre un verre le Jeudi soir



Comité de Pilotage



Marie-Astrid Boutet

Chargée de Recherche

RMeS INSERM UMRS 1229 - Nantes Université - ONIRIS



Christophe Blanquart

Directeur de Recherche

CRCI2NA INSERM UMRS 1307 - Nantes Université



Aurélie Moreau

Chargée de Recherche

CR2TI INSERM UMRS 1064 - Nantes Université



Yves Delneste

Directeur de Recherche

CRCI2NA INSERM UMRS 1307 - Université d'Angers



Valérie Lecureur

Professeur des Universités

IRSET INSERM UMRS 1085 - Université de Rennes



Karine Crozat

Chargée de Recherche

MOBIDIC UMR1236 INSERM CNRS - Université de Rennes



Ronan Kapetanovic

Directeur de Recherche

ISP UMR1282 INRAE Val de Loire - Université de Tours

Invité (Guest Speaker)



Johan GARAUDE

Equipe Mitochondrial Biology and Innate Immunity
ImmunoConcEpT
Univ. Bordeaux, CNRS UMR5164, INSERM ERL1303

Johan GARAUDE, who earned a Ph.D. in molecular endocrinology in 2007 from the University of Montpellier, studied the molecular mechanisms involved in leukemogenesis and T-cell activation. In 2008, he joined Julie Magarian Blander's laboratory in New York to explore antitumor immune responses. His work has notably helped demonstrate the role of dendritic cells in the natural differentiation of Th17 cells.
In 2011, Johan was hired as a Research Fellow at INSERM. There, he conducted research on cellular metabolism and mitochondrial biology in innate immune cells. That same year, Johan became a visiting researcher at the Centro Nacional de Investigaciones Cardiovasculares in Spain. Upon his return to France in 2017, Johan worked in Bordeaux on rare diseases, genetics, and metabolism. He is currently continuing his research at ImmunoConcept, where he studies host-pathogen interactions and the role of mitochondria in innate immunity.

Title: **Microbial viability drives immunometabolic responses of macrophages**

Abstract:

During bacterial infection, macrophages successively encounter and engulf live and killed microbes, and trigger appropriated host responses to eradicate the threat and restore tissue homeostasis. Despite the critical role of phagocytosis during this event, the fate of phagocytosed microbial cargo and its impact on host cell is poorly understood. Our investigation reveals that phagocytosis of bacteria provides bioenergetic and biosynthetic precursors that are differentially utilized by macrophages depending on microbial viability. This highlights the capacity of phagocytic cells to adjust their cellular metabolism to the 'fueling' capacity of the ingested cargos and how, together with the sensing of microbial viability, it regulates immunometabolic adaptations to shape host response intensity to the course of microbial infection.

Oral Presentation

Title: Modulation of innate immune signaling pathways in ASFV-infected primary alveolar macrophages

Auteurs: Ferdinand Roesch *(INRAE, UMR1282 ISP, Tours)*

Abstract:

African swine fever virus (ASFV) is a major threat to global pig production. Infection with virulent ASFV strains causes a severe hemorrhagic disease in pigs, characterized by dysregulated inflammation and high mortality. Myeloid cells like monocytes, dendritic cells, and macrophages are major targets of ASFV both in vitro and in vivo.
In particular, macrophages play a central role in viral replication, sensing of infection, and the inflammatory response that contributes to disease outcome. Using different OMICS approaches and cell-based assays, we investigate how ASFV virulence factors modulate innate immune signaling in primary macrophages. We compared the profiles of expression of host and viral genes in primary alveolar macrophages (PAMs) infected with ASFV strains of differing virulence. We found that attenuated ASFV strains generally induce stronger type I interferon and NF-κB responses than virulent ones. Confocal microscopy analyses of ASFV-infected PAMs supported these observations, and overexpression assays were used to investigate the contribution of individual viral factors to this phenomenon. In parallel, yeast two-hybrid screening of the ASFV ORFeome identified novel candidate interactions between ASFV proteins and host regulators of the NF-κB pathway such as ABIN2. Finally, we are developing a platform based on induced pluripotent stem cell derived macrophage to define the Pattern Recognition Receptors (PRRs) involved in ASFV sensing. Together, these approaches aim to understand how ASFV remodels innate immune responses in macrophages. This knowledge may support the rational design and evaluation of safer live attenuated ASFV vaccine candidates.

