BIO594 – Summary

Topic: Adaptive Phenotypic Plasticity and Epigenetics

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Phenotypic plasticity can be adaptive, neutral, and maladaptive in populations under environmental change. It is postulated that epigenetic mechanisms, non-genetic factors, can regulate transcription and potentially be the driver behind phenotypic plasticity. As this is an emerging field, epigenetic processes should provide new insight of how organisms can adapt to environmental change. Ghalambor et al. 2015 (GH) discusses that plasticity constrains evolution in the Trinidadian guppy (*Poecilia reticulata)*, thus suggesting that non-plastic traits amplifies the strength of directional selection. Ryu et al. 2018 (RY) compared the methylome and the trancriptome of *Acanthochromis polyacanthus* under 4 different transgenerational scenarios to identify the differentially methylated regions that could potentially explain the changes in physiology. Liew et al. 2018 (LI) showed how the epigenome (DNA methylation) is altered under differential pH scenarios in the coral *Stylophora pistillata*, which is correlated with changes in phenotype. This summary will aim to answer the following questions: (1) is plasticity adaptive in any of the three papers? (2) What is different in the interpretation of whole-genome methylation data between LI and RY? (3) Can epigenetic data be used to fully describe phenotypic plasticity?

*Is plasticity adaptive in these papers?*

In GH, non-adaptive plasticity is postulated to promote evolution, as the majority of the transcripts identified showed non-adaptive plastic changes in their expression. Differences in gene expression transcripts of *P. reticulata* with ancestors from high predator environments and reared in low predator environments had signals of parallel divergence patterns as individuals from low predator environments. This suggests that phenotypic plasticity is non-adaptive in *P. reticulate* populations in regards to predator environments, and can promote evolution through strengthening directional selection. In RY, there is evidence that the rate of warming can induce transgenerational plasticity in *A. polyacanthus*, creating differential phenotypes that can be explained by changes in the epigenome. If these changes are occurring in germline cells, epigenetic inheritance could lead to beneficial phenotypes in changing environments and potentially lead to selection. In this case, transgenerational plasticity could create beneficial phenotypes that would be adaptive. In LI, it is difficult to determine if the phenotypic changes due to changes in pH are adaptive, as it is ecologically depended (i.e. multi-variable environment) and are these changes even heritable? It is unclear if corals have germlines, therefore epigenetic inheritance may not exist. In terms of being adaptive, reductions in pH could decrease the robustness of coral skeletons, potentially leading to mortality. Therefore, this could be non-adaptive plasticity that could select for a particular phenotype in response to low pH conditions.

*What is different in the interpretation of whole-genome methylation data between LI and RY?*

RY used a vertebrate study system where as LI used an invertebrate system. DNA methylation can change transcription different ways between vertebrates and invertebrates, potentially adding another layer of complexity when comparing epigenomic interpretations. DNA methylation in vertebrates typically occurs on CpG islands, which are usually situated on promoter regions of the DNA and regulate transcription. This is showcased in the RY paper, as most of the methylated regions were CpG sites. Invertebrate DNA methylation can occur in multiple different variations, contributing to differential layers in complexity. Roberts and Gavery (2012) described that invertebrates can have sparse methylation patters that can result in: alternative start sites, sequence mutation, exon skipping, and transient methylation. Therefore, when interpreting the whole-genome methylation data in invertebrates, it is difficult to make the connection between the methylated region and the expressed gene, which is simpler to interpret in the vertebrate systems.

*Can epigenetic data be used to fully describe phenotypic plasticity?*

Epigenetic data can be used to make inferences about how an organism can be altering its phenotype in response to environmental change, however this it must be interpreted with caution. For example, RY discusses that epigenetic effects could be strongest during the developmental period of an organism, which may not be reflected as an epigenetic change in the adult. Additionally, epigenetic mechanisms tend to work together, as methylated regions on the DNA can recruit histone modifiers that can change chromatin structure and thus transcription. Therefore, future studies should compare multiple epigenetic factors together to understand the mechanistic response between the epigenome and phenotype.