

MULTI-OMICS WORKFLOW TO CHARACTERISE OXIDATIVE STRESS AT THE MOLECULAR LEVEL USING *IN VITRO* MODELS

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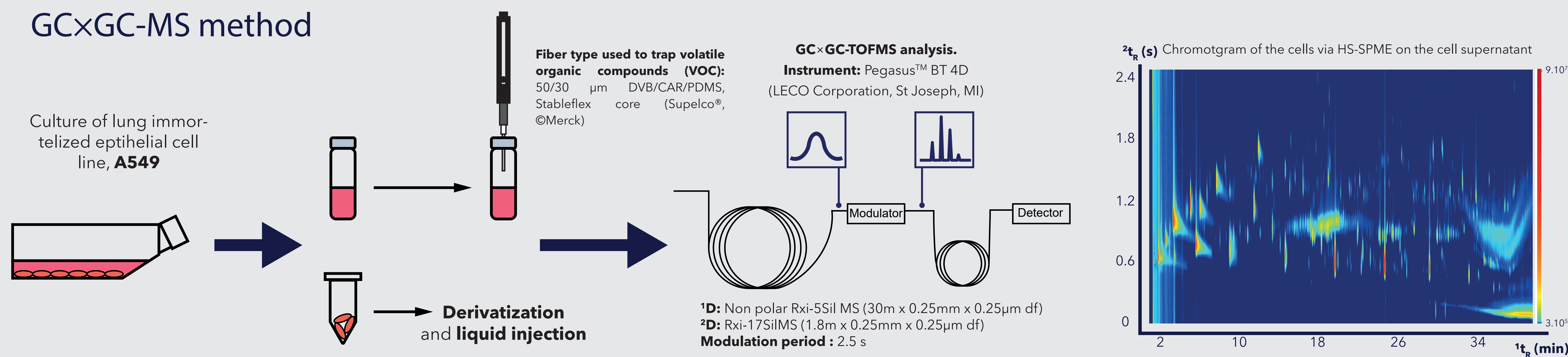
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Context

Oxidative stress is a pathological condition that arises when there is an imbalance between reactive oxygen species (ROS) production and cellular detoxification ability [1]. This condition has been linked to various diseases such as asthma and cancer, making it an important area of research for better diagnosis and treatment of inflammatory diseases. *In vitro* cell cultures have become an essential tool to comprehend the intricate mechanisms of oxidative stress involved in inflammatory reactions [2]. The use of *in vitro* cell cultures provides an ethical and controlled environment where the effects of oxidative stress can be studied independently of other confounding factors. The challenge lies in establishing optimal oxidative conditions, as induced by H₂O₂, without triggering apoptosis or necrosis of the cells. However, achieving analytically reproducible conditions with biological materials is challenging. In this ongoing research, we are striving to replicate and refine a robust analytical workflow for the optimal oxidation of A549 epithelial cell lines using H₂O₂.

