Copy Number Variation and Divergence in Color and Morphology in a Three-spine Stickleback Stream-Anadromous Pair

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Background

- The three-spine stickleback is a teleost that has undergone recurrent adaptive radiations from marine to freshwater environments.
- The Little Campbell stream-anadromous pair is an example of recently diverged, but closely related, morphs. One way in which they are divergent is in their red throat coloration. Females in the stream population often have characteristic red throats, whereas anadromous females lack this trait.
- Diploid organisms typically carry two copies of each gene. However, differences in the number of copies of chromosomal segments exist in the form of Copy Number Variation (CNV) which has arisen as a key feature of evolutionary diversification.

Methods

- Collected fish, Little Campbell Stream (LCS) and Little Campbell Anadromous (LCA), from British Columbia.
- Extracted DNA from fin clips.
- Sequenced DNA using Illumina paired-end sequencing (30x depth), aligned reads to the reference stickleback genome.
- GATK CNVcaller was used to identify deletions and duplications in relation to the reference genome.
- Statistically verified CNV differences between populations and color morphs. Identified CNVs in 18 specific genes, previously identified in Newsome et al. unpublished by scanning VCF files.

Results, Interpretation

- Average Number of Deletions
  - Little Campbell Stream: Red - 24000, Dull - 22000
  - Little Campbell Anadromous: Red - 26000, Dull - 24000
  - Significantly more deletions in Little Campbell Anadromous females than in Little Campbell Stream females.

- Average Number of Duplications
  - Little Campbell Stream: Red - 15000, Dull - 14000
  - Little Campbell Anadromous: Red - 16000, Dull - 15000
  - No significant difference in duplications between red and dull females.

Conclusions

- Stream individuals show lower levels of deletions indicating that they can act as reservoirs for ancient alleles selected out of marine populations (Lowe et al., 2018).
- Freshwater (stream) individuals generally have more gene copies than anadromous, possibly providing new gene functions for freshwater invasion (Hirase et al., 2014).
- There were no CNV differences found between the red and dull females.
- We found very few CNVs within genes. This is expected as it is thought that around 95% of CNVs are in noncoding regions (Lowe et al., 2018).

Future Direction

- Hope to search more thoroughly for CNVs in intronic regions near genes of interest.
- Will include more study populations to enhance and assess generality.
- Use additional calling programs and molecular technique to validate calls.