

Transcriptome analysis of color common carp: insight into molecular mechanisms of body colors

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Body color is an important phenotypic trait in fish; however, its molecular mechanism remains unclear. The Oujiang color common carp (*Cyprinus carpio* var. *color*) is a widespread variant of common carp found in the Oujiang River basin of Zhejiang Province, and is characterized by numerous body color patterns. In the present study, transcriptome profiling analysis of skins of two carp strains, “white” and “red-black”, was conducted using the 454 RNA pyrosequencing. We obtained 408,928 and 328,173 high-quality reads in “red-black” and “white” fishes, respectively, with an average length of 232 bp. These reads were assembled into 49,417 EST clusters, with 405 bp on average and the largest length of 6,262bp. A total of 40,755 protein coding sequences (CDSs) were predicted from all these EST clusters and 16,795 (41.2%) of them were assigned to biological functions. In addition, 17,233 CDSs were classified into 25 KOG categories, with the category ‘Signal transduction mechanisms’ as the largest one, containing 2,632 CDSs. Gene ontology terms were assigned to 12,260 CDSs. Comparison of the gene expression between “red-black” and “white” revealed that 497 EST clusters were significantly up-regulated in the “white” strain, while 823 EST clusters were significantly up-regulated in “red-black” strain. Proteins encoded by these 1,320 EST clusters were enriched in category ‘Cytoskeleton’ ($p < 0.001$), which contains 1,049 EST clusters. 119 EST clusters showed significant expression variation between the two color patterns, including actin, myosin and troponin genes. Our preliminary results provide fundamental information for subsequent studies on the molecular mechanisms in determining body color pattern of common carp.

Keywords: *Cyprinus carpio* var. *color*, body color, RNA-Seq, differential gene expression analysis