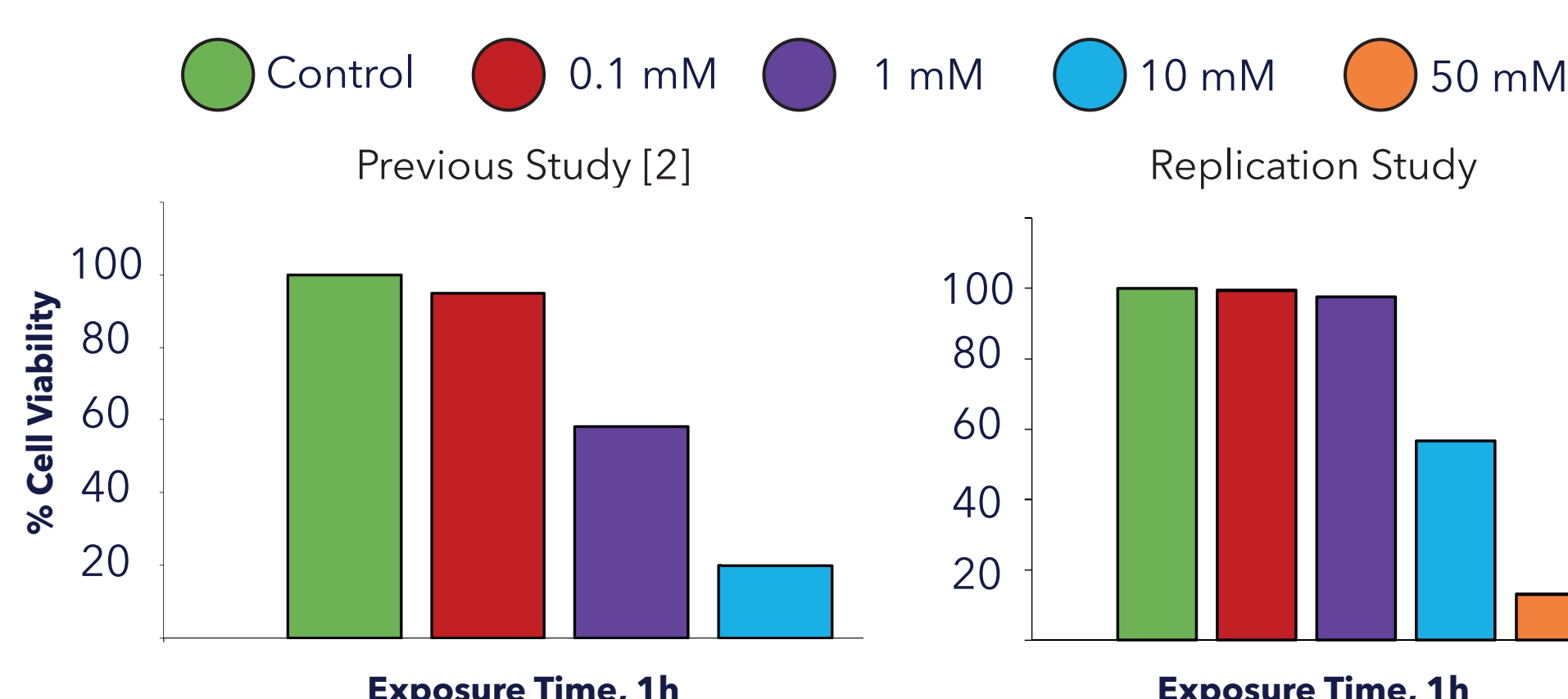
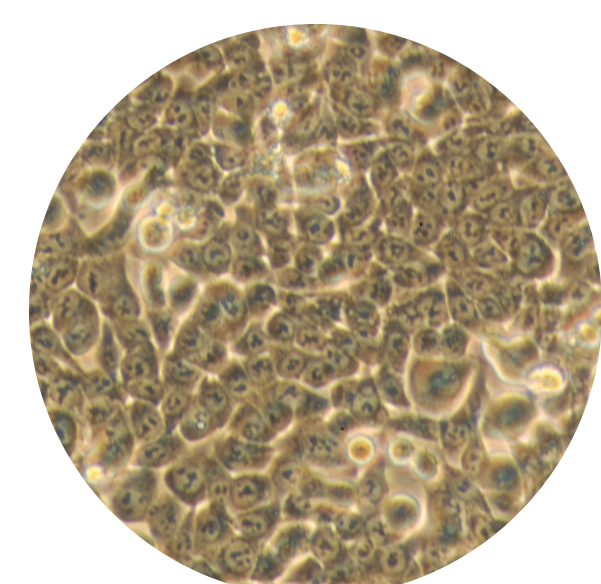
GCxGC-MS method



