Hypoxia Biomarkers In *Notothenia coriiceps*

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BACKGROUND & SIGNIFICANCE

Antarctic fishes have developed adaptations that make them especially well suited to the cold, thermally stable environment of the Southern Ocean.[2] This may have led to trade-offs, weakening their ability to respond to a rapidly changing environment.[1][3][6] With current ocean warming trends, hypoxic events are expected to increase in frequency and intensity,[4] and the ability of Antarctic fishes to withstand these events is not yet known. In this study, we measured glycogen and lactate levels in brain, heart ventricle and liver tissues of *Notothenia coriiceps* held at normoxia and exposed to hypoxia to characterize the hypoxia response, as depleted glycogen stores and elevated lactate concentrations indicate a metabolic shift toward anaerobic energy production.[5]

Yellowbelly rockcod, *Notothenia coriiceps*

OBJECTIVES

- Characterize the hypoxia response experimentally by:
  - Measuring lactate and glycogen levels in normoxic and hypoxic fish
- Quantify changes in mRNA levels using RNA-Seq

RESULTS

- **A switch to anaerobic metabolism was observed in the liver only:**

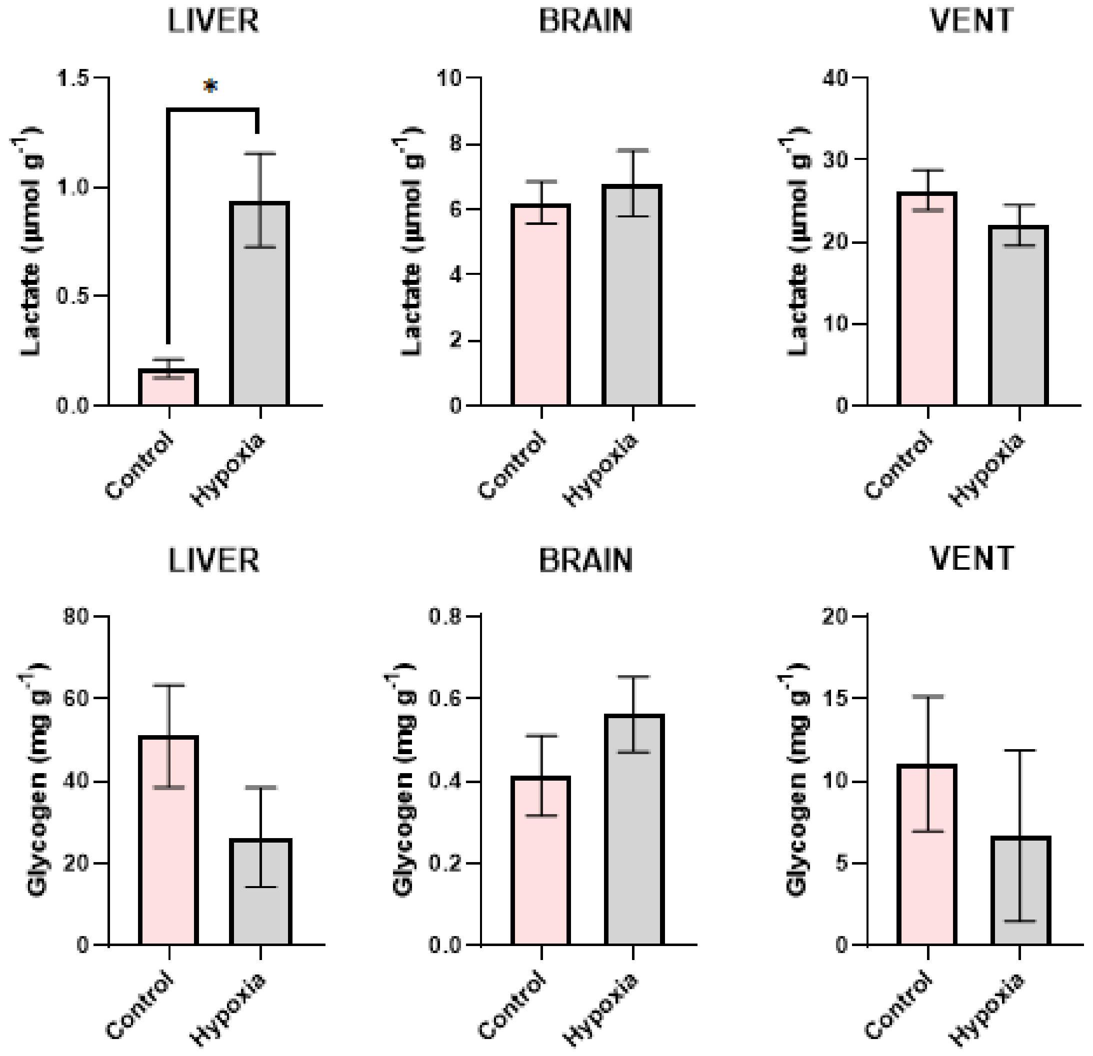

Figure 1. Lactate levels remained unchanged in heart ventricle and brain but were significantly higher ($p<0.05$) in the liver of fishes exposed to hypoxia compared to those held at normoxia. Glycogen levels did not change in response to hypoxia but tended to decrease in the liver ($p=0.19$).

