INFRAFRONTIER Webinar: Complex *in vitro* Modelling Technologies

19 October 2026 | 13:00-16:00 CET | Online webinar

13:00 **Introduction by Dr. Michelle Stewart, MLC Harwell**

13:10 **iPSC Generation and Quality Control**
by Dr. Lenka Hromadkova, Czech Centre for Phenogenomics

Human induced pluripotent stem cells (hiPSCs) are widely used to study human diseases and to develop complex *in vitro* models (CIVMs). Established hiPSC lines can be obtained from repositories or collaborators and have usually undergone extensive characterization. However, regular quality control is still needed to monitor pluripotency, genomic stability and differentiation capacity. New hiPSC lines can also be generated in-house by reprogramming primary cells. This is especially useful for studying patients with rare genetic variants that are not represented in available cell collections. Genome editing can also be used to generate isogenic hiPSC lines, reducing the effect of different genetic backgrounds in disease studies. We will provide an overview of hiPSC generation, characterization and quality control, with emphasis on both established and newly generated lines. Their use in disease modelling and in the development of 2D and 3D CIVMs will be also discussed.

13:40 **Lung Organoid Microarrays for Precision Infection Modelling and Drug Development**
by Dr. Ana Zarubica, PHENOMIN-CIPHE

Biomedical research is advancing rapidly, yet translating discoveries into reliable, reproducible, and human-relevant models remains a major challenge. Combining the strengths of animal models, human cell-based systems, and computational approaches offers new opportunities to accelerate the path from discovery to therapy. Within the PRIMTECH-3R project, supported by Infrafrontier and the 3Rs framework, and in collaboration with Dr. Edwin Rosairo-Olivieri at New York University, we have established lung organoid microarrays at CIPHE as a scalable platform for precision infection modelling. These stem cell-derived models enable the study of lung development, host–pathogen interactions, infection dynamics, tissue responses, and therapeutic efficacy in a controlled and multiplexed format. We will present their development within the CIPHE Immunology and Infection programs, highlighting the potential of lung organoids to bridge and complement in vitro and in vivo approaches, providing more human-relevant models alongside animal studies. Integration of transcriptomic, proteomic, imaging, and cellular profiling will support model characterization and comparison with in vivo systems. As a future perspective, we aim to incorporate immune, stromal, and endothelial cells to better recapitulate the complexity of the lung microenvironment. Together, these approaches will contribute to refined preclinical research, improved disease modelling, and more predictive drug screening and development.

14:10 **Glioblastoma in 3D: Unlocking Therapeutic Breakthroughs Through Advanced Coculture Modeling**
by Dr. Fabio Mammano & Dr. Daniela Marazziti, CNR Italy

Glioblastoma (GBM) remains the most commonly occurring malignant primary brain tumor in adults, characterized by diffuse invasion, profound cellular heterogeneity, resistance to standard therapies and near certainty of relapse. We are developing a standardized three-dimensional co-culture platform based on the Alvetex polystyrene scaffold. The system enables co-culture of murine or patient-derived GBM cells with mESC-derived neurons and astrocytes, offering a comprehensive platform to study GBM invasion, tumor-associated neurotoxicity, and the efficacy of novel therapeutics. Moving beyond conventional cell-killing assays, it provides a dynamic, high-resolution view of tumor interactions with the brain's cellular architecture. By integrating mass spectrometry, advanced imaging, and quantitative viability assays, the model enables generation of robust multiparametric datasets that support preclinical drug discovery and deepen our understanding of the mechanisms driving brain cancer progression.

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14:40 **Break**

14:55 **Integrated 3D bioprinted muscle model to study cancer cachexia (MuTu)**

by Dr. Agnese Bonato & Dr. Giulia Vigato, CNR Italy

Cancer cachexia is a metabolic wasting syndrome with no effective treatment, affecting up to 80% of solid cancer patients. To date, cancer cachexia lacks representative *in vitro* and *in vivo* models. We developed an integrated *in vitro* muscle model incorporating an appropriate tendon-like attachment system and cancer organoids to study muscle-cancer crosstalk in a dynamic and versatile platform (MuTu). This Complex *In Vitro* Model (CIVM) allows assessing functional and molecular alterations in muscle fibres co-cultured with colon cancer organoids. *In vitro* morphological, molecular, and functional validation of platform performance will be performed, followed by *in vivo* comparison with animal models of cancer cachexia. This model is also expected to enable further studies of muscle function in other muscle-related pathologies. Overall, MuTu will support drug testing and therapeutic research in a reproducible and ethically responsible system, reducing animal testing while providing a reliable, cost-effective, and time-saving in vitro platform.

15:25 **A high-throughput BBB platform modeling glucose transport deficiency for CNS therapeutic development**

by Dr. Chiara Parisi, CNR Italy

We are developing a standardised, scalable, high-throughput mouse stem cellbased GLUT1-BBB Cell-In-Vitro Model (CIVM) that reproduces key functional features of the blood–brain barrier in a physiologically relevant 3D microenvironment. The model is designed for biomedical studies investigating BBB function and glucose transport, with particular relevance to GLUT1 deficiency syndrome (GLUT1 DS) and neurodegenerative diseases associated with impaired glucose transport across the BBB. Its direct validation through *in vitro–in vivo* comparison of glucose permeability supports its use as a reliable experimental platform. The CIVM enables scalable assessment of BBB integrity and permeability through complementary readouts, including barrier integrity and fluorescent glucose transport. Moreover, the platform can be adapted to different mouse genetic backgrounds, enabling the development of disease specific BBB models and providing a versatile tool for mechanistic studies and preclinical research.

15:55 **Closing remarks**

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