Full length article

Metabolic energetic adaptation of Atlantic salmon phagocytes to changes in carbon sources and exposure to PAMPs

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https://doi.org/10.1016/j.fsi.2024.109926 Get rights and content

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Abstract

Phagocytic cells are pivotal for host homeostasis and infection defense, necessitating metabolic adaptations in glycolysis, the tricarboxylic acid (TCA) cycle, and oxidative phosphorylation (OXPHOS). While mammalian phagocytes shift towards glycolysis and glutaminolysis during polarization, research on fish phagocyte metabolic reprogramming is limited. To address this, the Atlantic salmon phagocytic cell line, SHK-1, serves as a valuable model. Using the Seahorse XFe96 Flux Analyzer, this study compares SHK-1 bioenergetics under glucose-restricted (L-15 medium) and glucose-supplemented (PM) conditions, providing insights into metabolic characteristics and responses to *Piscirickettsia salmonis* bacterium Pathogen-associated molecular patterns (PAMPs). A standardized protocol for the study of real-time changes in the metabolism study of SHK-1 in PM and L-15 media, determining oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) is shown. Exhibiting metabolic adaptations, SHK-1 cells in the PM medium have higher basal and maximal OCR and spare capacity (SRC), while those grown in the L-15 medium favor OXPHOS, showing minimal glycolytic function. Despite metabolic differences, intracellular ATP levels are comparable, highlighting the metabolic plasticity and adaptability of SHK-1 cells to various carbon sources. Exposure to PAMPs from *Piscirickettsia salmonis* induces a metabolic shift, increasing glycolysis and OXPHOS, influencing ATP, lactate, glutamine, and glutamate levels. These findings highlight the role of mitochondrial bioenergetics and metabolic plasticity in salmon phagocytes, offering novel nutritional strategies for host-pathogen interventions based on energy metabolism.