Notes:

Title: Metal meets microbe: exploring zinc-mediated immunity in chicken macrophages

Auteurs: Etienne Boucard[1], Quentin Meffre[1], Matthew Sweet[2], Isabelle Virlogeux-Payant[1], Ronan Kapetanovic[1]
[1] *INRAE, Université de Tours,*
[2] *Institute for Molecular Bioscience (IMB), University of Queensland, Brisbane, QLD, Australia.*

Abstract:

Salmonella is a Gram-negative bacterium and a major cause of foodborne illness worldwide. It is commonly transmitted to humans through contaminated pork, chicken meat or eggs, and salmonellosis was the second most reported zoonosis in the European Union in 2024. However, Salmonella contamination is difficult to detect in livestock, as pigs and chickens are usually asymptomatic. Understanding their immune responses is therefore essential to enhance their ability to defend against *Salmonella*.

During bacterial infection, macrophages are among the first immune cells to respond and deploy various antibacterial mechanisms. One involves intracellular zinc mobilisation to poison bacteria. Zinc is distributed by two major families of transporters: SLC30A (ZnT) exporters and SLC39A (ZIP) importers. Although their role in antibacterial defence has been documented in human and murine macrophages, particularly for SLC30A1, their involvement in chicken macrophages remains poorly characterised. We investigated the zinc response in chicken HD-11 macrophages following LPS treatment using Fluozin-3-AM and a bacterial fluorescent reporter of high zinc concentrations. Unlike human macrophages, chicken macrophages displayed zinc vesicles at rest, whose number increased after LPS stimulation. We also measured SLC30A and SLC39A expression following LPS stimulation and found that SLC30A1, a key zinc transporter in human macrophages, was highly expressed at rest. We are currently overexpressing this transporter using exogenous mRNA and investigating E. coli and Salmonella during macrophage infection. Infection assays showed that a Salmonella mutant lacking the zinc exporter ZntA was more sensitive to zinc toxicity and more efficiently eliminated by HD-11 macrophages. Zinc sensitivity also varied between *Salmonella* serovars. Altogether, our results highlight the role of zinc toxicity in chicken macrophage defence against Salmonella and suggest that this response may differ from that in mammals.

Notes:

Title: GAG from Aspergillus fumigatus modulates human macrophage responses through TLR2-MMR signaling and inflammasome activation

Auteurs: Maaike Suuring [1], Perrine Bomme [2], Sergey Samsonov, Elise Biquand [1], Thierry Fontaine, Benoit Briard [1,*]

[1,] *UMR Inserm U 1100 - Centre d'Etude des Pathologies Respiratoires (CEPR)*

Abstract:

Aspergillus fumigatus causes invasive aspergillosis, a life-threatening infection of immunocompromised hosts. Alveolar macrophages provide early defense against fungal spores. However, A. fumigatus has developed strategies to evade immune clearance, making it important to understand how fungal components influence macrophage signaling and inflammation. Galactosaminogalactan (GAG), an A. fumigatus cell wall polysaccharide, contains galactose and acetylated or deacetylated galactosamine residues (NAG or deGAG) that modulate immunity. We investigated their effects on macrophage activation and inflammation response. In murine bone marrow-derived macrophages (BMDMs), GAG activated MAPK signaling and the NLRP3 inflammasome. Molecular modeling predicted a stable GAG-TLR2 interaction, and TLR2 knockout BMDMs showed reduced NLRP3 inflammasome activation. In human macrophages, GAG and deGAG induced IL-1β and TNF-α release, but deGAG induced stronger cytokine production and cell death. TLR2 neutralization reduced cytokine release but not cell death. Phenotypic analysis showed that deGAG reduced mannose receptor (MMR) expression, and MMR neutralization decreased deGAG induced cell death without affecting cytokines, suggesting that MMR-mediated uptake contributes to cytotoxicity.

