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Developmental Biology

In order to understand the complexities that come with evolutionary development, we must first understand the complex mechanisms that operate the appearance and disappearance of certain phenotypes. Development is largely regulated and executed through gene regulatory networks (GRNs), a web of interacting genes, transcription factors, and enhancers. All of which either activate or repress genes around them through network connections in order to maintain and fine tune a variety of processes such as body formation and photosynthesis. One of the most well studied organisms, with regards to GRNs, is body formation in sea urchin.

In Israel *et al*. (2016), they examined and compared the development of lecithotrophic urchin larvae to planktonic feeding urchin larvae. In their study, they examined the gene expression of two planktonic feeding urchins and one lecithotrophic urchin, where one of the planktonic urchins represented the outgroup. They found that there were more alternations in the GRN for lecithotrophic urchins than those that were planktonic, regardless of relationship. In addition, they found that there were more “small” changes rather than “large” changes in the network. For the lecithotrophic urchins they found that Wnt8, Abopec, and VEGFR was inhibited reducing the production of micromeres, development of a functional gut, and the simplification of the skeleton respectively. In addition, they found that FoxC was accelerated while ScratchX was lost, inducing the adult body plan much sooner than the planktonic feeding urchin larvae. In addition, the modifications to VEGFR, which also codes for lipids, led to a number of downstream effects leading to lecithotrophy. This study emphasized that there were significant adaptions in the lecithotrophic urchin while the two species of planktonic were relatively similar, indicating lecithotrophy occurred through compressed and rapid evolution.

Photosynthesis is also well studied with regards to GRNs, given that this process relies on the input of multiple components. In Imam *et al* (2014), they focused on a subset of transcription factors (which were thought to be responsible for photosynthesis) and examined the expression of these transcription factors in the photosynthetic bacteria, *R. sphaeroides*. They found that while all these previously recorded transcription factors where involved with photosynthesis, some were more central to the process than others. Furthermore, they discovered several transcription factors/genes that were also important to photosynthesis. In addition, they also found examples of duplication, such as with FrnL and CrpK. They found that while these two share several functions such as photosynthetic growth, CrpK cannot detect oxygen, which led them to believe CrpK is a duplicate of FrnL. This is an important example because it emphasizes the point that the creation of new phenotypes is not the result of new gene or transcription factors. Instead, they are the result of slight modifications in genes already present. In addition, genes that have these alterations are usually duplicated, preserving the original ancestral gene. This provides a second copy in the case that the newer, modified one was to malfunction. An example of this is seen with Hox genes, which are also crucial for body formation in a number of organisms.

While both studies examined GRNs, each had a different focus. The photosynthesis paper focused on a select group of transcription factors responsible for photosynthesis, determined from previous studies, and cross checked those with the transcription factors that were being expressed in *R. sphaeroides.* Whereas the urchin paper compared which genes or transcription factors were being expressed between the three urchin species. Additionally, the urchin paper was focused more on the evolution of the lecithotrophic sea urchin, whereas the photosynthesis paper was focused on understanding the mechanisms behind photosynthesis. This was evident because the urchin paper compared the expression of certain transcription factors between three species, where the photosynthesis paper only focuses on one species.

Both studies emphasized the point that in GRNs, there is no “new gene” created, nor is a gene destroyed. Instead, new phenotypes arise from a slight shift or single mutation in transcription factors or less central genes. While these changes can be relatively large as seen with the sea urchins with Elov6.3, they cannot be too large, or the organism will not survive. As a result, most of these changes tend to be smaller affecting less crucial genes. In addition, this slight change could impose a cascading effect where the loss of a gene (i.e. ScratchX or VEGFR) may result in another gene not being repressed or not being activated. Due to the complex nature of these networks, it is feasible to see how a seemingly insignificant alteration can have a massive impact on the development of an organism and species.