Study Workflow

1. Attempt to replicate the previous study [2]

Oxidation condition:
0.1 mM of H₂O₂ for 1 h



1.a Viability Test

1.b SPME analysis on the cell supernatant

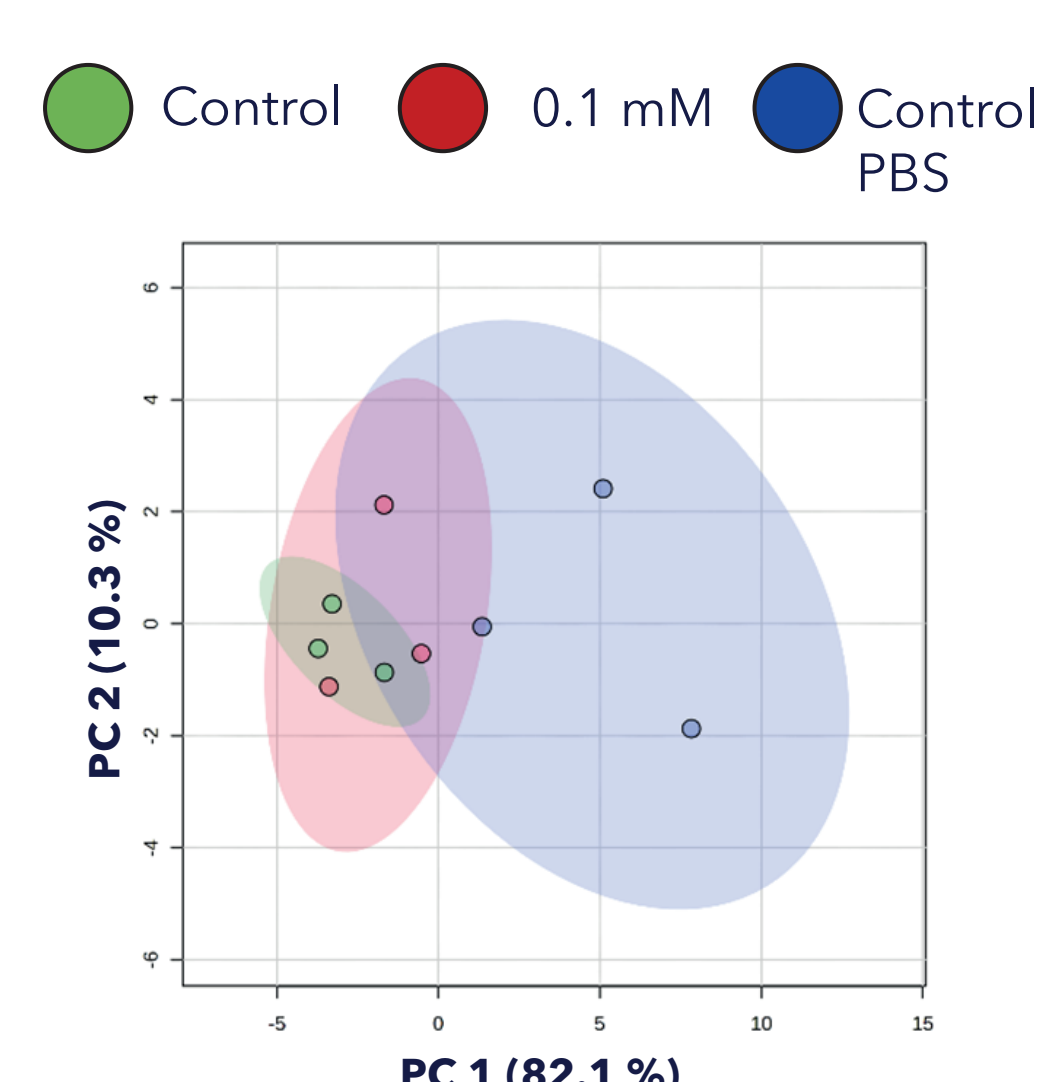
1.c Results of the SPME part

Expectations

- Confirmation of the previous oxidation condition (0.1 mM of H₂O₂ for 1h)
- Same viability for the cell with the same oxidation conditions
- Unambiguous clustering in the PCA for the different conditions

Outcomes

- The profile of the viability test is different (shifted)
 - There is no clear separation across the different oxidations conditions
 - This concentration seems too «soft» to trigger any oxidation event
- Are we sure about the concentration of H₂O₂?**



Solution: Titration of H₂O₂ and try to oxidize with a higher concentration!