We discovered that GAG induced cell death is caspase-dependent, whereas deGAG induced death is associated to necroptosis. Microscopy images confirmed increased intracellular vesicular structures following deGAG stimulation, suggesting possible internalization. RNA sequencing revealed an immunomodulatory profile induced by GAG, cellular stress and necroptosis induced by deGAG and enhanced IL-1 specific response induced by NAG. These results reveal distinct roles of galactose and galactosamine residues in macrophage inflammation and cell death. TLR2 drives immunomodulation and inflammasome activation, whereas MMR is linked to necroptotic cytotoxicity.

Future transcriptomic analyses using TLR2- and MMR-neutralizing antibodies should clarify these mechanisms and identify therapeutic targets.

Notes:

Title: Human Alveolar Macrophages Constitute a Previously Unrecognized Replication Niche for Influenza Virus Abstract

Auteurs: Charles VERNEY*, Camille DAVID*, [...], Antoine GUILLON (* equal contribution)

[1,] *UMR Inserm U 1100 - Centre d'Etude des Pathologies Respiratoires (CEPR)*

Abstract:

Alveolar macrophages (AMs) play a critical role in lung innate immunity and homeostasis, yet their role during influenza infection remains unclear. To date, evidence suggest that even though the virus initiates genome replication and protein synthesis, the production of new virions does not occur, ending to an abortive viral influenza cycle in AMs. Here, we performed ex vivo influenza infection in both human AM and human precision cut lung slices. In contrast to what is observed using murine AMs, we showed that the viral cycle in human AMs was highly productive and influenza-infected human AMs contributed to efficient viral egress of numerous infectious particles from both influenza A and B strains. We demonstrated that the absence of virion release by murine AM was not explained by lack of acquired phenotypes such as AMs maturity (so called trained immunity) or aging but was rather an inter-species difference.

Expansion microscopy and transmission electronic microscopy of influenza-infected human macrophages allowed to characterize the extensive budding at their cell surface. So far, airway epithelial cells were considered as the only significant replication niche for influenza viruses.

Here, we reveal that AMs are a significant second source for virions production in the human lungs.

Notes:

Title: **Autologous Tolerogenic Dendritic Cells induces Treg through lactate secretion**

Auteurs: Maël SEITE[1], Alison DUMONT[1], Laurence DELBOS[1],Claire Pecqueur[2], Aurélie MOREAU[1]
[1.] *CR2TI*
[2.] *CRCI2NA*

Abstract:

Objective: Kidney graft survival is limited by chronic rejection and the adverse effects of long-term immunosuppression. Tolerogenic dendritic cells (DC) represent a promising strategy to promote immune tolerance. Autologous Tolerogenic Dendritic Cells (ATDC), generated from monocytes cultured with low concentrations of GM-CSF, display a glycolytic profile and produce lactate. A first-in-human Phase I trial demonstrated the feasibility and safety of ATDC administration in kidney transplant recipients and was associated with an increased proportion of regulatory T cells (Treg). Previous in vitro studies showed that ATDC exert their immunomodulatory effects mainly through secreted metabolites. We therefore investigated how the ATDC secretome promotes Treg accumulation.
Methods: Total and naïve $CD4^+$ T cells were stimulated with ATDC secretome.
Treg induction and proliferation were assessed by flow cytometry, and the role of lactate was investigated by pharmacological inhibition of lactate production. Metabolic changes were evaluated using mitochondrial and lipid probes. Treg induction and suppressive capacity were also assessed in a conventional iTreg model. Results: The ATDC secretome increased Treg frequency among total $CD4^+$ T cells independently of lactate and classical cytokine-mediated mechanisms. In isolated naïve $CD4^+$ T cells, Treg induction was de novo and lactate-dependent. The secretome increased mitochondrial polarization, mitochondrial ROS and lipid content in Treg generated from total $CD4^+$ T cells, whereas only mitochondrial polarization increased in Treg generated from naïve $CD4^+$ T cells. Finally, the secretome enhanced iTreg induction and suppressive capacity. Conclusion: The ATDC secretome promotes Treg induction through lactate-dependent and -independent mechanisms and induces metabolic changes associated with enhanced Treg function, providing new insights into ATDC-mediated immune tolerance.