- **RNASeq data shows an enhanced hypoxia response in liver, suggesting that this organ may play an important role in mitigating the effects of hypoxia:**

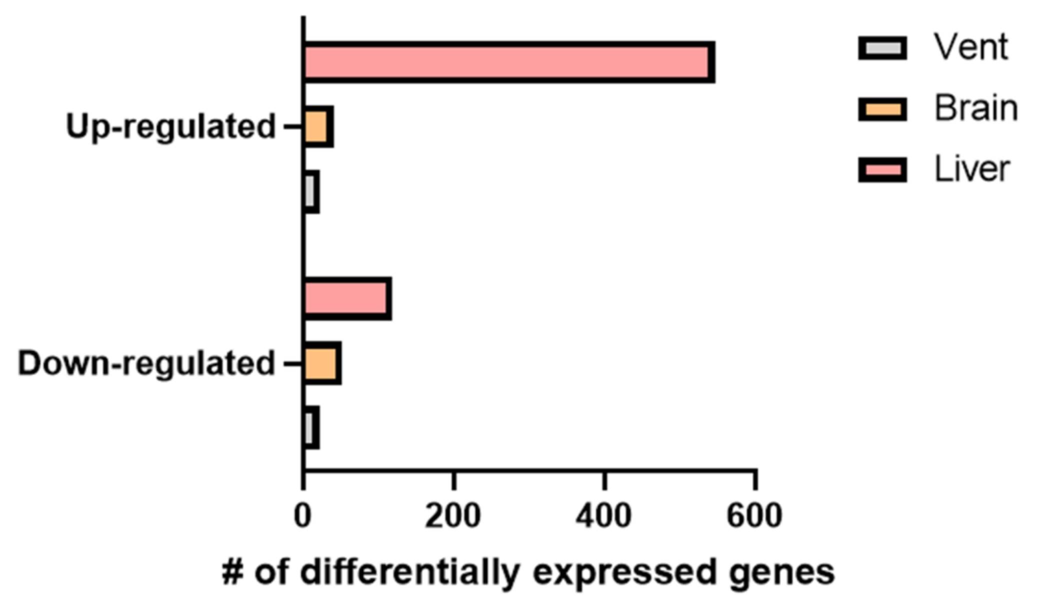

Figure 2. Up and down-regulated genes of liver, brain and heart ventricle from RNASeq data analysis.

RESULTS, CONT.

- **Very little overlap of differentially expressed genes was observed among tissues in response to hypoxia, indicating that the response is highly tissue-specific:**

