Liver transcriptome of diploid and triploid Atlantic salmon (*Salmo salar* L.)

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Main findings

- We found a relatively small number of differentially expressed genes (DEGs) between ploidy groups, suggesting a close similarity in liver transcriptome between diploid and triploid Atlantic salmon. In contrast, the effect of ontogeny assessed by comparing fry, parr and smolt showed large differences in liver transcriptome response for both diploid and triploid fish.
- In both ploidy groups, the majority of significantly enriched biological processes for Gene Ontology (GO) terms down-regulated in fry compared to parr were related to nucleotide and energy metabolism, while immune system processes were significantly down-regulated in parr when compared to smolts (Fig. 1).
- The striking resemblance in GO terms for both ploidies could be due to a mechanism of genome dosage compensation involved in polyploidy regulation.

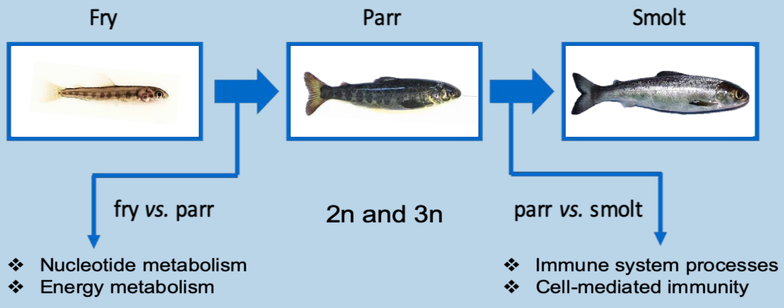

Fig.1: Summary of functional categories for comparisons of diploid (2n) and triploid (3n) ´fry vs. parr´ and ´parr vs. smolt´

Introduction

- Triploid fish are of interest to solve key issues for the sustainable development of Atlantic salmon (*Salmo salar* L.) farming in Norway and other producing countries, namely the impact of farmed escapees on wild stocks and pre-harvest sexual maturation. However, uncertainties regarding the performance of cultured triploid stocks have hindered the widespread adoption of triploid salmon by the industry, except in Tasmania.
- The liver is the main organ involved in fish metabolism and plays roles in detoxification and immunity with effects on fish health, welfare and growth.
- In this study, we compared the liver transcriptome of diploid and triploid salmon fed a standard fishmeal commercial diet from fry stage to the completion of parr-smolt transformation.

Materials and Methods

- A detailed description of the experimental set up, fish and feed used in this experiment is provided by Peruzzi *et al*. (2018). Fish were sampled at 21, 30 and 38 weeks post start-feeding (1455-2745 day-degrees post start-feeding) corresponding to fry, parr and smolt stage, respectively.
- The transcriptome analysis involved the extraction and use of total RNA from fish liver for RNA-seq library preparation, next-generation sequencing on the NextSeq500 (Illumina). TopHat2 and DESeq2 were used for mapping and for differential expression, respectively (Kim *et al*. 2013; Love *et al*. 2014).

Results

- The PCA plot for sequenced data did not indicate clustering by ploidy; instead, the data clustered according to ontogeny stage (Fig. 2).

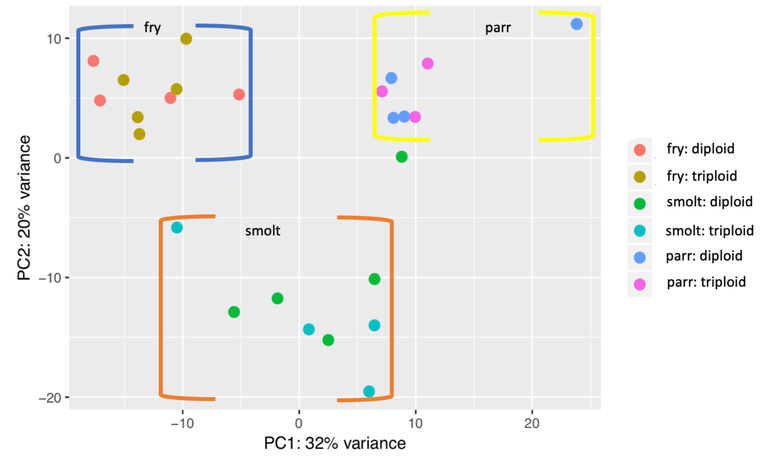

Fig.2: Principal Component Analysis (PCA) plot for individual samples (n=4-5 fish/ploidy/stage) of diploid and triploid fish.

