**Matías Gómez Words: 753**

Distinguishing between phenotypic plasticity and evolutionary change in species is crucial to better understand and predict organismal changes and their implications to potential adaptation to new environments. A plastic response occurs when individuals within a population, with a particular genotype, undergo a prompt change in phenotype as a result of new environmental conditions. Meanwhile, adaptive evolution takes place when shifts in allele frequencies in a population vary the phenotype as a product of natural selection. Until recently, phenotypic and environmental interactions have been focused on readily measured morphological traits, overlooking much more subtle trait fluctuations that may underpin the actual plastic response, such as immunity, physiology, parasitic load or local habitat heterogeneity. Furthermore, elucidating the relationship between plasticity and adaptation has been confounded by this multiple level of organismal response. However, the coupling of experimental evolutionary biology with gene expression profiling casts a broader net across likely significant traits underlying acclimation and could ultimately illuminate adaptive mechanisms.

The studies by Bernal et al. (2018) and Walworth et al. (2016) aimed to test whether phenotypic plasticity could aid in adaptive change by studying transgenerational variation in traits of interest and transcriptomics under laboratory conditions. The first study investigated damselfish´s (*Acanthochromis polyacanthus*) metabolic reaction to gradual temperature increase across two generations, finding that metabolic compensation can occur if fish are raised in warmer water than their parents, but the physiological process is not the same in fish where parents and offspring experience the same elevated temperature. Genes involved in inflammation, apoptosis and stress response were differentially expressed in transgenerational fish exposed to + 3°C with respect to Control, which was accompanied by an increase in liver size, suggesting a compounded response to the increased temperature. The authors acknowledged that gene expression in other non-studied tissues may clarify their findings. Likewise, the second study evaluated the transition from plasticity to adaptation under elevated CO2  settings in the marine nitrogen fixer (*Trichodesmium*) across ~570-850 (~4.5 y) generations, discovering that a short-term response to higher CO2  concentration can reached fixation in the long-term, exemplified by the loss of the plasticity in the newly adapted individuals when exposed to low CO2. Gene expression analysis identified decreased differential regulation of RNA polymerase sigma factors in low vs high CO2 cultures that alter metabolism of Nitrogen and Carbon. This genome´s species is known to contain repetitive and transposable elements that could mediate adaptation. Although the authors accepted the inherently difficulty in quantify gene expression of these elements when applying short-read (50-150 bp) technologies, they binned those sequences with ≥70% identity into clusters and measured the expression of each cluster across treatments. Their findings showed no dissimilarities in expression of such elements across clusters, putatively indicating that they are devoid of selection.

Contrastingly, Lohma et al. (2017) set off to disentangle phenotypic plasticity and local adaptation in stickleback (*Gasterosteus aculeatus*) under natural settings and test gene expression in migrants to new habitats. Despite populations under study (lake vs stream) exhibit divergently morphology, SNPs and immune gene (MHC) allele frequencies, no clear differences were found in transcriptomic profiles in reciprocal transplants. Interestingly, individuals with local MHC alleles are more heavily parasitized than those with foreign ones when translocated between habitats. Since ontogeny contributes to overall adaptation, the authors recognized that disparities in sticklebacks’ transcriptional reaction norms may not allow to identify a definitive genetic cause underlying this observation. Theoretically, plasticity would evolve in more heterogeneous habitats, but greater transcriptomic plasticity was found in lake fish, which inhabit the more stable habitat. Overall, fish that migrate to the novel environment will display a gene expression profile characteristic of that habitat, suggesting that transcriptomic plasticity mitigates the physiological stress caused by different conditions.

In conclusion, these studies exemplify the power of harnessing reciprocal transplants or manipulative experiments with transcriptomic tools as a way to bridge the gap between ongoing organismal responses to shifting conditions and their phenotypic response, as well as telling apart such plasticity from true evolutionary change in real or simulated environmental conditions. Although the advent of gene RNA-seq has opened a new avenue for dissecting finer and hitherto unforeseen physiological responses, there are still caveats pertaining the time and origin of genetic sample that might confound transcriptomic profiling and the ensuing inferences based upon these methods. Likewise, there is an ongoing need to scale physiological experiments where more environmental variables and their interplay are taken into account, not to mention the inclusion of clear-cut fitness measures as proxy of real transitions in the genome from a phenotypic state to an adaptive one.

**References**

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