A Protein-Protein Interactome for an African Cichlid

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CCS CONCEPTS

• **Applied computing** → **Computational transcriptomics**; **Biological networks**.

KEYWORDS

Comparative genomics, protein-protein interactome, ethology

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1 INTRODUCTION

Protein-protein interactomes (PPIs) have been used extensively to classify and predict genes associated with complex phenotypes. PPI approaches have been successful for organisms with well-annotated genome features, but are more challenging for non-model organisms due to a lack of available experimental data. To address this challenge, labs have created PPIs for non-model organisms by inferring "interologs", or orthologous protein-protein interactions [1].

African cichlids are a diverse clade of fishes that have been used to study rapid evolutionary divergence [3]. This project presents an interolog-based method of building an African cichlid-specific PPI from an existing zebrafish interactome [1]. As a case study, we use a cichlid PPI to study the transcriptomic signatures of mouthbrooding, an acute period of parental care accompanied by voluntary starvation [3]. Brain transcriptome data from mouthbrooding *Astatotilapia burtoni* were used to weight the resulting interactome. This project presents a method to characterize transcriptomic changes in a non-model organism using resources from model organisms.

2 METHODS

The zebrafish interactome was downloaded from FunCoup, a database of functional couplings between proteins that uses a variety of confirmed and inferred evidence sources [1]. We generated orthologs between *A. burtoni* and zebrafish using OrthoFinder [2]. We converted interactions using the following rule: for zebrafish proteins that have an interaction z_1, z_2 with corresponding ortholog sets $T_1 = \{i_1, i_2, ...i_k\}$, $T_2 = \{j_1, j_2, ...j_k\}$, create a set of interactions between all $t_1 \in T_1$ and all $t_2 \in T_2$. Finally, we mapped gene expression data from mouthbrooding *A. burtoni* onto the PPI.

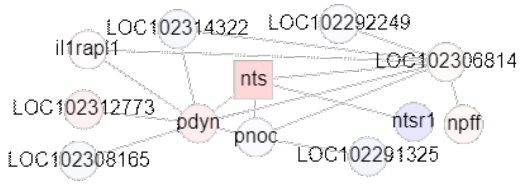

Figure 1: Red/blue intensity increases with increasing or decreasing log2 fold change, respectively. White nodes represent neutral expression or no available gene expression data.

3 RESULTS AND DISCUSSION

The resulting network contained 10,838 genes, 1,778,361 interactions with an average node degree of 322, and maintains similar topology to the zebrafish interactome. Analysis of RNA-seq data revealed 2,987 differentially expressed (DE) genes between the brains of brooding and non-brooding fish, 30 of which being significant when corrected for false discovery rate. Among the most relevant DE genes was neurotensin (nts), a peptide involved in both feeding behavior in parental care. Its immediate subnetwork contains various opioid and glutamate receptors, with members of the former all showing the same expression trend (Fig. 1). Neurotensin modulation during mouthbrooding by its neighbors in the network may be a key component to understanding the complex parental behavior. The resulting network allows for further computational analyses on the molecular substrates of complex behaviors in a non-model organism.

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