

## ESTABLISHING ZEBRAFISH AS A NOVEL EXERCISE MODEL

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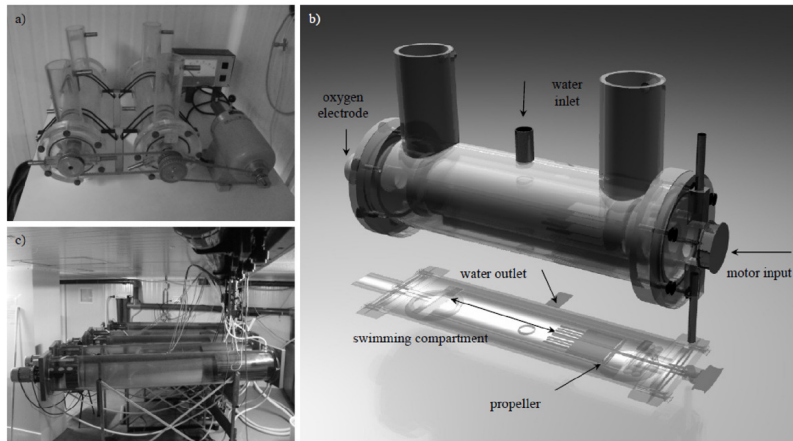
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### Introduction

Zebrafish has been largely accepted as a vertebrate multidisciplinary model but its usefulness as a model for exercise physiology has been hampered by the scarce knowledge on its swimming economy, optimal swimming speeds and cost of transport. Therefore, we have performed individual and group-wise swimming experiments to quantify swimming economy and to demonstrate the exercise effects on growth in adult zebrafish.

### Methodology/Principal Findings

Individual zebrafish ( $n=10$ ) were able to swim at a critical swimming speed ( $U_{crit}$ ) of  $0.548 \pm 0.007 \text{ m s}^{-1}$  or  $18.0$  standard body lengths (BL)  $\text{s}^{-1}$  (Palstra et al., 2010). The optimal swimming speed ( $U_{opt}$ ) at which energetic efficiency is highest was  $0.396 \pm 0.019 \text{ m s}^{-1}$  ( $13.0 \text{ BL s}^{-1}$ ) corresponding to  $72.26 \pm 0.29\%$  of  $U_{crit}$ . The cost of transport at optimal swimming speed ( $COT_{opt}$ ) was  $25.23 \pm 4.03 \mu\text{mol g}^{-1} \text{ m}^{-1}$ .



Small Blazka-type swimming tunnels to swim individual zebrafish and large ones to perform group-wise experiments. Source: Palstra et al., 2010.

A group-wise experiment was conducted with zebrafish ( $n=83$ ) swimming at  $U_{opt}$  for 6 h  $\text{day}^{-1}$  for 5 days  $\text{week}^{-1}$  for 4 weeks vs. zebrafish ( $n=84$ ) that rested during this period (Palstra et al., 2010). Swimming zebrafish increased their total body length by 5.6% and

body weight by 41.1% as compared to resting fish. For the first time, a highly significant exercise-induced growth is demonstrated in adult zebrafish.

Expression analysis of a set of muscle growth marker genes revealed clear regulatory roles in relation to swimming-enhanced growth for genes such as growth hormone receptor b (*ghrb*), insulin-like growth factor 1 receptor a (*igflra*), troponin C (*stnnc*), slow myosin heavy chain 1 (*smyhc1*), troponin I2 (*tnni2*), myosin heavy polypeptide 2 (*myhz2*) and myostatin (*mstnb*) (Palstra et al., 2010).

Recently, we have finalized single color microarray analyses to elucidate the changes taking place in the white muscle transcriptome in response to exercise (earray design ID 021626; 4x44K; total of 43,863 genes). We have performed microarray analysis of 8 individual swimmers vs. 8 individual resters. The number of differentially expressed genes was 2,354 (5.4%;  $P < 0.01$ ;  $< 0.5$  and  $> 2$  fold change), of which 1,778 genes (76%) were down-regulated and 576 (25%) were up-regulated. At this moment, we are performing Gene Ontology analysis. Immunohistochemical techniques are also being applied on white muscle of exercised zebrafish to demonstrate changes in fibre composition, capillarity and anaerobic vs. aerobic metabolism.

### Conclusions/Significance

From the results of our study we can conclude that zebrafish can be used as an exercise model for enhanced growth, with implications in basic, biomedical and applied sciences, such as aquaculture. This is of major importance because the existing data on commercially interesting species like Atlantic salmon (Totland et al., 1987) and yellowtail kingfish (Brown et al., 2011) also indicate that sustained exercise at optimal speeds enhances muscle growth. Moreover, optimal exercise has important consequences for flesh quality. Potential added benefits of sustained exercise may be delay of ovarian development and stimulation of immune status. Exercise could represent a natural, non-invasive and economical approach to improve growth, flesh quality as well as welfare of aquacultured fish (Palstra and Planas, 2011): a FitFish for a healthy consumer.

### References

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