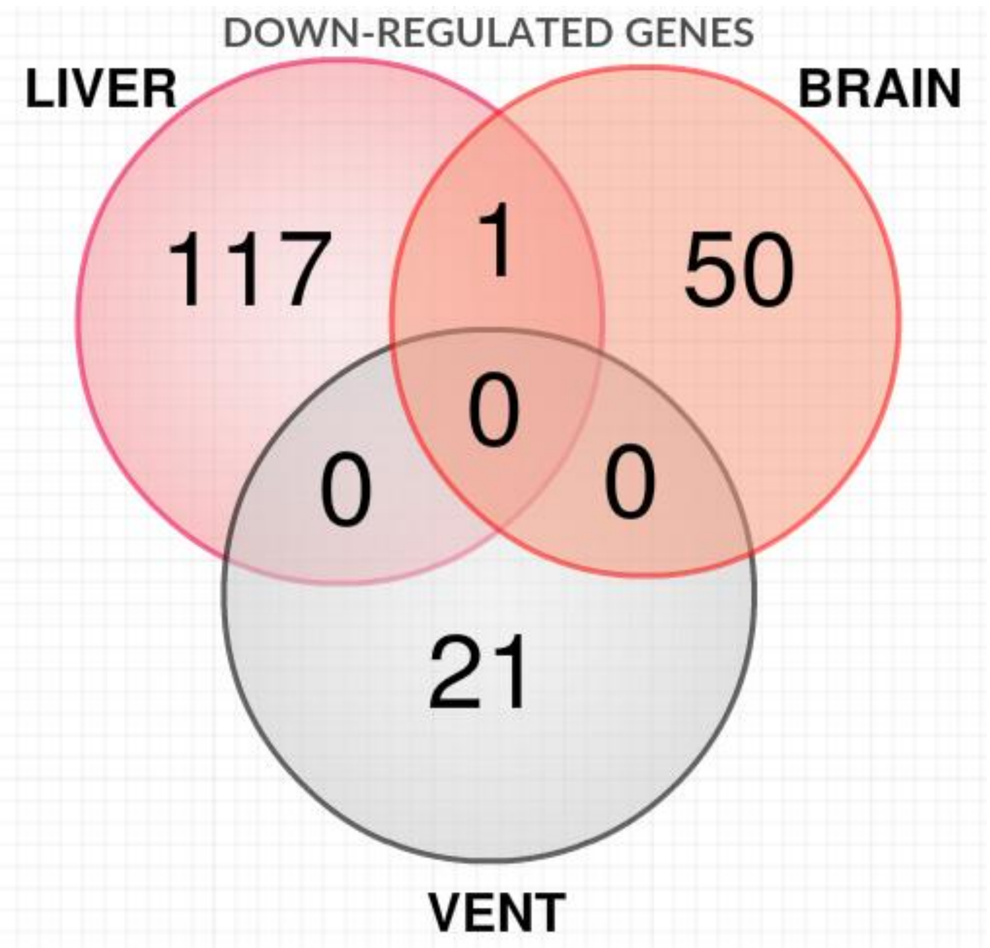

Figure 3. Overlap of down-regulated genes among the three tissues studied.

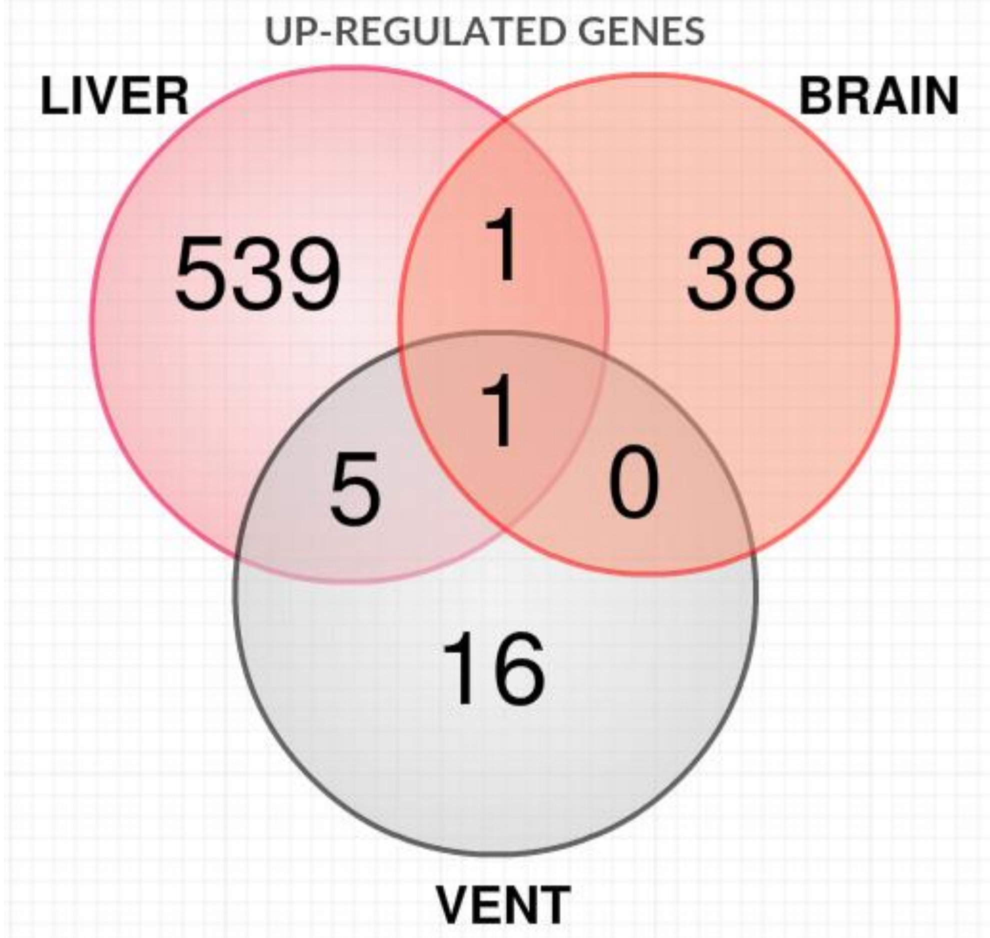

Figure 4. Overlap of up-regulated genes among the three tissues studied.

MATERIALS AND METHODS

- *N. coriiceps* were collected & exposed to either normoxia (12 hrs at 10 mg L^{-1} O_2)(n=6) or hypoxia (12 hrs at 2 mg L^{-1} O_2)(n=6).
- Tissues (brain, heart ventricle, liver) were collected, flash frozen and stored at -80°C.
- Spectrophotometric assays to quantify lactate and glycogen were performed using commercially available kits.
- Two-tailed t-tests were used to assess significance between treatment groups ($p<0.05$).
- Transcript levels were quantified with RNA-Seq.

FUTURE RESEARCH

- Further analysis of RNA-Seq data to associate specific differentially expressed genes to the hypoxia response.
- Quantification of HIF-1α protein levels. HIF1-α is a master transcriptional regulator of genes involved in the hypoxia response.

CONCLUSIONS

- The hypoxia response in *N. coriiceps* is tissue-specific and enhanced in the liver.
- The otherwise oxygen-sensitive brain and heart tissues surprisingly did not respond as strongly to hypoxia as liver, suggesting other protective mechanisms.

ACKNOWLEDGMENTS AND REFERENCES

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