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**HEPATIC MICRORNA PROFILE IN ‘GLUCOSE INTOLERANT’ RAINBOW TROUT AND PREDICTED CONSEQUENCES FOR THE INTEGRATION OF ENDOCRINE SIGNALS.**

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Rainbow trout are a widely-used research model in the endocrine and nutritional regulation of energy metabolism. Due to their poor utilization of dietary carbohydrates characterized by a prolonged hyperglycemia following the ingestion of carbohydrate-rich diets, rainbow trout are generally considered to be ‘glucose-intolerant’. In addition to the investigation of endocrine signaling, mRNA and protein abundance and function of rate-limiting enzymes in energy metabolic pathways, recent studies have pointed to metabolic roles of microRNAs. MicroRNAs are short, non-protein-coding RNA molecules with roles in the regulation of energy metabolism in both, mammals and rainbow trout. Taking advantage of a recent annotation of the rainbow trout miRNA repertoire and genome-derived UTR target sequences in this species, we used a transcriptome-level approach to identify hepatic miRNA abundance in response to dietary carbohydrate regimes inducing hyperglycemia. Using *in silico* methods, we provide evidence for the emerging hypothesis that altered hepatic miRNA profiles in response to a high dietary carbohydrate load may result in differential endocrine regulation of carbohydrate metabolism in the liver, thus contributing to a ‘glucose intolerant’ metabolic phenotype. Acknowledgements: Supported by: A University of Ottawa start-up grant to JAM and financial support from the INRA PHASE Department to SP and LM.

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