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Nutritional impact of dietary iron on the molecular regulation of iron uptake and homeostasis in larval and adult zebrafish *Danio rerio*

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Zebrafish was used for testing the nutritional impact of dietary iron through two experimental diets, varying in the content of a novel iron-containing protein and thus having high and low iron content, specifically on the molecular regulation of iron uptake and homeostasis.

In an unbiased approach, RNAseq using an Illumina HiSeq2000 was performed on the intestines of larval fish fed with the experimental diets from 6 to 21 dpf. 328 genes were differentially expressed: expression of 114 genes was up-regulated and 214 genes down-regulated in larvae fed at high vs. low iron level. Dominant gene groups representing ribosome components and activity and transport were down-regulated in these larvae. 27 genes were identified as involved in iron homeostasis but were non-differentially expressed at a fold change 0.27 – 1.54.

In a biased approach, qPCR was performed on individual intestines and livers of adult fish fed with the experimental diets for one month. Intestine expression of marker gene hepcidin antimicrobial peptide 1 (*hamp1*) was significantly higher, and of hephaestin-like 1 significantly lower in fish fed at high vs. low iron level. Liver expression of marker genes transferrin a and *hamp1* was significantly higher, and of ferritin heavy polypeptide 1a significantly lower in fish fed at high vs. low iron level. These expression profiles, supported by data on body composition, suggest that in fish fed at higher iron level, less dietary iron uptake occurs, less iron is released in the circulation, and less iron is taken up and stored in the liver.

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