Gene Expression and RNA-Seq Summary

Maggie Schedl

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Studying differences in populations or treatments between groups often has to do with investigation phenotypic plasticity: the differences in phenotypes seen by the same genotype. This can be elucidated by measuring differences in gene expression, however there might not always be a causal relationship between the two (ie. Epigenetic effects). Experiments on gene expression between “treatment” groups, pertaining to climate change variables, are seen in Lee et al. (2016) and Bernal et al. (2018). In contrast, Lohman et al. (2017) use gene expression differences to study local adaptation and decreased selection pressure against invaders into a locally adapted environment.

Our desire to understand what our natural populations have to face, and how they will face it, is a major driver of research into using gene expression analysis to study projected environmental conditions that will occur with this planet’s climate change trajectory. For marine systems, two variables are most commonly studied: temperature increase (Bernal et al. 2018), and ocean acidification (Lee et al. 2016). A great strength of both of these studies is that they used transgenerational approaches when measuring phenotypic plasticity. Bernal et. al (2018) used stepwise increases in water temperature to compare the expression patterns of damselfish. They also compared expression patterns with phenotypic measurements, such as metabolic rate and aerobic scope. This allowed them to have confidence in their observation of upregulated Gene Ontology (GO) enriched terms for metabolism in the step +3.0 degree fish, because they also had the higher increased basal metabolic rate measurements. Transgenerational increases in temperature had a different effect on gene expression than sustained or harsh increases, thus Bernal et. al (2018) showed the importance of studying climate change scenarios on a more realistic scale.

Lee et. al (2016) went a step further in their experimental design; because they studied the bacteria *Trichodesmium* after 4 years of treatment to varying CO2 regimes, they could investigate the long-term change of phenotypic plasticity to adaptation, or genetic assimilation to their original plastic response. Their experimental design allowed them to elucidate this by comparing the differentially expressed genes (DEGs) between high CO2 selected, acute CO2 stress, and high CO2 selected transferred to low CO2 expression. These all had the same expression pattern, suggesting genetic assimilation to the high CO2. They further observed sigma factor expression change only in the high CO2 selected treatment, and they concluded that that was only due to adaptation and not phenotypic plasticity. An important consideration for both Lee et. al (2016) and Bernal et. al (2018) is the considerable effort it may take to associate GO enriched terms with the treatment experienced, the many DEGs that do not have annotations or terms, and the limitations that still occur with transgenerational plasticity (Donelson et al. 2018).

Lohman et. al (2017) investigated phenotypic plasticity as a homogenizing agent in migration and local adaptation in lake and stream sticklebacks. If populations are locally adapted, phenotypic plasticity could dampen the fitness differences between populations allowing gene flow to persist. Their approach was threefold: to see if there were expression differences between populations, observe expression pattern changes with transplantation, and measure the convergence of expression pattern of foreign populations to local expression patterns. They showed that both stream and lake populations exhibited phenotypic plasticity that brought their transplanted expression patterns closer to the native population’s, however neither stream nor lake modulated expression to the same degree. Lake populations had a greater degree in plasticity, however expression changes in both population groups varied most by original ecotype.

These three papers are excellent examples of the wide variety of questions that can be answered with gene expression studies. The use of GO analysis bridges the gap between genetic information and functional biological processes, which is incredibly important when assessing the potential effects of climate change. Climate change scenarios are not the only way to utilize gene expression, although it may seem urgent now, many other environmental factors and biotic effects that influence gene expression are worth of studying, and may provide insight on processes that happened in the past. Lohman et. al (2017) and Lee et. al (2016) both used gene expression techniques to look at broader and longer-term processes of adaptation and population change, even though their approaches were very different. Athough Bernal et. al (2018) used multiple generations of damselfish, their main focus was plastic changes triggered by rapid environmental disturbance. That may be applicable for short term stress events, such as low salinity pulses from heavy rains, but stresses that persist may change expression in the long term. Moving forward from this type of research, studies like Lee et. al (2016) may be the most useful, because the effects of climate change are not going to be short stress events; most future CO2 projections do not show any decrease from current warming levels (Jones, 2017). Studies such as Lohman et. al (2017) that uses expression to uncover why populations remain divergent despite phenotypic plasticity, and Lee et. al (2016) that attempt to link plastic to genomic changes long term leverage the capabilities of gene expression research to reach far beyond the scope of the time point the expression was quantified. These techniques make expression data amiable to answering a broad variety of questions.

References

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