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De novo Transcriptome Assembly of Lumpfish (Cyclopterus lumpus L.) Brain Towards Understanding their Social and Cognitive Behavioural Traits

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Abstract : Understanding fish behavior is essential to improve animal welfare in aquaculture research. Behavioral traits can have a strong influence on fish health and habituation. To identify the genes and biological pathways responsible for lumpfish behavior, we performed an experiment to understand the interspecies relationship (mutualism) between the lumpfish and salmon. Also, we tested the correlation between the gene expression data vs. observational/physiological data to know the essential genes that trigger stress and swimming behavior in lumpfish. After the de novo assembly of the brain transcriptome, all the samples were individually mapped to the available lumpfish (Cyclopterus lumpus L.) primary genome assembly (fCycLum1.pri, GCF_009769545.1). Out of ~16749 genes expressed in brain samples, we found 267 genes to be statistically significant ($P > 0.05$) found only in odor and control (1), model and control (41) and salmon and control (225) groups. However, genes with $|LogFC| \geq 0.5$ were found to be only eight; these are considered as differentially expressed genes (DEG's). Though, we are unable to find the differential genes related to the behavioral traits from RNA-Seq data analysis. From the correlation analysis, between the gene expression data vs. observational/physiological data (serotonin (5HT), dopamine (DA), 3,4-Dihydroxyphenylacetic acid (DOPAC), 5-hydroxy indole acetic acid (5-HIAA), Noradrenaline (NORAD)). We found 2495 genes found to be significant ($P > 0.05$) and among these, 1587 genes are positively correlated with the Noradrenaline (NORAD) hormone group. This suggests that Noradrenaline is triggering the change in pigmentation and skin color in lumpfish. Genes related to behavioral traits like rhythmic, locomotory, feeding, visual, pigmentation, stress, response to other organisms, taxis, dopamine synthesis and other neurotransmitter synthesis-related genes were obtained from the correlation analysis. In KEGG pathway enrichment analysis, we find important pathways, like the calcium signaling pathway and adrenergic signaling in cardiomyocytes, both involved in cell signaling, behavior, emotion, and stress. Calcium is an essential signaling molecule in the brain cells; it could affect the behavior of fish. Our results suggest that changes in calcium homeostasis and adrenergic receptor binding activity lead to changes in fish behavior during stress.

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