Notes:

Title: **Deciphering macrophage heterogeneity with mass cytometry immunophenotyping in a mouse model of alveolar echinococcosis**

Auteurs: Brice Autier[2], Maya Katby[1], Bérenger Raoul[1], Christelle Manuel[1], Sarah Dion[1]
[2]*Univ Rennes, CHU Rennes, Inserm, EHESP, Irset*

Abstract:

Background and aims: Echinococcus multilocularis is a tapeworm whose larvae can infect the liver and cause a severe disease alveolar echinococcosis (AE). In AE, periparasitic granuloma formation is a key pathological feature, characterized by infiltration of immune cells, including macrophages. Macrophages are suspected to play dual role during the course of infection, however, their clear role remains poorly defined. Using complementary approaches we described the heterogeneity of macrophage populations during AE. Methods: A murine peritoneal AE model was used to characterize macrophage populations by mass cytometry immunophenotyping, integrated with RTqPCR and immunofluorescence imaging. In parallel, we evaluated the effect of E. multilocularis antigen on human macrophages derived from Peripheral Blood Mononuclear Cells using RTqPCR and multiplex cytokine dosage, in order to compare to mouse findings.

Results: Mass cytometry immunophenotyping revealed F4/80HiCD64- macrophages subtypes at early stages of infection, some expressing atypical markers CD31 and DC-SIGN. As infection progressed, these subtypes were replaced by F4/80Lo/intCD64+ macrophages with classical M1 (Ly6C+CD206-) or M2 (Ly6C-CD206+) profile. Integrating these data with RTqPCR and immunofluorescence imaging suggested that early recruited macrophages are transforming into epithelioid cells (expression of E-cadherin) while macrophages present at late stages are transforming into fibrocyte-like cells (expression of COL1A1 and FN1). Antigen stimulation favored a pro-inflammatory macrophage profile rather than M2 like, epithelioid or fibrocytic phenotypes, but also stimulated production of VEGFA and Galectin-3. Conclusion : Altogether, these results highlight the heterogeneity of macrophages during AE and suggest that stage specific macrophage populations can affect disease progression. However, the precise role of these populations remain to be investigated.

Notes:

Title: Efferocytosis in systemic sclerosis: from physiopathology to therapeutic approaches

Auteurs: LECUREUR Valérie[a], ERAZO-BORRAS Lucia[a], LELONG Marie[a], LE TALLEC Erwan[a,b], ADDA Corentina, ZIMMERMANN François[a,b] , BALLERIE Alice [a,b] and LESCOAT Alain [a,b]

a Univ Rennes, INSERM, EHESP, IRSET (Institut de recherche en santé, environnement et travail) – UMR_S 1085, F-35000 Rennes, France.

b Univ Rennes, CHU Rennes, INSERM, EHESP, IRSET (Institut de recherche en santé, environnement et travail) – UMR_S 1085, 35000 Rennes, France.

Abstract:

Macrophages are professional phagocytes capable to clear apoptotic cells, in a process called efferocytosis. This mechanism takes place in 3 steps: recognition, ingestion and digestion of the apoptotic cells. Defects in efferocytosis have been observed in systemic autoimmune diseases, including systemic sclerosis (SSc), which is characterized by vasculopathy, inflammation and fibrosis impacting the skin and internal organs, such as the lungs.

We characterized the efferocytosis defects and associated mechanisms found in patients with SSc, in mouse models of SSc, and in mice exposed to crystalline silica — a mineral dust described as the primary environmental risk factor for developing SSc.

