

P23—Circular RNAs as Potential Growth Biomarkers in Nile Tilapia

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Summary

Circular RNAs (circRNAs) are non-polyadenylated, non-coding RNAs produced by alternative back-splicing. They are considered as potential biomarkers in different biological processes and efficient in participating in microRNA (miRNA) sponging and epigenetic regulation of gene expression. There are some reports in farm animals (sheep, goat, chicken) that describe the functional roles of circRNAs in muscle growth [1]. However, our knowledge of their expression in muscle and functional mechanisms related to growth is still limited in teleosts. Fast and enhanced fish muscle growth is one of the main traits of interest for the global aquaculture industry, which is currently targeted mainly through diet improvements and selective breeding. In this study, we used fast- and slow-growing Nile tilapia from the third generation of our in-house domestication program, which have been reared in a freshwater recirculating aquaculture system. Nile tilapia having an average total length of 29.28 ± 2.15 cm and 13.8 ± 1.98 cm were considered fast- and slow-growing fish, respectively. We profiled mRNA, miRNA and circRNA expression in muscle tissue to provide insights into their potential function in muscle growth.

The results showed that 1947 mRNAs, 9 microRNAs and 8 circRNAs were differentially expressed between fast- and slow-growing Nile tilapia individuals. Gene ontology and KEGG analysis revealed that the differentially expressed mRNAs are involved in the regulation of myoblast differentiation, striated muscle cell development, mRNA splicing via spliceosome and spliceosomal snRNP complex; the last two processes are import components in circRNA production during pre-mRNA splicing. Bioinformatic target prediction revealed *oni-miR-34*, *oni-miR-130b* and *oni-miR-202* have complementary binding sites for *circMef2c* and muscle growth-associated mRNAs. A ceRNA network was constructed through integrative analysis of the interplay between *circMef2c*, 3 miRNA and 65 mRNAs. Potential interactions were found in *circMef2C-oni-miR-34-Igfbp2*, *circMef2C-oni-miR-130b-5p-myod1* and *circMef2C-oni-miR-202-fgf14*, which likely play an important role in muscle gain throughout ontogeny. Our data suggest that these circRNAs may prove to be novel growth biomarkers with potential application in the aquaculture sector.

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References

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