CHRD 2024: Abstract Submission Form

Presenter Name
Floriane Houenagnon

Presenter Status
Masters Student

Role in the project
Design
Perform Experiments
Analyze Data
Write Abstract

Research Category
Basic Science

Title
The Impact of Omega-3 fatty acids on glucose metabolism in macrophage cell models

Background
Obesity is associated with a state of chronic inflammation, which is a risk factor for progression to diseases such as Type 2 Diabetes. Macrophages play a key role in obesity-associated inflammation. Common n-3 PUFA, such as docosahexaenoic acid (DHA) and α-linolenic acid (ALA), have anti-inflammatory effects. In monocytes, this is associated with changes to catabolic pathways. Their impact on metabolic pathways in macrophages remains unclear.

Objective
To describe the effects of n-3 PUFA on glucose metabolism by glycolysis and mitochondrial respiration in macrophages.

Methods
Macrophages, including murine RAW 264.7 cells and human THP1-derived macrophages (TDM), were treated with the following: Vehicle, DHA, ALA, and Oleic acid (OA, a monounsaturated fatty acid control) for 24 hours. Then, the ATP rate assays were conducted using a Seahorse XFe24 instrument. Data were normalized by measuring protein content via BCA assay or by cell counting using the Cytation 5 cell imaging multimode Reader. Cell viability was assessed using the CYQUANT XTT assay.

Results
TDM and RAW macrophages have different metabolic phenotypes. Examining vehicle-treated conditions shows that the ratio of total ATP produced from mitochondrial respiration to glycolysis is ~15:1. In RAW 264.7 cells, that ratio is ~ 1:1. In TDM, DHA significantly increases the percent of ATP derived from glycolysis. In RAW 264.7 cells, neither n-3 PUFA significantly altered the balance of catabolic pathways. The XTT assay showed that DHA significantly increased TDM viability by approximately 25%, highlighting the importance of accurate normalization of Seahorse data.

Conclusion
The results highlight the heterogeneity between the cell lines. Further comparison of the basal metabolic differences between macrophage models will allow us to see which cell line model best mimics the primary macrophage cells.

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No

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