Additionally, we evaluated the role of efferocytosis in the therapeutic effects of allogeneic mesenchymal stromal cells via intravenous injection in a bleomycin mouse model of SSc, and in the reprogramming of the phenotype of human monocyte-derived macrophages from healthy donors and SSc patients.

Overall, these findings suggest that enhancing efferocytosis by favouring the resolution of inflammation and promoting immune tolerance could be a promising therapeutic strategy in systemic autoimmune diseases such as SSc.

Notes:

Poster/Flash Presentations

Title: Pro-resolving mediators and macrophages: toward an extracellular vesicle-based drug delivery strategy

Auteurs: Jamoneau.J, Tessier.S, Guicheux.J, Delplace.V, Gaudin.A

Abstract:

Pulpal inflammation is an essential response to bacterial or traumatic injury, but its resolution is crucial for preserving pulp vitality and supporting tissue repair. Specialized Pro-resolving Mediators (SPMs), including lipoxin A4 (LXA4) and resolvin E1 (RvE1), promote inflammatory resolution by limiting pro-inflammatory cytokine production, reducing neutrophil infiltration, and stimulating the clearance of apoptotic cells by macrophages (efferocytosis). However, their limited stability and bioavailability restrict their therapeutic application. This PhD project aims to use extracellular vesicles (EVs) derived from stem cells of the apical papilla (SCAP) as carriers for SPM delivery. We first investigated the effects of LXA4 and RvE1 on human THP-1-derived macrophages in different activation states to assess their pro-resolving activity.

Inflammatory responses were assessed by RT-qPCR and ELISA, while the NF-κB signaling pathway was evaluated by Western blotting. Macrophage efferocytic capacity was also analyzed. LXA4 and RvE1 decreased IL-6, TNF-α, and IL-1β expression and increased IL-10 expression. RvE1 also reduced NF-κB pathway activation, as shown by decreased p-p65 levels by Western blotting, and enhanced the efferocytic capacity of macrophages. These findings support the potential of these mediators to modulate macrophage inflammatory responses, with RvE1 additionally promoting efferocytosis. The next step is to load SPMs into SCAP-derived EVs and assess whether their biological activity on macrophages is preserved or enhanced. This strategy aims to combine the pro-resolving activity of SPMs with the intrinsic biological properties of EVs and their ability to deliver their own molecular cargo, which may promote pulp cell proliferation and differentiation. The goal is to modulate macrophage responses while supporting pulp tissue repair and regeneration.

Notes:

Title: Anti-Pseudomonas antibody induces innate immune memory hallmarks in alveolar macrophages

Auteurs: Alphonse Noémie, El Jamali Chaymae, Heuzé Vourc'h Nathalie and Sécher Thomas
(Université de Tours, CEPR-Inserm U1100)

Abstract:

Therapeutic antibodies (Abs) are increasingly used to treat disease, but their immunomodulatory effects during infection remain poorly understood. We previously showed that pulmonary delivery of the anti-Pseudomonas aeruginosa Ab mAb166 during respiratory infection generates immune complexes (ICs) that block primary infection and provide prolonged protection against secondary infection. Here, we demonstrate that mAb166–P. aeruginosa ICs induce hallmarks of innate immune memory in alveolar macrophages. Primary macrophages exposed to ICs displayed enhanced pro-inflammatory cytokine production and gene expression upon subsequent PAMP restimulation. Consistent with these findings, bronchoalveolar lavage cells from mice treated with ICs showed enhanced inflammatory responses, with more than 1,500 genes upregulated and enrichment of cytokine–cytokine receptor pathways. This response was accompanied by a metabolic shift toward glycolysis, consistent with the acquisition of an innate immune memory state in BAL cells. IC treatment also altered bone marrow progenitor populations, characterized by a reduction in multipotent progenitors, suggesting an effect on hematopoiesis. Overall, these findings reveal an additional, previously undescribed role of therapeutic antibodies in inducing hallmarks of innate immune memory.

