Discussion Paper Summary: RNA-seq

RNA sequencing (hereafter RNA-seq) is a powerful tool that can be used to answer many diverse questions relating to gene expression in individuals and populations. Bernal et al. (2018) used RNA-seq to study the effects of step-wise temperature increase on the damselfish, *Acanthrochromis polyacanthus,* while Lohman, Stutz, and Bolnick (2017) used it to understand adaptation and phenotypic plasticity in lake and stream populations stickleback ﻿(*Gasterosteus aculeatus*). Similarly to Lohman, Stutz, and Bolnick, Walworth et al. (2016) used RNA-seq to test for adaptation and phenotypic plasticity in the cyanobacterium, *Trichodesmium*, selected for high and low CO2 environments.Using similar methods in RNA-seq, all three studies were able to gain an in-depth understanding of the complex evolutionary processes shaping the phenotype of their study organism. Their research questions spanned different themes relating to the evolutionary history and future of these organisms.

All three studies sought to better understand the mechanisms behind phenotypic responses to novel environments in their organism of study. Bernal et al. focused on short-term responses to climate change over three generations. There was already some research done on the transgenerational effects of climate change on damselfish, however, Bernal et al. sought to model the fish’s response to increased temperature in a more realistic way, with temperature increasing with each successive generation. Bernal et al. tested if transgenerational and developmental responses could interact to allow the fish to adapt to increasing temperature. Walworth et al. were also interested in the effects of climate change in their study organism, *Trichodesmium*. However, they took a different approach. The researchers here were able to select for high and low CO2-adapted cyanobacteria over hundreds of generations, and later expose the cultures to the opposite treatment on a short-term basis to observe any plastic responses. Contrastingly, Lohman, Stutz, and Bolnick studied the mechanisms behind phenotypic responses to novel environments due to migration, rather than organismal responses to climate change. They sought to better understand how the stickleback in lake and stream populations would react phenotypically when migrating (or transplanted) to the opposite environment within a single generation. The three studies were similar in theme but varied in scope.

The organism of study greatly impacted the specific questions that researchers were able to investigate. Laboratory experiments for both the damselfish and the cyanobacteria studies lasted for about four years. However, in that time frame the researchers studying the damselfish were only able to model organismal response to climate change over three generations, while the cyanobacteria study in the same time frame was able to capture the population’s response to climate change over the course of over 570 generations. The life span of the organism in question greatly impacted the scope of the experiments in these two cases. Due to the longer life span of the damselfish, Bernal et al. were only able to capture phenotypic response over the course of a few generations. Because their study was on a shorter evolutionary time scale, they looked more in-depth to the types of evolutionary mechanisms behind these responses such as transgenerational acclimation, developmental acclimation, and acute responses and learn how these responses to environmental change compare to phenotypic response to step-wise temperature increases. Due to the longer evolutionary time scale of the cyanobacterial study, they were able to examine phenotypic and genotypic responses to climate change more generally. Instead of looking at different types of phenotypic responses, they were interested in learning whether phenotypic plasticity persisted in the cyanobacteria over several hundred generations of selection. Like Walworth et al., Lohman, et al. were interested in phenotypic plasticity, however, because they were dealing with wild fish, they assumed the stickleback were already adapted to each habitat. This meant that the researchers did not have to raise several generations of fish to study differences in plasticity among the different ecotypes.

The three studies above all used RNA-seq to examine phenotypic response to some sort of environmental change over three different timelines. The power of RNA-seq to study such vastly different research themes lies in its ability to be combined with other tools such as Gene Ontology, DNA sequencing, and metabolome profiling to better understand the complex network of mechanisms that result in the phenotypic output of an organism. These tools and the questions under study are limited by the nature of the organism of study. However, when combined, they can be used to answer a plethora of relevant questions relating to organismal and population responses to environmental change.

References:

Bernal, M. A., Donelson, J. M., Veilleux, H. D., Ryu, T., Munday, P. L., & Ravasi, T. (2018). Phenotypic and molecular consequences of stepwise temperature increase across generations in a coral reef fish. *Molecular Ecology*, *27*(22), 4516–4528. https://doi.org/10.1111/mec.14884

Lohman, B. K., Stutz, W. E., & Bolnick, D. I. (2017). Gene expression stasis and plasticity following migration into a foreign environment. *Molecular Ecology*, *26*(18), 4657–4670. https://doi.org/10.1111/mec.14234

Walworth, N. G., Lee, M. D., Fu, F.-X., Hutchins, D. A., & Webb, E. A. (2016). Molecular and physiological evidence of genetic assimilation to high CO2 in the marine nitrogen fixer Trichodesmium. *Proceedings of the National Academy of Sciences of the United States of America*, *113*(47), E7367–E7374. https://doi.org/10.1073/pnas.1605202113