

Dear Editors,

Dear Authors,

In the reviewed study authors conducted an extensive analysis of microRNA (miRNA) genes in pikeperch (*Sander lucioperca*) at various developmental stages and organs. Small RNA libraries from 20 pikeperch samples, including six developmental stages and four organs of adult fish, were sequenced. Moreover, the study assessed the diversity of mature miRNAs across different developmental stages and organs. The comprehensive analysis of the pikeperch miRNAome presented in this study holds significant importance for both basic biological understanding and practical applications in aquaculture. The identification and characterization of numerous unique miRNA sequences shed light on the intricate regulatory mechanisms governing developmental processes, organ-specific functions, and responses to environmental stress, thereby advancing our fundamental knowledge of fish biology.

The applicability of the presented data in the future is multi-faceted. Firstly, the insights gained into the conserved and novel miRNAs in pikeperch contribute to the broader understanding of miRNA evolution across teleost species. This knowledge is crucial for deciphering the molecular basis of vertebrate development and adaptation. In the context of aquaculture, the identified miRNAs, especially those associated with immune responses and stress, offer potential applications for enhancing the health and resilience of pikeperch populations in fish farms. Understanding the regulatory roles of specific miRNAs opens avenues for targeted interventions to improve growth rates, disease resistance, and overall well-being in aquaculture settings. This could lead to the development of innovative strategies for sustainable and efficient fish farming practices.

The introduction chapter effectively communicates the background, significance, and objectives of the study, providing accurate information in a clear and organized manner. However, there are a few areas where improvements can be made:

1. Providing more recent data, if available, on aquaculture production trends or advancements in genetic research could strengthen the manuscript's context;
2. The study's aim is clear, but specifying the expected outcomes or potential applications of the research could enhance reader engagement. Please provide more details on expected outcomes or applications;
3. Please provide more detailed information about the mentioned problems mentioned within the lines 65-67.

The provided Materials and Methods chapter is detailed and generally well-written.

However, there are a few points that require attention:

1. Provide more details on the selection criteria for samples, especially in terms of developmental stages and organs;
2. Lines 495-496 you wrote "Processed reads from all 20 samples were mapped to the reference applying STAR aligner software (v.2.5.2b)." What do you mean mapped to what? If you determined a comprehensive list of miRNAs, including their sequences (Supplemental File 1), and the goal is to quantify the expression of these specific miRNAs, mapping to a reference genome may seem unnecessary. Instead, a more straightforward approach would be to directly align the processed reads to the known miRNA sequences provided in the supplemental file;
3. Line 459 – should be supplementary table S6 I guess.

The Results and Discussion chapter provides a detailed account of the identification and characterization of miRNA genes in pikeperch, their diversity across different developmental stages and organs, and their differential expression patterns. Overall, the chapter is generally clear and logically structured, connecting results to the broader context. However, the authors may want to discuss potential implications of their findings in the broader context of pikeperch biology, aquaculture, or evolutionary perspective.

The conclusion chapter provides a concise summary of the key findings and implications of the study. While the conclusion outlines the potential applications of miRNAs in aquaculture, it could be strengthened by discussing specific traits of interest and how the identified miRNAs might play a role in improving those traits.

The abstract provides a comprehensive overview of the study, covering key aspects of the pikeperch miRNA repertoire. No remarks.

The title is concise and informative, providing potential readers with a clear understanding of the main subject matter of the research.

As the reviewed manuscript contributes valuable information about the miRNA landscape in pikeperch, shedding light on its diversity, differential expression patterns, and potential functional roles in different developmental stages and organs, including responses to hypoxia stress, I recommend the article for possible publication in the IJMS periodical after minor revision.

Best regards,