Genome sequencing of the perciform fish
Larimichthys crocea provides insights into molecular and genetic mechanisms of stress adaptation

With the support by the National 863 Project, National Natural Science Foundation of China, and National Basic Research Program of China, Prof. Chen Xinhua's laboratory at the Key Laboratory of Marine Biogenetic Resources, Third Institute of Oceanography, State Oceanic Administration, reported the genome sequencing of the perciform fish *Larimichthys crocea* (*L. crocea*), which was published in *PLOS Genetics* (2015, 11(4): e1005118).

The *L. crocea* is one of the most economically important marine fish in China and East Asian countries. It also exhibits peculiar behavioral and physiological characteristics, especially sensitive to various environmental stresses, such as hypoxia and air exposure. To understand the molecular and genetic mechanisms underlying the adaptation and response of *L. crocea* to environmental stress, the genome of *L. crocea* was sequenced and assembled using a bacterial artificial chromosome and whole-genome shotgun hierarchical strategy. The final genome assembly was 679 Mb, with a contig N50 of 63.11 kb and a scaffold N50 of 1.03 Mb, containing 25,401 protein-coding genes. Approximately 2,528 immune-relevant genes were annotated in the *L. crocea* genome, including 819 innate immune-relevant genes and 1,709 adaptive immune-relevant genes. Strikingly, *L. crocea* was found to have not only a relatively complete innate immune system, but also a well-established adaptive immune system, because the majority of the CD4+ T-helper type 1 (Th1), CD4+ T-helper type 2 (Th2) and CD8+ T cell-related genes were found. Transcriptome analyses of the hypoxia-exposed *L. crocea* brain revealed new aspects of neuro-endocrine-immune/metabolism regulatory networks that may help the fish to avoid cerebral inflammatory injury and maintain energy balance under hypoxia. Proteomics data demonstrate that skin mucus of the air-exposed *L. crocea* had a complex composition, with an unexpectedly high number of proteins (3,209), suggesting its multiple protective mechanisms involved in antioxidant functions, oxygen transport, immune defence, and osmotic and ionic regulation. These results reveal the molecular and genetic basis of fish adaptation and response to hypoxia and air exposure. The data generated by this study will provide valuable resources for the genetic improvement of stress resistance and yield potential in *L. crocea*.
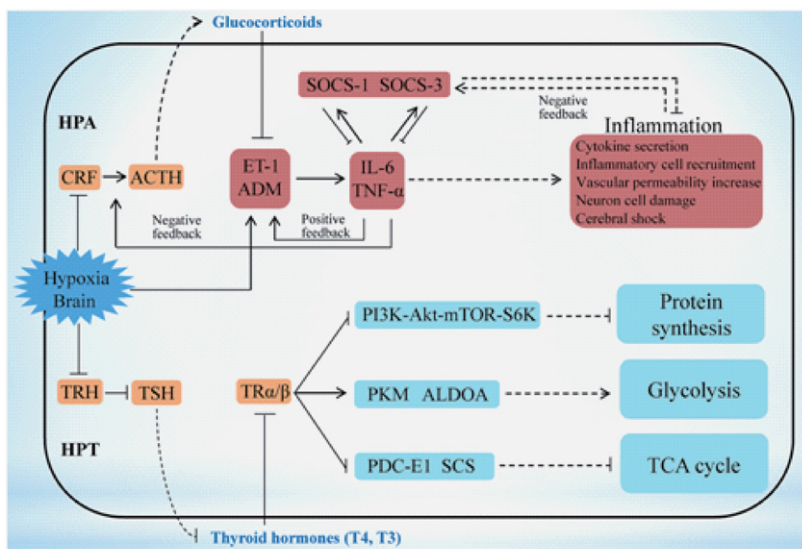

Figure Hypoxia stress exerts responses involved in the HPA and HPT axes. Under hypoxia, the potential neuro-endocrine-immune/metabolism networks contribute to the regulation of moderate inflammation and the maintenance of energy balance. Genes related to the neuro-endocrine system (orange), immunity (red), and metabolic system and protein synthesis (blue) are indicated. The outer border indicates the brain of *L. crocea*. The arrow represents promotion, and the interrupted line represents inhibition. Solid lines indicate direct relationships between genes. Dashed lines indicate that more than one step is involved in the process.