Research Proposal, BIOL7263
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Introduction

This project would primarily focus on comparative transcriptomics involving the Gouldian finch (*Erythrura gouldiae*), a species known to have three naturally-occurring head color morphs (red, black, and yellow heads). The maintenance of multiple morphs in this species has been of special interest, with recent studies probing the genetic links to black or red plumage presentation and what allows for metabolic conversion of substrate pigments to those observed pigments in bird plumage for the red and black morphs (Kim et al. 2019). However, the genetic and biochemical underpinnings of the least-populous yellow morph remains unknown, and is of interest (Kim et al. 2019). The yellow morph exhibits yellow-orange pigment in both its head and breast feathers, though each patch features different types of yellow-orange carotenoids (M. Toomey, pers. comm.). In the Gouldian finch head feathers, 3'-dehydrolutein is present, while in the belly feathers, lutein is more strongly expressed, though the genes involved in this differential expression are unknown (M. Toomey, pers. comm.). In other finch species, DHRS13 is a gene hypothesized to be involved in the conversion of lutein to 3'-dehydrolutein (Toomey, pers. comm.).

Research Questions

We would like to know if genes known to be relevant to converting red and yellow carotenoids in other finch species are present in Gouldian finch transcripts—CYP2J19, TTC39B, BDH1L, namely (Toomey et al. 2022). If that is the case, then we are especially interested in understanding whether those genes are differentially expressed for belly and head feathers, aiming to understand the biochemistry behind yellow plumage in Gouldian finches. Of special interest is the gene DHRS13, since it is hypothesized to be involved with conversion of key carotenoids in Gouldian yellow plumage. If these genes are differentially expressed, then they may be plausible candidates for the biochemical conversion to yellow carotenoids in yellow morph Gouldian finches, and an essential part of solving the pathway to the third morph phenotype. Additionally, we aim to improve annotation of the Gouldian finch genome for future use, by using comparisons to Zebra finch transcripts.

Methods

I will create a database of Zebra finch transcripts, then use a `blastn` command to query with Gouldian finch cDNA transcripts. From the predicted genes, I will both search for target genes as well as compile organized predictions to expand annotation for the Gouldian finch genome. To see if DHRS is expressed in Gouldian finches, I will assemble a database of Gouldian cDNA transcripts and I will use a `tblastn` command to query with the protein sequence for DHRS13. Using the returned list of transcripts for DHRS13 present in the Gouldian, statistics for differential expression can be used to determine whether the sequence expression differs among tissues.

Expected Outcomes

We expect that homologs for all target genes (DHRS13, TTC39B, CYP2J19, and BDH1L) will be expressed in the Gouldian finch transcripts, with DHRS13 being differentially expressed for different tissues.

References

1. Kim, K.-W., Jackson, B. C., Zhang, H., Toews, D. P., Taylor, S. A., Greig, E. I., Lovette, I. J., Liu, M. M., Davison, A., Griffith, S. C., Zeng, K., & Burke, T. (2019). Genetics and evidence for balancing selection of a sex-linked colour polymorphism in a songbird. *Nature Communications*, *10*(1). https://doi.org/10.1038/s41467-019-09806-6

2. Toomey, M. B., Marques, C. I., Araújo, P. M., Huang, D., Zhong, S., Liu, Y., Schreiner, G. D., Myers, C. A., Pereira, P., Afonso, S., Andrade, P., Gazda, M. A., Lopes, R. J., Viegas, I., Koch, R. E., Haynes, M. E., Smith, D. J., Ogawa, Y., Murphy, D., … Corbo, J. C. (2022). A mechanism for red coloration in vertebrates. *Current Biology*, *32*(19). https://doi.org/10.1016/j.cub.2022.08.013