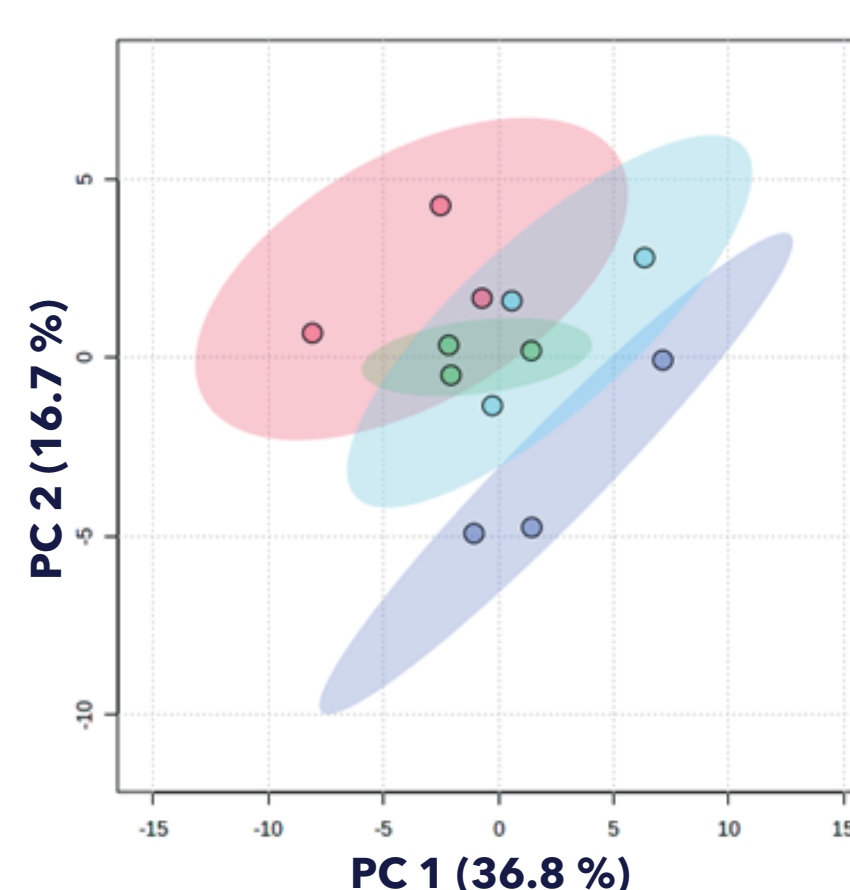
2.c Results of the SPME part

Expectations

- By controlling the H₂O₂ concentration, the results are more robust
- By increasing the concentration and the exposition time, the oxidation will be triggered

Outcomes

- The viability of the cells is high for all the conditions, even the 0.9 mM for 2 h
- There is no clear separation across the different oxidations conditions
- This concentration seems again too «soft» to trigger any oxidation event
- A small trend can be observed between the control group (dark blue) and the rest. However, it can be linked to the dilution when adding H₂O₂ to the media



● 0.9 mM for 2 h ● 0.9 mM for 1 h
● Control ● Control PBS

2.a Viability Test

The viability is around **98 %** for all the conditions



2.b SPME analysis on the cell supernatant

2. Increase the concentration and set up 2 exposures times

Oxidation condition:
0.9 mM of H₂O₂ for 1 h and 2 h

Developpement of an **analytical workflow** to ensure the **correct H₂O₂ concentration** with a titration by KMnO₄ previously calibrated by a fresh solution of oxalic acid

3. Study of the impact of the cell starving step for long exposition times

Oxidation condition:
0.1 mM of H₂O₂ for 1 h and 2 h with or without a starving step of FBS 2% for 24h

3.a Viability Test

The viability is around **96 %** for all the conditions



3.b SPME analysis on the cell supernatant

ONGOING

Context: Cells require serum (typically 10 % FBS/FCS) for growth and to maintain viability. However, during the oxidation process, the medium containing the oxidative agent is serum-free. Prolonged exposure, such as 24 h, would likely lead to cell death regardless of the oxidative agent used. The serum-starvation step allows the cells to adapt to a lower serum concentration, typically around 2 % for 24 h.

Next Step/Ongoing

- Developing an analytical derivatization workflow for the cellular pellet (utilizing metabolomic and lipidomics approaches)
→ **Comparing the VOC and approach with the derivatization/liquid approach**

- Advancing to the development of an organoid model to further enhance our understanding of the oxidation at a molecular level