Notes:

Title: Linking Copper and Oxidative Stress: Investigating a new host antimicrobial strategy against *Salmonella*

Auteurs: Soraya SADIQI, Ronan KAPETANOVIC, Isabelle VIRLOGEUX-PAYANT

INRAE, ISP, Université de Tours,

Abstract:

Salmonella enterica serovar Typhimurium is a major foodborne pathogen known to cause diseases ranging from gastroenteritis to systemic infections in humans and animals. As a facultative intracellular pathogen, it survives by adapting to hostile intracellular environments and evading host defenses. However, host cells combat it using antimicrobial mechanisms such as reactive oxygen species production or the accumulation of metal ions like copper.

In *Salmonella*, copper homeostasis is maintained partly by *cueP*, a predicted periplasmic metallochaperone uncommon among other enteric bacteria. It is regulated by the copper sensor CueR and the CpxA/CpxR two-component system, which responds to envelope stress. Yet the role of CueP in *Salmonella*'s survival and replication within host cells is still unclear. Thus, our objective is to characterise the spatial and temporal dynamics of copper and oxidative stresses in the intracellular host environment and how these signals are perceived by *Salmonella*.

To investigate the role of CueP during infection, we performed macrophage survival assays using a *cueP* deletion mutant. Preliminary *in vitro* results showed that the absence of CueP affects bacterial survival as early as 2 hours post-infection in RAW264.7 macrophages, suggesting that CueP plays an important role during the early stages of infection. To further characterize the bacterial stress responses underlying this phenotype, we are generating fluorescent reporter strains of *E. coli* and *S.* Typhimurium expressing GFP under the control of the *copA* (copper efflux transporter), *cpxP* and *cueP* promoters. Infection experiments using these reporter strains in RAW264.7 macrophages are currently underway to monitor the kinetics of intracellular copper and oxidative stress responses during infection.

Deciphering how host cells use copper and oxidative stress to control infection and how *Salmonella* adapts to these stresses will provide insights into immune cell antimicrobial strategies and host-pathogen interactions.

Notes:

Title: **Discovering new antimicrobial pathways: mitochondrial dynamics and lipid droplets drive immune responses in macrophages**

Auteurs: **Ronan Kapetanovic**†, Syeda Farhana Afroz†, James EB Curson†, Ina Kirmes, Divya Ramnath, Stephan Nothjunge, Jinting Liu, Jordan D Atkinson, Arnaud Ahier, Karoline D Raven, Marta Bosch, Bernhard Keller, Grace MEP Lawrence, Kaustav Das Gupta, Melanie R Shakespear, Charles Ferguson, Claudia J Stocks, Nilesh J Bokil, Gabriele Matthias, Tam TK Nguyen, Zeinab G Khalil, Robert C Reid, Karl A Hansford, Philip M Hansbro, Matthew A Cooper, Mark A Schembri, Antje Blumenthal, Kate Schroder, David P Fairlie, Albert Pol, Patrick Matthias, Robert G Parton, Steven Zuryn, Matthew J Sweet *†These authors contributed equally to this work.*

Abstract:

Mitochondria were originally described as organelles that produce energy, but are now tied to several critical cellular functions. They play a central role in signalling and metabolic pathways, as well as in the response to virus infection via the MAVS pathway. Here, we present a new role for mitochondria in host defence. We discovered that bacterial infection induces fragmentation of the mitochondrial network (mitochondrial fission). This stress response increases the production of mitochondrial reactive oxygen species (mitoROS) but also activates the mitochondrial unfolded protein response (UPRmt) and the production of antimicrobial lipid droplets. We also found that pathogens such as *Salmonella* actively block mitochondrial dynamics in order to survive within macrophages. However, promoting mitochondrial fission using pharmaceutical or genetic approaches restores an efficient antimicrobial response. In particular, targeting the enzyme HDAC6 allows to promote mitochondria fission. Overall, our findings have identified an evolutionarily conserved pathway that could be targeted to enhance the antibacterial response in macrophages.

Kapetanovic, Afroz, Curson et al Sci Immunol, 2026 Apr 24;11(118):eaed2623.

Notes: