Transcriptome analysis of the brain and liver of fast-and slow-growing phoenix barb (Spinibarbus denticulatus) for identifying genes for growth

Xi Xie*[1], Jiamiao Zhuang*[1], Xianping Liao[2], Zhengsheng Xu[2], Wenlang Liang[2], Yilin Su[2], Li Lin[3], Jungang Xie[2], Weiqiang Lin[2]
[1]College of Light Industry and Food, Zhongkai University of Agriculture and Engineering, Guangzhou, China; [2]Fishery Research Institute of Zhaoqing, Zhaoqing, China; [3]College of Animal Science Technology, Zhongkai University of Agriculture and Engineering, Guangzhou, China; *These authors contributed equally to this work

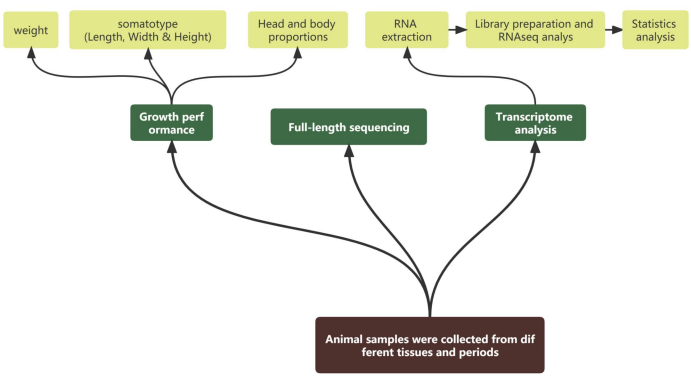
Abstract

- KEGG enrichment analysis showed that differentially expressed genes with different growth rates in the brain were enriched in pathways associated with brain growth, Th 17 cell differentiation, estrogen signaling, Protein processing in endoplasmic reticulum, cell adhesion molecules (CAM), Valine,leucine and isoleucine degradation, Fatty acid eiongation and circadian rhythms.
- The differentially expressed genes of different growth rates in liver were concentrated in liver growth, Protein processing in endoplasmic reticulum, Th 17 cell differentiation, Valine,leucine and isoleucine degradation, Fatty acid eiongation, estrogen signaling, lipid metabolism and AMPK signaling pathway.
- Individuals with different growth rates expressed different genes in the same growth period, and the same genes were expressed early in the fast-growth group and late in the slow-growth group.

Introduction

- Phoenix barb is a kind of freshwater fish distributed in different provinces in southern China. It is famous for its variety, mixed bait, strong stress resistance, tender meat, delicious taste and rich nutrition. It has become an important commercial fish in southern China. In addition, growth rate is one of the most important traits in commercial fish farming. Similarly, genetic makeup plays an important role in body size development. Although phoenix has been cultivated in different parts of southern China, the molecular mechanism of its growth rate has been poorly studied. In this paper, we analyze the transcriptome of the brain and liver tissues of both fast and slow-growing individuals and elucidate the molecular mechanisms that regulate the growth of this species.

Experimental process



Results

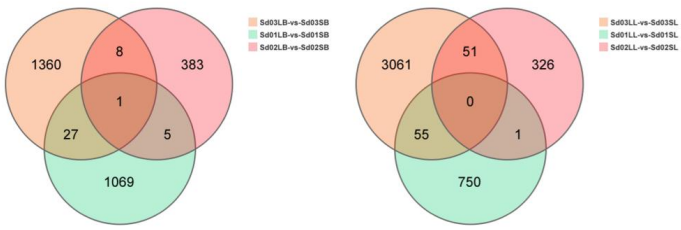


Figure 1 Venn diagram profile of differentially expressed genes in different tissues at different times (Left: Brain; Right: Liver)

- **1.** There were 1069/750, 383/326 and 1360/3061 differentially expressed genes in the brain/liver at 90, 150 and 300 DAHs, respectively. Furthermore, there were 27/55 differentially expressed genes shared by the 90DAH and 300DAH brain sites. (Figure 1)

