

13. Symmetry of Ohnolog gene expression in the Interferon Stimulated Pathways of the tetraploid common carp

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The common carp (*Cyprinus carpio*) is a species that came into existence due to a hybridization of two different cyprinid species about 12 MYA ago. The common carp, therefore, contains two sub-genomes (A and B) of different ancestral origin, referred to as allo-tetraploidy. Recent studies have shown that the common carp has retained a considerable part of its duplicated genes within its genome, but questions remain as to which degree these duplicated genes have remained active in both subgenomes over time. To study the functionality of duplicated genes that originated from the hybridization event, referred to as ohnologs, required thorough understanding of the genes phylogenetic history and function. To this end, we selected a core set of interferon stimulated genes (ISGs) to explore subgenome functionality. ISGs are suitable to study function due to their ability to be induced by interferon type-1 (IFN) following viral infection. In this way we can relate inducibility directly to gene function. Next, our core set of genes is shared between zebrafish and human, demonstrating that our core set is highly conserved and their phylogenetic relationships are known. With these conditions in place, we studied ISG ohnolog retention and inducibility by use of transcriptomics. Next, we used chromatin accessibility as a measure, to explore epigenetic regulation of the two subgenomes. Based on our analysis, single sub-genome dominance does not appear to be most evident in common carp. Rather, in most cases both ohnologs appear of more or less equal importance for coordinating complex physiological responses.