

Integrative bioinformatics data analysis of Nile Tilapia microRNAs

Luiz Augusto Bovolenta¹, Danilo Pinhal¹, Simon Moxon², Arthur Casulli de Oliveira³, Pedro Gabriel Nachtigall¹, Marcio Luis Acencio⁴, Cesar Martins⁵ and Ney Lemke⁶

¹*Department of Physics and Biophysics, Institute of Biosciences of Botucatu, São Paulo State University -*

UNESP, Brazil; ²*Department of Genetics, Institute of Biosciences of Botucatu, São Paulo State University -*

UNESP, Brazil; ³*School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich,*

United Kingdom; ⁴*Department of Cancer Research and Molecular Medicine, Faculty of Medicine, Norwegian*

University of Science and Technology - NTNU, Trondheim, Norway; ⁵*Department of Morphology, Institute*

of Biosciences of Botucatu, São Paulo State University - UNESP, Brazil.

MicroRNAs (miRNAs) are considered essential regulators of several biological processes, such as development, body axis patterning, immune responses, cell fate, proliferation and death. MiRNAs are small RNA molecules that contain approximately 22 nucleotides that are originated from longer hairpin-like RNA molecules (pri-miRNAs). These small RNA molecules silence gene expression either via mRNA degradation or preventing mRNA from being translated. In teleosts, miRNAs have been mainly associated with sexual differentiation, diseases markers, developmental and growth regulatory elements and environmental modulation effects. The Nile tilapia (*Oreochromis niloticus*), an teleostei species, has been globally recognized as a commercially valuable fish due to its phenotype characteristics, such as high endurance, easy adaptability, good consumer acceptance and rapid growth in a variety of aquaculture systems. In this sense, miRNA data are valuable to unravel molecular mechanisms responsible for phenotypes with economic value, specifically how miRNAs could enhance Nile tilapia productivity. To identify known and novel miRNAs associated with interesting phenotypes in Nile tilapia (sex differentiation, muscle growth and disease resistance), we performed an integrative bioinformatics analysis in attempt to unravel biological mechanisms of miRNAs discovered by RNAseq of 16 different samples taken from Nile tilapia adult tissues and developmental stages. In the first step of this analysis, we clustered miRNAs by their expression profiles using Mapman and identified 40 and 12 clusters considering only expression data from, respectively, adult tissues and developmental stages. Then we predicted putative miRNA-mRNAs interactions with TargetScan (version 6) and applied filters based on the evolutionary conservation of interactions and on the experimental evidence of expression of the target mRNAs (SRP009911) to create a collection of high confidence 11,168 miRNA-mRNAs interactions among 326 known miRNAs, 60 novel miRNAs and 3,805 mRNAs. Next, we performed a functional enrichment analysis for each set of targets of each miRNA within each of the 52 clusters using g:Profiler with Gene Ontology (GO) terms and, taking into consideration shared targets or similar enriched GO terms, we could infer putative functions to the novel miRNAs such as, for example miR-n483-5p predicted with MYOG gene, which can be involved in muscle development processes (“skeletal muscle tissue development” and “muscle organ development” terms). For miR-n941-5p, we identified a putative regulatory role in muscle dysfunctions (“Abnormal muscle tone” and “Hypopigmentation of the skin” terms). Finally, we can infer the miR-n741-5p regulatory roles at liver (“liver development, lipid metabolic process and fatty acid biosynthetic process” terms).

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