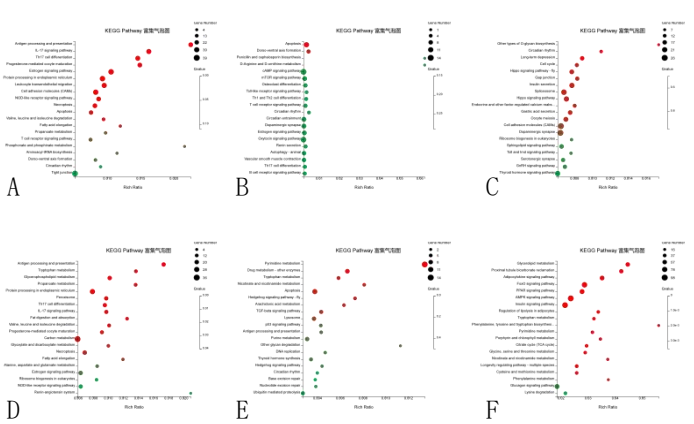


Figure 2 KEGG enrichment analysis of differentially expressed genes in different tissues at different times (A: 90DAH Brain; B: 150DAH Brain; C: 300DAH Brain; D: 90 Liver; E: 150DAH Liver; F: 300DAH Liver)

- 2. Genes linked to Th17 cell differentiation, estrogen signaling, Protein processing in endoplasmic reticulum, Valine, leucine and isoleucine degradation and Fatty acid elongation are crucial for regulating growth in the brain and liver in the early stages (90DAH). (Figure 2)

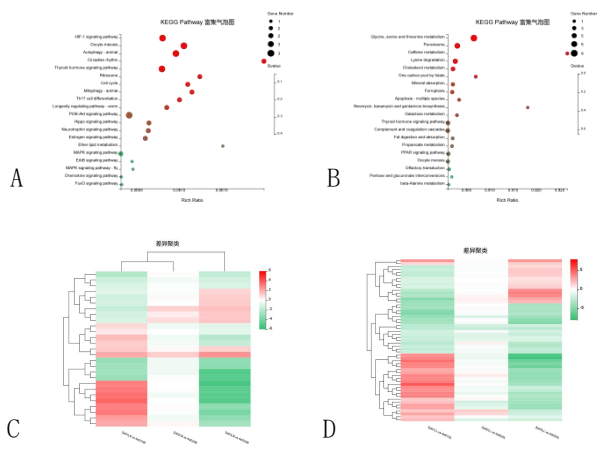


Figure 3 KEGG enrichment analysis and cluster plots of the same differentially expressed genes in different tissues at different times (A: KEGG enrichment map of the brain; B: KEGG enrichment map of the liver; C: cluster map of the brain; D: cluster map of the liver)

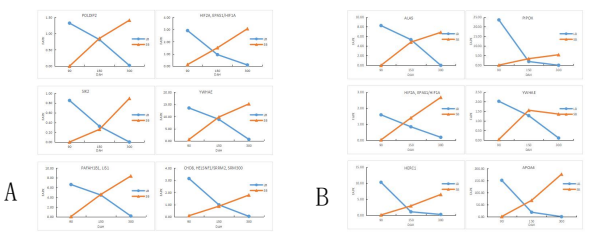


Figure 4 Analysis of typically differentially expressed genes at different growth rates and stages (A: Brain; B: Liver).

- 3. At the brain level of 90 DAH, compared with slow fish, fast fish were significantly enriched in individual genetic information processing, environmental information processing, organic systems, environmental information processing and lipid metabolism ($P < 0.01$). At 90 DAH in the liver, compared with slow fish, fast fish were significantly enriched in their individual amino acid metabolism, environmental information processing, genetic information processing, and organic systems ($P < 0.01$). By calculating FPKM at three time points, the expression patterns of these genes in different parts of fast fish and slow fish were compared.(Figure 3 and 4)

Conclusion

- In summary, the transcriptome of fast-growing and slow-growing individuals at different growth stages was investigated, and the molecular mechanisms of brain and liver development and growth were clarified by comparison. Results showed that different tissues and growth stages are regulated by multiple genes, most of which are involved in growth and development regulation. The KEGG pathway analysis revealed that the two groups of fast and slow growth were significantly more abundant in the three stages of biological metabolism-related signaling pathways. In addition, fast-growing individuals were more abundant in metabolism-related genes related to growth traits in the early growth stage compared to slow-growing individuals. This suggested that metabolism or metabolism-related genes may be connected to individual growth and development. Based on the aforementioned, these findings aid in understanding the molecular mechanisms driving Chinese phoenix barb development regulation and in identifying breeding target genes.

Acknowledgements

- This project was funded by the National Natural Science Foundation of China (grant no. 42106130), the Natural Science Foundation of Guangdong Province, China (grant no. 2020A1515110237), the Administration of the Fisheries Refined Oil Price Subsidy Special Fund, China and the Zhaoqing Institute of Fisheries Science (grant No. 2022N006)