- There were 34 DEGs for comparisons which define the ploidy effect. In contrast, comparisons between ontogeny stages from fry to smolt within each ploidy resulted in 5642 DEGs (Fig. 3).

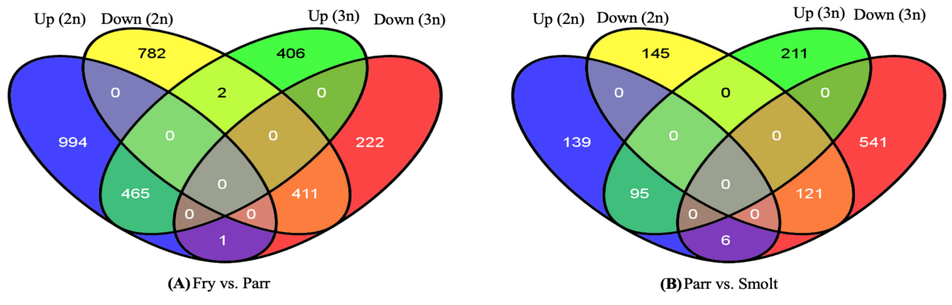

Fig.3: Venn diagrams for differentially expressed genes identified for comparisons between 'fry vs. parr' (A) and 'parr vs. smolt' (B) of diploid and triploid groups with an absolute fold-change > 2 and an adjusted p-value < 0.05.

- Further GO enrichment analysis for all DEGs returned no significantly enriched GO terms associated with ploidy, while comparisons for ontogeny in each ploidy group showed significantly enriched GO terms within down-regulated DEGs only (Fig. 4).

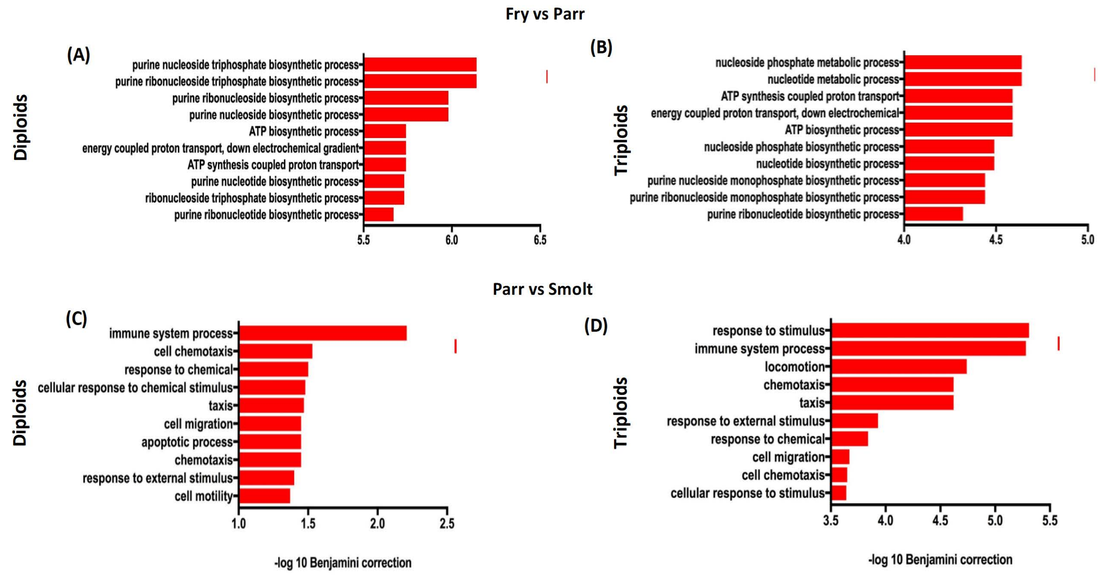

Fig.4: GO enrichment of down-regulated DEGs in 'fry vs. parr' (A,B) and 'parr vs. smolt' (C,D) for diploid and triploid fish (Benjamini correction < 0.05).

References

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