PROFILING OF FAST MUSCLE MICRORNAS ASSOCIATED WITH SEXUAL MATURATION AND PHOTOPERIOD TREATMENT IN ATLANTIC COD

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SUMMARY

Understanding the transcriptomic network regulating myogenesis may help us to improve the growth performance of farmed Atlantic cod. MicroRNA (miRNA) regulation is a post-transcriptional mechanism to downregulate the target mRNA transcription. In brief, the mature single strand miRNA binds to target mRNAs leading to their degradation, destabilization or transcriptional repression. Since miRNAs are found in a wide variety of species, developmental stages and tissue types, this mechanism could be involved in most biological processes. Despite their biological importance, the involvement of miRNAs in muscle growth has received scant attention in teleosts, particularly in commercially important species.

In the present report, we reared two-year old Atlantic cod for an additional year and sequenced the miRNAome of the fast skeletal muscle of both sexes at different seasons (August, November, February, March and May) throughout the reproductive cycle. In addition, we conducted photoperiod manipulation for 6 months with Atlantic cod juveniles and sequenced the fast muscle miRNAome throughout the photoperiod treatment (0, 8 hours, 1 day, 1 week, 1, 2, 4, 6 months). For photoperiod treatment, one fish group was kept under continuous illumination whereas the other was reared under a light regime that corresponded to natural photoperiod conditions in Bodø (Norway). Small cDNA libraries were used for emulsion PCR as a template and sequenced on the SOLiD 4 deep-sequencing platform. In the 10 miRNA libraries for the muscle at five different seasons for both sexes, 1.8 to 3.7 Million (M) reads per library were obtained. Then, 0.8 to 1.9 M reads (approximately 40% of total reads per library) were annotated to zebrafish miRNA data downloaded from miRBase 17. The comparison of expression levels in reads per kilobase of exon model per million mapped reads (RPKM) revealed that miR-206, miR-1, miR-100, miR-99, miR-22, miR-150, miR-214 and miR-133 were the top 8 highly expressed miRNAs. Notably, miR-206 has been identified as the most abundant miRNA through the maturation cycle for both of sexes, suggesting its biological importance in muscle growth. In addition, it is noteworthy that miR-1 and miR-133 that are reported as muscle specific microRNAs were in the top 8 list. Interestingly in males muscle, miR-1 expression reached a peak in November, whereas in females muscle its expression gradually increased and reached a peak in March. The 6-month photoperiod treatment produced significant difference in mean weight amongst the two groups of juvenile cod. The mean weight of continuous light group was 15 and 10 % higher than the natural photoperiod group at 4 and 6 months, respectively. The fast muscle miRNA transcriptomes from these samples will be further annotated, and their expression levels will be verified by qPCR. The data obtained in the present study will provide a significant contribution to our limited understanding of the molecular regulation of muscle growth in Atlantic cod and how it is affected by photoperiod and sexual maturation.