Phenotypic Plasticity and Epigenetics Summary

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Phenotypic plasticity has become a fervently studied topic in ecology and evolutionary biology recently; it is “﻿is the capacity for an individual genotype to produce different phenotypes in response to environmental variation” (Ghalambor et al. 2015). It is particularly amiable to eco-evo research because investigating phenotypic plasticity necessarily includes interactions with the environment and can often provide explanations of evolutionary processes. There can be many underlying mechanisms that influence phenotypic plasticity, and these mechanisms can be related as well, such as gene expression and DNA methylation. DNA methylation falls under the umbrella of Epigenetic mechanisms and can be a process that underlies gene expression patterns. Importantly, phenotypic plasticity can play a role in an organism’s response to a new environment or changing conditions; this is a critical area of research in terms of climate change, other human-caused disturbances, and conservation.

Phenotypic plasticity is likely prevalent in most organisms, however it can be hard to study without discrete phenotypes, which are often lacking in questions that pertain to stress responses, like those due to projected climate change conditions. These traits may be polygenic, which might also increase the potential for plasticity. Gene expression data, via techniques such as RNA-Seq, is one of the main ways to investigate phenotypic plasticity, especially when there is no clear phenotype measurement that a researcher can quantify. For example, the expression patterns between guppies living with or without predators (Ghalambor et al. 2015), can be a greater indicator of differences between those populations if there is no measurable trait known to be different or variable between them. The use of PC axis can separate out patterns with eigenvectors instead of discrete phenotypes (Fig. 1 Ghalambor et al. 2015). However, if one has prior knowledge of a plastic trait, investigating associations between the trait and potential drivers of plasticity, such as DNA methylation, can add more power to ones’ conclusions. Ryu et al. (2018), studied differentially methylated genes and their correlation with measures of aerobic scope (Fig. 2 Ryu et al. (2018) in coral reef fish raised over multiple generations with varying ocean warming treatments. Even further associations can be made if a researcher finds an association between gene expression, differential methylation, and a phenotype of ecological interest. Liew et al. (2018) did this for the coral *S. pistillata*, where they found a positive correlation between gene expression level and DNA methylation, and additionally found a relationship between increased methylation and cell size in corals subjected to decreasing seawater pH.

There seem to be two main questions that underlie these three papers and their topics: whether phenotypic plasticity is adaptive, and whether DNA methylation is a process or phenomenon that underlies phenotypic plasticity, and thus adaptation. All three of these studies do not go through enough generations to effectively show evolutionary change in gene frequencies, and no study even looked at genotypes; although Ryu et al. (2018) did look at specific genes for methylation. Directional plasticity may affect evolutionary trajectory in many ways. Plasticity may allow an organism to survive in a rapidly changing environment and reproduce, while the modification of the organism with natural selection takes more time to have effects. On the other hand, plasticity may dampen the effect of selection because selection acts on the phenotypes, and not the genes beneath them, thus failing to alter gene frequencies. However, there is a third option: non-adaptive phenotypic plasticity, which Ghalambor et al. (2015) demonstrated with guppies. Guppies with a population background of being raised with predators present in their water had a gene expression response to non-predator water that was the opposite of the expression response that non-predator adapted guppies exhibited. Since non-predator experiencing fish originally came from predator-experiencing populations, this could have caused a large selection pressure against many in the newly predator-free population, and drove the expression pattern to be so different. However, Ghalambor et al. (2015) did not have a phenotype in mind to study, and did not investigate possible functional reasons for differential expression, which left a gap open in their story.

In contrast, both Ryu et al. (2018) and Liew et al. (2018) used both phenotypes and epigenetic signals to understand plastic responses to climate change variables. And, when including previous research in Donelson et al. (2018), both also associated gene expression data. Goals of these two studies differed though, where Liew et al. (2018) aimed to determine if, and if so how, DNA methylation associated with plastic responses to pH stress. For *S. pistillata,* gene body methylation correlated with increased gene expression and increased modulation of expression. The authors argued that detailed modification of expression and reduction of transcriptional noise in genes associated with cell growth pathways likely produced the adaptive and plastic response. Because their study looked at corals only in one generation, the methylation patterns observed were an example of epigenetic effect. Ryu et al. (2018) looked at methylation patterns over multiple generations, moving past short plastic responses, into transgenerational epigenetics. They found profound differences in methylation in genes related to insulin and metabolic pathways in the temperature stressed fish. However, and they do acknowledge this, they did not test for true transgenerational epigenetic inheritance because fish offspring from high temperature treatments were never put back into normal temperatures. Other limitations, and general considerations for these three studies are, that differentially methylated genes do not necessarily correlated to differentially expressed genes (Ryu et al. 2018). Another is the general scope of the question being asked, for Ghalambor et al. (2015), their question pertained to the evolutionary histories of guppy populations experiencing different amounts of predator stress. Transplant or reciprocal transplant experiments are more applicable to studying the history of populations. Experimental treatments are often used to investigate the “what if” future questions. Although very different areas of study, both can gain insights from investigating phenotypic plasticity and epigenetics.

References

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