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► To cite this version:

Jan A. Mennigen, Stéphane Panserat, Lucie Marandel. Hepatic microRNA profile in "glucose" intolerant rainbow trout and predicted consequences for the integration of endocrine signals. 18. International Congress of Comparative Endocrinology, Jun 2017, Alberta, Canada. , 147 p., 2017, ICCE18. hal-01603132

HAL Id: hal-01603132

<https://hal.science/hal-01603132v1>

Submitted on 2 Jun 2020

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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.
