

### 3. Symmetry of homolog 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. Genes located on sub-genome B appear to have higher expression levels than their counterparts on sub-genome A, suggesting a degree of subgenome dominance. These differences in expression are small, however. To more thoroughly interpretate the ploidy effects on gene expression, a new carp genome was assembled. The well-annotated carp genome facilitated the zooming in on subgenome expression levels by studying, in particular, interferon-stimulated genes (ISGs) as a collective and well-characterized group of genes commonly expressed in response to interferon type-1 following viral infection. Specifically, we looked at 83 ISGs with ancestral origins before the hybridization event, therefore maximising the chance that both ancestors of the common carp would have had a complete set of these genes present in their genome. Using gene expression analysis we show that both sub-genomes express an almost complete set of ancestral ISGs. We also demonstrate that the ISG homologs present on both sub-genomes show diverse degrees of inducibility. Based on our analysis of an ancestral functional pathway, part of complex immune responses to viruses, single sub-genome dominance does not appear to be most evident in allo-tetraploid common carp. Rather, both subgenomes present in common carp, and in most cases both gene copies appear of more or less equal importance for coordinating complex physiological responses.